

Bacterial Community Succession in Earthworm Mucus and Sludge Compost and its Relationship with Environmental Factors

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This study investigated the effects of adding earthworm mucus on the changes in sludge compost bacterial community structure and its response to environmental factors. The results showed that adding earthworm mucus improved the composting effect of sludge, reducing nitrogen loss and increasing nutrients; nitrogen loss decreased by 5.55%, and potassium and phosphorus increased by 10.23 and 16.28%, respectively. Firmicutes, Chloroflexi, Actinobacteria, and Proteobacteria were the main bacterial phyla in the sludge, with a combined relative abundance of over 60%. The addition of earthworm mucus significantly impacted bacterial community structure and composting activity, increasing the relative abundance of dominant bacteria during the process. Redundancy analysis showed that environmental factors significantly impacted the changes in bacterial community structure during composting. The results indicate that the addition of earthworm mucus increases the relative abundance of advantageous bacteria playing essential roles in sludge composting, enhancing the fertility and maturity of sludge composting products by significantly reducing nitrogen loss and increasing potassium and phosphorus. Based on the response relationship between environmental factors and bacterial communities, the bacterial community structure in sludge composting can be improved by regulating environmental factors (such as pH and moisture content), enhancing the effectiveness of sludge composting.

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Introduction

Sewage sludge is a semi-solid waste generated from urban sewage treatment that contains high concentrations of pollutants such as heavy metals, pathogens, and organic compounds. It necessitates appropriate management, and how this sludge can properly be disposed of has become a critical environmental issue [1-3]. At present, there are three main methods for sludge disposal: chemical treatment (adding chemical components), thermal treatment (incineration, pyrolysis, gasification), and biological treatment (earthworm composting, composting, anaerobic digestion, autothermal thermal aerobic digester [3], and others). The three disposal methods have different advantages and disadvantages. Chemical treatment is simple to operate with minor nitrogen loss, but it is costly and increases the dry weight of residual sludge. Heat treatment takes a short time with a high weight reduction ability and the ability to recover carbon; however, it is technically complex, costly, and requires control of emitted gas pollutants [4]. Considering other factors such as cost and recycling capacity, biological disposal appears to be a suitable method for disposing of sludge [5].

Composting is a biological treatment method involving the controlled decomposition of organic waste under aerobic conditions through the use of the enzymatic activity of microorganisms [6, 7]. Recycling sludge compost for agricultural use and soil improvement is often one of the most convenient, effective, and cost-effective disposal options [1, 8]. During the composting process, harmful substances and pathogens in sludge can be eliminated, and nutrients such as nitrogen and phosphorus can be recovered and converted into organic fertilizers [9]. The physical and chemical properties of sludge are unsuitable for direct composting, meaning it can only be recycled into high-quality products through co-composting [10]. Many studies have added improved materials to sludge compost to achieve synergistic effects in stabilizing waste, and in recent years, significant achievements have been made in co-composting sludge with various additives to improve the quality and maturity of compost, such as rice husks, earthworms, biochar, and sawdust. [7, 8, 11, 12].

Research into earthworm composting began in the late 1970s and is considered an effective, environmentally friendly technology for treating sewage sludge [13]. Due to the complex composition of the initial sludge and the high-temperature environment formed during fermentation, it is often necessary to pre-compost the sludge when using earthworm composting to avoid killing the worms. To get around this issue, some scholars have shifted their focus from earthworm addition to adding only earthworm mucus, a lubricant secreted from the epidermis of earthworms that is mainly composed of water, lipids, carbohydrates, sugars, proteins, and amino acids [14, 15]. It plays a crucial role in earthworm movement, feeding, excretion, osmotic regulation, defense, and reproductive activities [16-18]. Bityutskii

et al. have demonstrated that earthworm mucus in soil can drive the mineralization and humification of plant residues [19]. In addition, studies have also found that adding earthworm mucus to earthworm compost can change the bacterial community structure and accelerate the mineralization and humification of compost materials [20]. Although earthworm mucus has been proven to have significant utilization value, there have been no reports on the direct use of earthworm mucus in sludge composting, and it is necessary to explore whether the direct addition of earthworm mucus could positively affect the sludge composting process.

Decomposition by microorganisms plays a crucial role in the transformation and stability of organic matter (OM) during composting. Bacteria are one of the most important types of microorganisms, and understanding their community changes during composting is of great significance for understanding the overall process as well as the microbiological mechanisms involved. To date, scholars have explored the changes in microbial community structure in composting systems, however, most have used human or livestock manure as raw materials and biochar or microbial agents as additives. In addition, some scholars have studied the effect of earthworm mucus on sludge composting, but this study is based on earthworm composting [20].

