

Sustainable valorization of traditional Chinese medicine residues via semi-permeable membrane composting: The impacts of nitrogen sources

Di Cui

jscz_dd@hotmail.com

Harbin University of Commerce

Peipei Gao

Harbin University of Commerce

Chunyan Li

Harbin Institute of Technology

Xiaoqi Wu

Harbin University of Commerce

Zeyi Chen

Harbin University of Commerce

Ang Li

Harbin Institute of Technology

Research Article

Keywords: Traditional Chinese medicine residues, Semi-permeable membrane, Aerobic composting, Peanut meal, Nitrogen source

Posted Date: September 15th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10936628/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Additional Declarations: No competing interests reported.

Abstract

Driven by global disease challenges, the traditional Chinese medicine (TCM) industry has flourished, however, the massive surge in TCM residues has emerged as a major bottleneck to its sustainable development. Semi-permeable membrane aerobic composting provides a key technology for TCM residue valorization, which typically relies on exogenous nitrogen supplementation to optimize the carbon-to-nitrogen (C/N) balance. Nevertheless, a systematic understanding of how differentiated nitrogen sources impact this composting process remains lacking. To address this, this study introduced distinct nitrogen sources as co-substrates for semi-permeable membrane aerobic composting to elucidate their modulation of key physicochemical parameters and microecological succession. The results demonstrated that peanut meal exhibited the optimal composting performance compared to alfalfa meal, soybean meal, and urea. Specifically, its thermophilic phase ($> 55^{\circ}\text{C}$) persisted for over 7 days, and total organic carbon (TOC) degraded most rapidly and stably, achieving a reduction rate of 49.82%. At maturity, the ammonium nitrogen ($\text{NH}_4^{+}\text{-N}$) content and electrical conductivity (EC) dropped to as low as 81 mg/kg and 2606 $\mu\text{S/cm}$, respectively, while the peak total nutrient content reached 5.79%. Meanwhile, the dynamic trend of the E4/E6 ratio aligned with typical aerobic composting patterns, indicating a high degree of humification. Community analysis revealed that *Bacillus*, *Bifidobacterium*, and *Cupriavidus* were key bacterial taxa driving composting efficiency, whereas fungi dominated by *Thermomyces*, *Mycobacterium*, and *Aspergillus* played pivotal roles in $\text{NH}_4^{+}\text{-N}$ and lignocellulose degradation, significantly accelerating compost maturation. Overall, this study provides critical microecological insights and a practical nitrogen optimization strategy for efficient and sustainable TCM residue composting.

1. Introduction

The escalation of global disease burdens and public health demands has propelled the rapid expansion of the traditional Chinese medicine (TCM) industry (Huang et al. 2021). However, accompanied by the continuous growth of the TCM market, the output of TCM residues (TCMR) has increased annually, with China's annual production exceeding 35 million tons (Wang et al. 2026). Currently, TCMR disposal still heavily relies on traditional methods such as open dumping, landfilling, and incineration (Tao et al. 2013). These extensive practices not only cause severe resource waste of residual lignocellulose and active components in TCMR, but also trigger secondary ecological pollution including malodorous gas emissions and leachate generation, contradicting the internationally advocated low-carbon circular development philosophy (Li et al. 2026a, Li et al. 2026b, Park et al. 2025). Therefore, establishing a green and recyclable TCMR valorization system to achieve synergistic ecological and economic disposal has emerged as a critical bottleneck for the sustainable development of the TCM industry.

Semi-permeable membrane-covered aerobic composting, an emerging organic solid waste management technology, exhibits prominent advantages in suppressing odor and greenhouse gas emissions, preventing local anaerobic fermentation, intensifying microbial degradation, and enhancing carbon retention efficiency, making it highly compatible with TCMR valorization (Kou et al. 2024, Xu et al. 2023,

Zhang et al. 2024). However, TCMR typically possesses structural features characterized by a high carbon-to-nitrogen ratio (C/N) and high lignocellulose content, resulting in severe nitrogen deficiency during the composting process (Bohacz 2018). Existing studies demonstrate that adding exogenous co-substrates can significantly alter substrate bioavailability, modulate the abundance of lignocellulose-degrading bacteria, and reshape physicochemical dynamics throughout biodegradation (Belyaeva and Haynes 2010, Liu et al. 2024b, Lu et al. 2022a). Although peanut meal, alfalfa meal, soybean meal, and urea are nitrogen-rich co-substrates widely applied in municipal and rural solid waste co-disposal (Mirzababaei and Hassani 2024, Zhan et al. 2024, Zhang et al. 2024), a systematic understanding of how distinct nitrogen sources affect the maturation performance of TCMR during semi-permeable membrane composting remains lacking.

Microbial communities serve as the core functional drivers in composting systems, dominating organic matter transformation processes including enzymatic catalysis, carbon mineralization, and humification, which directly determine compost maturity and product quality (Li et al. 2025, Lu et al. 2024, Ma et al. 2024, Tang et al. 2025, Wei et al. 2022, Xu et al. 2024). In aerobic composting, functional taxa such as *Firmicutes*, *Actinobacteria*, and functional fungi constitute the primary engine for decomposing complex lignocellulosic matrices by secreting highly synergistic extracellular enzymes (e.g., cellulase and lignin peroxidase) (Fang et al. 2022, Meng et al. 2022). Initial feedstock composition and operational parameters direct the targeted succession of functional microorganisms across different fermentation stages (Yan et al. 2025). Although macroscopic correlations between microbial community structure and physicochemical parameters (e.g., C/N ratio, temperature dynamics, pH gradient, and humification index) are well recognized (López-González et al. 2015), the microecological succession patterns and their responsive mechanisms with complex physicochemical properties during TCMR composting optimized by distinct nitrogen co-substrates remain to be elucidated.

To bridge these knowledge gaps, semi-permeable membrane-covered aerobic composting systems were constructed using TCMR as the primary substrate with the addition of distinct nitrogen co-substrates. The specific objectives were to: (1) systematically monitor the dynamic evolution of temperature, C/N ratio, pH, $\text{NH}_4^+\text{-N}$, and germination index (GI), evaluating the comprehensive impacts of different nitrogen sources on compost maturity and humification efficiency; and (2) track the structural evolution and functional guild shifts of both bacterial and fungal communities across the composting life cycle, elucidating the biological mechanisms driving efficient TCMR maturation. The findings of this study are expected to provide critical theoretical support for building a resource-saving and environment-friendly circular economy system for TCM resources, as well as scientific guidance for the high-value, sustainable recycling of organic waste in the TCM industry.

2. Materials and methods

2.1 Composting reactors

The composting reactor system (Fig. S1) consists of a primary vessel (53×35×25 cm) with integrated functional components. Internally, A layer of plastic film liner minimizes hygroscopic losses, while an externally mounted semi-permeable membrane facilitates selective gas exchange. A hermetic sealing interface between the membrane and reactor body ensures operational integrity under thermophilic conditions.

An air pump was connected to one side of the apparatus to achieve continuous aeration at a flow rate of 2 L/min. During the composting process, the compost pile was turned every 3 days to prevent anaerobic fermentation, and water was added periodically to maintain the moisture content at 60%-70%. Samples were collected daily throughout the entire composting process until the completion of fermentation. The semipermeable membrane, purchased from Heilongjiang Jinsen Bioengineering Co., Ltd., was composed of polytetrafluoroethylene (PTFE) with a pore size of 0.25 ~ 0.35µm.

2.2 Sample collection and analyses

The Chinese medicine residues (CMRs) were obtained from the decoction preparation room of the second affiliated hospital of Heilongjiang University of Chinese Medicine, which were prepared with more than 40 species of Chinese medicinal herbs as the main raw materials, including *Chuanxiong*, *Fuling*, *Taizishen*, *Gancao*, *Huangqi* and *Huangqin*. Four nitrogen-containing auxiliary materials, namely peanut meal powder, alfalfa meal powder, soybean meal and urea, were all purchased from the Harbin market. The initial carbon content, initial nitrogen content, C/N ratio and final feeding ratio of the different nitrogen sources are presented in Table S1.

The temperature at the top, middle and bottom of the reactor was measured regularly every day, and the average value was taken as the reactor temperature. The materials were dried in an oven at 105°C to constant moisture, and the moisture content was determined accordingly. Aqueous extracts of each solid material were prepared to determine their electrical conductivity (EC), pH value, E4/E6 ratio and seed germination index (GI). The pH value, electrical conductivity and E4/E6 ratio were determined in accordance with the National Standard Method NY525-2021. The C/N ratio was measured using an Elementar Vario EL elemental analyzer (Elementar, Germany). A pH meter (DELTA320A, Mettler-Toledo, Switzerland) was employed for the determination of pH and EC values. The E4/E6 ratio was assayed via the T6 spectrophotometer method. The germination index (GI) of seeds treated with CMR compost was determined using the paper towel culture method (Yang et al. 2021). Total organic carbon (TOC) was determined by incineration in a muffle furnace at 500°C for 5 h, and total carbon (TC) and total nitrogen (TN) were analyzed using a CN Analyzer (2100S, Analytik Jena AG, Germany).

2.3 Analysis of microbial community structure

High-throughput sequencing technology was employed to evaluate the microbial diversity in fertilizer samples containing different nitrogen sources, and the structure and key characteristics of the dominant microbial communities under different nitrogen source conditions and during the fermentation process were investigated. These samples were submitted to Shanghai Meinuo Biopharmaceutical Technology

Co., Ltd. for high-throughput sequencing. The sampling time and quantity for each pile sample are presented in Table 1.

Table 1
Sample sequencing

Nitrogen source	Sample time	Sample number
Alfalfa meal	Initial phase (0 d)	E1
	Temperature-rise phase (1–2 d)	E2
	Thermophilic phase (2–8 d)	E3
	Maturation phase (8–20 d)	E4
Peanut meal	Initial phase (0 d)	F1
	Temperature-rise phase (1–2 d)	F2
	Thermophilic phase (2–8 d)	F3
	Maturation phase (8–20 d)	F4
Urea	Initial phase (0 d)	G1
	Temperature-rise phase (1–2 d)	G2
	Thermophilic phase (2–8 d)	G3
	Maturation phase (8–20 d)	G4
Soybean meal	Initial phase (0 d)	H1
	Temperature-rise phase (1–2 d)	H2
	Thermophilic phase (2–8 d)	H3
	Maturation phase (8–20 d)	H4

2.3 Statistical analyses

The mean values and standard deviations of triplicate measurements for each physicochemical parameter are reported. Origin 2018 software was employed to visualize temporal variations in indicator. Both 16S rRNA and its analyses were conducted on the Majorbio platform. All sequencing data were deposited in the NCBI SRA database under accession number PRJNA1511876 and PRJNA1511898.

3. Results and discussion

3.1 The impact of different nitrogen sources on maturity indicators

3.1.1 C/N and temperature dynamics

Throughout the entire composting process, the C/N ratios of all four compost piles decreased gradually (Fig. 1a), a trend consistent with the findings of previous studies on the aerobic composting of traditional Chinese medicine residues (Xie et al. 2026). Microbial activity degrades organic carbon in the compost into CO₂, leading to carbon loss. Meanwhile, nitrogen loss occurs via the volatilization of ammonia, nitric oxide (NO) and other nitrogen-containing gases. The C/N ratio decreases when the loss of organic carbon surpasses that of nitrogen (Fang et al. 2022). The most remarkable variation in the C/N ratio was observed in the urea treatment, which presented a substantial initial increase. This is attributed to the higher nitrogen content of urea compared with other compost materials. After the completion of composting, the C/N ratios of all four piles fell below 20, which confirmed the maturity of the composting process (Zhang et al. 2019).

In the thermophilic phase, the temperatures of all four piles exceeded 50°C and were maintained above this threshold for 5–6 days (Fig. 1b). The peanut meal (organic nitrogen source) and urea (inorganic nitrogen source) piles exhibited the fastest temperature rise, with the urea pile reaching the highest temperature among all treatments on the 2nd day. This is due to the relatively higher nitrogen content of urea compared with other materials, which enables more direct utilization by microorganisms (Mirzababaei and Hassani 2024). Among the organic nitrogen treatments, temperatures of the peanut meal pile maintained above 50°C for the longest duration (up to 8 days), including 2 days at 60°C. Its performance during the thermophilic phase was superior to that of the wood chip and spent mushroom substrate treatments (Wang et al. 2024). From the 19th to the 20th day, the temperatures of all four compost piles dropped to near ambient levels, indicating the completion of aerobic fermentation. This observation is consistent with the results of recent studies (Belyaeva and Haynes 2010, Liu et al. 2024a). The peanut meal and urea piles showed a temperature rebound after turning and secondary fermentation, with the peanut meal pile sustaining temperatures above 50°C for the longest period. This suggests that peanut meal and urea are more readily utilizable by microorganisms than alfalfa meal and soybean meal, thus rendering them more suitable for fermentation.

3.1.2 Moisture content and pH

The moisture content of all compost piles with different nitrogen sources showed a decreasing trend throughout the composting process (Fig. 1c). The excessively rapid temperature rise led to accelerated moisture loss, while the semipermeable membrane applied in the aerobic fermentation process effectively mitigated such loss. Microbial metabolism within the piles facilitated the rapid degradation of organic matter, accompanied by the generation of metabolic water. A transient increase in moisture content was observed when the rate of water production exceeded that of evaporation (Robledo-Mahón et al. 2019). Either excessively high or low moisture content during composting exerts an adverse effect on microbial activity (Meng et al. 2022). The moisture contents of the peanut meal, alfalfa meal, soybean meal and urea piles decreased from the initial 71.65%, 70.53%, 70.18% and 71.23% to the final 53.60%, 61.43%, 58.27% and 62.25%, respectively. Among these piles, the peanut meal pile maintained a

relatively high porosity for an extended period, resulting in the most significant moisture loss. Its final moisture content was lower than those of straw compost treated with different inoculants (Liu et al. 2020b). Furthermore, the composting cycle of peanut meal was significantly shorter than that of wheat straw compost, demonstrating that peanut meal has superior fermentation characteristics as an organic nitrogen source.

During composting, the pH value reflects the balance between acidic and alkaline substances in the pile. The pH values of the four compost treatments rose above 8.0 on the 5th day and then tended to stabilize (Fig. 1d). The increase in pH during the thermophilic phase can be attributed to the microbial decomposition of organic matter, which induces ammonia production and the volatilization of organic acids (Qian et al. 2014). Driven by microbial activity, the pH of traditional Chinese medicine residues composted with different nitrogen sources finally became alkaline (pH 8–9), which is consistent with previously reported findings (Tao et al. 2022).

