

A Comparative Study of Swine Tissue Composting With Woodchips, Rice Husk And Wheat Straw

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Abstract

This study evaluated the performance of woodchips (WS), rice husk (RH) and wheat straw (ST) in swine tissue composting. The ST treatment was shown to first reach the highest temperature (55°C) at 12 d of composting and lasted 9 days. The total nitrogen content (TN) was higher and nitrogen loss was lower in ST than in WS or RH treatment. Ammonium nitrogen content (AN) analysis demonstrated lower NH₃ emission in ST than in WS or RH treatment. Bacterial community analysis indicated that bacterial diversity was higher in ST than in WS or RH treatment. The most dominant genera in all composting treatments were *Pseudomonas*, *Streptomyces*, *Brevibacterium*, *Saccharoporysora*, *Acinetobacter*, *Sphingobacterium*, *Devosia*, *Rhizobium*, *Microbacterium* and *Sanguibacter*. The dominant bacteria were *Pseudomonas*, *Staphylococcus* and *Sphingobacterium* in ST treatment, *Streptomyces*, *Acinetobacter* and *Sphingopyxis* in WS treatment, and *Sanguibacter*, *Pedobacter* and *Gordonia* in RH treatment. Spearman correlation analysis revealed positive relationship of *Brevibacterium*, *Devosia*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* to temperature; *Brevibacterium* and *Staphylococcus* to TN; *Brevibacterium*, *Devosia*, *Microbacterium*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* to AN. This research provides useful information for improving the efficiency of swine tissue composting.

Introduction

Aerobic composting can convert organic waste into a stabilized final product by microbial degradation, free of phytotoxicity and pathogens and with certain humic properties (Albrecht et al., 2010; Wei et al., 2014). Thus, it is considered as an environmentally friendly and economically viable alternative method for treating solid organic wastes, especially livestock and poultry manure (Zhang et al., 2019a). Animal carcasses are of high mass, high moisture content, high nitrogen content and zero porosity (Wilkinson, 2007), suggesting their difference from livestock and poultry manure in composting processes. Animal carcasses can not be mixed with materials evenly, which are usually placed in the center of the compost and covered with animal manure or some materials of good porosity, high carbon, low nitrogen (straw, corn silage or wood shavings) (Gilroyed et al., 2016). The composting of pig carcasses needs to undergo two processes: static stacking of carcass degradation and a maturation stage similar to the composting of livestock and poultry manure (Harper et al., 2009). By simulating field-scale livestock mortality composting systems, Akdeniz et al. (2010) designed a laboratory scale composting system with aerobic and anaerobic test units and tested the state and completion of the process by observing the gas concentrations of volatile organic compounds generated inside biosecure swine mortality composting units filled with six different materials. Glanville et al. (2016) assessed the potential of a passively-ventilated plastic-wrapped composting system for biosecure disposal of poultry mortalities caused by avian influenza as an emergency disposal option for disease-related swine mortalities. Ki et al. (2018) proposed a modified soil burial technique by covering swine carcasses to a final compost bed of 1.0–1.2 m, with the temperature in the bed increasing gradually to 35–45°C after 200 days.

Numerous bulking agents, including woodchips, wheat straw, sawdust, rice husk, rice bran, chopped hay, wood shavings, and peanut shells, had been mixed with waste materials to adjust the moisture content,

C/N ratio, and void spaces between particles (Adhikari et al., 2009; Gea et al., 2007; Iqbal et al., 2010; Kim et al., 2008). These bulking agents have been reported to not only modify the physical properties of the composting feedstock, but also change the biodegradation kinetics and composting performance (Adhikari et al., 2008; Kim et al., 2008; Kulcu and Yaldiz, 2007; Yanez et al., 2009). Woodchips, rice husk and wheat straw are the most commonly used carbon sources owing to their less cost and recycling necessity. Woodchips might improve compost efficiency by increasing convective airflow through windrows to increase the supply of oxygen and enhance aerobic decomposition. Wheat straw has a high crystallinity and a high degree of polymerization (Snelders et al., 2014; Sun et al., 2014), whose degradability was retarded under natural conditions owing to chemical stability and high C:N ratio (Chen, 2014), but promoted in co-compost of cow manure (Awasthi et al., 2019). Rice husk acts as a sort of conditioner by providing structural support and exhibits best performance in reduction of antibiotic resistance genes (ARGs) in chicken manure and improving the efficiency of the treating process (Xiao et al., 2009; Zhang et al., 2019b).

Complex microbial communities play a key role in composting (Xi et al., 2015). Understanding the dynamic changes of microbial communities in the composting process is extremely important for efficient composting. In our previous work, *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, and *Actinobacteria* were identified as the main phyla in the co-composting of wood shaving and swine carcasses (Yang et al., 2019). *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Acidobacter* and *Chloroflexi* were determined as the dominant phyla in the co-composting of rice straw and cow manure (Sun et al., 2019). However, composting materials vary in their efficiency and microbial composition in the composting process. The purpose of this study was to compare the performance of woodchips, rice husk and wheat straw in the swine mortality composting process, determine the major microbial communities and their correlation to key environmental factors, and provide a theoretical basis for selecting effective carbon source materials to improve composting efficiency.

Materials And Methods

2.1. Composting materials and experimental set-up

The composting process was carried out from July 2, 2018 to April 25, 2018 at the pig breeding farm of Huazhong Agricultural University, Wuhan, Hubei province, China (30°28'28.96"N 114°20'12.24"E). The main materials for composting were woodchips, rice husk, wheat straw and swine carcasses. The woodchips, rice husk and wheat straw were collected from woodworking factories (Wuhan, China). Swine tissue were collected from the National Pig Breeding Center (Hongshan District, Wuhan, China). Every pile contained 20 kg carcass tissue (no internal organs). Before composting, wheat straw was shredded to a size of 20–30 mm by a fiber cutter SBJ-800F from Xinhang machinery Co.LTD (Qingzhou, China).