There have been few reports on directly adding earthworm mucus to sludge compost and exploring the succession of bacterial communities that occur in response. Considering the potential utilization value brought by the complex components and special functions of earthworm mucus, this study evaluated the impact of earthworm mucus on sludge composting, especially the changes in bacterial composition that occur and their responses to environmental factors, to provide new directions for sludge resource utilization using this treatment method.

Materials and Methods

Test Materials

The municipal sludge used originated from a wastewater treatment plant in Huainan City, Anhui Province, China, with a moisture content after deep dewatering of 75-80%. The test sludge was fresh and was immediately transported back to the laboratory for composting testing after sampling. Earthworms produced the mucus used in the experiment after electrical stimulation at 5 V and 10 mA; the earthworms used were Taiping II *Eisenia fetida* purchased from the Jurong Earthworm Breeding Base in Jiangsu Province, China, commonly known as red earthworms. They had a fresh weight of ~0.5 g per worm. Each experimental material's basic physical and chemical properties are shown below (Table 1). Analytical methods are described in Section 2.3.

Materials	Sludge	Rice husk	Earthworm mucus
Electrical conductivity ($\mu\text{S}\cdot\text{cm}^{-1}$)	215.00	1142.33	495.00
Potential of hydrogen	7.31	6.58	7.85
Moisture content (%)	76.04	4.97	98.92
Organic matter (%)	43.73	41.78	0.39
Total nitrogen ($\text{g}\cdot\text{kg}^{-1}$)	20.62	3.20	0.09
Total phosphorus ($\text{g}\cdot\text{kg}^{-1}$)	13.45	0.39	0.03
Total potassium ($\text{g}\cdot\text{kg}^{-1}$)	3.56	3.78	0.01

The sludge was composted alone to establish a control (CK) with a total sludge weight of 4 kg, and 80 mL of earthworm mucus was added to the test group (M) [20], both of which were supplemented with approximately 200 g of rice husk to regulate the carbon to nitrogen ratio of the sludge. All treatments were set up in three parallel samples. The composted substrate was placed in a compost box with a length \times width \times height of 24 \times 21 \times 26 cm and was composted for 35 days. A compost box was used to control the temperature throughout the composting process, which was maintained at 40 $^{\circ}$ C on day 0, at 50 $^{\circ}$ C on days 1-8, and then decreased by 5 $^{\circ}$ C per day after day 9 until room temperature was reached. The box then entered a natural decay phase until the end of the composting process. During the first 15 days, the piles were turned twice a day and ventilated five times (at a rate of 0.5 L \cdot min $^{-1}$), then ventilated twice daily for the next 20 days and turned every 2 days.

Compost temperature (T) was measured in the morning and evening every day, and the average value was recorded as the temperature of the heap for that day. Samples were taken on days 0, 4, 8, 13, 19, 26, and 35, and around 150 g of samples were collected each time. Portions (10 g) of samples were stored in a refrigerator at 4 °C for the determination of physicochemical properties such as pH, EC, moisture content, and OM; 130 g were naturally air-dried for the determination of total nitrogen, total phosphorus, and total potassium; and 10 g were stored in a refrigerator at -80 °C for bacterial community analysis.

Moisture content (MC) was determined by weight loss in an oven at 105 °C. pH and electrical conductivity (EC) were determined by a benchtop acidimeter (PHS-3C, Shanghai Precision Scientific Instrument Co., Ltd., China) and a benchtop conductivity meter (DDS-307A, Shanghai Yidian Analytical Instrument Co., Ltd., China), respectively, using the methods reported by Jining et al. [21]. Total nitrogen (TN) and total phosphorus (TP) were determined using the alkaline potassium persulfate digestion-UV spectrophotometric method and the ammonium molybdate spectrophotometric

DNA Extraction and PCR Amplification

Microbial DNA was extracted from mouse feces specimens using the FastLee DNA kit for Feces (Hangzhou Legenomics Bio-Pharm Technology Co., Ltd., Hangzhou, China) according to the manufacturer's instructions. The V3-V4 region of the bacteria 16S ribosomal RNA gene was amplified by PCR (95 °C for 2 min, followed by 25 cycles at 95 °C for 30 s, 55 °C for 30 s, and 72 °C for 30 s, and a final extension at 72 °C for 5 min) using primers 341 F 5'-barcode- CCTAYGGGRBGCASCAG)-3' and 806 R 5'-GGACTACNNGGTATCTAAT-3', where the barcode was an eight-base sequence unique to each sample. The PCR reactions were performed in triplicate with 4 µL of 5X FastPfu Buffer, 2 µL of 2.5 mM dNTPs, 0.8 µL of forward primer (5 µM), 0.8 µL of reverse primer (5 µM), 0.4 µL of FastPfu Polymerase, 0.2 µL of BSA, and 10 ng of template DNA, topped up with ddH2O to a final volume of 20 µL. Amplicons were extracted from 2% agarose gels and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, U.S.) according to the manufacturer's instructions and quantified using QuantiFluor™-ST (Promega, U.S.).

