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The Effect of Feedstock Concentration on the Microbial Community Dynamics During Textile Waste Composting

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In this study, the effect of initial feedstock concentration on the microbial community structure and dynamics during textile waste composting processes was investigated using the next-generation sequencing approach. For this, three mixtures were prepared with different textile waste concentrations mixed with green waste and paper and cardboard waste for composting, to choose the proportion that will provide a mature final compost. A comprehensive characterization of the microbial communities associated with different textile waste concentrations during composting was achieved. It was noted that by increasing the concentration of textile waste, microbial communities (bacterial and fungal) change. Genera and species belonging to Actinobacteria, Firmicutes, Chloroflexia, Rozellomycota, Mortierellomycota, Aphelidiomycota, Ascomycota, and Mucoromycota were the most abundant in the mixtures containing either 40 or 60% of textile waste, whereas some of the species were absent at 80% of textile waste in the mix; this difference was also reflected by their enzymatic activities. Generally, these phyla are associated with composting, and they play a major role in recalcitrant molecular decaying. Ultimately, it can be concluded that the shift most likely occurred in microbial communities during composting probably owing to the interaction between changes in the nutrient concentration and microbial communities. This investigation proves that the concentration of textile waste significantly affects the microbial communities and demonstrates that a high concentration of textile waste is not suitable to grant a good maturity of compost.

Keywords: textile waste, feedstock concentration, microbial communities, next-generation sequencing, enzymatic activities

INTRODUCTION

Textile waste is considered a serious environmental and health problem worldwide due to its high concentration of chemical products including heavy metals (Talouizte, 2014; Talouizte et al., 2017; Biyada et al., 2019). Otherwise, these wastes are a treasure trove of organic matter, which can be converted into a nutrient-rich organic fertilizer and consequently contribute to the rehabilitation

of soils by its soil-improving qualities (Biyada et al., 2020a, 2021). To recover these wastes and understate or even eliminate their harmful effect on the environment and public health, various strategies have been proposed and developed to transform them into usable resources (Neher et al., 2013). Wherefore, composting is considered as one of the most sustainable management technologies for organic waste, which is a biological process that degrades organic matter into a useful product aerobically (Soobhany et al., 2015; Temporal-lara et al., 2016).

Successful composting is dependent on microbial community changing, which is affected by physical-chemical conditions and nutritional characteristics of feedstock composted (lignocellulosic compounds, protein, etc.) (Partanen et al., 2010). The correct management of all these factors could be attributed to the generation of a suitable final compost (Partanen et al., 2010). The identity of the microbial communities associated with the composting process, and therefore their metabolic abilities for organic matter biodegradation, depends considerably on the nutritional properties of feedstock composted (Maccready et al., 2013; Song et al., 2014). In fact, many studies devoted the effect of changing the nature of feedstock on microbial communities during composting (Neher et al., 2013; Song et al., 2014). Contrariwise, there is still a narrowed understanding of how microbial communities are affected by changing the concentration of feedstock that occurs during the composting process and their metabolic pathways. In this regard, a deeper understanding of the microbial communities depending on the variation feedstock concentration would significantly contribute to improving their efficiency. This goal could be achieved using the high-throughput sequencing approach; this molecular method has become popular recently due to its high potential to provide a complete genome of all microbial communities (bacterial and fungal) in the compost (Quast et al., 2013; López-gonzález et al., 2015).

No previous studies have been conducted to describe the microbial communities (bacterial and fungal) and their enzymatic activities in the case of industrial waste in general and textile waste especially, using different concentrations of the initial feedstock. Following the above mentioned, this study depicts a comprehensive comparison of both bacterial and fungal communities associated with compost from textile waste mixed with green waste, paper, and cardboard using a high-throughput sequencing approach, and the identification of the different enzymatic activities associated with the microbial communities present in compost mixture. During this investigation, the influence of the feedstock concentration on the change in microbial community structure and their metabolic pathways was highlighted, thus allowing to choose the best combination for improving the composting performance of the textile waste and produce maturity.

