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Succession of the microbial community during the process of mechanical and biological pretreatment coupled with a bio-filter for removal of VOCs derived from domestic waste: a field study

Jiaqi Hou,^{ab} Chengze Yu,^{ab} Fanhua Meng,^{ab} Xiaosong He,^{ab} Yong Wang,^{ab} Wangmi Chen^{ab} and Mingxiao Li^{ID *ab}

Changes in the microbial community can not only reflect the efficiency of waste disposal, but also reveal the effect of odor control during the treatment process. This study aimed to evaluate the removal efficiency of volatile organic compounds (VOCs) by the process of mechanical and biological pretreatment (MBP) coupled with a bio-filter (BF). An interesting phenomenon was found that the VOCs were effectively reduced through the MBP process. To understand the removal mechanism of VOCs, the abundance and diversity of microbial bacteria and fungi in the biological dehydration (BD) process, biological fermentation process, and BF process were explored. The abundance and diversity of microbes in the BF were relatively high, of which the bacteria such as *Lactobacillus*, *Bacillus* and *Candida* were the dominant species for VOCs treatment. The proposed technical process and the positive effects observed in this study indicate that it could be applied to the control of VOCs in the treatment of domestic waste.

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1. Introduction

The rapid growth of domestic waste with high moisture content and large fluctuations in composition has brought tremendous pressure and challenges to its treatment. Disposal methods for domestic waste include stacking, landfilling, composting, incineration and so forth.^{1,2} Since landfill will occupy a large amount of land and incineration will cause pollution such as dioxins, composting has become the main technical method for domestic waste treatment in recent years. Numerous studies have shown that domestic waste is separated before composting to ensure the quality of the composting products.^{3–5} Therefore, mechanical biological treatment (MBT), which is composed of mechanical screening and biological fermentation, has become an emerging technological hotspot. For example, single-stream or separated-stream MBT has been applied in Italy for waste treatment.⁶ Also, in the domestic waste plants in Phitsanulok, Thailand, MBT is used as a process to turn household waste into fertilizers or fuels.⁷ However, the high moisture content of domestic waste in China increases the length of the composting time. Simultaneously, domestic waste has also suffered from dehydration, which ultimately slows down the humification rate. Furthermore, if the front-end mechanical screening effect

is not good, it will seriously restrict the back-end composting effect.

To overcome this difficulty, a quality classification and utilization technology (QCU) that adds the mechanical biological pretreatment (MBP) link on MBT has become an improved new technology adopted by Chinese factories in accordance with the characteristics of Chinese waste. MBP is mainly composed of mechanical sorting and biological dehydration (BD). Mechanical sorting is very necessary due to its advantages of being relatively harmless, showing an obvious reduction effect and having low processing costs.⁸ The water content of domestic waste can be reduced by the BD process, making the final humic acid content derived from humified fermentation higher and fertilizer efficiency better. Then, domestic waste pretreated by MBP is further treated by secondary mechanical refinement and humified fermentation to improve its classification and utilization, and ensure the effective control of secondary pollutants such as volatile organic compounds (VOCs).

Various toxic and harmful gases (such as ammonia, hydrogen sulfide, and toluene) and a large amount of VOCs (e.g., dimethyl disulfide, dimethyl sulfide, benzene, 2-butanone, limonene, and methylene chloride) can be generated during domestic waste treatment,^{9,10} causing environmental pollution in and around the domestic waste plant. Removing inorganic odors and VOCs is important in the quality classification and utilization of domestic waste and secondary pollution control.^{11–13} In the research on the removal of VOCs under the

^aState Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing 100012, China. E-mail: limingxiao8122@163.com

^bState Environmental Protection Key Laboratory of Simulation and Control of Groundwater Pollution, Beijing 100012, China



bio-filter (BF) treatment, there are numerous reports about the removal rate, as well as the influence of process parameters such as inlet, gas flow, microbes and pressure drop.^{14–16} However, in the process of domestic waste treatment, the types and quantities of VOCs produced at different processing stages have a great influence on the treatment effect of the BF, but there are few relevant studies.

The specific microbes in the BF can mineralize VOCs into carbon dioxide and water,^{17–20} or convert target pollutants into intermediate products and final products that are less harmful.²¹ Some reports have examined the microbial action mechanism in the treatment of VOCs by evaluating microbial population dynamics.^{22,23} Zhang *et al.* used a BF to treat the gases produced by domestic sewage and found that overall or functional microorganisms can explain the difference in fine purification performance.²⁴ Zheng *et al.* used a BF to remove ammonia and sulfurated hydrogen from landfills and found that the microenvironment within the packing materials is an important factor in the removal performance of the BF.²⁵ Therefore, the microbial changes in the processing stage and the BF are critical to the evaluation of the removal potential of VOCs.

This study was performed in a domestic waste treatment plant in Shanghai. The types and quantities of VOCs produced in gases from the MBP process were analysed. The succession of the microbial community was also studied to evaluate the performance of the technology of QCU for the removal of VOCs.