The prepared compost material base was placed in the center without overlapping, followed by addition of each compost material until reaching the initial dimensions of the whole pile (1.2 m long, 0.8 m wide and 0.5 m high). The initial moisture content was set at 60%. A total of three treatment groups (WS,

woodchips + swine carcasses; RH, rice husk + swine carcasses; ST, wheat straw + swine carcasses) were set up (length 0.1m, width 0.6 m and height 0.3 m). Five-point sampling methods were used to collect subsamples at three different depths and five samples were obtained from each depth at day 0, 6, 12, 21, 30 ... 78. Then, the subsamples were mixed and divided into two portions, with one portion used for physical and chemical parameter determination and the other stored at -20°C for further high-throughput sequencing analysis.

2.2. Physical and chemical parameter analysis

The temperature was measured by inserting an electronic thermometer into the core of the piles and thermometer is calibrated before use and the ambient temperature is measured. The temperature is measured once a day during mesophilic and thermophilic phase and once every 2–3 days during the cooling phases. The moisture content was determined by drying at 105°C for 24 h. The pH value was determined in a 1:10 compost/water (w/v) suspension using a pH meter (FiveEasy Plus FE28, Mettler Toledo, Switzerland) after 1 h of equilibrium with shaking. The total nitrogen (TN) and total organic carbon (TC) was measured using an isotope ratio mass spectrometer (ISOPRIME 100, Elementar, Germany). The content of ammonium nitrogen (AN) was detected using a flow injection analyzer (Smartchem 200, AMS, Italy) (Supplementary table 1). Neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL) were determined by using the British Ringbio filter bag technology fiber analyzer. Hemicellulose was estimated as the difference between NDF and ADF. Cellulose was estimated as the difference between ADF and ADL content. Lignin was estimated as the difference between ADL and ash content.

2.3. Illumina high-throughput sequencing data analysis

The composting samples were subjected to DNA extraction using the MoBio PowerSoil® DNA Isolation Kit (12888). The V4 region of the 16S rRNA genes was amplified using the following primers: Forward 5'-AYTGGGYDTAAAGNG-3' and Reverse 5'-TACNVGGGTATCTAATCC-3'. The PCR products were separated by 2.0% agarose gel electrophoresis and were purified with the Axygen Axy Prep DNA Gel Extraction kit (AP-GX-500). After purification, the PCR products were quantified with Quant-iT PicoGreen dsDNA Assay Kit, Invitrogen (P7589) following the manufacturer's protocol. Next, the PCR products were pooled to construct amplicon libraries. The DNA library (≥ 2 nM) was diluted to 15–18 pM and subjected to DNA sequencing on an Illumina MiSeq machine with 2×300 bp reads. Sequence quality was analyzed using the sliding window method to remove reads with an average Phred score lower than 20 or ambiguous bases or sequence length shorter than 150 bp or mismatched primers. In addition, chimeras were removed with USEARCH using Qiime software. The obtained sequence fragments were assembled using the Flash software. Valid sequences were extracted according to the index information. The high-quality sequences were classified into operational taxonomic units (OTUs) with UCLUST using Qiime software at a 97% similarity setting (Caporaso et al., 2010; Edgar, 2010). Finally, the taxonomic classification was performed using the Qiime pipeline.

Alpha diversity parameters, including Chao 1 estimator, ACE estimator, Shannon index, and Simpson index were measured for the five samples from each treatment using the Qiime software. Spearman

correlation analysis was used to elucidate the relationship between the compost physiochemical properties and the patterns of bacterial community structure.

2.4. Statistical analysis

Spearman correlational analysis was performed using SPSS 20.0 (IBM Co., Armonk, NY, USA). Statistical calculations and data analysis were performed with the SPSS 22.0 statistical software package (IBM, USA) and GraphPad Prism version 7.0 for Windows (GraphPad Software, San Diego, CA, USA). A total of 5 replicates, 9 treatments. Results were presented as the mean \pm standard error from at least three independent experiments. P-values of < 0.05 and < 0.01 were considered as significant and highly significant, respectively.

Results And Discussions

3.1. Comparison of temperature, moisture and pH of samples

In Fig. 1, the pile temperature of wheat straw + swine tissues treatment (ST) rapidly increased and reached the thermophilic phase in the first 12 days of the process. The thermophilic phase was shorter in woodchips + swine carcass (WS) and rice husk + swine carcass (RH) treatments than in wheat straw + swine carcasses(ST) treatment. Moreover, the highest temperature in three composting treatments was in the order of ST (55°C) $>$ WS (42.6°C) $>$ RH (30.8°C). This might be due to the initial C/N ratio of ST treatment (close to 30) (Table S1), which was determined as a better condition for reproduction of microorganisms (Hashemi and Han, 2019).

In Fig.2a, the sharpest decrease of moisture content among the three treatments was observed in the RH treatment in the first 30 d of composting, probably due to the compensation for the evaporation of moisture via the production of metabolic heat and water by biodegradation. After 30 d, the moisture continued to decline in the ST treatment, probably due to its longer thermophilic stage, resulting in the greatest decreasing rate of moisture content among the three treatments. In Fig.2b, the pH value was shown to decrease rapidly in the RH treatment in the first 12 d, probably due to the microbial activity on easily biodegradable organic matter and the release of organic acids in the materials (Robledo-Mahon et al., 2019; Tang et al., 2020; Lopez-Gonzalez et al., 2015). As composting progressed, the pH increased to around 7.0 at the end of the process, indicative of proper stabilisation of organic matter (Robledo-Mahon et al., 2019; Liu et al., 2018).

3.2. Comparison of total organic carbon of samples

The total organic carbon (TOC) was detected to decrease gradually during the composting process in all the three treatments. The initial TOCs of 48.84%, 41.75% and 38.69% decreased to 44.32%, 36.32% and 32.42% in the final composts of WS, RH and ST, respectively (Fig. 3). The TOC decrease percentage was in the order of ST (15.9%) $>$ RH (12.99%) $>$ WS (9.32%). Compared with WS and RH, the ST feedstock exhibited slightly faster decomposition based on TOC reduction, probably attributed to more easily degradable organics contained in ST than in WS and RH (Qian et al., 2014).

