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Research Article

Response of Bacterial Community Structure in the Bulk Soil and Rice Straw Residues under Different Crop Rotation Systems

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This study investigated the effect of upland crop rotation on soil bacterial community in bulk soil and rice straw residues in the alluvial soils. Soil samples and rice straw residues in two crop rotation models including triple rice and rice-upland crops were collected for incubation under anaerobic and aerobic conditions. Data were analyzed from Denaturing Gradient Gel Electrophoresis band patterns. The results showed that the composition and diversity of communities colonizing the rice straw residues differed from those inhabiting the bulk soil. The bacterial community composition and diversity were only moderately affected by rice straw residues in the bulk soil. Especially, this study indicated that the composition of the bacterial community associated with the bulk soil and rice straw residues was dynamic in two incubation conditions (aerobic or anaerobic) and the different crop rotation models. The findings of this study demonstrated that the bacterial diversity was not affected by the difference in continuous paddy rice cultivation compared to the upland crop rotation system.

1. Introduction

Soil bacterial communities—an essential component of soil—are the primary driver of soil nutrient cycling through their metabolic activities [1]. Bacteria are critical in many biological, chemical, and physical processes that drive terrestrial ecosystems. Their metabolic activities are fundamental in energy flow, cycling of elements, and organic matter turnover in soil and affect soil fertility and plant growth [2–4]. Previous studies reported that the activity and diversity of soil microbial communities are affected by the soil conditions such as organic resources, oxygen requirement, moisture, and temperature [5–7].

In the agricultural systems, several management practices including crop monocultivation, fertilizer application, soil preparation, and various crop rotation systems such as triple rice or rice-upland crops have been found with significant impacts on the structure and diversity of microbial communities in the soil [8–12]. Recently, farmers in the Vietnamese Mekong Delta (VMD) region have converted the intensive rice cultivation system into the rice-upland crops rotation model due to the change in environmental conditions [13–16]. Previous studies reported that bacterial communities had been associated with the decomposition of rice straw residues in flooded rice soil microcosms [15, 17–19]. For instance, Dung and Diep [20] employed the combination of the unweighted-pair group method using arithmetic averages (UPGMA) and 16S ribosomal ribonucleic acid (rRNA) gene-based Denaturing Gradient Gel Electrophoresis (DGGE) to investigate the diversity of microbial community diversity under two cropping models were mono-rice cultivation and rice-upland crop rotation. Their study indicated that the diversity of bacterial communities in the rice-upland crops rotation model was significantly higher than mono-rice cultivation system [20]. Besides, their results showed that the average Shannon diversity index (H) was highest in the rice-upland crops model compared to the triple rice cultivation. Several studies have been performed that analyzed the microbial community composition and diversity in either bulk soil [21–24] or on rice straw residues in both microcosm and field situations

[25–28]. However, a study comparing the microbial community structure in the bulk soil compared to rice straw under diversity cropping systems in the VMD region is limited.

The objectives of this study were to investigate the influence of the diversity of crops in the rice-upland crop rotation on the structure of a bacterial community in bulk soil and rice straw residues by comparing bacterial communities from continuous paddy rice cultivation. This study conducted a field experiment in Tien Giang province, which is located in the VMD. The soil and rice straw were collected in two cropping models including triple rice and rice-upland crops (baby corn and mungbean) system. The bacterial community was determined using DGGE to analyze the bacterial 16S rRNA gene sequences amplified by targeted PCR and the sequences of 16S rRNA gene clone libraries created from selected samples.

2. Materials and Methods

2.1. The Characteristics of Soil and Rice Straw. The field experiment was conducted at Tien Giang province, Vietnam. The soil is Aeric Tropaquept (USDA). In 0–20 cm soil depth, pH ranged from 4.9 to 5.5, and soil organic carbon (SOC) ranged in low levels for paddy rice (2.5%–3.3%C) according to Metson [29]. The soil characteristics before the experiment are described by Dung et al. [15].

Soil samples were collected in the fields of two cropping models including triple rice (SR) and rice-upland crop rotation (SB) system after 60 days after sowing. Soil samples were taken by soil auger at the depth of 0–20 cm from three different replicate plots, well-mixed and stored at 4°C in the dark till use.

The straw residues were collected from fresh stems at the harvest stage. The straw was stored at room temperature for 1 week until a water content of 10%. It were divided into pieces measuring about 2–3 cm and filled small litter bags with pores of 200 μm, and then sterilized at 121°C for 20 min. The other characteristics of straw residues are described by Dung et al. [15].

2.2. Microcosm Experimental Set-Up and Sampling. Two major microcosm setups were used in the experiment, both of which were carried out in the laboratory with three replicates. For the aerobic microcosm setup (SR-AE and SB-AE) and anaerobic setup (SR-AN and SB-AN), the soils were incubated under aerobic (AE) and anaerobic (AN) conditions, respectively. The soils were sieved through a 2-mm mesh sieve after being dried at room temperature. Then, 160 mL glass vials were filled each with 50 g of the sieved soil with addition of 3 L bags containing rice straw residues. In addition to the microcosms with rice straw residues, four other microcosms were set-up without rice straw, including CTSR-AE, CTSB-AE for aerobic condition setup, and CTSR-AN, CTSB-AN for anaerobic condition setup, respectively).