2. Materials and methods

2.1 Sample collection

The QCU used in the domestic waste treatment plant included the following processes: mechanical sorting–biological dehydration–secondary mechanical refinement–humified fermentation (Fig. 1). The cycle of the QCU of domestic waste takes approximately two months. Initial domestic waste underwent BD for 20 days after mechanical sorting, and then the dehydrated waste was further processed by a secondary mechanical refinement to ensure the proportion of organic materials. Finally, the high organic waste was humified fermented for 35 days to produce organic fertilizers. The difference between mechanical sorting and secondary mechanical refinement was the sieve diameter of the trommel screen. The VOCs in the gases from MBP were analysed in this study. Also, the VOCs in the gases produced in the process were collected by the BF. The BF included an upper compartment and a lower compartment, and each compartment had three layers. In each layer, 3 points were randomly selected and mixed into one sample of 300 g. The samples were immediately taken to the laboratory and stored in a refrigerator at -80°C .²⁶ The collected samples for the process of the QCU and BF are shown in Table 1.

2.2 Analysis method

2.2.1 Volatile organic compounds. The VOCs of gases generated from the QCU were determined by gas

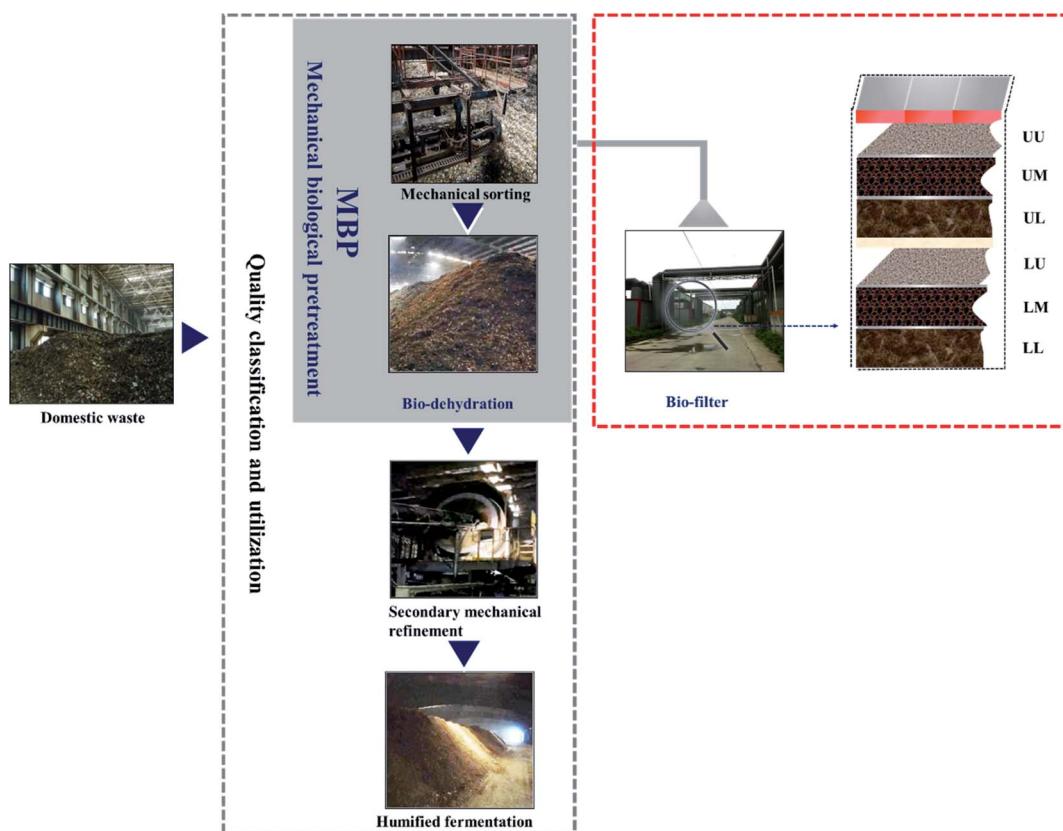


Fig. 1 Quality classification and utilization of domestic waste and BF for odor removal.



Table 1 Sample name and sampling time

Sample ID	Sampling
FW	Fresh waste
BD1	Biological dehydration for 1 day
BD7	Biological dehydration for 7 days
BD20	Biological dehydration for 20 days
HF1	Humified fermentation for 1 day
HF20	Humified fermentation for 20 days
HF35	Humified fermentation for 35 days
UU	Up layer from the upper compartment of the BF
UM	Middle layer from the upper compartment of the BF
UL	Low layer from the upper compartment of the BF
LU	Up layer from the lower compartment of the BF
LM	Middle layer from the lower compartment of the BF
LL	Low layer from the lower compartment of the BF

chromatography-mass spectrometry (GC-MS).²⁷ The VOCs were pre-concentrated using the solid-phase micro-extraction (SPME) method. An SPME fiber coated with 75 μ m carboxen-polydimethyl-siloxane (Supelco, PA, USA) was used to capture VOCs in Tedlar bags. The SPME fiber was manually inserted into the bag for 30 min. Then, the SPME fiber coating containing VOCs was inserted into the GC inlet and kept at 230 °C for 3 min.