3.1.3 EC and TOC

As an important indicator of salt content in the composting system, electrical conductivity (EC) value can reflect the plant toxicity level and potential plant growth inhibition. The EC variation patterns of the three organic nitrogen fertilizer treatments were similar, all showing a trend of first increasing and then gradually decreasing (Fig. 1e). The early increase in EC may be attributed to the rapid organic matter mineralization by microbial activities, which produced a large amount of NH_4^+ and other ions in the initial stage of composting (Zhang and Sun 2014). During the thermophilic phase, NH_4^+ -N was converted to NH_3 , leading to an increase in cation exchange capacity, a downward trend in EC, and gradual stabilization (Liu et al. 2020a). At this stage, the most significant decrease in EC occurred in peanut meal compost, which may be due to the increased utilization of nutrient ions (e.g., NH_4^+) by microorganisms (Lu et al. 2022b). After composting, the EC values of peanut meal, alfalfa meal, and soybean meal were 2606 $\mu\text{S}/\text{cm}$, 4830 $\mu\text{S}/\text{cm}$, and 4112 $\mu\text{S}/\text{cm}$, respectively. The EC value of compost with peanut meal as the nitrogen source was lower than 4000 $\mu\text{S}/\text{cm}$ after composting, indicating maturity and higher safety (Li et al. 2017, Wang et al. 2018). The final EC value of peanut meal compost was lower than that of garden waste compost with cow dung added (2960 $\mu\text{S}/\text{cm}$) (Gong et al. 2019) and Chinese medicine residue compost with microbial inoculants added (2694 $\mu\text{S}/\text{cm}$) (Wang et al. 2021), suggesting that the use of peanut meal in medicinal plant cultivation can reduce the risk of root damage. Therefore, both peanut meal and urea are more suitable as compost nitrogen sources.

The TOC contents of all four treatments exhibited a consistent decreasing trend, reaching the minimum values at the late stage of fermentation (Fig. 1f). These observations are consistent with the composting results previously reported in the literature (Awasthi et al. 2016, Wang et al. 2021). After composting, the TOC contents of the four piles decreased to 49.65%, 53.34%, 54.48% and 46.32%, respectively, all exceeding 30%, which complies with the NY/T525-2021 National Standard for Organic Fertilizers. During composting, the TOC contents of the peanut meal (organic nitrogen source) and urea (inorganic nitrogen source) treatments decreased more rapidly and stably than those of the alfalfa meal and soybean meal

treatments. This indicates the enhanced decomposition of organic matter and microbial utilization in the compost, which in turn results in an increase in carbon dioxide emission.

3.1.4 NH_4^+ -N and Total Nutrient Contents

In all compost piles, the NH_4^+ -N content initially increased (Fig. 2a), which can be attributed to the microbial mineralization and decomposition of organic nitrogen compounds into NH_4^+ -N (He et al. 2011). Compared with other compost treatments, the urea treatment showed a marked release of NH_4^+ -N caused by the significant accumulation of nitrogenous compounds, due to its higher nitrogen content. The NH_4^+ -N contents of all four piles exhibited a declining trend after 8 days, which may result from the volatilization of NH_3 in the reactor and the microbial transformation of NH_4^+ -N serving as a nitrification substrate (Demeestere et al. 2002). At the maturation stage, the NH_4^+ -N contents of the four compost treatments were 81 mg/kg, 85 mg/kg, 213 mg/kg and 281 mg/kg, respectively. All these values were below the standard NH_4^+ -N content for mature compost (< 400 mg/kg) (Zeng et al. 2012). Among the four compost treatments, peanut meal compost exhibited superior maturity, with a lower NH_4^+ -N content compared to pig manure compost using wheat straw as a bulking agent (Assandri et al. 2021).

The total nutrient content of raw traditional Chinese medicine residues was below 5% before composting (Fig. 2b), failing to meet the minimum requirement (5%) specified in China's National Standard for Organic Fertilizers (NY 525–2021). After composting, the final total nutrient contents of the peanut meal, alfalfa meal, soybean meal and urea treatments were 5.79% (57.9 g/kg), 4.83% (48.3 g/kg), 5.16% (51.6 g/kg) and 6.39% (63.9 g/kg), respectively. Notably, the alfalfa meal treatment failed to reach the 5% threshold required for organic fertilizer certification. Among the three organic nitrogen source treatments, the peanut meal treatment had the highest total nutrient content. Furthermore, the total nutrient content of traditional Chinese medicine residue compost produced via semipermeable membrane aerobic composting with peanut meal or urea as the nitrogen source was higher than that of the multi-pile aerobic composting system with different C/N ratios (Ajmal et al. 2021). This phenomenon can be explained by the enhanced microbial metabolic activity and significant decomposition of organic matter during the thermophilic phase.

3.1.5 Seed germination index and E4/E6 ratio

All four treatments exhibited an increasing trend in GI (Fig. 2c), which was consistent with the observations from the thermophilic composting of green waste (Liu et al. 2018). In the initial fermentation stage, aerobic microorganisms degraded large organic molecules into phytotoxic short-chain molecules that inhibit seed germination. With the progression of fermentation, sustained microbial activity facilitated the further decomposition of these short-chain organic molecules, thereby reducing phytotoxicity (Zhang et al. 2020). After composting, the GI values of all four treatments exceeded the national standard ($\text{GI} \geq 70\%$), reaching 113.6%, 99.5%, 98.2% and 151.6%, respectively. No significant phytotoxicity was observed, and the measured GI values were higher than those reported for straw

compost (Chen et al. 2024). Among the tested reactors, the one with peanut meal as the nitrogen source matured the earliest, exhibiting the highest maturity, optimal fermentation performance and the most efficient removal of phytotoxic substances.

The E4/E6 ratio can serve as an indicator of the polymerization degree of humic acid during compost fermentation (Fig. 2d). A lower E4/E6 ratio corresponds to a higher degree of condensation and aromatization of humic acid in the compost (Liu et al. 2018). During aerobic composting, the E4/E6 ratio decreases gradually with the increase in compost maturity (Fernandez-Bayo et al. 2018). The measured values of the four treatments increased initially and then decreased. From days 10 to 17, the E4/E6 ratio in the traditional Chinese medicine residue fermentation reactor with peanut meal as the nitrogen source remained consistently lower than that of the other three treatments. This indicates that the addition of peanut meal can promote the formation of macromolecular humic acid in traditional Chinese medicine residues and enhance the humification process of the reactor (Dong et al. 2016). In the maturation stage, the E4/E6 ratio decreased gradually, a trend consistent with that observed in green waste composting (Liu et al. 2018).

3.2 Microbial community structure with different nitrogen sources

3.2.1 Diversity analysis of bacterial community structure in composting

Venn diagrams were constructed to compare the microbial communities of the four compost piles across different fermentation stages (Fig. 3). As shown in Fig. 3a, although all composts were prepared with traditional Chinese medicine residues as the raw material, nitrogen sources significantly altered the *bacterial* community structure. A total of 103 unique operational taxonomic units (OTUs) were identified in F1-F4 (peanut meal), 240 in G1-G4 (urea), and 300 in H1-H4 (soybean meal). All compost piles exhibited a consistent pattern (Fig. 3b): the initially high number of unique taxa decreased during the thermophilic phase and then increased in the maturation stage. This indicated an increase in the complexity of bacterial communities at the maturation stage, which could be attributed to the proliferation of functional bacteria and the emergence of new microbial populations (Grenier et al. 2023).

Analysis of the microbial diversity indices (ACE, Chao1, Shannon and Simpson indices) for different nitrogen source treatments (Table S2) revealed that at the initial stage of composting, the microbial richness and diversity were similar across all four treatments, with the Shannon index exhibiting an overall increasing trend. During the thermophilic phase, the Shannon index of the three treatments (excluding alfalfa meal) showed a positive correlation with temperature dynamics. Notably, in comparison with other treatments, the peanut meal treatment maintained a higher temperature for a longer duration during the thermophilic phase, which highlighted the thermotolerant characteristics of *Bifidobacterium thermophilum* and *Pseudomonas*, and this property was conducive to the aerobic composting of traditional Chinese medicine residues.

Non-metric Multidimensional Scaling (NMDS) analysis of the bacterial community structure (Fig. 3c) revealed a tight clustering among the four treatments, indicating a similar composition of the initial bacterial microbiome. With the progression of composting, the bacterial community structures underwent distinct changes, and the E2-H2 samples deviated from their initial positions during the heating phase. As the process entered the thermophilic phase, the thermophilic functional bacterial communities became dominant. The peanut meal treatment exhibited the longest thermophilic duration and the most significant structural divergence from the heating phase (F2). In contrast to the peanut meal treatment, the other treatments showed a shorter thermophilic phase and lower fermentation activity, which was attributed to the nitrogen sources being unfavorable for the growth of thermophilic microorganisms. After the heating phase, the alfalfa meal treatment presented the minimal structural variation in functional bacterial communities, which was consistent with its slower temperature rise rate and limited thermophilic duration. During the maturation process, the bacterial community structures of the soybean meal and urea treatments were the most similar.

3.2.2 Characteristics of bacterial community structure during composting

High-throughput 16S rRNA gene sequencing results (Fig. 3d) revealed significant differences in the bacterial community structure during composting with different nitrogen sources. At the initial stage of composting (E1, F1, G1 and H1), the four compost treatments exhibited a similar bacterial community structure, in which the relative abundance of *Bacteroidetes* was far higher than that of *Proteobacteria* and *Actinobacteria*. Throughout the thermophilic phase and maturation stage, the relative abundance of *Proteobacteria* increased rapidly. Notably, the relative abundance of *Proteobacteria* in the compost piles with peanut meal and urea as nitrogen sources increased by 34.2% and 14.8%, respectively. Among all compost treatments, the one with peanut meal as the nitrogen source showed the most remarkable increase in the relative abundance of *Proteobacteria*. After the completion of composting, the relative abundance of *Actinobacteria* increased to varying degrees in the piles treated with organic nitrogen sources. In contrast, the population abundance of *Firmicutes* decreased significantly in all four nitrogen source treatments. These findings indicated that *Proteobacteria* and *Actinobacteria* are the key functional microbial phyla driving the composting process. Notably, *thermotolerant Proteobacteria* actively promote the mineralization of organic matter, thereby facilitating the degradation of traditional Chinese medicine residues (Zhang et al. 2025). Metabolites secreted by *Actinobacteria* exhibit antimicrobial activity and significantly accelerate the degradation of lignocellulose (Meng et al. 2022).

An in-depth analysis of the bacterial communities at the genus level in the four compost treatments with different nitrogen sources revealed that *Bacillus*, *Bifidobacterium thermophilum* and *Pseudomonas* were the dominant functional microbial groups (Fig. 3e). At the early stage of composting, the bacterial community structures of all piles were similar. With the increase in composting temperature, the microbial communities in the piles with organic (peanut meal) and inorganic (urea) nitrogen sources exhibited greater similarity. Notably, the relative abundance of *Bacillus* in the peanut meal and urea piles decreased significantly by 24.6–75.4% and 40.2–64.7%, respectively. In contrast, the relative abundance

of *Bifidobacterium thermophilum* in the peanut meal pile increased from 37.5% to 43%, and that of *Pseudomonas* increased from 0.6% to 4.0-25.4%.

Based on the analysis of compost fermentation indices and bacterial community structure, *Bacillus* was found to be dominant in the microbial communities of all four compost treatments at the initial composting stage. As a thermophilic genus, *Bacillus* exhibits high activities of protease, lipase and cellulase (Caballero et al. 2020, Moharana et al. 2019). At this stage, the four compost treatments showed similar physicochemical properties (e.g., C/N ratio and temperature), indicating that *Bacillus* and other microorganisms are primarily responsible for decomposing organic matter in traditional Chinese medicine residues. These microbes facilitate the degradation of proteins and recalcitrant organic carbon components (e.g., lignocellulose), thereby enhancing compost fertility and sustaining the proper function of the fermentation system (Caballero et al. 2020, Wang et al. 2023). During the heating, thermophilic and maturation stages of composting, the treatment with peanut meal as the nitrogen source exhibited a rapid temperature rise and a prolonged thermophilic duration. The pH, GI and EC values showed an increasing trend, while the $\text{NH}_4^+\text{-N}$ content, E4/E6 ratio and TOC content presented a decreasing trend, accompanied by an increase in the relative abundances of *Bifidobacterium thermophilum* and *Pseudomonas*. The observed increases in pH and EC, together with the reduction in $\text{NH}_4^+\text{-N}$, could be attributed to the microbial degradation of organic matter, which releases inorganic ions (causing an increase in EC) and simultaneously promotes the production of $\text{NH}_4^+\text{-N}$ and the volatilization of ammonia, thus elevating the pH of the compost piles (Pan et al. 2026).

In the maturation stage, the decrease in temperature facilitated microbial nitrification, which promoted the conversion of $\text{NH}_4^+\text{-N}$ to $\text{NO}_3^-\text{-N}$. This process reduced ammonia volatilization and nitrogen loss during composting, thereby decreasing the $\text{NH}_4^+\text{-N}$ content (Ding et al. 2020). In urea-based compost, the higher nitrogen content inhibited the decomposition of $\text{NH}_4^+\text{-N}$ by microorganisms such as *Bifidobacterium thermophilum* and *Pseudomonas*, leading to higher residual $\text{NH}_4^+\text{-N}$ levels compared with organic nitrogen source treatments. *Bifidobacterium thermophilum* and *Pseudomonas* contribute to the decomposition of complex organic matter, driving a continuous decrease in TOC during the composting process. Microbial enzymes under neutral to alkaline conditions play a key role in the degradation of lignocellulose, promoting humification and increasing the E4/E6 ratio during the thermophilic phase (Liu et al. 2018, Zhang et al. 2021). These microbial activities also generate a large amount of metabolic energy, which explains the prolonged thermophilic duration in peanut meal compost, particularly due to the remarkable metabolic activity of *Pseudomonas* (Zhang et al. 2021).

3.3 Fungal community structure with different nitrogen sources

3.3.1 Diversity analysis of fungal community structure in composting

Venn diagrams of the fungal community structure among the four compost treatments (Fig. 4a) revealed a large number of unique fungal species in each group. A total of 58 unique fungal species were identified in F1-F4 (peanut meal), 58 in G1-G4 (urea), and 76 in H1-H4 (soybean meal). During the composting process, the number of unique fungal genera in each treatment decreased gradually, indicating that a considerable proportion of fungal populations were eliminated through the fermentation process.

Table S3 presents the fungal α -diversity indices of the four compost treatments. Throughout the entire fermentation process, the Ace, Chao1 and Shannon indices exhibited a decreasing trend, and the Shannon index showed a negative correlation with the Simpson index. Both the richness and diversity of the fungal community declined during composting, which was negatively correlated with temperature dynamics. In the thermophilic phase, the three indices (Ace, Chao1 and Shannon) increased, which could be attributed to the proliferation of thermophilic fungal populations with the rise in temperature (Di Piazza et al. 2020). At the maturation stage, the fungal abundance and diversity decreased to their lowest levels.