The anaerobic and aerobic setups were prepared differently in this experiment. The 80% of the soil's water-holding capacity was filled with sterile distilled water for the aerobic setup. In contrast, for the anaerobic setup, the soil was saturated with 45 mL of sterile distilled water. The water height was adjusted to be ~8–10 cm above the soil surface. The bottles were sealed with latex stoppers and crimped shut to ensure that the soil and water mixture was evenly distributed. They were then given a handshake that was rather vigorous. The microcosms were produced and incubated at a constant temperature of 25°C in the dark.

At set times, that is, after 0, 15, 30, and 50 days of incubation, triplicate vials were sacrificed for rice straw analysis and soil analysis. The litter bags, containing the straw which were used for PCR-DGGE bacterial community analysis, were washed with potassium phosphate buffer (7.5 mM, pH 7). In addition, each piece of rice straw was washed thoroughly with the buffer to remove soil particles. In addition, 0.4 g samples were taken from the bulk soil for bulk soil bacterial community structure analysis.

2.3. Total Deoxyribonucleic Acid Extraction, PCR Amplification, and DGGE Analysis. The total deoxyribonucleic acid (DNA) was isolated from rice straw residues and soil according to Boon et al. [30]. From each bag, 0.4 g rice straw and from bulk soil, 0.4 g soil was mixed with 0.6 g beads (0.10–0.11 mm diameter) and 0.8 mL of 0.1 M Na_3PO_4 (pH 8) in 2.2 mL micro tubes. The mixture was treated five times for 90 s at 27,000 rpm in a bead beating apparatus. 32 μL of a lysozyme solution (50 mg mL^{-1} Tris-HCl 10 mM, pH 9) was added. Subsequently, 60 μL of 20% SDS and 0.2 mL of 8 M ammonium acetate (pH 7.2) were added, followed by 10 min head over-end shaking. After centrifugation at 7,000 rpm for 15 min, the three supernatants recovered from the three bags taken from the same plot at the same time were pooled and purified with 0.8 mL chloroform-isomylalcohol (24 : 1) by shaking the mixture for 60 min head over-end and centrifugation at 15,000 rpm for 15 min. The aqueous phase was transferred to a fresh tube and 0.8 volume of isopropanol was added for overnight precipitation of the DNA at −20°C. After centrifugation at 10,000 rpm for 30 min, the pellet was dried at room temperature for 30 min and resuspended in 250 μL TE-buffer (10 mM Tris, 1 mM EDTA, pH 8). The crude DNA extract was purified with the Wizard DNA clean-up kit by means of a vacuum manifold (Promega), as described by the manufacturer. The purified DNA was finally recovered in 50 μL TE-buffer and stored at −20°C until use. Before PCR analysis, 30 μL of the DNA extract was cleaned from humic acid by adding 2 mg acid-washed polyvinyl-polypyrrolidone (PVPP) and 30 μL TE-buffer. The mix was vortexed and centrifuged at 11,000 rpm during 5 min. After centrifugation, the supernatant was recovered and subjected to PCR amplification.

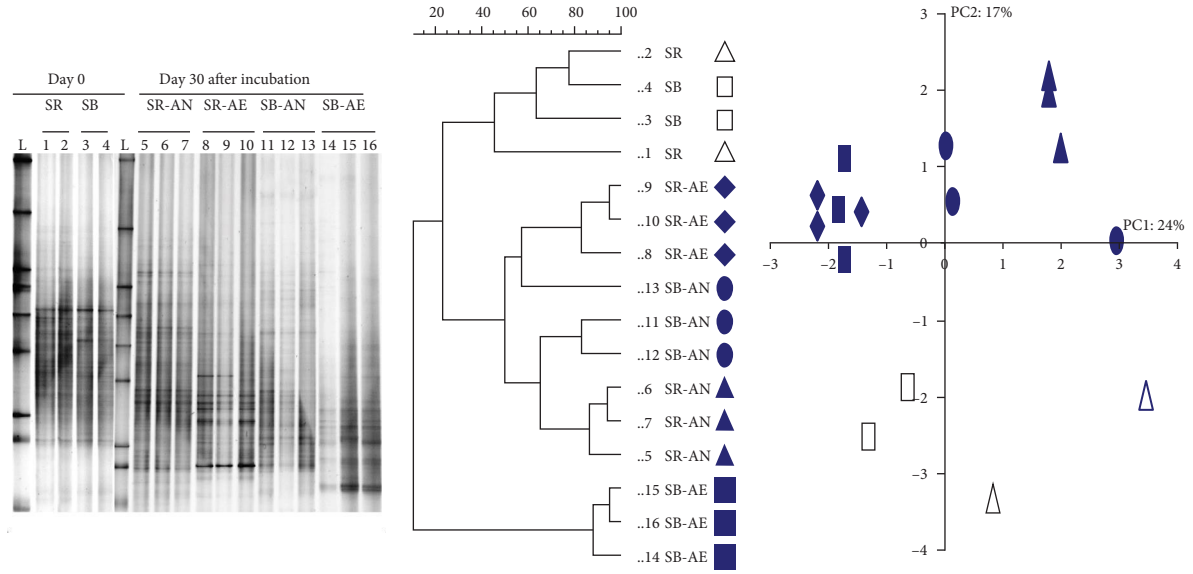
The primer pairs F984-GC and R1378 were utilized for PCR amplification of bacterial 16S rRNA gene fragments (Table 1), which were described by Heuer et al. [31]. The PCR mixture was denaturated, thermal cycles, and finished with an extension step at 72°C for 10 min, according to Gomes et al. [32].