3.3. Comparison of cellulose and lignin content of samples

Figure 4 shows the cellulose and lignin contents of the three treatments throughout the 78-day natural composting period. In Fig. 4a, the final cellulose degradation rate was seen to be in the order of ST (16.25%) > WS (14.08%) > RH (13.01%). In Fig. 4b, the final lignin degradation rate was shown to be ordered as ST (45.05%) > RH (25.33%) > WS (0.79%). Both the lignin and cellulose degradation rates were significantly higher in ST than in WS or RH. A more favorable condition in ST may improve the microbial activity of cellulose-decomposing microorganisms (Sun et al., 2016; Yu et al., 2007; Zhao et al., 2016). The aforementioned results indicate that wheat straw could significantly promote lignocellulose degradation during swine tissue composting.

3.4. Comparison of nitrogen profile of samples

With the degradation of swine tissues, the total nitrogen content of the three groups all showed an upward trend (Fig. 5a). At the end of composting, the total nitrogen content of the straw group was the highest. It may be that straws have high nitrogen content and are rich in phosphorus, potassium, calcium, and magnesium, which are suitable for the growth of microorganisms and promote the degradation of organic matter

In Fig. 5b, the ammonium nitrogen (AN) content of ST and RH treatments showed an increase and reach a peak value, followed by a decrease throughout the composting process. Previous studies have indicated that the increase of ammonium nitrogen (AN) can be attributed to the mineralization and ammonification of organic nitrogen. up to 53d, the straw group had the highest ammonium nitrogen content among 3 groups, which further confirmed that the conversion efficiency of organic nitrogen was high and the composting process was good at the straw group. The ammonium nitrogen content of the woodchips group gradually increased, indicating that the composting process of the woodchips group was slow, but the woodchips has a larger void ratio, which can absorb NH_4^+ (Hashemi et al., 2016), resulting in the highest final ammonium nitrogen content.

3.5. Comparison of bacterial communities

As shown in Table 1, the sequences of each sample were clustered as Operational Taxonomic Units (OTU) with over 97% identity. Among the three treatments, ST showed the highest OTU number in the samples at thermophilic stage, while the lowest OTU number in initial stage. In terms of Shannon index, ST showed a greater increase and decrease trend than WS or RH. The decrease of Shannon index from ST1 to ST2 might be due to the death of some species during the mesophilic phase, and the marked rise from ST2 (5.78) to ST3 (8.82) was related to the contribution of sufficient nutrients to the growth of some thermophilic or thermotolerant microorganisms (Sun et al., 2019) (Meng et al., 2019). The obvious drop of Shannon index after thermophilic phase was in line with the changes of Chao 1 index. In general, the highest diversity was shown by ST3 in the ST treatment, RH3 in the RH treatment, and WS4 in the WS treatment.

Table 1

Effects of different treatments on Observed Sequences, OTU number, estimated indices (Simpson, Chao 1, ACE and Shannon) and coverage in five sampling stages.

Sample	Sequence	OTUs	Simpson	Chao1	ACE	Shannon
WS1	45760	155	0.976902	1004.21	1046.8	7.47
WS2	44242	199	0.975829	1184.18	1236.44	7.49
WS3	31531	178	0.990941	2024.78	1970.42	8.84
WS4	34659	262	0.99608	2591.25	2602.74	9.52
WS5	34223	218	0.991009	2181.46	2333.1	9.15
RH1	38100	153	0.970149	967.56	1018.12	7.01
RH2	30279	193	0.979968	1302.64	1397.27	7.62
RH3	31768	247	0.992569	1953.25	2061.54	9.15
RH4	28314	206	0.968353	1325.03	1327.73	8.02
RH5	36626	234	0.991915	1942.27	1911.68	8.78
ST1	30948	169	0.968464	1125.01	1211.52	7
ST2	34252	173	0.93199	711.65	741.55	5.78
ST3	50685	399	0.990531	1979.12	2081.65	8.82
ST4	34685	266	0.989882	1712.15	1682.66	8.46
ST5	32329	194	0.991996	1345.6	1360.71	8.67

Note: Chao1 richness estimation index (Chao1) indicates the number of species in the community; the ACE richness estimation index (ACE), the number of species in the community; Shannon diversity index (Shannon), the richness and evenness of the community; Simpson diversity index (Simpson), community diversity. The first column in the table is the sample name, followed by indexes of Observed Sequences, OTU number, Chao1, ACE, Shannon, and Simpson coupled with the results of samples in the same sequencing depth. 1, 2, 3, 4, 5 represent samples at five different periods, including the initial phase, the warming phase, the high temperature phase, the cooling phase, and the maturity phase. WS = woodchips + swine carcasses; RH = rice husk + swine carcasses; ST = wheat straw + swine carcasses.

3.6. Comparison of bacterial community composition at phylum and genus level

Figure 6 presents the classification of 16S rRNA gene sequences at the phylum and genus level. For all the samples at the phylum level (Fig. 6a), the most dominant phyla included *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Cyanobacteria*, *Chloroflexi*, accounting for over 99% of the total 16S rRNA gene sequences in each sample. The first four dominant taxonomic phyla were also found in composting of other wastes (Antunes et al., 2016; de Gannes et al., 2013; Wei et al., 2018).

Proteobacteria was incredibly diverse and contained members of great importance to carbon, sulfur, and nitrogen cycles of the planet (Wei et al., 2018; Zhong et al., 2018; Yang et al., 2019). The abundance of *Proteobacteria* showed a downward trend in WS and RH treatments, but a trend of first rise and then fall in the ST treatment at the thermophilic phase, possibly due to the great importance of *Proteobacteria* phylum to global C, N and S cycling (Burges et al., 2020).