Non-metric Multidimensional Scaling (NMDS) analysis of the four compost treatments (Fig. 4c) revealed that E1, F1, G1 and H1 exhibited similar structural characteristics. During the composting process, the soybean meal and urea piles displayed a consistent fungal community structure in both the thermophilic and maturation stages, whereas the peanut meal and alfalfa meal piles showed a similar fungal composition during the heating and thermophilic phases. Notably, in comparison with the other three composts, the alfalfa meal compost exhibited a distinct fungal community structure during the thermophilic and maturation stages, which confirmed the differential distribution of functional fungi as illustrated in Fig. 4b. *Aspergillus* was identified as the common functional fungal genus across all four composting systems. However, the relative abundances of thermophilic functional fungi (thermophilic molds and *Cladosporium*) varied significantly among the different piles. Compared with the initial composting stage, all composts presented a distinct fungal community structure, indicating a temporal succession of the fungal community in response to temperature changes during the composting process.

3.3.2 Characteristics of fungal community structure during composting

The four treatments exhibited a similar fungal community structure at the initial, heating and thermophilic stages (E1, F1, G1, H1; E2, F2, G2, H2; E3, F3, G3, H3), with *Ascomycota* being the dominant phylum (Fig. 4c). At the maturation stage, the relative abundance of *Ascomycota* remained stable in the soybean meal treatment, while it increased to varying degrees in the alfalfa meal and peanut meal treatments. In contrast, the urea treatment (inorganic nitrogen source) showed a slight decrease in the relative abundance of *Ascomycota*. Nevertheless, *Ascomycota* remained the dominant phylum in all treatments at the maturation stage, with a relative abundance exceeding 90% in the late fermentation stage. The organic nitrogen source treatments maintained an especially high proportion of *Ascomycota*

(> 97%), which could be attributed to the enzymes secreted by this phylum that facilitate the rapid degradation of organic matter (Meng et al. 2019), rendering *Ascomycota* a major lignocellulose-degrading phylum during the thermophilic and maturation stages (Meng et al. 2022). Analysis of compost parameters confirmed the gradual maturation of all compost treatments, indicating that the presence of *Ascomycota* facilitated the maturation of traditional Chinese medicine residue compost (Wan et al. 2021).

The fungal community structures of the four compost treatments with different nitrogen sources are presented in Fig. 4d. At the initial fermentation stage, all treatments exhibited a similar fungal composition. During the heating stage, the relative abundance of *Aspergillus* increased significantly in the organic nitrogen source treatments (peanut meal and alfalfa meal). In the thermophilic and maturation stages, *Cladosporium* was absolutely dominant in the soybean meal and urea treatments, while the relative abundance of thermophilic molds increased sharply in the peanut meal and alfalfa meal treatments, with a dominant presence particularly in the peanut meal treatment. The relative abundance of *Aspergillus* decreased significantly in all treatments. Within this community structure, *Aspergillus* converts ammonium nitrogen to nitrate nitrogen and microbial Kjeldahl nitrogen (Wang et al. 2010), and the laccase it secretes promotes the decomposition of lignocellulose (Leonowicz et al. 2001), thereby accelerating the degradation of organic matter during the composting of traditional Chinese medicine residues (Huang et al. 2019). The changes in the abundances of thermophilic molds and *Cladosporium* were positively correlated with the compost pH. These thermophilic fungi produce thermostable cellulase, which participates in the decomposition of lignocellulose and promotes compost maturation (Basotra et al. 2016).

This study investigated the application effects of four nitrogen sources in the aerobic composting of Chinese medicine residues, and the results confirmed that peanut meal is the optimal organic nitrogen source for this composting system. Compared with other nitrogen sources, the thermophilic phase of composting in the peanut meal group lasted for more than 7 days, with the $\text{NH}_4^+\text{-N}$ content as low as 81 mg/kg, EC value as low as 2606 $\mu\text{S/cm}$, and total nutrient content peaking at 5.79%. Its total organic carbon (TOC) decreased the fastest and most stably, with a reduction rate of 49.82%. Meanwhile, the variation in its E4/E6 ratio conformed to the typical trend of aerobic composting, reflecting a relatively high degree of humification, and all key composting indicators in this group exhibited the optimal performance.

Microbial community analysis showed that there were significant differences in the abundance of *Bacillus* among different groups. In the compost with peanut meal as the nitrogen source, *Bacillus*, *Bifidobacterium*, and *Pseudomonas* were the key bacterial taxa affecting composting efficiency. Functional fungi dominated by *Thermomyces*, *Mycobacterium*, and *Aspergillus* played a crucial role in the degradation of ammonium nitrogen and lignocellulose, thereby accelerating the maturation of compost.

4. Conclusion

This study systematically demonstrates that among the four typical nitrogen sources tested, peanut meal serves as the optimal organic nitrogen source for enhancing the semi-permeable membrane aerobic composting of TCMR. Peanut meal amendment significantly improved the physicochemical properties and performance of the composting matrix: the thermophilic phase ($\geq 55^{\circ}\text{C}$) persisted for over 7 days, satisfying harmless disposal standards, upon maturity, the ammonium nitrogen ($\text{NH}_4^{+}\text{-N}$) content dropped to 81 mg/kg, effectively mitigating nitrogen loss via ammonia volatilization, while EC was maintained within a safe range, eliminating salinity-induced phytotoxicity risks. In terms of nutrient transformation, the peanut meal group achieved the highest TOC reduction rate (49.65%) and a consistently lower E4/E6 ratio, reflecting more complete organic matter conversion and enhanced humification; the final product reached a total nutrient content of 5.79%, fulfilling the premium grade requirements of agricultural industry standards. Mechanistic analysis revealed that peanut meal optimized the microbial community structure by establishing a bacterial core comprising *Bacillus*, *Bifidobacterium*, and *Pseudomonas*, which operated synergistically with a functional fungal guild dominated by *Thermomyces*, *Mycobacterium*, and *Aspergillus* to collectively drive efficient lignocellulose decomposition and favorable carbon and nitrogen transformations. Overall, utilizing peanut meal as a co-substrate for TCMR composting not only enhances compost quality but also achieves the valorization of oil-processing by-products, demonstrating substantial ecological and economic value.

Declarations

Declaration of 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.

Data availability

Data will be made available on request.

Author contribution statement

D. C. and C. L. wrote the main manuscript text. D. C. contributed to formal analysis, conceptualization and funding acquisition; C. L. performed formal analysis, methodology and investigation. P. G. provided resources. X. W. and Z. C. performed investigation. A. L. contributed to supervision, project administration and funding acquisition. All authors reviewed the manuscript.

Acknowledgments

This work was supported by Joint Guidance Project of Natural Science Foundation of Heilongjiang Province (No. PL2025E038), Open Project of State Key Laboratory of Urban-rural Water Resources and Environment, Harbin Institute of Technology (No. MS202530) and Youth Traditional Chinese Medicine

References

1. Ajmal, M., Shi, A., Awais, M., Mengqi, Z., Zihao, X., Shabbir, A., Faheem, M., Wei, W. and Ye, L (2021) Ultra-high temperature aerobic fermentation pretreatment composting: Parameters optimization, mechanisms and compost quality assessment. *J. Environ. Chem. Eng.* 9(4): 105453.
2. Assandri, D., Pampuro, N., Zara, G., Bianco, A., Cavallo, E. and Budroni, M (2021) Co-composting of brewers' spent grain with animal manures and wheat straw: Influence of two composting strategies on compost quality. *Agronomy-Basel.* 11(7): 1349.
3. Awasthi, M.K., Pandey, A.K., Bundel, P.S., Wong, J.W.C., Li, R.h., Zhang, Z.q (2016) Co-composting of gelatin industry sludge combined with organic fraction of municipal solid waste and poultry waste employing zeolite mixed with enriched nitrifying bacterial consortium. *Bioresour. Technol.* 213: 181–189.
4. Basotra, N., Kaur, B., Falco, M.D., Tsang, A., Chadha, B.S (2016) *Mycothermus thermophilus* (Syn. *Scytalidium thermophilum*): Repertoire of a diverse array of efficient cellulases and hemicellulases in the secretome revealed. *Bioresour. Technol.* 222: 413–421.
5. Belyaeva, O.N., Haynes, R.J (2010) A comparison of the properties of manufactured soils produced from composting municipal green waste alone or with poultry manure or grease trap/septage waste. *Biology and Fertility of Soils* 46: 271–281.
6. Bohacz, J (2018) Microbial strategies and biochemical activity during lignocellulosic waste composting in relation to the occurring biothermal phases. *J. Environ. Manage.* 206: 1052–1062.
7. Caballero, P., Macías-Benítez, S., Revilla, E., Tejada, M., Parrado, J., Castaño, A (2020) Effect of subtilisin, a protease from *Bacillus* sp., on soil biochemical parameters and microbial biodiversity. *Eur. J. Soil Biol.* 101: 103244.
8. Chen, S.M., Fan, Z.W., Li, Y.Y., Cai, H.G., Liang, Y., Wu, H.Y., Wang, L.C (2024) Straw additive enhances manure compost quality by promoting diverse aerobic bacteria and unitary thermophilic fungi. *Environ. Technol. Innov.* 36: 103818.
9. Demeestere, K., Van Langenhove, H. and Smet, E (2002) Regeneration of a compost biofilter degrading high loads of ammonia by addition of gaseous methanol. *J. Air Waste. Manage. Assoc.* 52(7): 796–804.
10. Di Piazza, S., Houbraken, J., Meijer, M., Cecchi, G., Kraak, B., Rosa, E. and Zotti, M (2020) Thermotolerant and thermophilic mycobiota in different steps of compost maturation. *Microorganisms.* 8(6): 880.
11. Ding, J.L., Wei, D., An, Z.Z., Zhang, C.J., Jin, L., Wang, L., Li, Y., Li, Q (2020) Succession of the bacterial community structure and functional prediction in two composting systems viewed through metatranscriptomics. *Bioresour. Technol.* 313: 123688.

12. Dong, Y.F., Li, J.H., Li, X.J. and Zhou, B.X (2016) The promotion effect of low-molecular hydroxyl compounds on the nano-photoelectrocatalytic degradation of fulvic acid and mechanism. *Nano-Micro Lett.* 8(4): 320–327.
13. Fang, C., Su, Y., Liang, Y.Y., Han, L.J., He, X.Q., Huang, G.Q (2022) Exploring the microbial mechanism of reducing methanogenesis during dairy manure membrane-covered aerobic composting at industrial scale. *Bioresour. Technol.* 354: 127214.
14. Fernandez-Bayo, J.D., Yazdani, R., Simmons, C.W., VanderGheynst, J.S (2018) Comparison of thermophilic anaerobic and aerobic treatment processes for stabilization of green and food wastes and production of soil amendments. *Waste. Manag.* 77: 555–564.
15. Gong, X.q., Li, S.y., Carson, M.A., Chang, S.X., Wu, Q., Wang, L., An, Z.f., Sun, X.y (2019) Spent mushroom substrate and cattle manure amendments enhance the transformation of garden waste into vermicomposts using the earthworm *Eisenia fetida*. *J. Environ. Manage.* 248: 109263.
16. Guo, T., Wang, Y., Zhu, Y.L., Zhang, Z (2013) The reutilization of herbal residues. *Adv. Mater. Res.* 726–731: 2993–2996.
17. Grenier, V., Gonzalez, E., Brereton, N.J. and Pitre, F.E (2023) Dynamics of bacterial and archaeal communities during horse bedding and green waste composting. *PeerJ.* 11: e15239.
18. He, H.B., Li, X.B., Zhang, W. and Zhang, X.D (2011) Differentiating the dynamics of native and newly immobilized amino sugars in soil frequently amended with inorganic nitrogen and glucose. *Eur. J. Soil Sci.* 62(1): 144–151.
19. Huang, K., Zhang, P., Zhang, Z.H., Youn, J.Y., Wang, C., Zhang, H.C. and Cai, H (2021) Traditional Chinese Medicine (TCM) in the treatment of COVID-19 and other viral infections: Efficacies and mechanisms. *Pharmacol. Ther.* 225: 107843.
20. Huang, Y., Li, D.Y., Wang, L., Yong, C., Sun, E.H., Jin, H.M. and Huang, H.Y (2019) Decreased enzyme activities, ammonification rate and ammonifiers contribute to higher nitrogen retention in hyperthermophilic pretreatment composting. *Bioresour. Technol.* 272: 521–528.
21. Kou, B., Huo, L., Cao, M.Y., Yu, T.Q., Wu, Y.M., Hui, K.L., Tan, W.B., Yuan, Y. and Zhu, X.L (2024) Applying kitchen compost promoted soil chrysene degradation by optimizing microbial community structure. *J. Environ. Manage.* 370: 122761.
22. Leonowicz, A., Cho, N.S., Luterek, J., Wilkolazka, A., Wojtas-Wasilewska, M., Matuszewska, A., Hofrichter, M., Wesenberg, D. and Rogalski, J (2001) Fungal laccase: Properties and activity on lignin. *Eur. J. For. Res.* 41(3–4): 185–227.
23. Li, C.Y., Meng, J., Zhao, H.P. and Li, A. (2026a) Overcoming thermodynamic limitations on anaerobic methanogenesis via DSF/c-di-GMP enhanced indirect interspecies electron transfer. *Water Res.* 304: 126402.
24. Li, C.Y., Tang, A.Q., Zhang, S.H., Mironov, V. and Li, A (2025) Bidirectional regulation of aerobic granular sludge through diffusible signal factor/bis(3'-5')-cyclic dimeric guanosine monophosphate crosstalk: Restoring stability and enhancing maturation at low temperatures. *Bioresour. Technol.* 434: 132823.