MATERIALS AND METHODS

Experimental Design

The details of composting methods were described previously (Biyada et al., 2020a). Mixtures were set up for composting with shredded wastes (between 20 and 30 cm) labeled "Mix A, B, and C." Different combinations used are summarized in **Table 1**, whereas the composition of feedstock used is summarized in **Table 2** (Biyada et al., 2020b). An in-silo composter of approximately 200 L was used for composting. Appropriate mixing of the feedstock has been achieved, and the silos were turned at least three times per week for 44 weeks. Samples were collected in triplicate according to the four cardinal positions, later placed in polyethylene bags, and stored at 4°C until further analysis.

Experimental Analysis

The C/N ratio of compost samples was computed by finding the percentage of total C and N which were analyzed using a TOC analyzer (Shimadzu-V CSN) (Mancinelli et al., 2017). The measurement of heavy metal concentrations was carried out using inductively coupled plasma spectrometry (ICP-AES) according to Alsac (2007). Cellulose activity was measured according to Biyada (Biyada et al., 2020b). Physical-chemical analysis was accomplished at various phases of composting (1 week and 44 weeks), and these data of the same sample were published previously (Biyada et al., 2020b; **Table 3**). The obtained results were tested statically using ANOVA (normalized ANOVA) using GraphPad Prism.

Identification of Microbial Species Using Next-Generation Sequencing of 16S rRNA and ITS Gene Amplicons

DNA was extracted directly from solid compost samples according to the PureLink Microbiome DNA Purification Kit recommendation. Amplification of 16S rRNA and ITS genes and sequencing was performed at the Genomic Analysis Platform Macrogen (South Korea). For amplification of 16S rRNA gene targeting the V3-V4 region from 16S rRNA primers specific to bacteria was used:

TABLE 1 | Different combinations of feedstock used during the composting of textile waste.

Feedstocks	Mix A	Mix B	Mix C
Textile waste (%)	40	60	80
Green waste (%)	30	20	10
Paper and cardboard waste (%)	30	20	10

TABLE 2 | Physical-chemical characteristics of the feedstock.

Physical-chemical parameters	Green waste	Textile waste	Paper and cardboard waste
Moisture %	60.56±0.04	50.26±0.05	10.23±1.06
pH	6.8±0.4	7.3±0.11	7.2±0.01
Total organic carbon %	44.56±0.6	30.26±0.36	40.26±0.04
Total kjeldahl nitrogen %	1.23±1	0.53±0.8	1.01±0.2
C/N ratio	36.22±0.01	57.09±0.15	39.86±0.18

Values designate mean ± SD based on three samples.

TABLE 3 | Contents of heavy metals (Cr, Cu, Zn, and Ni), C/N ratio, and cellulase activity throughout the textile waste composting process of Mix A, B, and C (Biyada et al., 2020b).

	Cr (mg/Kg)		Cu (mg/Kg)		Zn (mg/Kg)		Ni (mg/Kg)		C/N ratio		Cellulase activity (U g-1)	
	1 week	44 weeks	1 week	44 weeks	1 week	44 weeks	1 week	44 weeks	1 week	44 weeks	1 week	44 weeks
Mix A	220 ± 4	68 ± 6	520 ± 1	120 ± 4	454 ± 3	320 ± 4	1,000 ± 10	60 ± 2	32.56	16.30	7.82 ± 0.97	9.88 ± 0.81
Mix B	860 ± 10	65 ± 7	460 ± 6	160 ± 6	554 ± 8	210 ± 7	1,020 ± 10	51 ± 5	39.15	16.96	2.47 ± 0.89	7.00 ± 3.38
Mix C	780 ± 5	78 ± 4	480 ± 6	100 ± 4	820 ± 4	398 ± 2	400.0 ± 5	59 ± 1	58.29	21.39	0.41 ± 0.20	5.84 ± 1.43

Values designate mean ± SD based on three samples.

Forward: 5′-TCGTCGGCAGCGTCAGATGTGTATAAGAG ACAGCCTACGGGNGGCWGCAG

Reverse: 5′-GTCTCGTGGGCTCGGAGATGTGTATAAGAG ACAGGACTACHVGGGTATCTAATCC.