Actinobacteria plays an important role in degradation of refractory cellulose and lignin (Partanen et al., 2010; Peters et al., 2000; Su et al., 2015). *Bacteroidetes* plays a major role in organic matter degradation and C cycling (Wang et al., 2018); *Bacteroidetes* could break down lignocellulose into short chain fatty acids (Dodd et al., 2011; Zhong et al., 2018). *Firmicutes* is thought to play a major role in lignocellulose degradation (Pankratov et al., 2011). The relative abundance of *Bacteroidetes* and *Firmicutes* was both higher in ST than in WS or RH, implying more rapid degradation of cellulose and lignin in ST (Fig. 4a-b). *Cyanobacteria* is the main N₂ fixing organism in freshwater ecosystems (Li et al., 2019). *Cyanobacteria* showed higher abundance in ST than in WS or RH, providing support for N pollution control, remediation, and management. *Chloroflexi* contains aerobic and anaerobic thermophiles, filamentous anoxygenic phototrophs, and anaerobic organohalide respirers (Maymo-Gatell et al., 1997; Xu et al., 2019). *Chloroflexi* exhibited the highest relative abundance in ST5 among all the samples, promoting rapid biodegradation of organic substances and then humification. *Planctomycetes* is considered as slow-growing decomposers of organic matter and has a unique anaerobic ammonium oxidation trait (Kulichevskaya et al., 2012; Zhong et al., 2018). *Planctomycetes* had the highest abundance in WS5 among all the samples, and this phylum may contribute to net nitrification in the compost piles.

Figure 6b shows the top 20 genera in the composting samples. Among them, *Pseudomonas*, *Brevundimonas*, *Acinetobacter*, *Devosia* and *Rhizobium* belong to *Proteobacteria*. *Streptomyces*, *Brevibacterium*, *Saccharoporysora*, *Microbacterium*, *Sanguibacter* and *Brachybacterium* belong to *Actinobacteria*. *Sphingobacterium* belongs to *Bacteroidetes*. *Pseudomonas* is widely distributed in nature and can decompose complex polymers such as lignocellulose (de Gannes et al., 2013). The relative abundance of *Pseudomonas* was higher in ST than WS or RH, probably due to its longer thermophilic phase and higher degradation rate of lignocellulose than either of them. *Streptomyces* and *Acinetobacter* began to emerge at the initial phase of WS treatment and reached the highest level at maturity phase. *Streptomyces* was a dominant bacterium during composting of swine carcasses and woodchips (Yang et al., 2019), which was related to the consumption and assimilation of ammonia (Kim et al., 2013; Yang et al., 2019). A comparison of these three treatments revealed the highest relative abundance of *Brevibacterium* in RH3 sample, which was consistent with the rise of total nitrogen content at the high temperature period. *Brevibacterium* was related with total nitrogen and ammonium nitrogen content in swine carcass composting (Yang et al., 2019). Overall, the total abundance of the top 20 dominant genera was the higher in ST than in WS or RH, indicating that the wheat straw treatment environment is more suitable for microbial growth. The dominant bacteria were *Pseudomonas*, *Staphylococcus* and *Sphingobacterium* in ST treatment, *Streptomyces*, *Acinetobacter* and *Sphingopyxis* in WS treatment, and *Sanguibacter*, *Pedobacter* and *Gordonia* in RH treatment.

3.7. Correlation analysis between bacterial communities and selected factors

Environmental factors are the main drivers for the development of microbial communities (Maeda et al., 2010). The potential effects of various physicochemical parameters (pH, AN, MC, temperature, TC, TN, cellulose, hemicellulose and lignin) on the bacterial community structure throughout the composting process were evaluated by Spearman analysis of the relationship between environmental factors and top 20 genera (Fig. 7). The variables of AN, MC, TN, hemicellulose and lignin and composting temperature were shown to have different (positive/negative) impacts on bacterial communities. *Pseudomonas* was positively related to MC and hemicellulose, but negatively related to temperature and AN. *Brevibacterium* was positively related to temperature, TN and AN. *Saccharoporysora* showed a negative correlation with temperature. *Brevundimonas* showed a significant and positive correlation with pH and cellulose. *Devosia* showed a positive correlation with AN and temperature. Those observations corroborated our analysis results of physicochemical parameters. In terms of compost product, *Pseudomonas*, *Brevibacterium*, *Devosia*, *Staphylococcus*, *Microbacterium*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* all showed a positive correlation with N content, suggesting the high quality of the compost product. Among them, *Brevibacterium*, *Devosia*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* all showed a positive correlation with temperature, suggesting the high maturity of the compost product.

Conclusion

In this study, the environment of ST treatment is more suitable for microbial growth and swine tissue composting efficiency is higher than WS or RH treatments. The dominant bacteria were *Pseudomonas*, *Staphylococcus* and *Sphingobacterium* in ST treatment, *Streptomyces* *Acinetobacter* and *Sphingopyxis* in WS treatment, and *Sanguibacter*, *Pedobacter* and *Gordonia* in RH treatment. Spearman analysis revealed that bacterial species compositions in different composting materials were all significantly influenced by temperature, TN, MC, cellulose, lignin and AN. *Pseudomonas*, *Brevibacterium*, *Devosia*, *Staphylococcus*, *Microbacterium*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* all showed a positive correlation with N content. Among them, *Brevibacterium*, *Devosia*, *Sanguibacter*, *Brachybacterium* and *Promicromonospora* all exhibited a positive correlation with temperature, implying that the compost product has high security. The environmental factors vary in their effect on each species, and microbial communities can be effectively regulated by adjusting relevant environmental parameters. This research facilitates our understanding of the influence mechanism of woodchips, rice husk and wheat straw on the efficiency of swine tissue composting and contributes to the develop of high efficient microbial agent.

Declarations

Data availability

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

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Contributions

Zhenzhen Han, Xinyi Ruan and Rong Zheng designed the study. Zhenzhen Han and Xinyi Ruan completed the entire experimental study. Zhenzhen Han and Xinyi Ruan wrote the manuscript with inputs from Rong Zheng and Jin Chai . Xuchen Yang and Yajing Shan helped with the statistical analysis, and the figures.