25. Li, C.Y., Wei, W., Meng, J. and Li, A (2026b) Unveiling switch coordinating wastewater anaerobic biological treatment: The role of quorum sensing and the potential thrust from signal molecule analogs. *Water Res*: 289, 124834.
26. Li, S.Y., Li, J.J., Yuan, J., Li, G.X., Zang, B. and Li, Y.Y (2017) The influences of inoculants from municipal sludge and solid waste on compost stability, maturity and enzyme activities during chicken manure composting. *Environ. Technol.* 38(13–14): 1770–1778.
27. Liu, D.X., Chen, G.S., Lu, X.R., Jie, M. H., Li, C., and Liang, Y. J (2024a) Greenhouse gases emissions and nutrient changes during aerobic composting with different manure sources. *Northern Horticulture*. 11: 70–78.
28. Liu, L., Wang, S.Q., Guo, X.P., Zhao, T.N., Zhang, B.L (2018) Succession and diversity of microorganisms and their association with physicochemical properties during green waste thermophilic composting. *Waste. Manag.* 73: 101–112.
29. Liu, S., Zeng, J.L., Cheng, Z.W., He, J.L., Pang, Y.L., Liao, X.D., Xing, S.C (2024b) Evaluation of compost quality and the environmental effects of semipermeable membrane composting with poultry manure using sawdust or mushroom residue as the bulking agent. *J. Environ. Manage.* 353: 120162.
30. Liu, T., Kumar Awasthi, M., Kumar Awasthi, S., Ren, X.N., Liu, X.Y., Zhang, Z.Q (2020) Influence of fine coal gasification slag on greenhouse gases emission and volatile fatty acids during pig manure composting. *Bioresour. Technol.* 316: 123915.
31. Liu, Y.W., Cheng, D.M., Xue, J.M., Weaver, L., Wakelin, S.A., Feng, Y. and Li, Z.J (2020b) Changes in microbial community structure during pig manure composting and its relationship to the fate of antibiotics and antibiotic resistance genes. *J. Hazard. Mater.* 389: 122082.
32. López-González, J.A., Suárez-Estrella, F., Vargas-García, M.C., López, M.J., Jurado, M.M., Moreno, J (2015) Dynamics of bacterial microbiota during lignocellulosic waste composting: Studies upon its structure, functionality and biodiversity. *Bioresour. Technol*: 175, 406–416.
33. Lu, M.L., Lin, B.F., Zhang, Y., Hao, Y.H., Li, K., Huang, Z., Li, J.B (2024) Insight into the molecular transformation pathways of humic acid in the co-composting of bagasse and cow manure after adding compound microorganisms. *Process Biochem*: 143, 23–33.
34. Lu, T., Yang, Y., Feng, W.J., Jin, Q.C., Wu, Z.G., Jin, Z.H (2022a) Effect of the compound bacterial agent on microbial community of the aerobic compost of food waste. *Lett. Appl. Microbiol*: 74, 32–43.
35. Lu, X.L., Yang, Y.X., Hong, C.L., Zhu, W.J., Yao, Y.L., Zhu, F.X., Hong, L.D., Wang, W.P (2022b) Optimization of vegetable waste composting and the exploration of microbial mechanisms related to fungal communities during composting. *J. Environ. Manage.* 319: 115694.
36. Ma, S.S., Shen, Y.J., Ding, J.T., Cheng, H.S., Zhou, H.B., Ge, M.S., Wang, J., Cheng, Q.Y., Zhang, D.L., Zhang, Y., Xu, P.X., Zhang, P.Y (2024) Effects of biochar and volcanic rock addition on humification and microbial community during aerobic composting of cow manure. *Bioresour. Technol*: 391, 129973.

37. Meng, L.X., Xu, C.x., Wu, F.L., Hu, H (2022) Microbial co-occurrence networks driven by low-abundance microbial taxa during composting dominate lignocellulose degradation. *Sci. Total. Environ.* 845: 157197.
38. Meng, Q.X., Yang, W., Men, M.Q., Bello, A., Xu, X.H., Xu, B.S., Deng, L.T., Jiang, X., Sheng, S.Y., Wu, X.T., Han, Y., Zhu, H.F (2019) Microbial community succession and response to environmental variables during cow manure and corn straw composting. *Front. Microbiol.* 10: 529.
39. Mirzababaei, N., Hassani, A (2024) Comparative evaluation of organic waste composting rate with urea and KOH application: Environment development and sustainability. *Environ. Dev. Sustain.* 26: 3889–3910.
40. Moharana, T.R., Pal, B., Rao, N.M (2019) X-ray structure and characterization of a thermostable lipase from *Geobacillus thermoleovorans*. *Biochem. Biophys. Res. Commun.* 508: 145–151.
41. Pan, M.Q., Yang, S.Y., Feng, L. and Zhang, L.Q (2026) Mitigation of greenhouse gas emissions mediated by functional microbial dynamics under optimized composting condition. *Environ. Res.* 303: 124777.
42. Park, H.-D., Wells, G.F., Lee, H.-S. and Love, N.G (2025) Environmental biotechnologies enabling a carbon-neutral circular economy. *ACS ES&T Eng.* 5(5): 1085–1087.
43. Qian, X.Y., Shen, G.X., Wang, Z.Q., Guo, C.X., Liu, Y.Q., Lei, Z.F. and Zhang, Z.Y (2014) Co-composting of livestock manure with rice straw: Characterization and establishment of maturity evaluation system. *Waste Manage.* 34: 530–535.
44. Robledo-Mahón, T., Martín, M.A., Gutiérrez, M.C., Toledo, M., González, I., Aranda, E., Chica, A.F. and Calvo, C (2019) Sewage sludge composting under semi-permeable film at full-scale: Evaluation of odour emissions and relationships between microbiological activities and physico-chemical variables. *Environ. Res.* 177: 108624.
45. Tang, A.Q., Li, C.Y., Feng, D.L. and Li, A (2025) Deciphering the code of temperature rise on aerobic granular sludge stability: A DSF-c-di-GMP mediated regulatory mechanism. *Environ. Res.* 267: 120705.
46. Tao, Z.D., Liu, X.C., Sun, L.L., He, X.X. and Wu, Z.S (2022) Effects of two types nitrogen sources on humification processes and phosphorus dynamics during the aerobic composting of spent mushroom substrate. *J. Environ. Manage.* 317: 115453.
47. Wan, J.X., Wang, X.F., Yang, T., Wei, Z., Banerjee, S., Friman, V.P., Mei, X.L., Xu, Y.C., Shen, Q.R (2021) Livestock manure type affects microbial community composition and assembly during composting. *Front Microbiol* 12: 621126.
48. Wang, J., Chen, Q., Wang, Y., Su, L., Tan, Z., Liu, D., You, S., Wu, H. and Cao, F (2026) Valorization of starch-rich traditional Chinese Herbal residues into 5-Keto-d-gluconic acid via multi-enzymes cascade. *Bioresour. Technol.* 455: 134806.
49. Wang, J., Jiao, M.N., Zhan, X.Y., Hu, C.H. and Zhang, Z.Q (2024) Humification and fungal community succession during pig manure composting: Membrane covering and mature compost addition. *Bioresour. Technol.* 393: 130030.

50. Wang, L.Q., Yu, Q.L., Huang, M.Y (2010) Screening and nitrogen transformation activity of ammonia-oxidizing molds during aerobic chicken manure composting. *Environ. Sci. J. Integr. Environ. Res.* 31: 2763–2767.
51. Wang, L.Y., Wang, T.F., Xing, Z.J., Zhang, Q.F., Niu, X.H., Yu, Y.S., Teng, Z.J., Chen, J.X (2023) Enhanced lignocellulose degradation and composts fertility of cattle manure and wheat straw composting by *Bacillus* inoculation. *J. Environ. Chem. Eng.* 11: 109940.
52. Wang, M.H., Liu, Y., Wang, S.Q., Wang, K., Zhang, Y (2021) Development of a compound microbial agent beneficial to the composting of Chinese medicinal herbal residues. *Bioresour. Technol.* 330: 124948.
53. Wang, X., Selvam, A., Wong, J.W.C (2016) Influence of lime on struvite formation and nitrogen conservation during food waste composting. *Bioresour. Technol.* 217: 227–232.
54. Wei, Z.M., Mohamed, T.A., Zhao, L., Zhu, Z.C., Zhao, Y., Wu, J.Q (2022) Microhabitat drive microbial anabolism to promote carbon sequestration during composting. *Bioresour. Technol.* 346: 126577.
55. Xie, M., Zhang, Y.X., Wang, D.R., Zeng, Y. and Feng, D.W (2026) Impacts of magnesium sulfate and calcium superphosphate on nitrogen conservation, humification, and fertilizer effectiveness during corn starch residue-soybean meal-oyster shell co-composting. *J. Environ. Chem. Eng.* 14(1): 120875.
56. Xu, C.J., Wu, B.W., Zhao, P.C., Wang, Y., Yang, H., Mi, Y.Z., Zhou, Y., Ma, T., Zhang, S., Wu, L.X., Chen, L., Zang, H.L., Li, C.Y (2023) Biological saccharification coupled with anaerobic digestion using corn straw for sustainable methane production. *Bioresour. Technol.* 367: 128277.
57. Xu, Z.M., Li, R.H., Liu, J., Xu, X.R., Wang, S.W., Gao, F., Yang, G.P., Yao, Y.Q., Zhang, Z.Q., Zhang, X., Zhang, Y., Quan, F.S (2024) The impact of ammonifying microorganisms on the stabilization and carbon conversion of cow manure and wheat husk co-composting. *Chem. Eng. J.* 490: 151626.
58. Yan, Y.P., Sun, Y.N., Cui, J.N., Gao, J.J., Chai, Y.N. and Liu, Z.Y (2025) Environmental factors and microbial interactions drive microbial community succession during solid-state fermentation of corn husk for microbial biomass protein production. *Front. Microbiol.* 16: 1646555.
59. Yang, Y., Wang, G., Li, G., Ma, R., Kong, Y. and Yuan, J (2021) Selection of sensitive seeds for evaluation of compost maturity with the seed germination index. *Waste Manage.* 136: 238–243.
60. Zeng, Y., De Guardia, A., Ziebal, C., De Macedo, F.J., Dabert, P (2012) Nitrification and microbiological evolution during aerobic treatment of municipal solid wastes. *Bioresour. Technol.* 110: 144–152.
61. Zhan, Y.B., Chang, S., Chen, Y.T., Chang, Y., Chen, P.Z., Chen, Y.F., Zhang, L.L., Yang, L., Xia, X.G., Li, J., Wei, Y.Q (2024) Effect of auxiliary materials on the formation of humic acid carbon and nitrogen and bacterial dynamics in kitchen waste composting. *J. Environ. Chem. Eng.* 12: 113190.
62. Zhang, B.X., Xu, Z.C., Jiang, T., Huda, N., Li, G.X., Luo, W.H (2020) Gaseous emission and maturity in composting of livestock manure and tobacco wastes: Effects of aeration intensities and mitigation by physiochemical additives. *Environ. Technol. Innov.* 19: 100899.
63. Zhang, J.P., Ying, Y., Yao, X.H (2019) Effects of turning frequency on the nutrients of *Camellia oleifera* shell co-compost with goat dung and evaluation of co-compost maturity. *PLoS One* 14:

64. Zhang, L., Sun, X.Y (2014) Changes in physical, chemical, and microbiological properties during the two-stage co-composting of green waste with spent mushroom compost and biochar. *Bioresour. Technol.* 171: 274–284.
65. Zhang, M.Y., Liang, W., Tu, Z.N., Li, R.H., Zhang, Z.Q., Ali, A., Xiao, R (2021a) Succession of bacterial community during composting: dissimilarity between compost mixture and biochar additive. *Biochar* 3, 229–237.
66. Zhang, Y., Shen, Y.J., Ding, J.T., Zhou, H.B., Cheng, H.S., Zhao, H., Qin, Y.W. and Ma, S.S (2025) Enhancing oil degradation and humification in food waste composting via *Fusarium proliferatum* inoculation. *Environ. Technol. Innov.* 40: 104513.
67. Zhang, Y.Z., Wang, N.Q., Wan, J.X., Jousset, A., Jiang, G.F., Wang, X.F., Wei, Z., Xu, Y.C. and Shen, Q.R (2024) Exploring the antibiotic resistance genes removal dynamics in chicken manure by composting. *Bioresour. Technol.* 410: 131309.

Figures

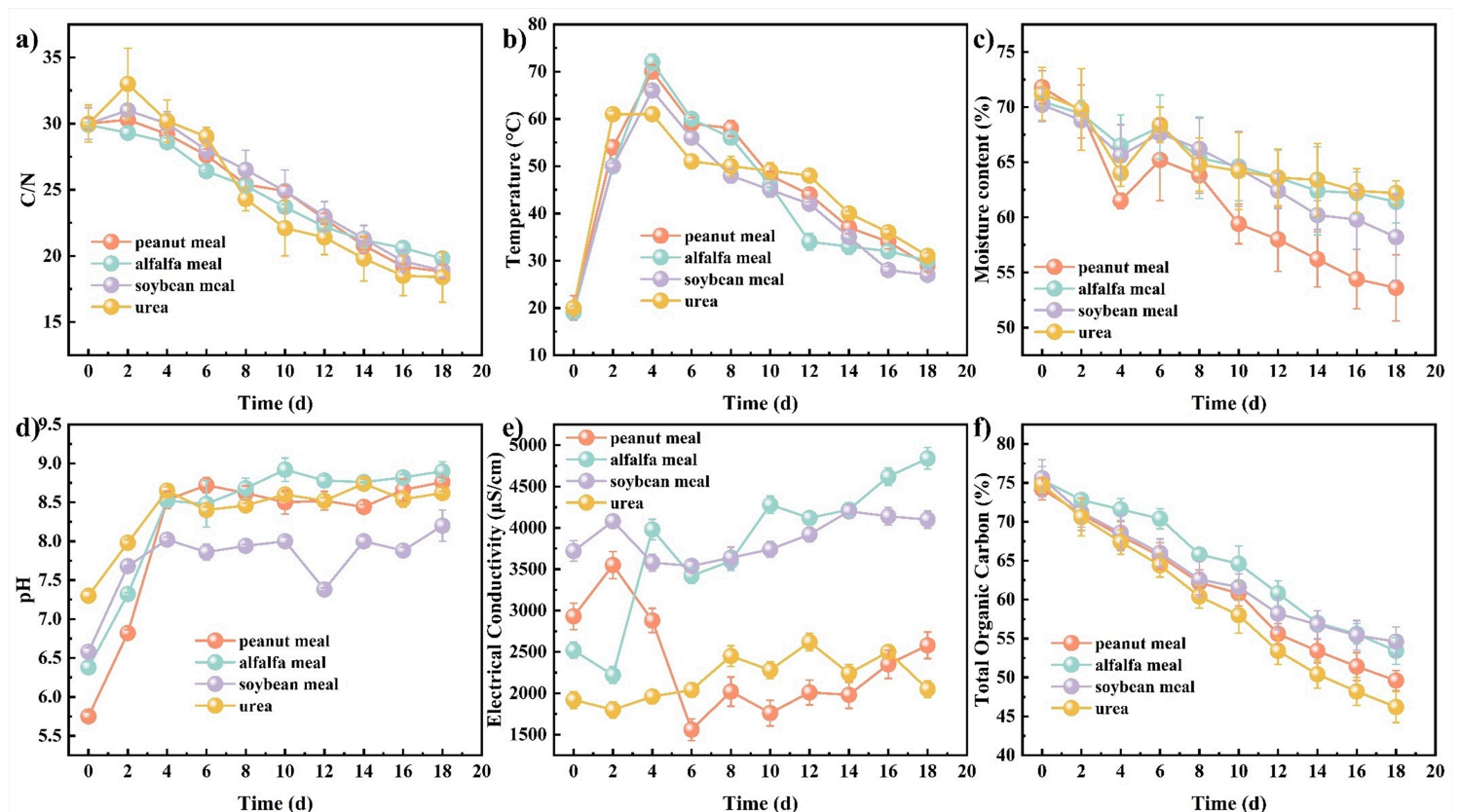


Figure 1

Changes in the C/N (a), temperature (b), moisture content (c), pH (d), electrical conductivity (e) and total organic carbon (f) in different composting treatments