Raw data processing and analysis were done using Excel 2021 and SPSS24. One-way analysis of variance (ANOVA) and least significant difference (LSD) were used to analyze the physicochemical properties as well as microbial community structure in the compost samples; physicochemical parameters and microbial abundance were plotted using Origin 2022. Redundancy analysis (RDA) plots were plotted via the Parnassian Genome Cloud platform (<https://www.genesccloud.cn>). The significance was set at 0.05 and 0.01.

to the intense competition between dominant bacteria. The abundance of Actinobacteria slightly increased from the high-temperature period to the maturation stage, mainly due to its ability to degrade complex organic compounds such as cellulose and lignin as well as its role in carbon and nitrogen conversion [43, 44]. After the high-temperature period until the end of composting, Bacteroidetes became one of the dominant phyla, while other dominant phyla remained unchanged. This phylum is crucial for the utilization of lignocellulose and the subsequent release of short-chain fatty acids, explaining their increasing relative abundance during the composting stage [45]. The relative abundance of dominant bacteria in the M treatment with the ability to degrade complex OM, such as lignin and cellulose, was higher than that in the CK treatment from the beginning of the composting process until maturity (0-18 days), indicating that adding earthworm mucus improved the composting efficacy.

To further explore the microbial community structure of composting, the horizontal distribution of bacterial genera was analyzed (Figure 5). During composting, the main dominant bacterial genera were *Bacillus*, *Caldicoprobacter*, *Saccharibacteria_Norank*, *Tepidimicrobium*, and *Ureibacillus*. In the early stage of composting (0 days), the dominant bacterial genera for CK and M treatments were *Anaerolineaceae_Uncultured*, *Caldilineaceae_Uncultured*, *Saccharibacteria_Norank*, *Saprospiraceae_Uncultured*, and *TK10_Norank*. When composting entered the high-temperature period, the horizontal distribution of bacterial genera underwent drastic changes, with *Bacillus*, *Caldicoprobacter*, and *Saccharibacteria_Norank*, *Tepidimicrobium*, and *Ureibacillus* becoming the dominant bacterial genera in both treatment groups, with the total combined relative abundance reaching 47.49 and 58.86% for CK and M treatments, respectively, on the fourth day. As the compost continued to ferment and mature, the main

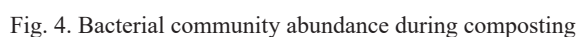


Fig. 4. Bacterial community abundance during composting

Changes in bacterial communities can significantly impact the composting process, especially its efficacy. Studies have reported that bacterial community succession is driven by changes in environmental conditions and substrate composition at each composting stage [50]. Understanding the impact of environmental factor changes during composting on microbial community succession is particularly important. The influence of environmental factors on the relative abundance of the top six phyla in earthworm mucus compost sludge was analyzed using RDA. As shown in Figure 6, the RDA1 and RDA2 axes explained 68.01 and 3.43% of the changes in bacterial community structure and environmental factors, respectively. Together, the two axes explained 71.44% of the sample information, indicating that physical and chemical factors are related to changes in bacterial community structure during composting. At the phylum level, the correlation order between environmental factors and bacterial community structure was EC>MC>pH>OM>TN>T, but the difference is minimal. Specifically, T, pH, and EC were positively correlated with Firmicutes, Actinobacteria, and Saccharibacteria but negatively correlated with

Compared with the CK treatment, the M treatment with added mucus showed a higher trend in the abundance of dominant bacterial genera throughout the entire composting process, mainly reflected in both *Bacillus* and *Ureibacillus*. *Bacillus* and *Ureibacillus* are the prominent representatives of Firmicutes, which are widely present bacterial community components during the composting stage. According to reports, *Bacillus* mainly survives in compost by forming endophytic spores that can tolerate high temperatures [46]. In addition, studies have shown that *Bacillus* can compete with other microorganisms because of its antifungal and protease activities [47, 48]. Rong et al. reported that *Ureibacillus* is an aerobic thermophilic bacterium that can degrade lignocellulose [49]. Adding earthworm mucus resulted in a more efficient macromolecular degradation system in the M treatment.