Bacterial 16S rRNA gene fragments were analyzed using DGGE on an Ingeny phor U-2 system located in Leiden, The Netherlands. A 30 μL portion of the PCR product was loaded onto an 8% (w : v) polyacrylamide gel with a denaturing gradient that ranged from 35% at the top to 65% at the bottom of the gel in Tris-acetate-EDTA (TAE) buffer. Electrophoresis was conducted at 60°C and 120 V for a duration

Table 1: The primer pairs F984-GC and R1378 for PCR amplification in this study.

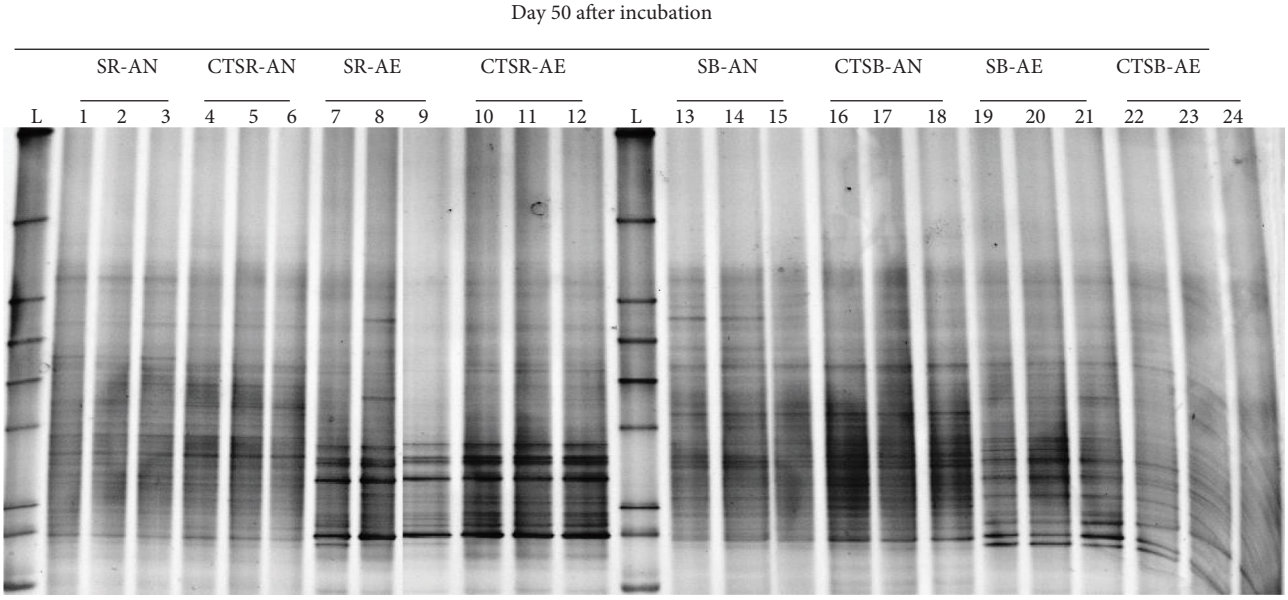
Primer	Target	Sequence (5′–3′)	Reference
F984-GC*	Bacteria—16S rRNA	GC.-AACGCGAAGAACCTTAC	Heuer et al. [31]
R1378	Bacteria—16S rRNA	CGGTGTGTACAAGGCCCGGGAACG	Heuer et al. [31].

*F984 contained GC clamp: CGC-CCG-GGG-CGC-GCC-CCG-GGC-GGG-GCG-GGG-GCA-CGG-GGGG at the 5′ site.



(a) (b) (c)

Figure 1: Bacterial 16S rRNA gene Denaturing Gradient Gel Electrophoresis (DGGE) profiles obtained from bulk soils in the different microcosm setups at 0 and after 30 days of (a) incubation, (b) corresponding UPGMA, and (c) PCA results. SR—rice soil; SB—baby corn soil; SR-AN, SR-AE, SB-AN, and SB-AN are treatments with: rice soil under anaerobic conditions, rice soil under aerobic conditions, baby corn soil under anaerobic conditions, and baby corn soil under aerobic conditions, respectively. In the PCA and UPGMA plots, the symbols used to correspond with particular treatments as follows: (solid triangle) SR-AN; (solid diamond) SR-AE; (solid circle) SB-AN; (solid square) SB-AE; (open triangle) soil SR at day 0; (open square) soil SB at day 0.



(a)

Figure 2: Continued.