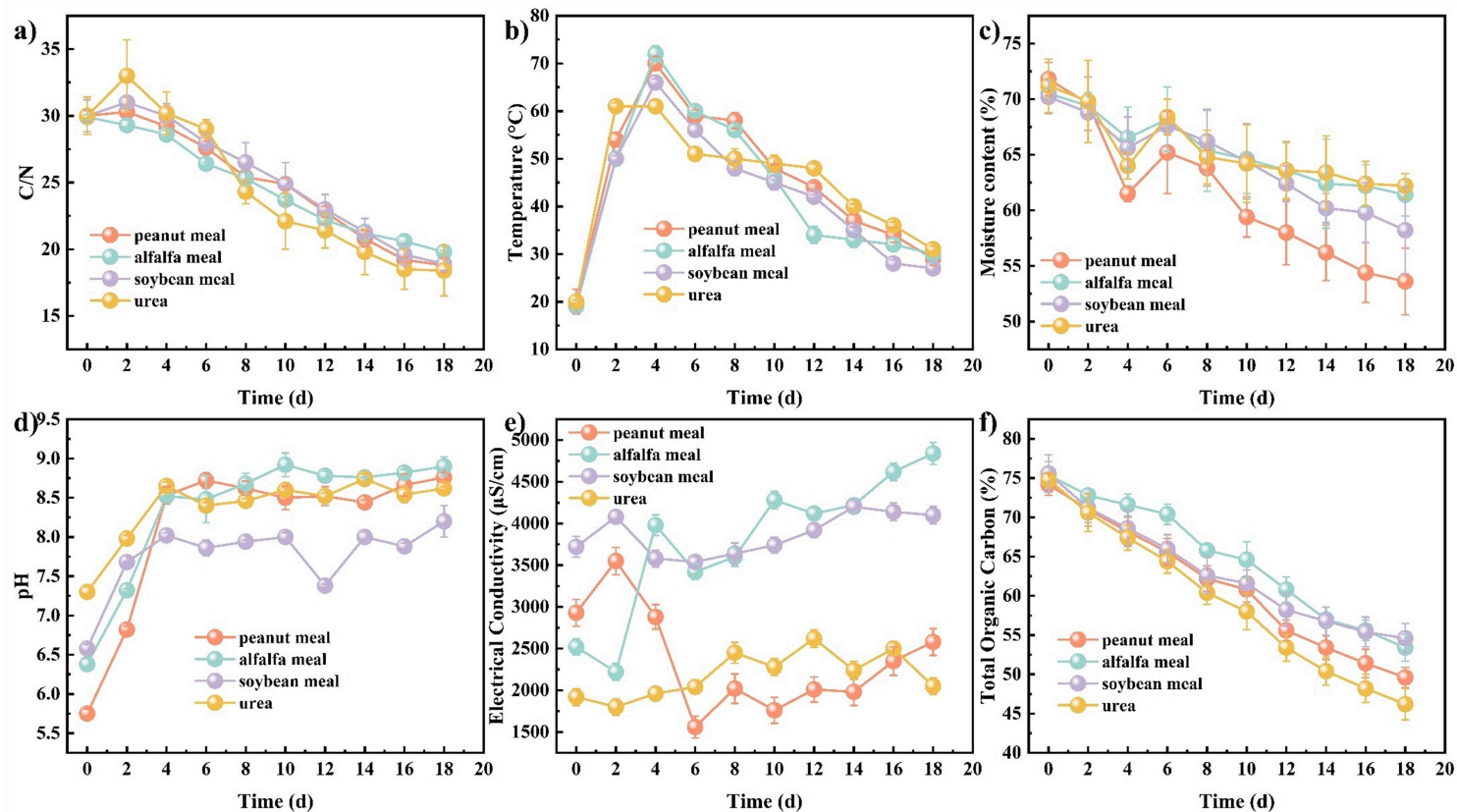


Figure 1

Changes in the C/N (a), temperature (b), moisture content (c), pH (d), electrical conductivity (e) and total organic carbon (f) in different composting treatments

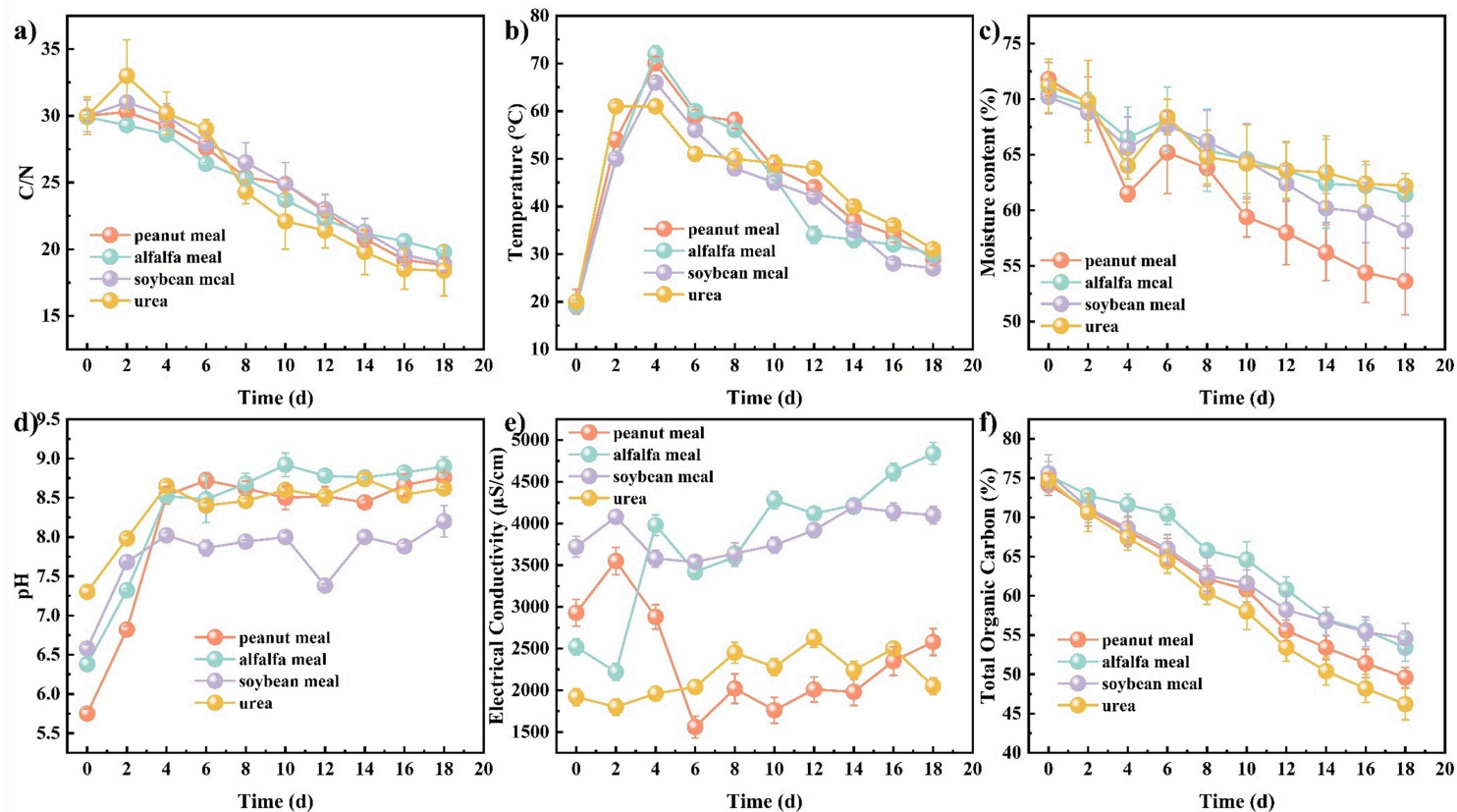


Figure 1

Changes in the C/N (a), temperature (b), moisture content (c), pH (d), electrical conductivity (e) and total organic carbon (f) in different composting treatments

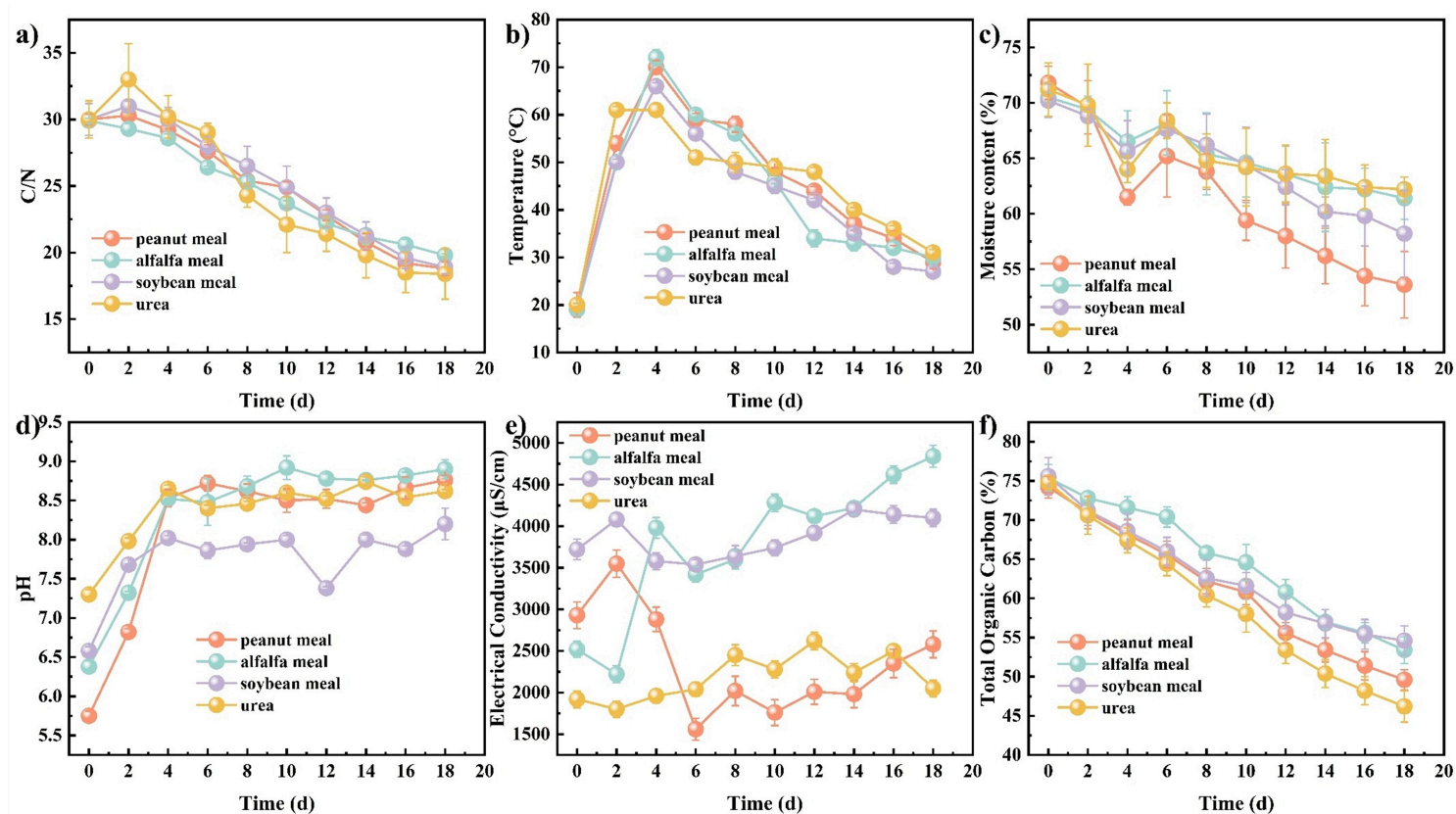


Figure 1

Changes in the C/N (a), temperature (b), moisture content (c), pH (d), electrical conductivity (e) and total organic carbon (f) in different composting treatments

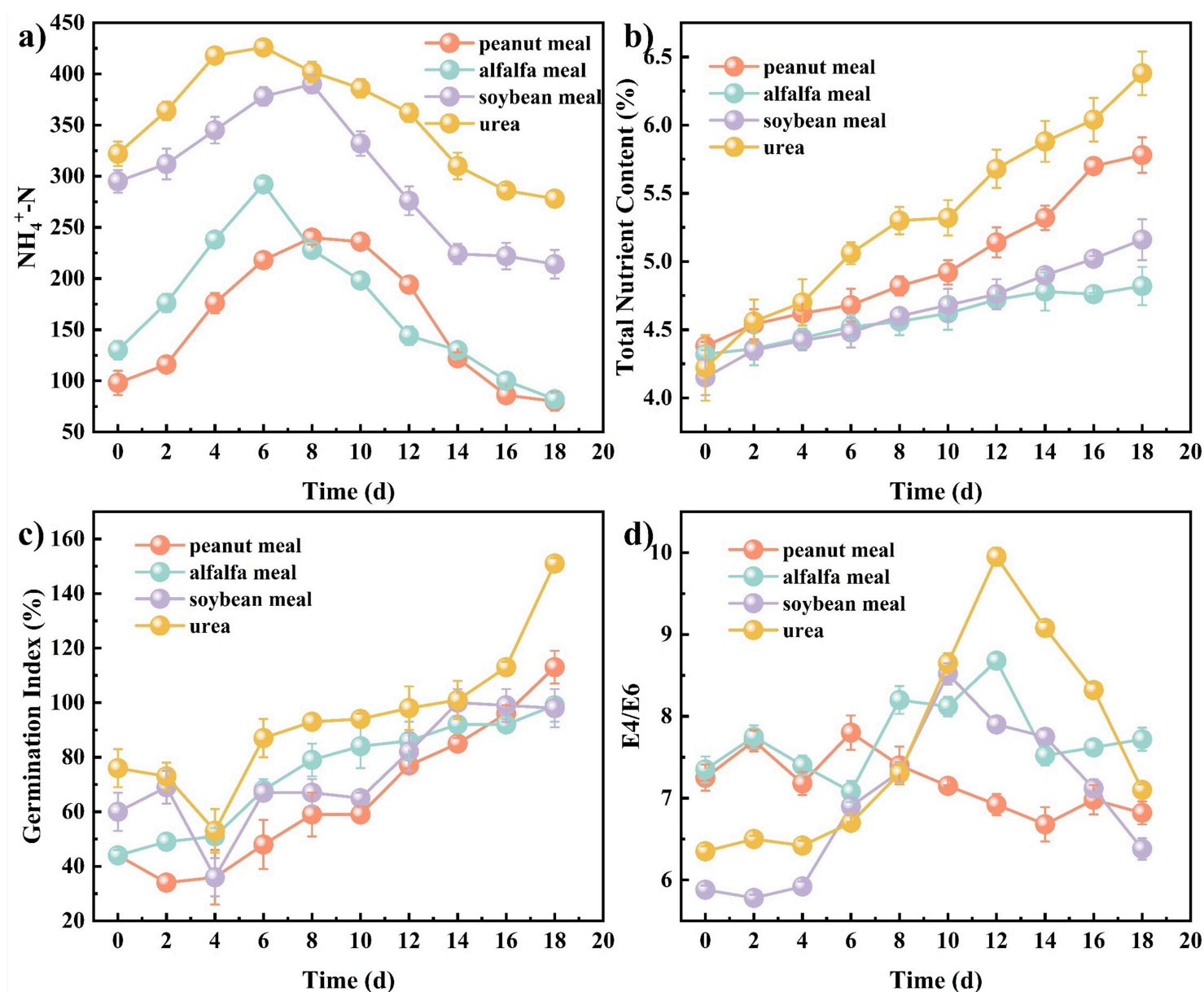


Figure 2

Changes in the $\text{NH}_4^+\text{-N}$ (a), total nutrient content (b), GI (c) and E4/E6 (d) in different composting treatments