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Ethics declarations

Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

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Figures

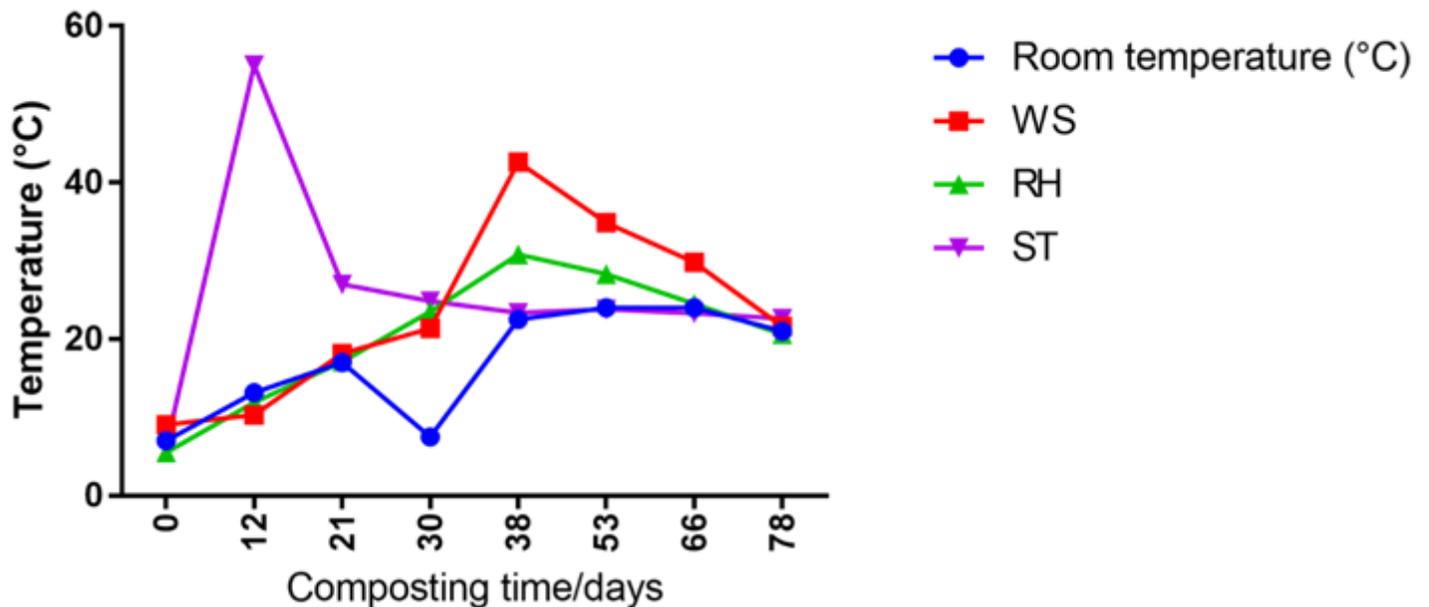


Figure 1

Temperature variations in WS, RH and ST during the composting process. WS = woodchips + swine carcasses; RH = rice husk + swine carcasses; ST = wheat straw + swine carcasses

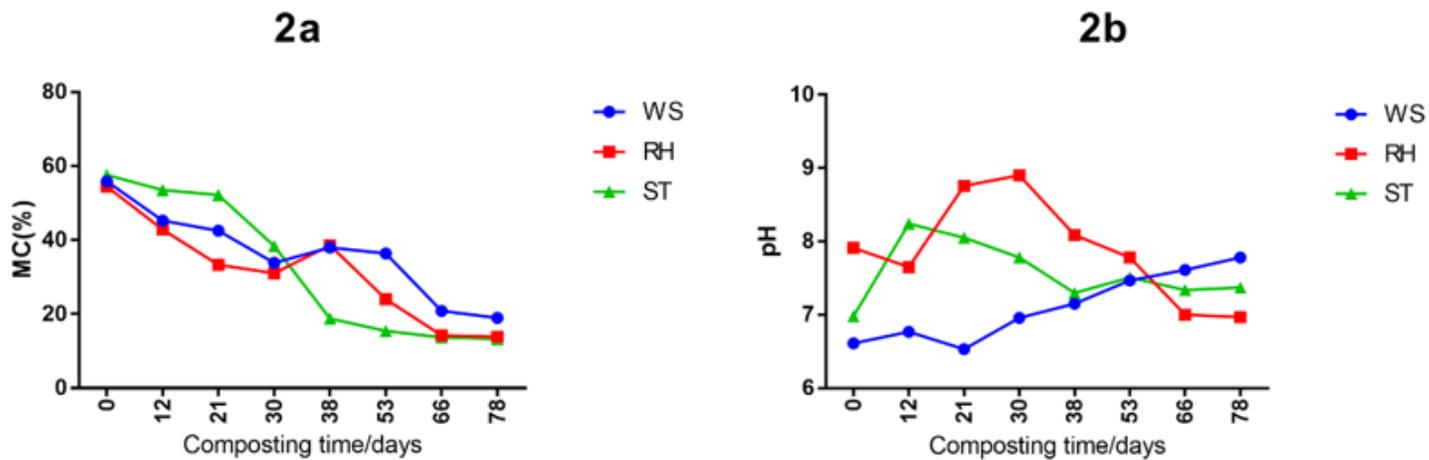


Figure 2

WS, RH and ST during composting process: (a) moisture content and (b) pH. WS = woodchips + swine carcasses; RH = rice husk + swine carcasses; ST = wheat straw + swine carcasses.