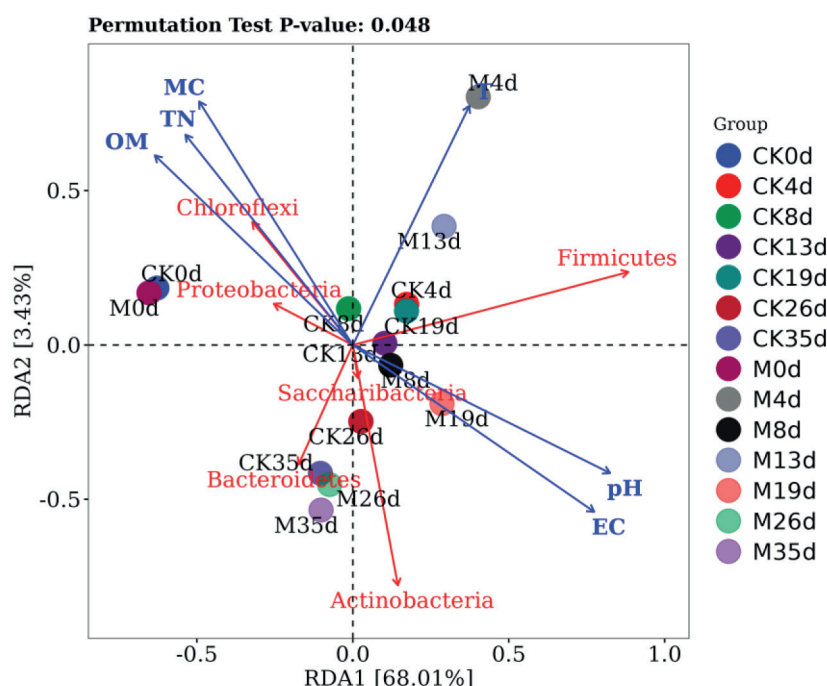


Fig. 6. Redundancy analysis of environmental factors and bacterial community structure during composting (gate level). The arrow length in the RDA graph represents the degree of correlation between environmental factors and sample distribution.

Chloroflexi and Proteobacteria; MC, TN, and OM were positively correlated with Chloroflexi and Proteobacteria, and negatively correlated with Firmicutes, Actinobacteria, and Saccharibacteria.

Although the impact of T on bacterial communities in this study is relatively small compared to other environmental factors, it has been reported that it is still an essential factor affecting microbial metabolism during composting [22, 42, 51]. Both high and low pH can seriously impact microbial activities. Lucas et al.'s research suggests that changes in pH can lead to changes in nutrient availability, such as calcium and magnesium, which may indirectly affect bacterial communities [52]. For this study, the above conclusions are directly reflected in the Firmicutes phylum, which had the highest relative abundance during the composting process, and pH was the environmental factor with the strongest positive correlation during the thermophilic stage. For Actinobacteria, which play a vital role in the decomposition of lignocellulose, the most negatively correlated environmental factor was MC. According to reports, Actinobacteria can survive in harsh environments, such as those with high temperatures and reduced water content, by forming spores [53, 54]. In this study, the MC content in the M treatment during the thermophilic stage was lower than that in the CK treatment, and correspondingly, the relative abundance of Actinobacteria was higher in MC. TN and OM were the environmental factors with the strongest positive correlation with Chloroflexi and Proteobacteria, respectively, indicating that the nutrient content (C, N) in compost changed with the continuous transformation of microbial metabolites [54]. The results indicate that appropriately increasing pH and reducing MC during

the high-temperature composting period could promote composting humification. Environmental factors (T, pH, MC, OM, TN, EC) in composting played a large role in the succession of bacterial community structure, as all kinds of bacteria are affected by environmental factors to different degrees. Regulating these environmental factors in the composting process may be an effective optimization method, especially in terms of improving bacterial community structure.

Conclusions

This study examined the addition of earthworm mucus to composting sludge to determine its effects on composting efficacy and the microbial community involved. The addition of earthworm mucus optimized sludge composting and played a prominent role in reducing nitrogen loss and increasing nutrients. Earthworm mucus increased the relative abundance of dominant bacteria in sludge compost, which is beneficial for sludge maturation. Environmental factors significantly impacted the bacterial community structure during sludge composting. These results indicate that sludge composting can be optimized for improved efficacy by regulating environmental factors.

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