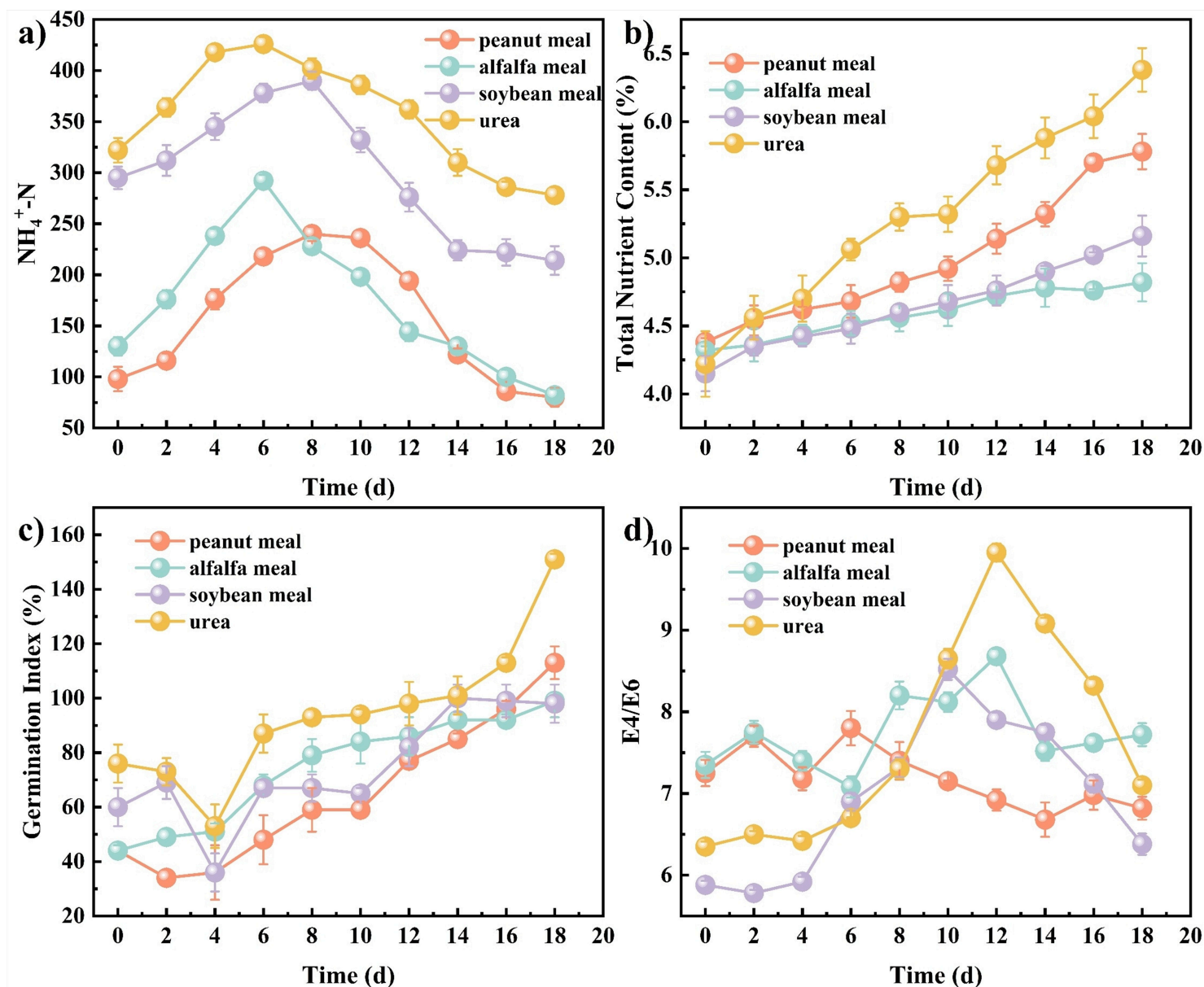


Figure 2

Changes in the $\text{NH}_4^+\text{-N}$ (a), total nutrient content (b), GI (c) and E4/E6 (d) in different composting treatments

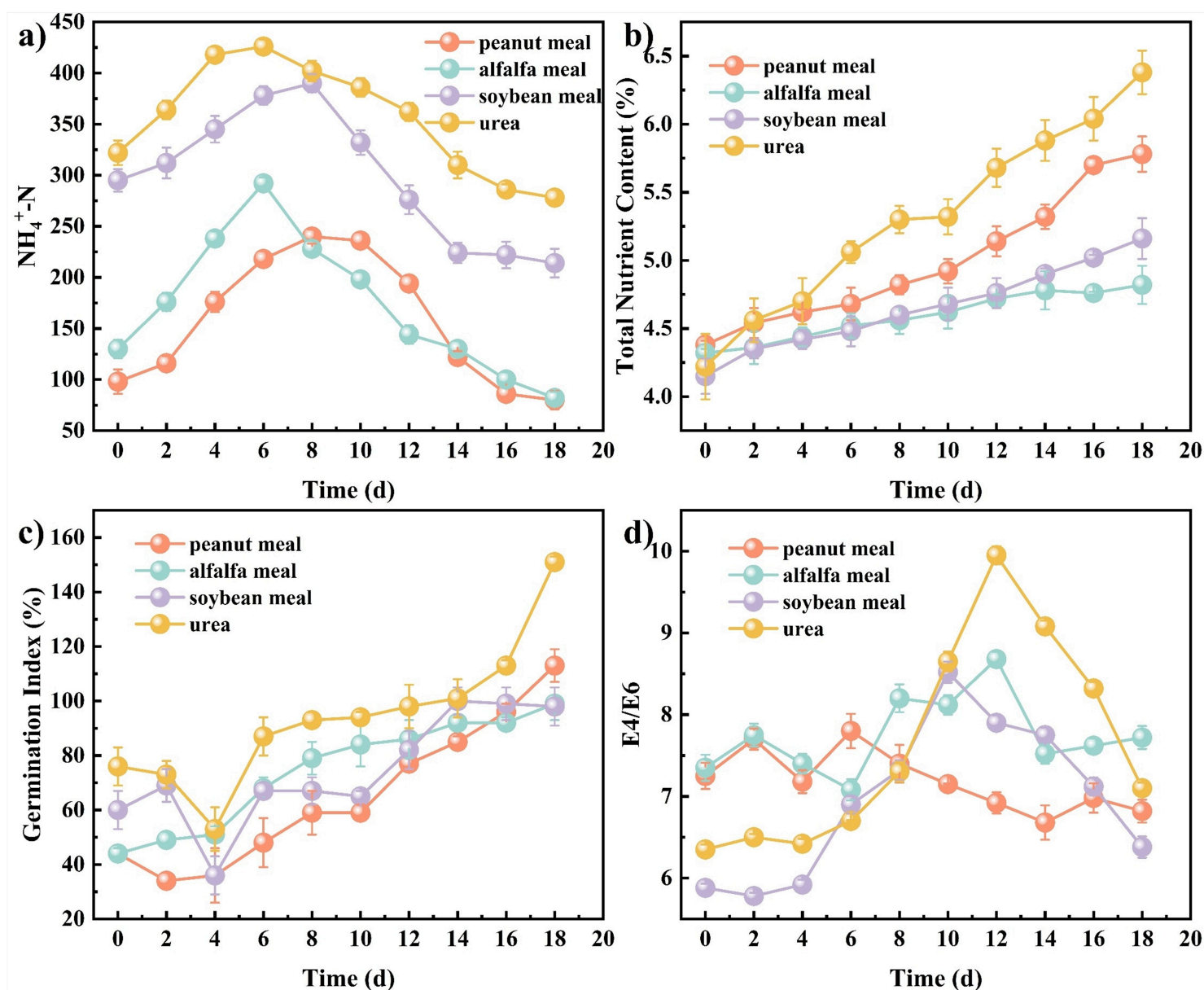


Figure 2

Changes in the $\text{NH}_4^+\text{-N}$ (a), total nutrient content (b), GI (c) and E4/E6 (d) in different composting treatments

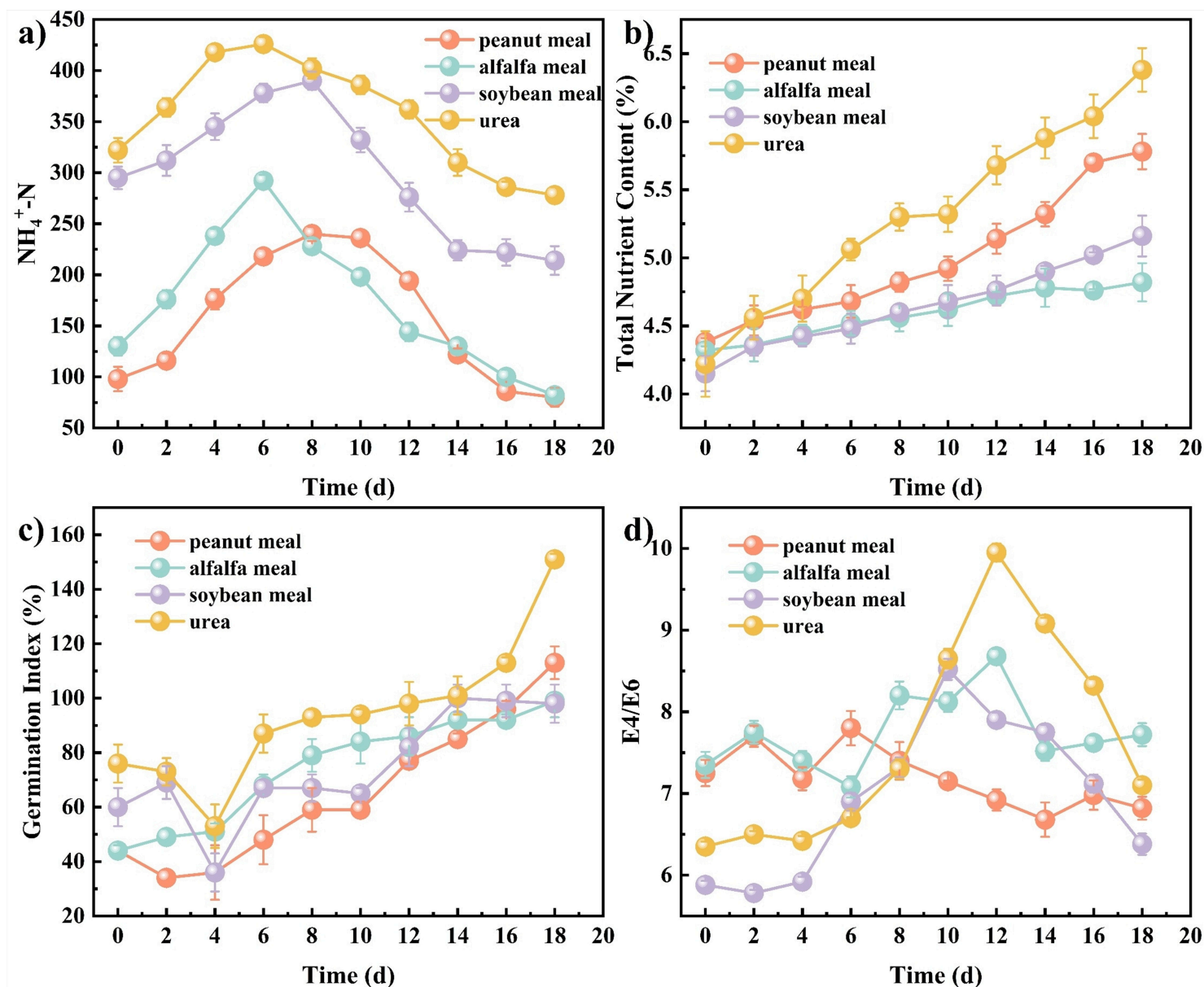


Figure 2

Changes in the $\text{NH}_4^+\text{-N}$ (a), total nutrient content (b), GI (c) and E4/E6 (d) in different composting treatments

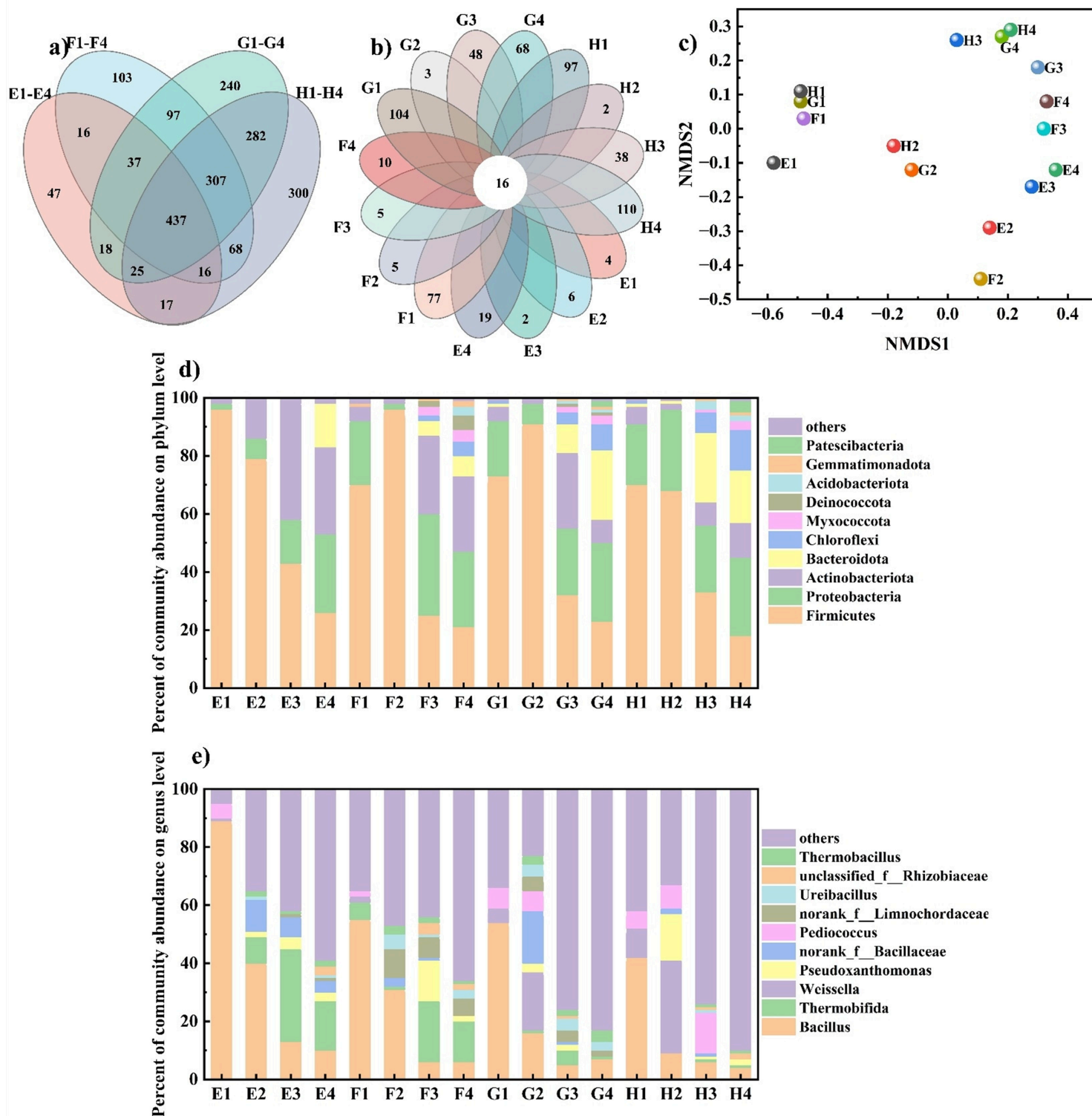


Figure 3

Venn diagram of bacterial community structure in (a) different piles, (b) different stages during the composting process, (c) NMDS analysis of bacterial communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