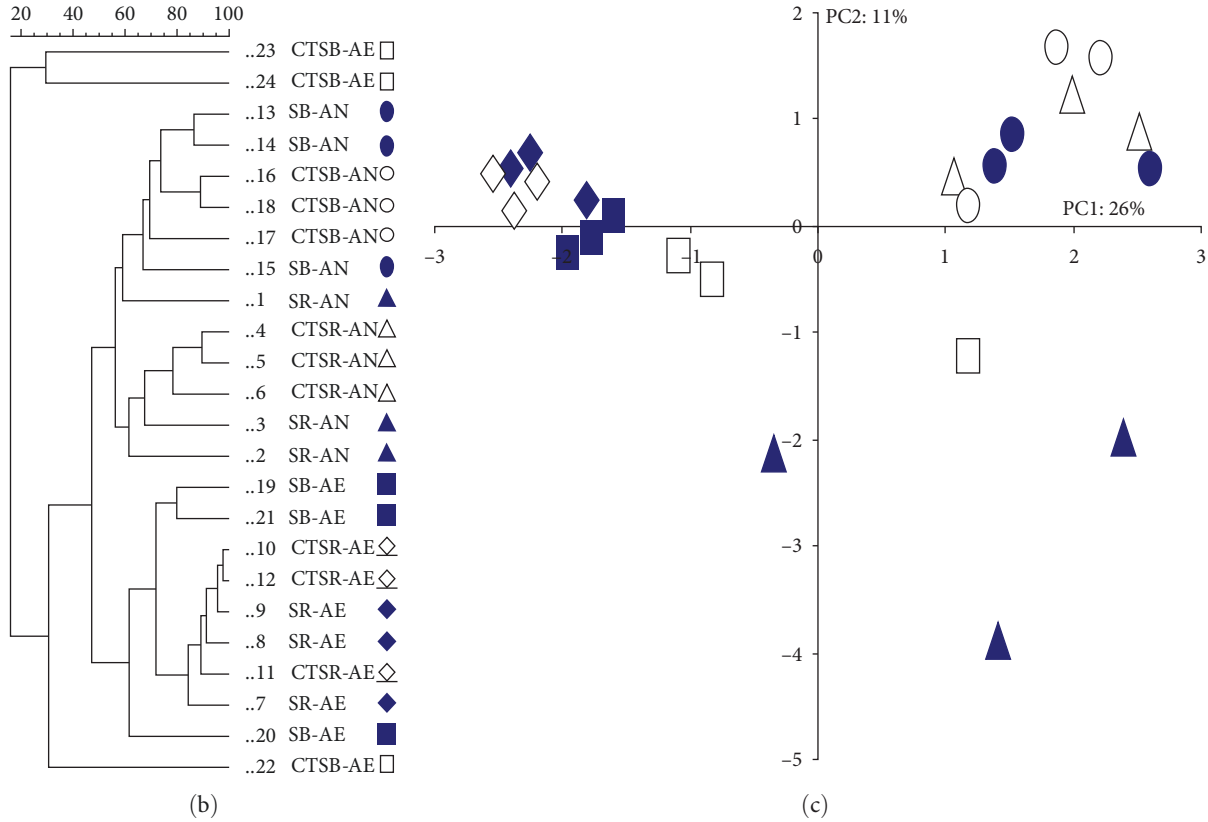


Figure 2: Bacterial 16S rRNA gene DGGE fingerprints (a) of the bacterial community in the bulk soil of the different microcosm set-ups, (b) corresponding UPGMA, and (c) PCA clustering at day 50. In the DGGE fingerprint, the microcosm setups from which the fingerprints originated are indicated above the lane numbers. Lane L: 16S rRNA gene DGGE ladder. In the UPGMA clustering, the number mentioned before the indicated microcosm setup corresponds to the lane number in the DGGE fingerprint. In the PCA analysis, the symbol corresponds with a particular microcosm setup as follows: (solid triangle) SR-AN; (open triangle) CTSR-AN; (solid diamond) SR-AE; (open diamond) CTSR-AE; (solid circle) SB-AN; (open circle) CTSB-AN; (solid square) SB-AE and (open square) CTSB-AE.

Table 2: The bacterial community's Shannon diversity index (H) in the bulk soil of the different microcosm setups at days 0, 30, and 50 after incubation.

Treatments	Shannon diversity index		
	Day 0	Day 30	Day 50
SR	1.05 ± 0.01^{a}	—	—
SB	0.97 ± 0.06^{a}	—	—
SR-AN	—	1.14 ± 0.03^{bc}	1.21 ± 0.06^{d}
SR-AE	—	1.01 ± 0.09^{ab}	0.92 ± 0.06^{ab}
SB-AN	—	1.23 ± 0.06^{c}	1.34 ± 0.06^{e}
SB-AE	—	0.96 ± 0.15^{a}	1.01 ± 0.04^{bc}
CTSR-AN	—	—	1.04 ± 0.06^{c}
CTSR-AE	—	—	0.99 ± 0.07^{bc}
CTSB-AN	—	—	1.00 ± 0.07^{bc}
CTSB-AE	—	—	0.87 ± 0.06^{a}

The value after ± showed the standard deviation ($n = 3$). Means in a column followed by the same letter are not significantly different. Means marked with different letters (a, b, c, d, e) are significantly different according to the T-test for day 0 and the Duncan's Multiple Range Test for day 30 and day 50 ($p < 0.05$).

of 15 hr. After electrophoresis, the DGGE gels were treated with 1xSYBR Gold (Molecular Probes, Leiden, The Netherlands) for 30 min and then captured through a GeneLink camera system (SYNGENE, Cambridge, United Kingdom) using a UV transilluminator.

2.4. Data Analysis. The bacterial 16S rRNA gene DGGE fingerprints were analyzed using Gelcompar II version 4.602 software from Applied Math's (SintMartens–Latem, Belgium) to generate dendrograms. The Pearson's correlation UPGMA was employed for constructing these dendrograms. The diversity of the microbial community was assessed using the Shannon–Weaver index of general diversity H, which was calculated using the densitometric curves of the DGGE profiles [30, 33], according to the formula:

$$H = -\sum(n_i/N)\log(n_i/N) \quad (1)$$

where n_i is the peak height, and N is the sum of all peak heights in the densitometric curve. The statistical Shannon index of different treatments were statistically analyzed with SPSS 13 using analysis of variance (One-way ANOVA). Only treatments with significant differences were submitted to the Tukey comparison test at the 5% significance level.