The desorption of the VOCs was performed on an Agilent 6890 gas chromatograph system coupled to a mass spectrometric detector (Agilent Technologies, CA, USA). The oven temperature was programmed from 40 °C (5 min) to 270 °C (20 min) by increasing the temperature at the rate of 5 °C per minute. The transfer line was heated at 280 °C. The carrier gas was helium at a constant flow of 1 mL min⁻¹ (mean velocity 36 cm s⁻¹). The mass spectrometer was operated in the scan mode (35–550 amu). The VOC concentration was calculated according to the regression equation of the identified pollutants.²⁸ The emission concentration lower than 0.0005 mg m⁻³ is regarded as undetected and no statistics were performed. This value is the detection limit. The detected VOCs were classified into six categories: saturated hydrocarbon, unsaturated hydrocarbon, aromatic hydrocarbon, sulfide, ketones, and ester. The classification details are shown in Table 2.

2.2.2 DNA extraction and PCR amplification. Genomic

DNA was extracted by a BIOTEKE silt genomic DNA rapid extraction kit (spin column type). Amplified products from the PCR reaction were mixture containing 5 μ L of 10 \times buffer, 4 μ L of dNTP, 1 μ L of per primer (10 μ M, respectively), 30–50 ng of template DNA, 1.5 U of Ex Tag (Takara, Dalian). Then, the quencher bacterial high-purity water was added to the reaction system until it reached 50 μ L. The GC-clamp of the bacterial 16S rRNA genes was 5'-GGCCCCGGCCG-

rDNA genes was 5'-CGCCGGGGCGGGGCGGGGGCACGGGG-3', and the primers of the bacterial 16S rDNA genes were 341F-GC (5'-GC-clamp-CCTACGGGAGGCAGCAG-3') and 534R (5'-ATTACCGCGGCTGCTGG-3').^{29,30} The GC-clamp of the bacterial 16S rDNA genes was 5'-CGCCCGCCGCGCCCCCGCGCCCCGGCCCGCCGCCCCCGCCCC-3',

and the primers of the 18S rDNA genes of the fungus were NS1 (5'-GTAGTCATATGCTTGTCTC-3') and GCfung (5'-GC-clamp-ATTCCCCGTTACCCGGTTG-3').³¹

The amplifying condition followed the touchdown PCR, and different amplification conditions were used for bacteria and fungi. The reaction conditions for bacterial amplification were as follows: an initial denaturation of 5 min at 94 °C, 10 cycles of 30 s at 94 °C, and annealing at 60 °C for 30 s (where each cycle drops 1 °C), and the annealing temperature dropped to 50 °C after 10 cycles, and then extended at 72 °C for 1 min, denaturation at 94 °C for 30 s, annealing at 58 °C for 30 s, extension at 72 °C for 1 min after 20 cycles, extension at 72 °C for 10 min. The reaction conditions for fungal amplification were as follows: an initial denaturation of 5 min at 94 °C, denaturation at 94 °C for 30 s, and annealing at 60 °C for 30 s (where each cycle drops 1 °C), the annealing temperature dropped to 50 °C after 10 cycles, and then extended at 72 °C for 1 min, denaturation at 94 °C for 30 s, annealing at 58 °C for 30 s, extension at 72 °C for 1 min after 20 cycles, and finally at 72 °C for 10 min. All PCR products were stored at 4 °C.

2.2.3 DGGE analysis and sequencing: A Dcode system (Bio-

2.2.5 DGGE analysis and sequencing. A Dcode system (Bio-Rad Laboratories) was used to analyze the PCR products. PCR samples were applied directly onto 8% (wt/vol) polyacrylamide gels in 1× TAE. The denaturant gradient of bacteria and fungi was 30–60% and 20–50%, respectively. Electrophoresis was performed for 16 h at 80 V, and the temperature was set at 60 °C.³² After electrophoresis, the gel was diluted at a ratio of 1 : 10 000 and stained with SYBR Green I for 30 min, and the images were taken using a Gel Doc-It TS imaging system (UVP, USA).

Bacterial sequencing results were compared with the compiled results of 16S rDNA genes in the Genbank database using BLAST, and the fungus sequencing results were compared using the compiled results of 18S rDNA genes in the Genbank database.³³ PCR was conducted using an Omnis-E programmable thermal cycler (Hybaid Ltd., Middlesex, UK).

2.3 Data analysis

SPSS 17.0 (SPSS International) and Origin 8.0 (IBM, USA) were used to analyze and process the data. Gene Quest and Quantity One 4.6.2 were used to analyze microbial data.