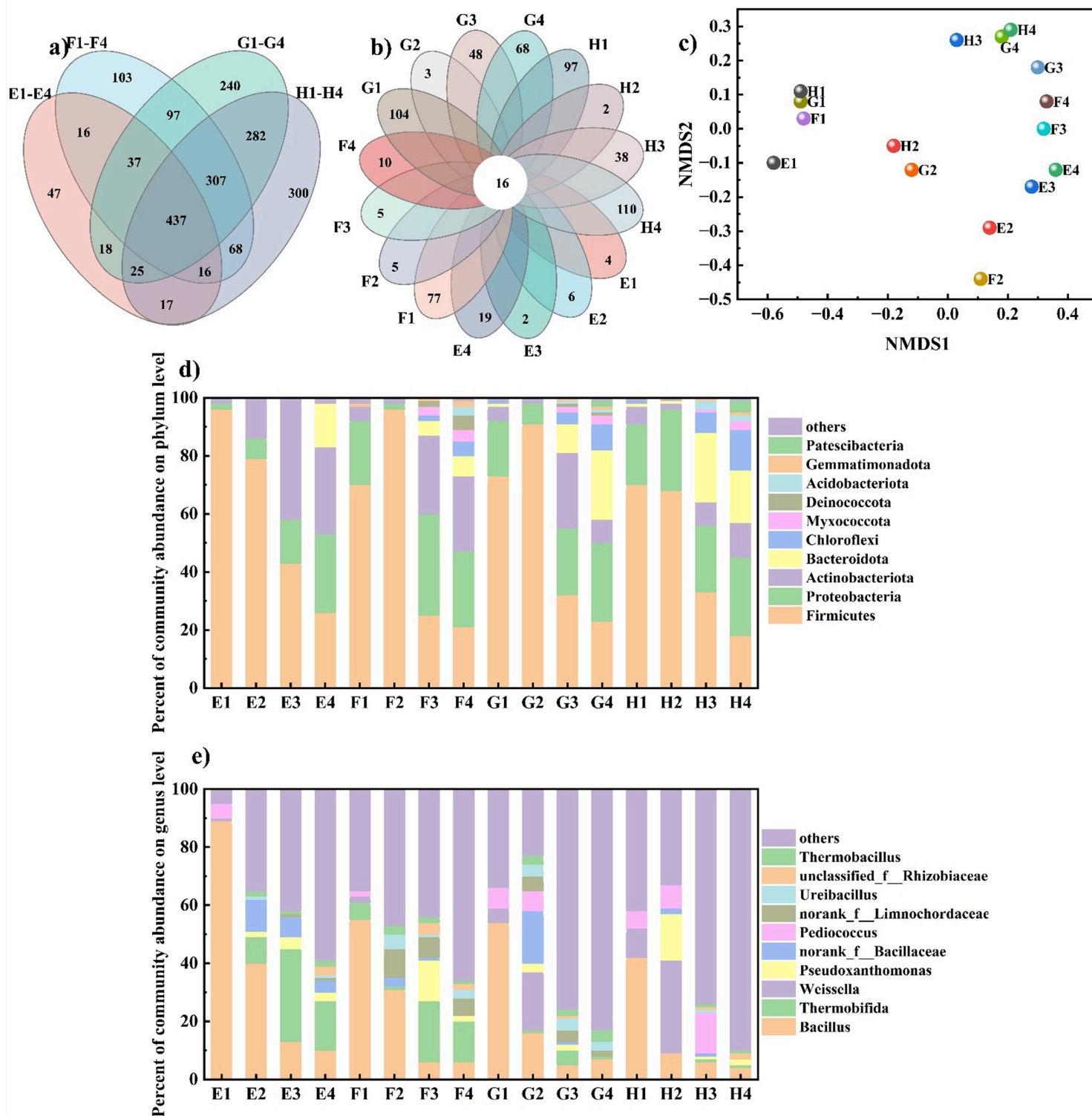


Figure 3

Venn diagram of bacterial community structure in (a) different piles, (b) different stages during the composting process, (c) NMDS analysis of bacterial communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

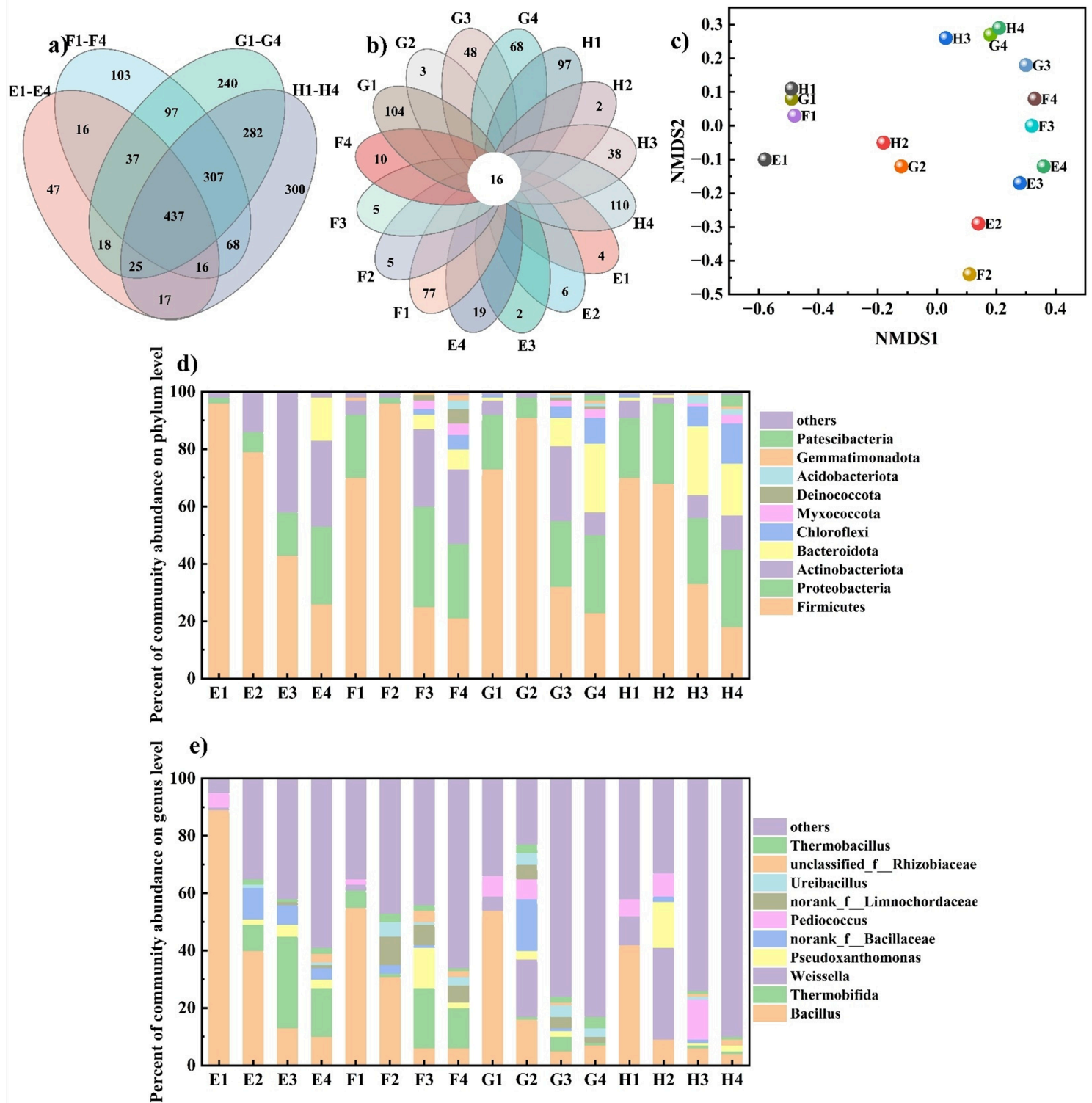


Figure 3

Venn diagram of bacterial community structure in (a) different piles, (b) different stages during the composting process, (c) NMDS analysis of bacterial communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

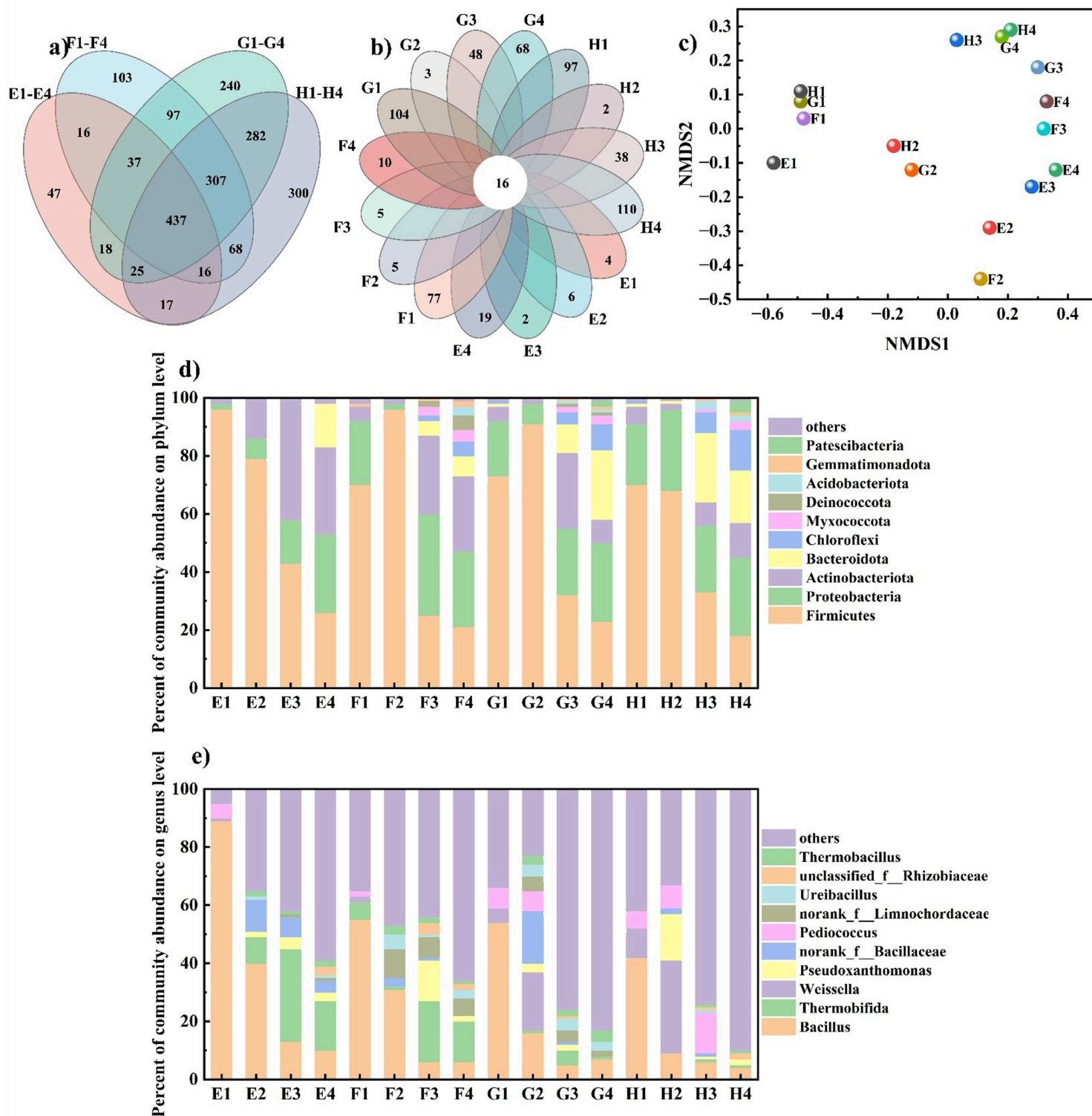


Figure 3

Venn diagram of bacterial community structure in (a) different piles, (b) different stages during the composting process, (c) NMDS analysis of bacterial communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