3. Results

3.1. Bacterial Community Structure, Diversity, and Shannon Diversity Index (H) in Bulk Soil. Figure 1 shows the bacterial 16S rRNA gene DGGE profiles obtained from bulk soils in

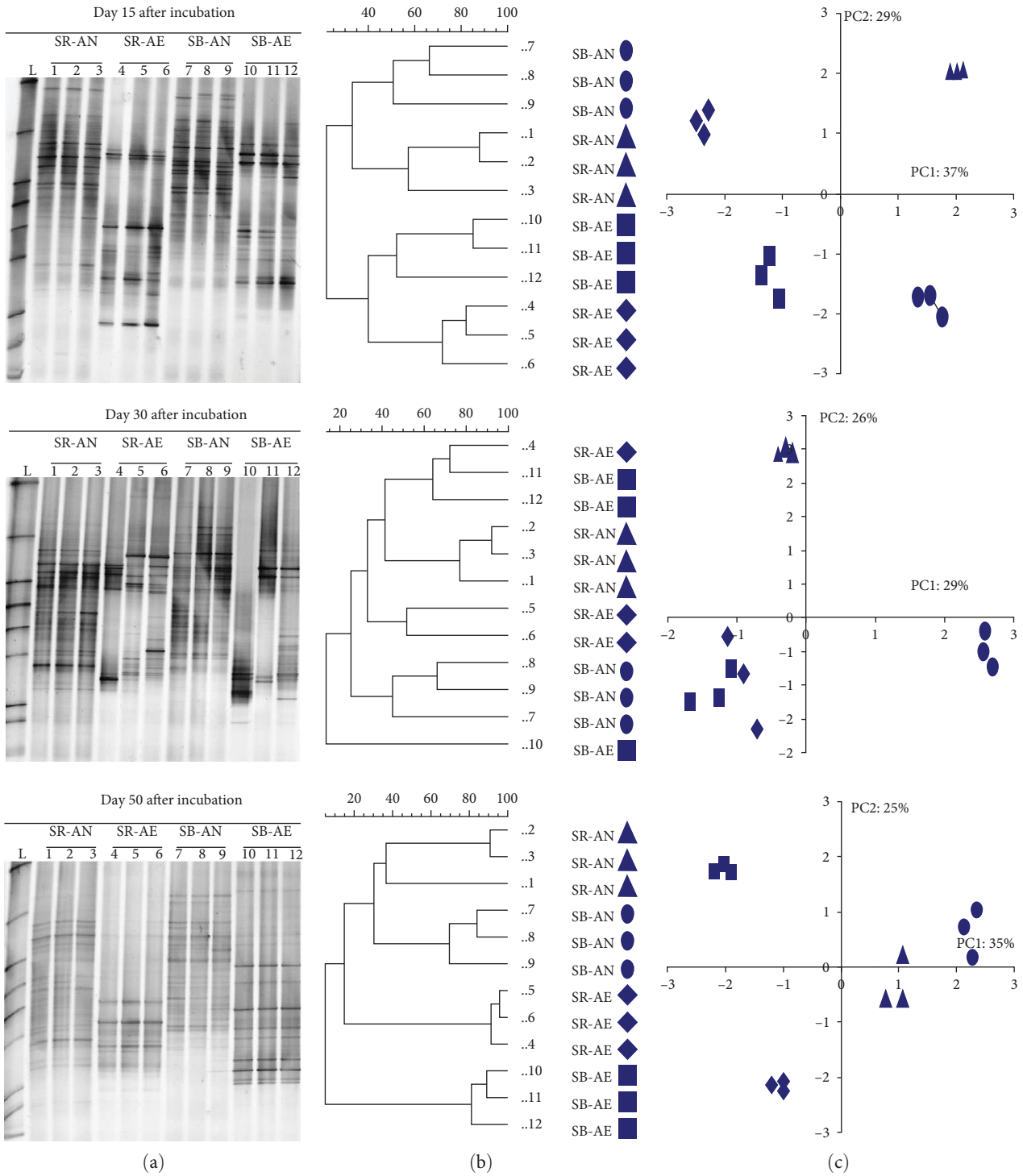


Figure 3: Bacterial 16S rRNA gene DGGE fingerprints (a) obtained from the communities present in the rice straw residues in various microcosm setups and results of the corresponding UPGMA cluster analysis (b) and PCA analysis (c) at day 15 (top), at day 30 (center) and day 50 (bottom) of incubation. In the DGGE fingerprint, the microcosm setups from which the fingerprints originated are indicated above the lane numbers. Lane L: bacterial 16S rRNA gene DGGE ladder. In the UPGMA clustering, the number mentioned before the indicated microcosm setup corresponds to the lane number in the DGGE fingerprint gel. In PCA analysis, the symbol corresponds with a particular microcosm set-up as follows: (solid triangle) SR-AN; (solid diamond) SR-AE; (solid circle) SB-AN and (solid square) SB-AE.

the different microcosm setups at 0 and after 30 days of incubation and the corresponding UPGMA and principal coordinate analysis (PCA) results. Figure 2 shows the results for the bulk soil community at day 50. The results showed that the bacterial bulk soil community composition at time 0 differed slightly between the SR and SB soil and that the community composition changed during incubation in both soils. At both days 30 and 50, the effect of the aerobic/anaerobic

Table 3: The diversity (H value) of the bacterial community colonizing rice straw residues in microcosm setups at days 14, 30, and 50 of incubation.