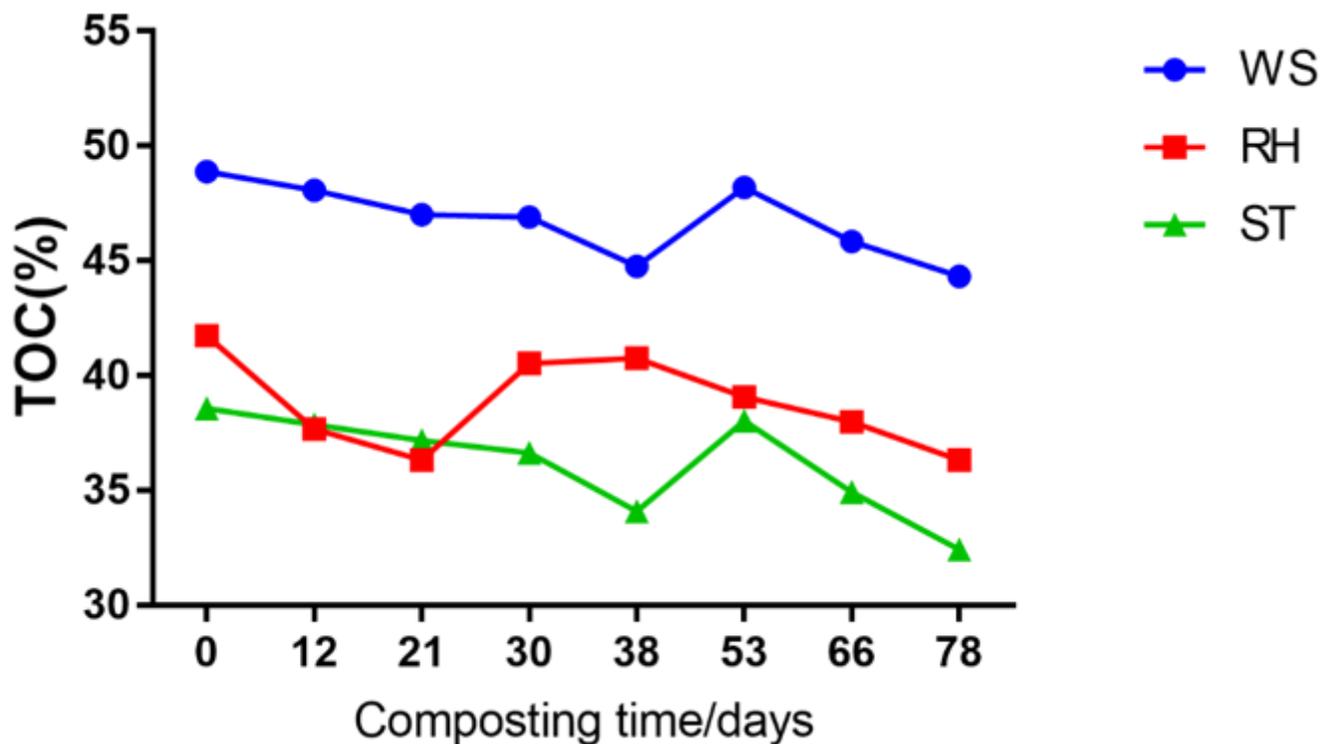


Figure 3

The content of total organic carbon during composting process. WS = woodchips + swine carcasses; RH=rice husk +swine carcasses; ST = wheat straw + swine carcasses.

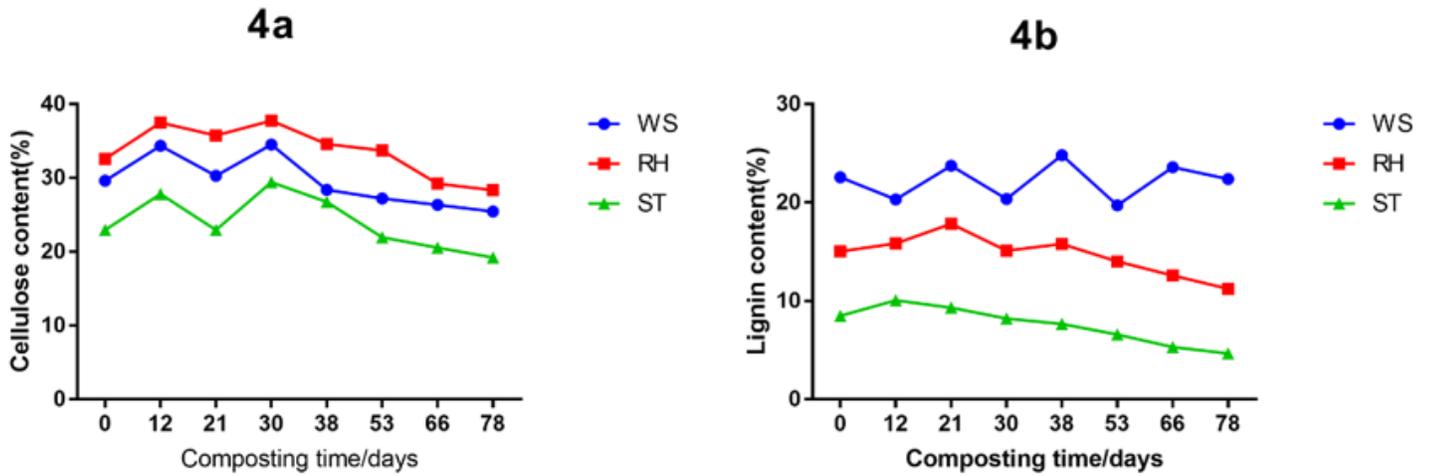


Figure 4

Variations in the cellulose and lignin content in three different treatments during the composting process. (a) cellulose content, and (b) lignin content. WS=woodchips+ swine carcasses; RH=rice husk +swine carcasses; ST=wheat straw+ swine carcasses.

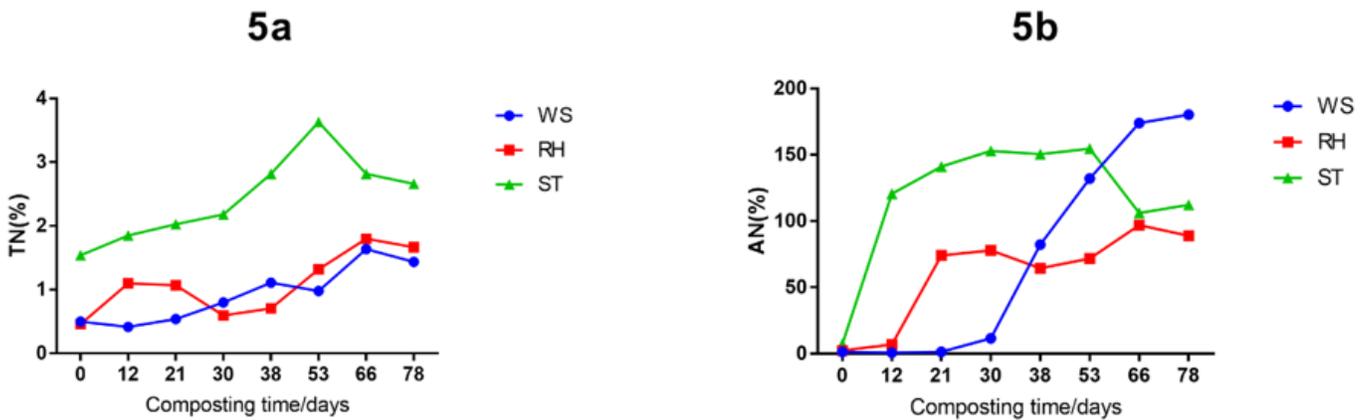


Figure 5

Variations of total nitrogen (TN) and ammonium nitrogen (AN) in three different treatments during the composting process: (a) total nitrogen content, and (b) ammonium nitrogen content. WS=woodchips+ swine carcasses; RH=rice husk +swine carcasses; ST=wheat straw+ swine carcasses.