3 Results and discussion

3.1 Removal of VOCs by OCU

The total content of VOCs in the gases from the initial domestic waste was 8.46 mg m^{-3} (Fig. 2). The VOCs in the gases released during domestic waste mechanical sorting mainly consisted of saturated hydrocarbons and aromatic hydrocarbons.³⁴ The content of aromatic hydrocarbons is a key issue in VOCs. The concentration of aromatic hydrocarbon was 3.63 mg m^{-3} , accounting for 42.9% of the total VOCs. Zhang *et al.*³⁵ showed that the content of aromatic compounds was higher than that of other VOCs in the municipal waste treatment. Compared with initial domestic waste, the contents of saturated hydrocarbons, aromatic hydrocarbons, ketones, and esters increased with

Table 2 Classification of the detected VOCs

Category	Volatile organic compounds
Saturated hydrocarbon	Trichloromethane, 1,1-dichloroethane, 1,2-dichloropropane, dichloromethane, cyclohexane, <i>N</i> -heptane, <i>N</i> -hexane
Unsaturated hydrocarbon	<i>cis</i> -1,3-Dichloropropene, hexachloro-1,3-butadiene, styrene, perchloroethylene, <i>trans</i> -1,3-dichloropropene, trichloroethylene
Aromatic hydrocarbon	Benzene, chlorobenzene, <i>M</i> -dichlorobenzene, <i>P</i> -dichlorobenzene, ethylbenzene, toluene, trimethylbenzene, xylene, 1-ethyl-4-methylbenzene
Sulfide	Carbon disulfide
Ketones	Acetone, methyl ethyl ketone, methyl isobutyl ketone, methyl <i>n</i> -butyl ketone
Ester	Ethyl acetate

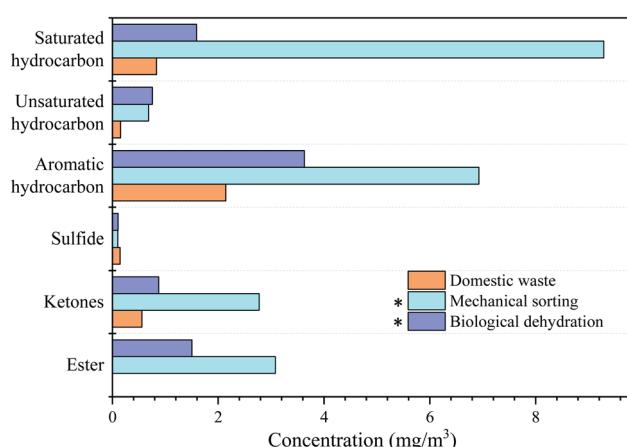


Fig. 2 Changes in the contents of VOCs during QCU. Saturated hydrocarbon (trichloromethane, 1,1-dichloroethane, 1,2-dichloropropane, dichloromethane, cyclohexane, *N*-heptane, and *N*-hexane), unsaturated hydrocarbon (*cis*-1,3-dichloropropene, hexachloro-1,3-butadiene, styrene, perchloroethylene, *trans*-1,3-dichloropropene, and trichloroethylene), aromatic hydrocarbon (benzene, chlorobenzene, *M*-dichlorobenzene, *P*-dichlorobenzene, ethylbenzene, toluene, trimethylbenzene, xylene, and 1-ethyl-4-methylbenzene), sulfide (carbon disulfide), ketones (acetone, methyl ethyl ketone, methyl isobutyl ketone, and methyl *n*-butyl ketone) and ester (ethyl acetate) were detected in VOCs. * Significant difference at $p < 0.05$.

mechanical sorting. For the mechanical motion, the content of saturated hydrocarbons after the mechanical sorting of domestic waste was 5.3 times that of the initial waste.³⁶ The increase in the content of some VOCs in the gases might also be attributable to the photodegradation caused by the operation of the drum screening machine for mechanical sorting.^{37,38}

The domestic waste was further subjected to BD to achieve the purpose of waste volume reduction. The content of total VOCs in the gases detected after BD was 3.81 mg m^{-3} , which was 2.2 times lower than that of the initial waste. As shown in Fig. 2, aromatic hydrocarbons, saturated hydrocarbons, and ketones were the key pollutants that should be controlled during this process. After BD, the content of saturated hydrocarbons decreased to one sixth of its initial value and the content of aromatic hydrocarbon was reduced to half of that of

mechanical sorting. However, BD did not contribute much to sulfide degradation but caused a slight increase in its content. The volatile sulfur compounds were the most important aromatic components produced by biodegradation.³⁹ Aromatic hydrocarbons are usually observed in transfer stations, landfills, and aerobic fermentation plants. Studies have shown that aromatic hydrocarbons were not produced through biodegradation but result from the chemically synthesized materials and household solvents contained in wastes.⁴⁰ BD had a better effect in controlling the release of VOCs compared with mechanical sorting. The results showed that in the MBP process, the content of target pollutants such as saturated hydrocarbons, aromatic hydrocarbons, ketones and esters had been reduced. However, the removal of VOCs in the gases from the MBP process was a synergistic BD and BF, which is the key aspect that needs to be explored through microbial changes.