Treatments	Shannon diversity index			
	Day 14	Day 30	Day 50	Average
SR-AN	1.18 ± 0.06^{a}	1.14 ± 0.03^{bc}	1.21 ± 0.06^{b}	1.18 ± 0.02^{b}
SR-AE	1.06 ± 0.05^{a}	1.01 ± 0.09^{ab}	0.92 ± 0.06^{a}	1.00 ± 0.01^{a}
SB-AN	1.33 ± 0.10^{b}	1.23 ± 0.06^{c}	1.34 ± 0.06^{c}	1.30 ± 0.04^{c}
SB-AE	1.13 ± 0.01^{a}	0.96 ± 0.15^{a}	1.01 ± 0.04^{a}	1.03 ± 0.06^{a}

The value after $\pm$ showed the standard deviation ($n = 3$). Means in a column followed by the same letter are not significantly different. Means marked with different letters (a, b, c) are significantly different according to Duncan's Multiple Range Test ($p < 0.05$).

conditions and the lesser degree of soil origin was indicated in the obtained DGGE profiles and in the UPGMA and PCA clustering results. Interestingly, as observed at day 50, bacterial community structure in the bulk soil seems to be poorly affected by the presence of the rice straw residues because almost no differences (except for a few bands in the anaerobic system) were found between bacterial community DGGE profiles recorded for the control microcosms without rice straw (CTSR and CTSB microcosms) compared to those recorded for microcosms containing rice straw.

Shannon diversity values calculated for the bacterial community from bulk soil incubated under various microcosm treatments are shown in Table 2. At time points day 30 and day 50, the average H of the bacterial communities in the anaerobic microcosm setups were significantly higher than those of the communities in the aerobic microcosm setups. Significant differences in H between soils SR and SB were only observed at time point 50 for the anaerobic microcosms containing rice straw. Significant differences of H also existed between the SR-AN and CTSR-AN, SB-AN and CTSB-AN, and SB-AE and CTSB-AE at 50 days, indicating that the addition of rice straw affects bacterial diversity in the bulk soil, especially under anaerobic conditions. However, at time point day 0, there was no significantly different in H between the SR and SB setups.

3.2. Bacterial Community Structure, Diversity, and Shannon Diversity Index (H) in Rice Straw Residues. Figure 3 indicates the results of the analysis of the bacterial 16S rRNA gene DGGE profiles obtained from the communities present in the rice straw residues across different microcosm setups and sampling times, as well as the UPGMA and PCA results. The effect of the implied aerobic or anaerobic conditions is visible in the DGGE profiles and was translated in the UPGMA and PCA clustering results at all sampling times. Moreover, apparent effects of the soil origin were demonstrated at 15 days (Figure 3-top) and 50 days (Figure 3-bottom) of incubation and to a lesser extent at 30 days (Figure 3-center).

The H values calculated for the bacterial community colonizing the rice straw incubated under various microcosm treatments are shown in Table 3. Overall, over the whole experimental period, H ranged from 0.92 to 1.34. The highest H was found in the SR-AN and SB-AN treatments. The average H for the bacterial community in the SB-AN microcosm setup was significantly higher than that of the communities in the other three setups at the time points of days 14 and 50. In addition, the average H value recorded across the experiments was highest for the SB-AN system, which was significantly different from the mean H value calculated for the other three systems. Moreover, the bacterial community inhabiting rice straw in SB soil was a significantly higher H value compared to that in SR soil.

Figure 4 showed the UPGMA and PCA clustering results of the DGGE profiles of both the bacterial communities colonizing rice straw residues (RS) and those in the bulk soil (S) in the different microcosm setups at day 30 (Figure 4-above) and day 50 (Figure 4-below) of incubation. The analyses separate the bacterial communities of the RS samples on the one hand and the S samples on the other hand. The data suggest that the rice straw determines in the first place of the community composition, followed by the incubation conditions (aerobic or anaerobic) and finally, the soil origin/history (SR or SB). Comparisons of H for the bacterial community between the RS and S samples are shown in Table 4. The H of the communities associated with rice straw residues was often higher than that in the bulk soil with often significant differences, indicating that rice straw provides a niche that increases bacterial diversity. This was especially the case for the anaerobic systems.