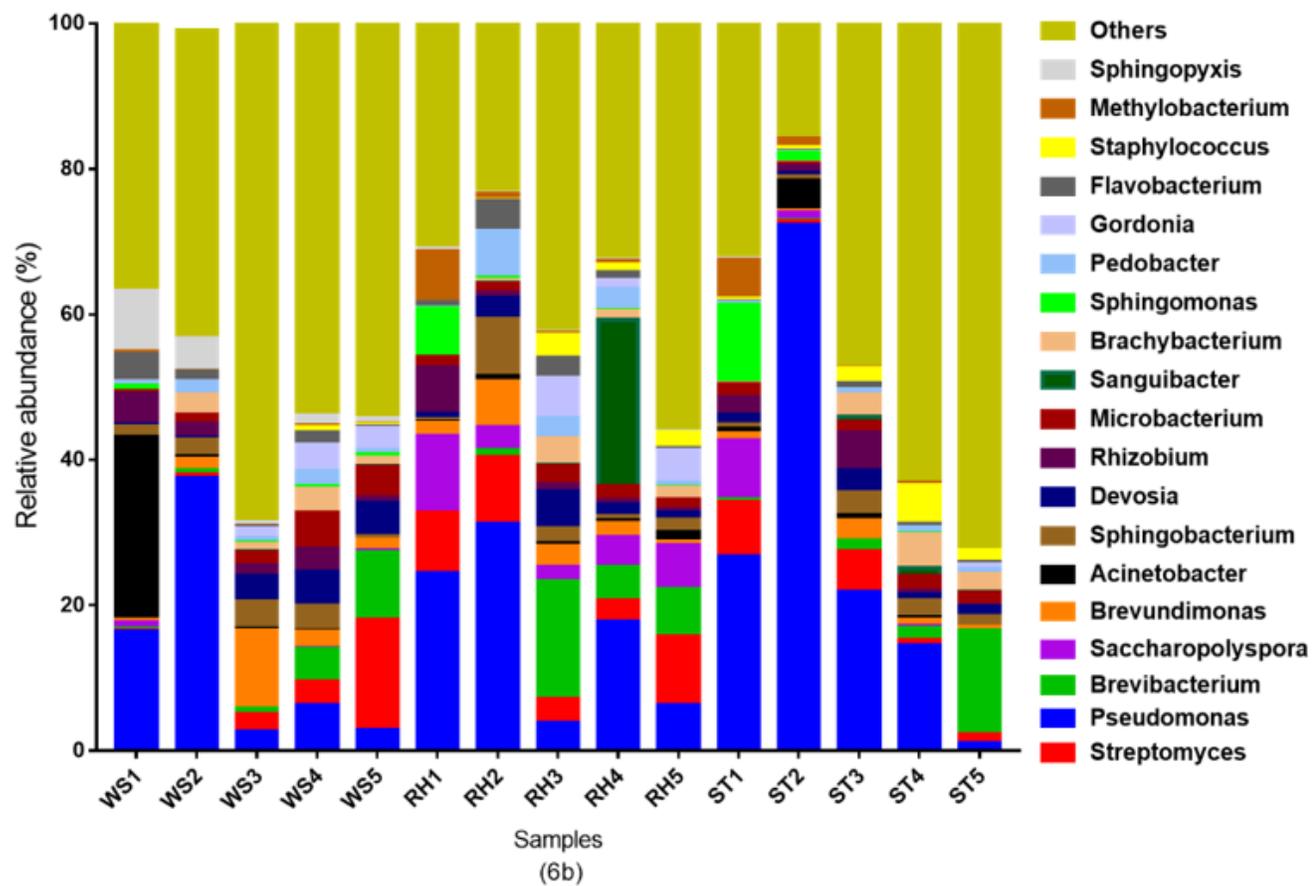
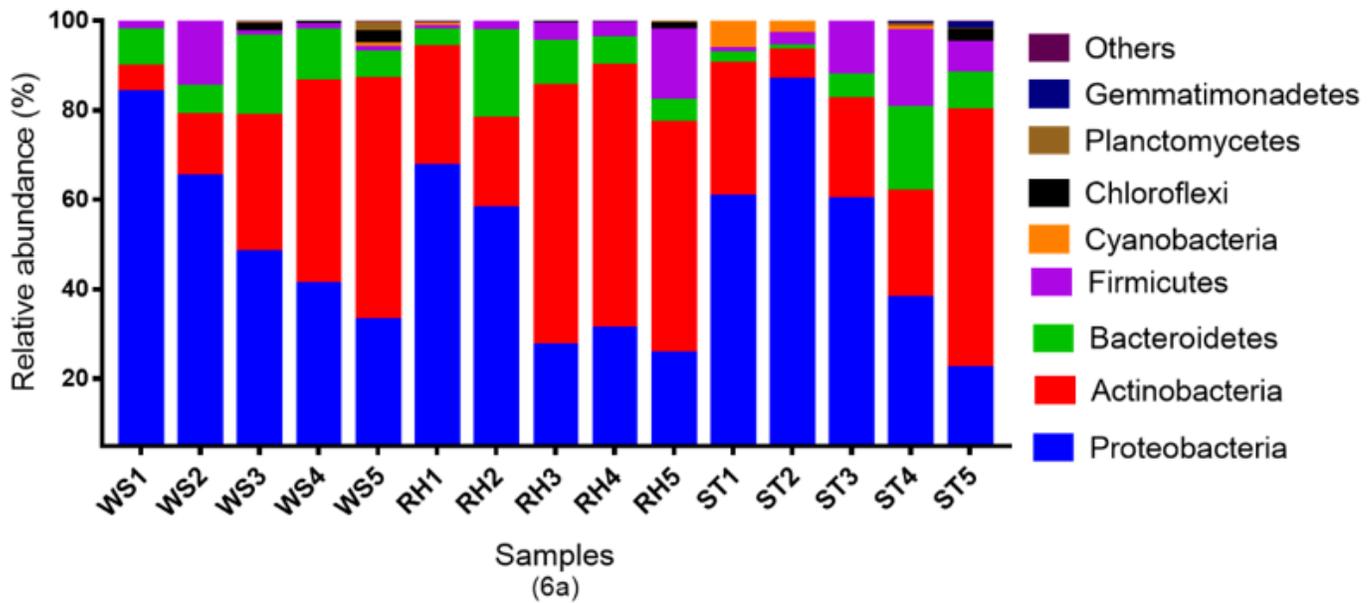