3.2 Denatured gradient gel electrophoresis profile analysis

The 16S rDNA and 18S rDNA gene fragments of bacteria and fungi were revealed by denatured gradient gel electrophoresis (DGGE) patterns (Fig. 3). The distribution of microbes corresponding to different samples can be judged according to the position, number and brightness of the bands. As illustrated in Fig. 3, bands r and cc were detected among all padding filters of the BF, while band d was detected throughout the BD and humified fermentation. In addition, bands m and o appeared only in the lower compartment of the BF, while band n was detected only in the upper compartment. The results also revealed that the bacterial diversity decreased with the increase in the height of the padding filter, which was consistent with previous findings.⁴¹ Regarding BD and humified fermentation, band v and bands j, l, and gg appeared separately in humified fermentation and BD. The dehydration and fermentation were important for organic matter degradation, thereby accelerating rotting.^{33,42,43} Significant differences between classification, utilization, and biofiltration were found in the bacterial profiles. It can be seen from the bacterial DGGE map that compared to BD, the BF got a better biodiversity.

As shown in Fig. 3b, bands l-r were located in the lower part of the DGGE profile, signifying that these fungi had a higher G + C content³³ and better deodorization ability. The numbers of bands were in the order of resource utilization > biofiltration,



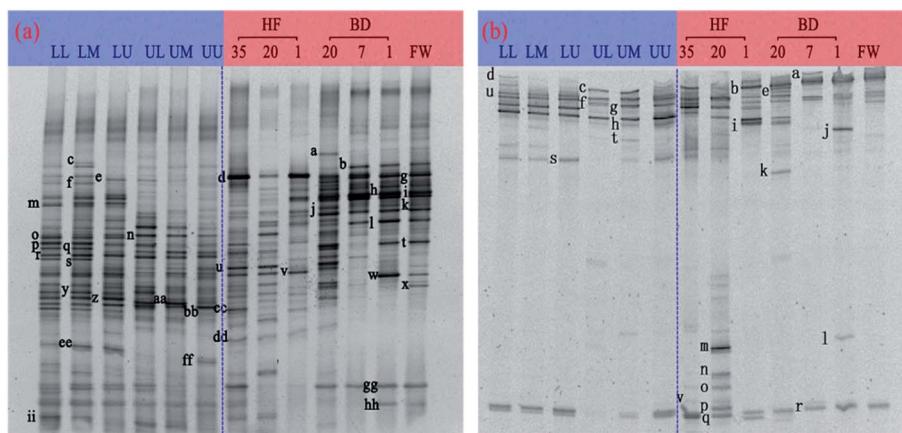


Fig. 3 DGGE maps of bacterial (a) and fungal (b) communities at different locations (purple area) and stages (red area). Samples of fresh waste (FW), biological dehydration for 1 day (BD1), biological dehydration for 7 days (BD7), biological dehydration for 20 days (BD20), humified fermentation for 1 day (HF1), humified fermentation for 20 days (HF20), up layer from the upper compartment of the BF (UU), middle layer from the upper compartment of the BF (UM), low layer from the upper compartment of the BF (UL), up layer from the lower compartment of the BF (LU), middle layer from the lower compartment of the BF (LM) and low layer from the lower compartment of the BF (LL) were detected.

which was consistent with the bacterial DGGE profile. The bands of the fungal DGGE maps of BD and BF were similar, and there was a small difference in the number of bands. The results showed that resource utilization could increase the amounts and types of the dominant fungi in the humified fermentation and BD. Regarding bands a–k from the top of the DGGE profile, band f appeared in both biofiltration and resource utilization, while band h occurred only in biofiltration. The number of bands in BD20 and HF20 was significantly higher than that in the other lanes. Among these, band k in BD20 and bands m–q in HF20 were the dominant species in their lane. Further analysis of the bands in the BF showed that bands u and s were typical in the lower compartment, and the types and numbers of these bands were in the order of lower compartment > upper compartment. The VOCs discharged by the QCU of the four-stage compartment preferentially passed through the lower compartment of the BF, where their air inflows were higher than those in the upper compartment of the BF. This is because VOCs are introduced into the BF, which has an inner effect on the microbes in the filter.⁴⁴

3.3 Dominant microbial communities of biofiltration

The number of bands and Shannon index of bacteria were more than those of fungi (Table 3). The number of bands in BD20 of bacteria was 26, which was 3.71 times that of fungi. The diversity (H) of bacteria was 3.19, which was 1.72 times that of fungi. The greater the diversity, the more abundant the species.⁴⁵ The diversity and abundance of the species decreased with the period of humified fermentation. Regarding biofiltration, the numbers of bands of lower padding filters were much more than those of upper padding filters, but the Pielou index of each padding layer did not show much difference, suggesting that the more abundant the species diversity, the more stable the biological community, which was consistent with the data in the PCR-DGGE analysis. The Shannon index of bacteria in the

lowest layer was 0.35 times higher than that in the highest layer. The filter material with the strongest bacterial diversity was the LL layer with a value of 3.48; however, for fungi, the filter material with the strongest fungal diversity was the LU layer with a value of 2.27. From the perspective of microbial abundance and diversity, bacteria in the BF and fungi in BD20 were more abundant.