4. Discussion

In this study, the composition of bacterial communities in the bulk soil and rice straw residues was different. This was observed both under aerobic and anaerobic conditions and for both soils. Previous studies have reported that bacteria community structure significantly correlate with soil water content [34–37]. Using PLFA on samples from a field experiment, Kimura and Asakawa [37] and Li et al. [38] indicated that the microbial communities found on rice straw residues were significantly different in composition from those in the bulk soil in both flooded and drained soils. Similarly, Asakawa and Kimura [17] also indicated that the bacterial communities associated with rice straw significantly differed from those in different water conditions. However, samples from the bulk soil and rice straw residues were taken at different time points and from soils with different treatments, making it difficult to compare the communities between the different compartments. Therefore, this study provides the results in comparing bulk soil communities and communities associated with plant residues incorporated in rice paddy soil, especially in the VMD region. Flooded paddy soil is always considered as an ecosystem with three major compartments of oxic-anoxic interface: soil surface, bulk soil, and rhizosphere. They provide different habitats for microbiota and together contribute to the high bacterial diversity found in rice paddy soils [10, 21, 39–41]. This study indicated that the rice straw residues itself present a distinct niche in rice paddy soil and add to the microbial community diversity. This is accentuated by the fact that in most cases, bacterial

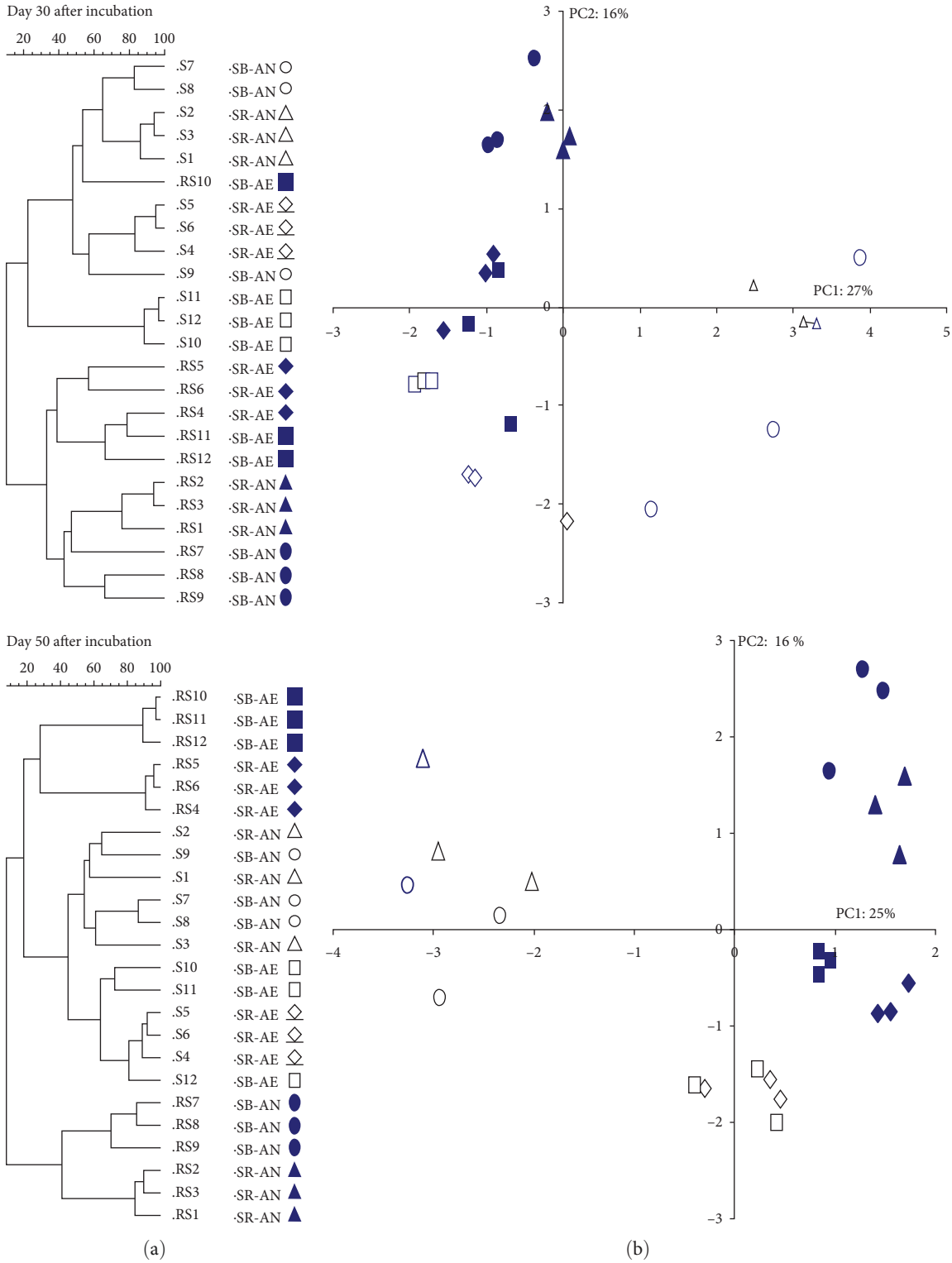


FIGURE 4: The UPGMA (a) and PCA (b) analyses of DGGE patterns of the bacterial community in the bulk soil (*S*) and those colonizing rice straw restudies (RS) at day 30 (above) and day 50 (below) of incubation of the different microcosm set-ups. In the UPGMA clustering, the marks mentioned before the indicated microcosm setup as follows: S1–S3: bulk soil of SR-AN; S4–S6: bulk soil of SR-AE; S7–S9: bulk soil of SB-AN; and S10–S12: bulk soil of SB-AN. RS1–RS3: rice straw residues of SR-AN; RS4–RS6: rice straw residues of SR-AE; RS7–RS9: rice straw residues of SB-AN; and RS10–RS12: rice straw residues of SB-AE. In PCA and UPGMA analysis, the symbol corresponds with a particular microcosm setup as follows: (solid triangle) RS-SR-AN; (open triangle) S-SR-AN; (solid diamond) RS-SR-AE; (open diamond) S-SR-AE; (solid circle) RS-SB-AN; (open circle) S-SB-AN; (solid square) RS-SB-AE and (open square) S-SB-AE.