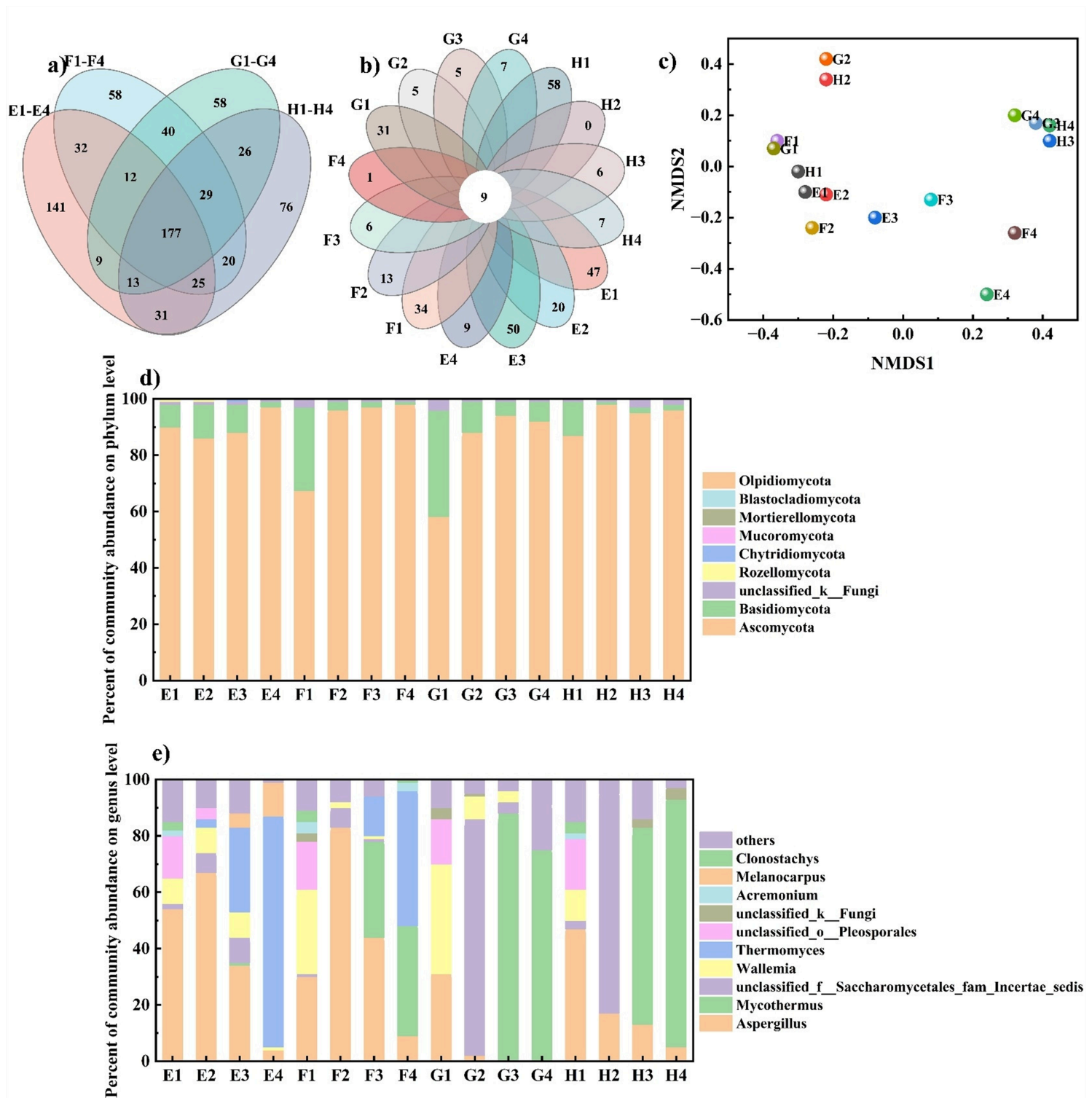


Figure 4

Venn diagram of fungal community structure in (a) different piles and (b) different stages during the composting process, (c) NMDS analysis of fungal communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

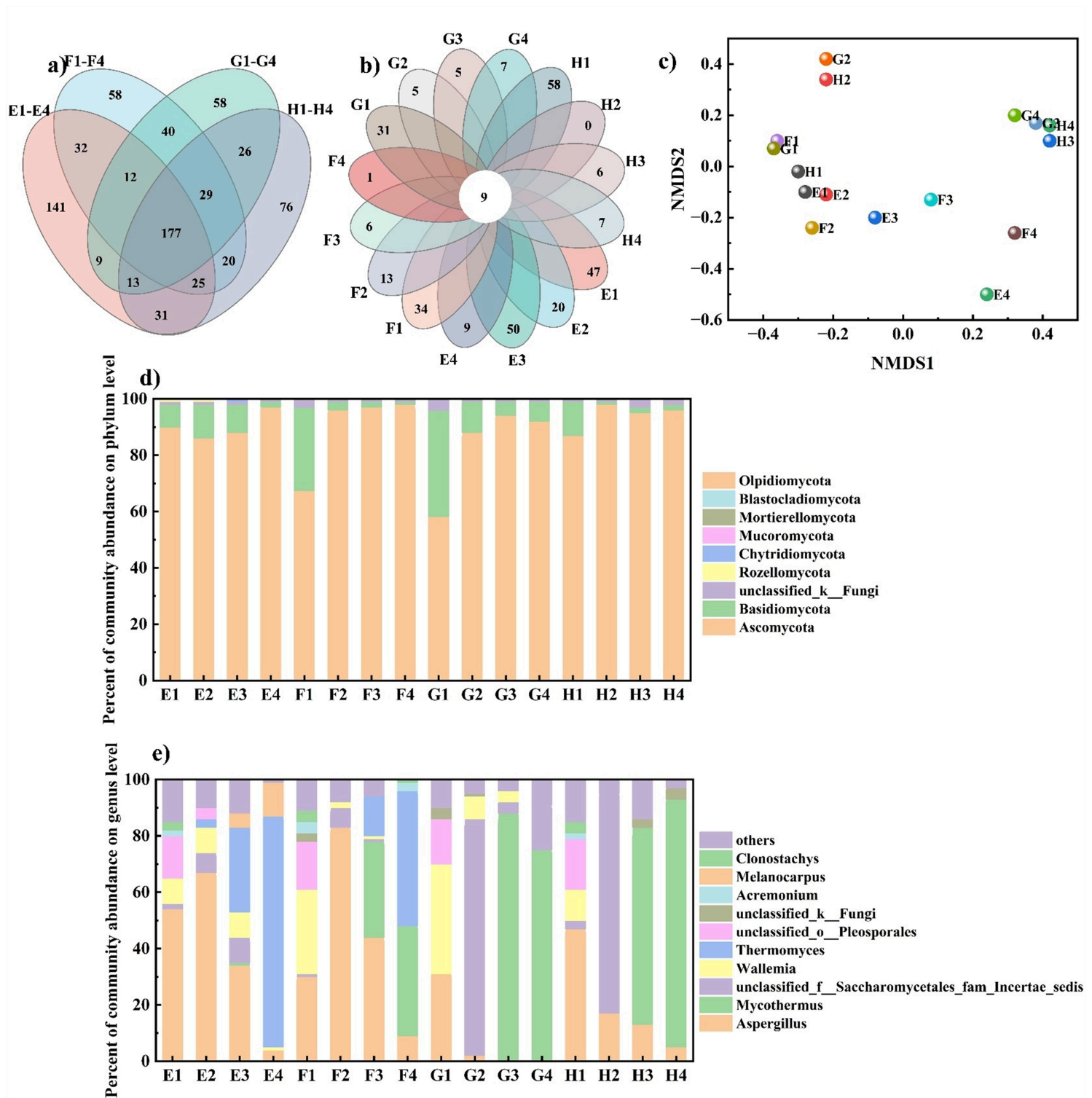


Figure 4

Venn diagram of fungal community structure in (a) different piles and (b) different stages during the composting process, (c) NMDS analysis of fungal communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

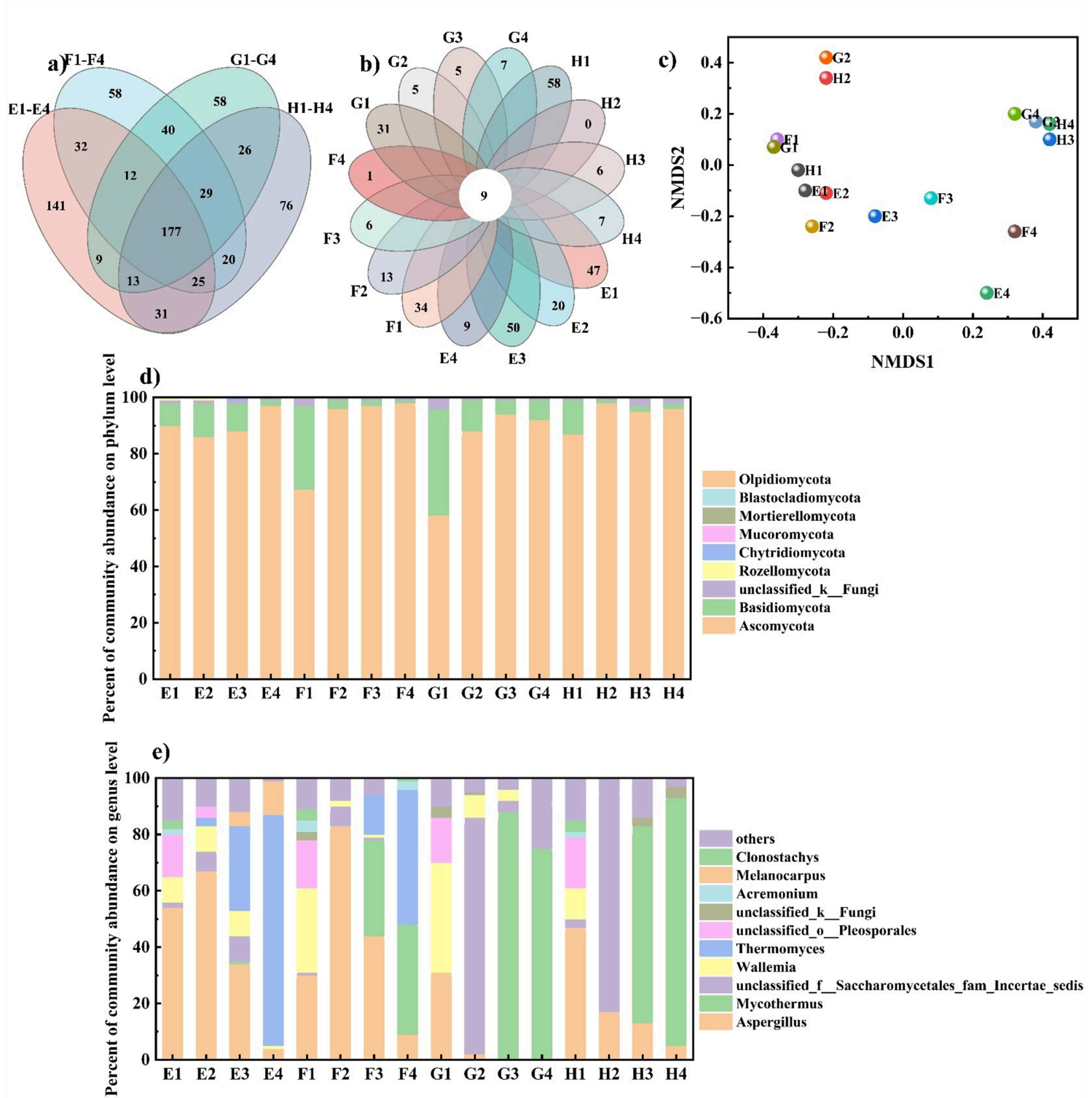


Figure 4

Venn diagram of fungal community structure in (a) different piles and (b) different stages during the composting process, (c) NMDS analysis of fungal communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

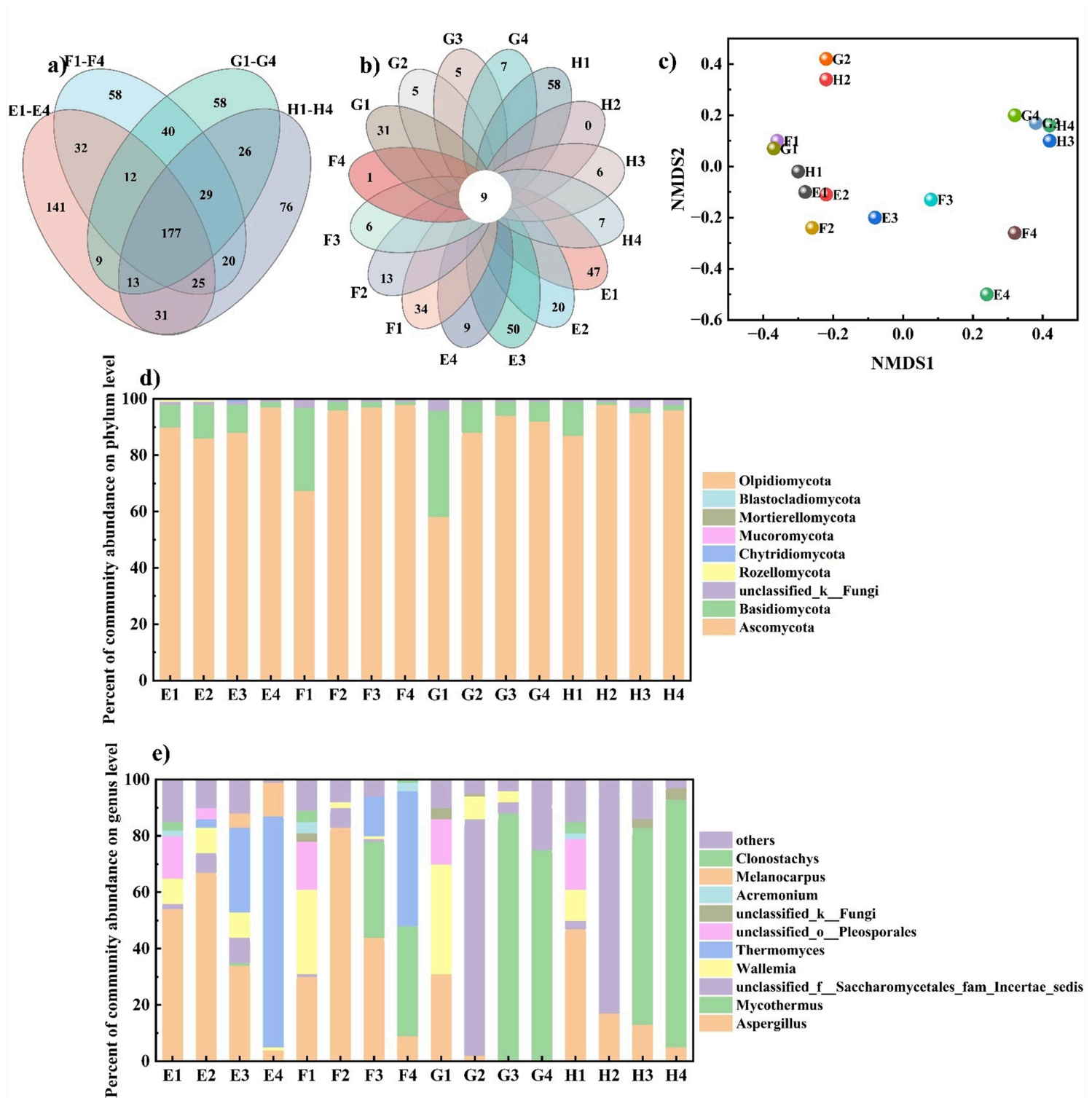


Figure 4

Venn diagram of fungal community structure in (a) different piles and (b) different stages during the composting process, (c) NMDS analysis of fungal communities at different stages of the composts, Fungal community composition at the (d) phylum level and (e) genus level during the composting process

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Supplementmaterials.docx](#)
- [Supplementmaterials.docx](#)
- [Supplementmaterials.docx](#)
- [Supplementmaterials.docx](#)