Table 4 presents the sequencing results of the dominant bands of bacteria, which were obtained after comparing the sequence of the bands with the National Center for Biotechnology Information (NCBI) database. The results showed that *Lactobacillus* and *Bacillus* were the dominant species. The main difference was that some dominant bacteria in upper-compartment samples had a lower abundance compared with that in the lower compartment such as *Lactobacillus* (Fig. 4). For the original domestic waste, *Lactobacillus*, *Bacillus*, and *Lactococcus* were dominant with the respective abundances of 40.71%, 10.65%, and 10.52%. After mechanical sorting, BD, secondary mechanical refinement, and 35 day humified fermentation, the proportion of *Lactobacillus* was 14.85%, which was quite different from that of the original domestic waste. During the deodorization process of the BF, *Bacillus* could effectively degrade sulfurated hydrogen and ammonia in gases.¹⁶ *Lactobacillus* is anaerobic, facultative anaerobic, or micro aerobic bacteria, which have good removal efficiency for ammonia and other odors.⁴⁶ *Thermobifida*, *Methylorum*, *Pseudoxanthomonas*, *Taibaiella*, *Enterococcus*, *Aerococcus*, and *Lactococcus* were also detected besides *Lactobacillus* and *Bacillus*. *Pseudoxanthomonas* and *Thermobifida* secreted xylanase and glucanase, which were involved in the degradation of cellulose and hemicellulose.⁴⁷ *Taibaiella* has an excellent effect on the removal of aniline, and it usually appears in the landfill leachate.⁴⁸ Therefore, during the classification and utilization of FW to HF35, they had always been dominant species. *Enterococcus* and *Lactococcus* were



Table 3 DGGE band diversity profiles of bacteria and fungi

Sample	Bacteria			Fungi		
	Band number	Shannon (H)	Pielou (E)	Band number	Shannon (H)	Pielou (E)
FW	19	2.85	0.97	5	1.57	0.98
BD1	11	2.35	0.98	7	1.87	0.96
BD7	10	2.22	0.97	5	1.47	0.92
BD20	26	3.19	0.98	7	1.85	0.95
HF1	7	1.87	0.96	4	1.35	0.98
HF20	17	2.81	0.99	11	2.37	0.99
HF35	8	2.02	0.97	5	1.52	0.95
UU	24	3.13	0.98	4	1.34	0.96
UM	19	2.90	0.99	7	1.84	0.95
UL	26	3.19	0.98	9	2.14	0.97
LU	30	3.35	0.99	11	2.27	0.95
LM	34	3.47	0.98	7	1.83	0.94
LL	34	3.48	0.99	5	1.56	0.97

pathogenic bacteria, which only existed in the initial stage of composting and disappeared as the temperature rises.⁴⁹ *Enterococcus* and *Lactococcus* were not detected in HF35, which meant that the QCU used in the domestic waste treatment

effectively removed pathogenic bacteria. Therefore, the dominant bacterial genera of BD and BF differ in composition. The dominant bacterial genera of BF are *Lactobacillus*,