Table 4: Shannon diversity index of the bacterial communities colonizing rice straw residues and bulk soil at days 30, 50 and the average of the two-time points.

Treatments	Shannon diversity index		
	Day 30	Day 50	Average
RS-SR-AN	1.14 ± 0.03^{bcd}	1.21 ± 0.06^{bc}	1.18 ± 0.02^{cd}
S-SR-AN	1.18 ± 0.06^{cd}	0.97 ± 0.20^{a}	1.07 ± 0.09^{bc}
RS-SR-AE	1.01 ± 0.09^{abcd}	0.92 ± 0.06^{a}	0.97 ± 0.03^{ab}
S-SR-AE	0.85 ± 0.23^{a}	0.93 ± 0.15^{a}	0.89 ± 0.08^{a}
RS-SB-AN	1.23 ± 0.06^{cd}	1.34 ± 0.06^{c}	1.28 ± 0.01^{d}
S-SB-AN	1.12 ± 0.21^{bcd}	1.10 ± 0.12^{ab}	1.11 ± 0.09^{c}
RS-SB-AE	0.96 ± 0.15^{abc}	1.01 ± 0.04^{a}	0.98 ± 0.09^{ab}
S-SB-AE	0.92 ± 0.03^{a}	0.90 ± 0.00^{a}	0.91 ± 0.02^{a}

The value after $\pm$ showed the standard deviation ($n = 3$). Means in a column followed by the same letter are not significantly different. Means marked with different letters (a, b, c, d) are significantly different according to Duncan's Multiple Range Test ($p < 0.05$).

diversity was higher in communities associated with rice straw than in bulk soil, especially under flooded conditions.

This study found that the composition of bacterial communities were dynamic in time for the communities in bulk soil and rice straw residues under both conditions and for both soil types. Other studies have also shown that the dynamic of bacterial communities colonizing rice straw residues ranges in different times both in flooded and dry conditions [12, 19, 42–44]. Weber et al. [19] showed that the bacterial community observed changes during the initial 15-day incubation period, but stability was observed during the remaining 71 days of incubation. Similarly, Ji et al. [44] reported that the microbial community structure strongly responded to rice straw incorporation in paddy soil, indicating the temporal dynamics of these communities in response to different soil conditions and amendments.

Under anaerobic conditions, the communities in bulk soil and associated with the rice straw of both soils changed in composition during the first 15 days but remained relatively stable. However, in the aerobic setups, especially the rice straw-associated soil community still changed considerably in composition after 15 days of incubation. This was then attributed to the dynamic character in the composition of rice straw residues due to the degradation itself. Several previous studies also reported the long-term dynamic character of the composition of bacterial communities in paddy soil under both flooded and upland conditions in a field experiment and showed the succession of soil bacterial communities degrading rice straw with time [17, 45–47].

During incubation, only slight differences in the composition of the bacterial communities were found between the bulk soil amended with and without rice straw residues. This was only for the soils incubated under anaerobic conditions. Under those conditions, rice straw amendment resulted in the appearance of only a few DGGE bands which were not seen in the microcosms without rice straw, also leading to differences in diversity index H. Those results indicated that the degradation of rice straw residues and products from first-stage hydrolysis are being decomposed and metabolized near the rice straw residues. Therefore, the exchange of substrates between the bulk soil compartment and the rice straw residue compartment seems minimal but can explain the minor community composition and diversity changes observed under anaerobic conditions in the bulk soil.

In addition to time and compartment, the bacterial communities were affected by the incubation conditions (either aerobic or anaerobic conditions) and the soil management history (either continuously cultivated with paddy rice or cultivated in a paddy rice-upland crop rotation system). Based on the UPGMA and PCA results, differences in community composition appear in the first place to be due to the incubation conditions more than to the soil history. Previous studies showed the effects of water saturation, drainage, and changing redox conditions on microbial community composition in wet tropical soil or wetland [48–50] and paddy soil [51, 52]. Furthermore, the SR and SB soils developed different compositions in the rice straw-associated bacterial community under aerobic conditions. In addition, also the composition of the bulk soil community in both systems with and without rice straw developed in different communities in the SR and SB soils. The communities in the SR and SB soils already showed differences in composition at time zero, but those differences increased with incubation, especially in the rice straw-associated communities. These observations are consistent with the idea that cropping and other land management practices can significantly affect soil microbial community characteristics [53, 54].

5. Conclusions

In this study, we investigated the effects of crop rotation on the bacterial community structure in the bulk soil and rice straw residues. We found that the composition and diversity of communities colonizing the rice straw residues were clearly different from those inhabiting the bulk soil with a positive effect of the availability of a rice straw niche on diversity. The bulk soil and rice straw-associated communities were dynamic in time. In bulk soil, the bacterial community composition and diversity were only moderately affected by the presence of rice straw residues. The composition of both the community in the bulk soil and the community associated with rice straw residues was affected by the incubation conditions (aerobic or anaerobic) as the soil history.

Data Availability

The data presented in this article are available from the corresponding author upon request.

Conflicts of Interest

All authors declare that there are no conflicts of interest regarding the publication of this paper.

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