Figure 6

Classification of 16S rRNA gene sequences at the phylum (a) and genus (b) level for each day of composting. The x-coordinate is arranged according to the sample name, with each column graph representing a sample and each taxon being distinguished by color. The y-coordinate represents the relative abundance of each taxon. The longer the column, the higher the relative abundance of the taxon in the corresponding sample. The samples were first clustered according to their mutual similarity, and

then arranged horizontally according to the clustering results. Likewise, taxonomic units were also clustered according to their mutual similarity in distribution in different samples and arranged vertically according to the clustering results. In the figure, red represents the genus with higher abundance in the corresponding sample, and green represents the genus with lower abundance. WS = woodchips + swine carcasses; RH = rice husk + swine carcasses; ST = wheat straw + swine carcasses.

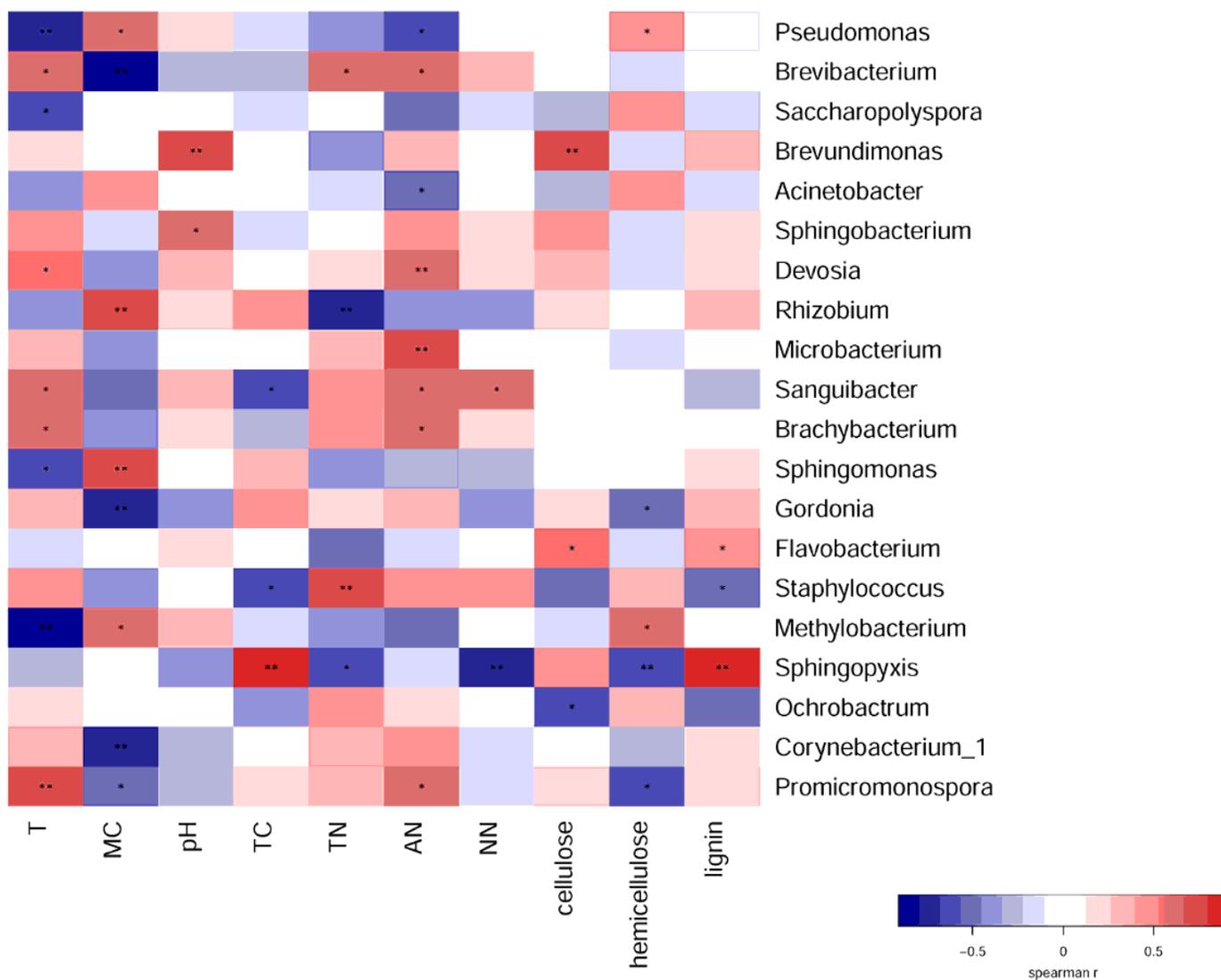


Figure 7

Spearman analysis of the relationship between environmental factors and top 20 genera. In the Spearman correlation heatmap, the R value is indicated by different colors, $0.01 < p \leq 0.05^*$, $0.001 < p \leq 0.01^{**}$, $p < 0.001^{***}$. T, temperature; MC, moisture content; TC, total organic carbon; TN, total nitrogen; NN, nitrate nitrogen.

Supplementary Files

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