Table 4 Sequencing analysis of 16S rDNA from bacteria

Sequences	Accession number	Species with the greatest similarity	Similarity, %
a	NR104932.1	<i>Erwinia billingiae</i> strain billing E63	100
b	NR113334.1	<i>Lactobacillus curvatus</i> strain NBRC 15884	99
c	NR109520.1	<i>Flavobacterium marinum</i> strain SW105	96.48
d	NR104708.1	<i>Aerococcus viridans</i> strain NBRC 12219	100
e	NR165710.1	<i>Mucilicibacter soli</i> strain R1-15	91.37
f	NR109509.1	<i>Chitinophaga cymbidii</i> strain R156-2	97.44
g	NR104573.1	<i>Lactobacillus plantarum</i> strain CIP	100
h	NR042438.1	<i>Lactobacillus graminis</i> strain G90 (1)	98.49
i	NR044702.2	<i>Lactobacillus amylophilus</i> strain DSM	98.47
j	NR115765.1	<i>Enterococcus faecalis</i> strain ATCC 19433	99.50
k	NR104926.1	<i>Lactobacillus bif fermentans</i> strain CIP 102811	99.49
l	NR113925.1	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> strain NBRC 100676	100
m	NR109732.1	<i>Fabibacter pacificus</i> strain DY53	91.62
n	NR108906.1	<i>Bacillus eiseniae</i> strain A1-2	96.02
o	NR133876.1	<i>Taibaiella koreensis</i> strain THG-DT86	98.45
p	NR074291.1	<i>Bordetella petrii</i> strain DSM 12804	95.98
q	NR043110.1	<i>Pseudoxanthomonas kalamensis</i> strain JA40	98.49
r	NR114009.1	<i>Galibibacter mesophilus</i> strain NBRC 101624	92.31
s	NR029151.1	<i>Bacillus thermoamylovorans</i> strain DKP	98.99
t	NR029261.2	<i>Lactobacillus sanfranciscensis</i> strain L-12	99.49
u	NR159904.1	<i>Bacillus lacus</i> strain AK74	97.99
v	NR133975.1	<i>Bacillus kokeshiformis</i> strain MO-04	95.98
w	NR112108.1	<i>Chroococcidiopsis thermalis</i> PCC 7203	89.83
x	NR117506.1	<i>Bifidobacterium longum</i> strain KCTC 3128	99.43
y	NR114899.1	<i>Methylorum populi</i> BJ001	98.28
z	NR044309.1	<i>Steroidobacter denitrificans</i> strain FS	96.98
aa	NR148571.2	<i>Chloroflexus islandicus</i> strain isl-2	88.44
bb	NR074876.1	<i>Dictyoglomus thermophilum</i> H-6-12	89.66
cc	NR112015.1	<i>Thermobifida fusca</i> strain IFO 14071	98.95
dd	NR137360.1	<i>Bacillus campisalis</i> strain SA2-6	98.47
ee	NR145530.1	<i>Actinoallomurus bryophytorum</i> strain NEAU-TX1-15 sequence	88.33
ff	NR042035.1	<i>Actinomadura umbrina</i> strain IMSNU 22165	89.27
gg	NR043148.1	<i>Lactobacillus oligofermentans</i> strain AMKR18	99.49
hh	NR113958.1	<i>Lactococcus lactis</i> subsp. <i>hordniae</i> strain NBRC 100931	100
ii	NR156918.1	<i>Luteitalea pratensis</i> strain HEG-639	88.83



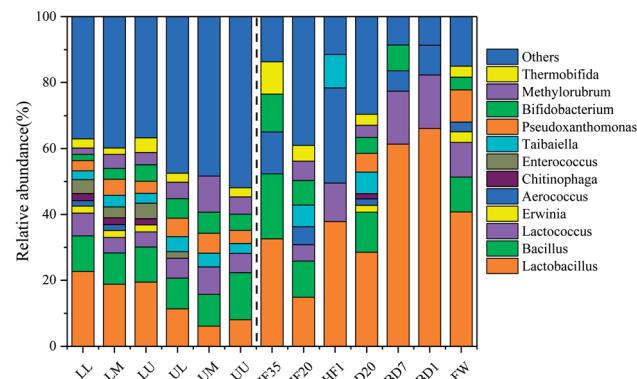


Fig. 4 Relative abundance of bacteria at the genus level. Samples of fresh waste (FW), biological dehydration for 1 day (BD1), biological dehydration for 7 days (BD7), biological dehydration for 20 days (BD20), humified fermentation for 1 day (HF1), humified fermentation for 20 days (HF20), humified fermentation for 35 days (HF35), up layer from the upper compartment of the BF (UU), middle layer from the upper compartment of the BF (UM), low layer from the upper compartment of the BF (UL), up layer from the lower compartment of the BF (LU), middle layer from the lower compartment of the BF (LM) and low layer from the lower compartment of the BF (LL) were detected.

Taibaiella, etc. These dominant bacterial genera play a positive role in the removal of target pollutants.

The similar values of sequences a, b, j, s, and u in Table 5 were all more than 99%. The 13 dominant fungal bands were classified as *Candida*, *Aspergillus*, and *Thermothelomyces*. *Candida* has a significant impact on the production and changes of VOCs.⁵⁰ As illustrated in Fig. 5, *Candida* has always been the dominant genus during the QCU process of domestic

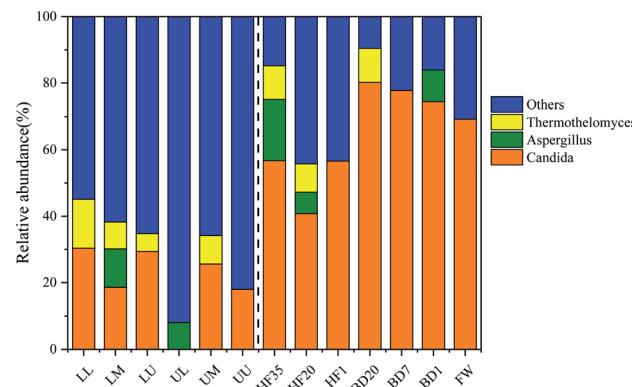


Fig. 5 Relative abundance of fungi at the genus level. Samples of fresh waste (FW), biological dehydration for 1 day (BD1), biological dehydration for 7 days (BD7), biological dehydration for 20 days (BD20), humified fermentation for 1 day (HF1), humified fermentation for 20 days (HF20), humified fermentation for 35 days (HF35), up layer from the upper compartment of the BF (UU), middle layer from the upper compartment of the BF (UM), low layer from the upper compartment of the BF (UL), up layer from the lower compartment of the BF (LU), middle layer from the lower compartment of the BF (LM) and low layer from the lower compartment of the BF (LL) were detected.

waste. It had the highest proportion of 80.27% in BD20, but it was not detected in the UL, indicating that VOCs were not conducive to the survival of *Candida*. *Aspergillus* can promote the removal rate of ammoniacal nitrogen and chemical oxygen demand in the landfill leachate and the activity of cellulolytic enzymes.⁵¹ The concentration of *Thermothelomyces* began to increase on the 20th day of biological dehydration, and it mainly existed in the padding filter of the BF for VOC degradation. *Thermothelomyces* was a common thermophilic genus,

Table 5 Sequencing analysis of 18S rDNA from fungi

No	Accession number	Species with the greatest similarity	Similarity, %
a	NG063407.1	<i>Candida sojae</i> JCM 1644	99.14
b	NG063416.1	<i>Candida quercitrusa</i> JCM 9832	99.43
c	NG064977.1	<i>Tritirachium cinnamomeum</i> IHEM 3714	89.82
d	NG062812.1	<i>Acremonium flavum</i> CBS 596.70	96.78
e	NG062131.1	[<i>Candida</i>] <i>fukazawai</i> JCM 1641	97.93
f	NG063411.1	<i>Candida austromarina</i> JCM 8894	95.42
g	NG064994.1	<i>Thermothelomyces hinnuleus</i> ATCC 52474	93.86
h	NG067668.1	<i>Megasporia hengduanensis</i> BJFC Cui 8076	97.20
i	NG063422.1	<i>Candida edax</i> JCM 9470	93.33
j	NG064802.1	<i>Aspergillus proliferans</i> CBS 121.45	99.14
k	NG065474.1	[<i>Candida</i>] <i>intermedia</i> JCM 1607	97.33
l	NG065472.1	[<i>Candida</i>] <i>pseudointermedia</i> JCM 1592	97.04
m	NG063232.1	<i>Aspergillus cervinus</i> NRRL 5025	80.5
n	NG063232.1	<i>Aspergillus cervinus</i> NRRL 5025	80.28
o	NG064802.1	<i>Aspergillus proliferans</i> CBS 121.45	98.56
p	NG063232.1	<i>Aspergillus cervinus</i> NRRL 5025	80.5
q	NG063419.1	<i>Candida viswanathii</i> JCM 9567	92.84
r	NG063242.1	[<i>Candida</i>] <i>glabrata</i> NRRL Y-65	98.57
s	NG064994.1	<i>Thermothelomyces hinnuleus</i> ATCC 52474	99.12
t	NG064938.1	<i>Aspergillus caninus</i> UAMH 10337	80.5
u	NG063242.1	[<i>Candida</i>] <i>glabrata</i> NRRL Y-65	99.43
v	NG064994.1	<i>Thermothelomyces hinnuleus</i> ATCC 52474	92.75



which has a significant catalytic oxidation effect on polycyclic molecules.⁵² *Thermothelomyces* also appeared in BD20, and the diversity of fungi in BD20 was high, indicating that BD also made a certain contribution to the removal of target pollutants.

4. Conclusions

This study compared the types and contents of VOCs in the gases from the original domestic waste, and illustrated that VOCs can be removed during the MBP process. It was recommended that VOCs produced in 20 days before BD should be monitored. *Lactobacillus* and *Bacillus* among bacteria, and *Candida*, *Aspergillus*, and *Thermothelomyces* among fungi were dominant with a positive role in the disposal of VOCs. In addition, the bacteria in the BF are the key step to remove VOCs in the gases, and the fungi in BD have also made a small contribution in the removal of VOCs. Moreover, inoculating *Lactobacillus*, *Bacillus*, *Candida*, *Aspergillus*, and *Thermothelomyces* into BF is expected to improve the removal efficiency of VOCs.

Author contributions

Jiaqi Hou: Data curation, Writing – original draft preparation, and Funding acquisition; Chengze Yu: Software and Formal analysis; Fanhua Meng: Validation and Software; Xiaosong He: Validation and Software; Yong Wang: Conceptualization and Methodology; Wangmi Chen: Reviewing and Editing; Mingxiao Li: Ideas and Supervision.

Conflicts of interest

There are no conflicts to declare.

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