For the fungal samples, the amplification of the internal transcribed spacer ITS2 region was carried out using the following primers:

Forward: ITS3 (5′-GCATCGATGAAGAACGCAGC-3′).

Reverse ITS4 (5′-TCCTCCGCTTATTGATATGC-3′).

Processing and Analyzing of Sequencing Data

To analyze the 16S rRNA gene fragments for bacteria, Mothur version 1.44.3 was used. To achieve this, raw sequences were filtered and aligned using the SILVA version 132 database (Schloss et al., 2009). For bacterial species identification, Ribosomal Database Project (RDP) 16S database was used. Fungal sequences were first trimmed using CUTADAPT and then analyzed using DADA2 Sequences that were identified using the UNITE version 8.2 database (Callahan et al., 2016). Enzymatic activities were identified using the UniProt (Universal Protein) database. For this, search queries containing identified species (bacterial and fungal) together with enzyme codes of interest were used to find records in the UniProt database.

RESULTS

Variation of Microbial Community Composition and Diversity During Composting

Twelve FASTQ files were generated by NGS and corresponded to the pair-end sequencing (forward and reverse) of compost samples from mixture A, B, and C. Six FASTQ files corresponded to 16S rRNA and the rest corresponded to ITS regions. **Tables 4**, **5** illustrate the amount of 16S rRNA and ITS sequences during the analysis by Mothur and DADA2. Bacteria and fungi rDNA libraries were built for each mixture. From the total of bacterial sequences, 6.87, 11.86, and 4.75% of Actinobacteria were obtained, respectively, for mixtures A, B, and C (**Table 4**).

Composition of the Bacterial Community in the Compost Identified by Mothur

The taxa were studied in order to reveal their relative abundance in the compost samples. **Figure 1** illustrates the bacterial community in the mixtures analyzed (A, B, and C), thus showing that the bacterial composition in the compost samples varied in taxonomic structure and diversity depending on the concentration of feedstock in each mixture.

Bacterial diversity was represented by four majority phyla, which were selected as the most dominant, with a maximum representation of Proteobacteria (25, 28, and 33%), Bacteroidetes (20, 19, and 19%), Actinobacteria (6, 11, and 5%), and Firmicutes (11, 9, and 0.5%), respectively, for composts A, B, and C (**Figure 1**), and these taxa have been commonly associated with compost. Within these phyla, the taxonomic distribution comprised mostly α-Proteobacteria (13, 18, and 10%), Bacilli (9, 6, and 0.3%), Actinobacteria (3, 7, and 3%), and γ-Proteobacteria (7, 7, and 20%), respectively, for mixtures A, B, and C, which were identified as the most abundant class.

Several classes such as β-Proteobacteria (0.8, 2, and 1%), Clostridia (1, 3, and 0.06%), and Flavobacteriia (5, 2, and 3%), respectively, for mixtures A, B, and C were present as a minority in compost samples. Even though the same trends were observed for all mixtures (dominance of Proteobacteria and Bacteroidetes), differences were detected from one mixture to another. In this regard, it was observed that the proportion of Actinobacteria, Firmicutes, and Chloroflexia was greater for mixtures A and B than mixture C.

Figure 2 illustrates the bacterial distribution at the genera level for each composting mix, and **Table 6** shows the most

TABLE 4 | Amount of 16S rRNA sequences generated and identified in each mixture A, B, and C using Mothur.

	Starting amount of sequences	Number of identified bacterial sequences	Number of actinobacteria (% of identified)
Mix A	124,995	66,280	6.87
Mix B	119,902	70,514	11.86
Mix C	115,761	71,752	4.75

TABLE 5 | Amount of ITS sequences generated in each mixture A, B, and C using DADA2.

	Starting amount of sequences	Amount of sequences after filter	Sequences proceed to classification (% of starting amount)
Mix A	177,965	76,525	57.75
Mix B	160,843	73,032	46.30
Mix C	212,891	143,141	68.86

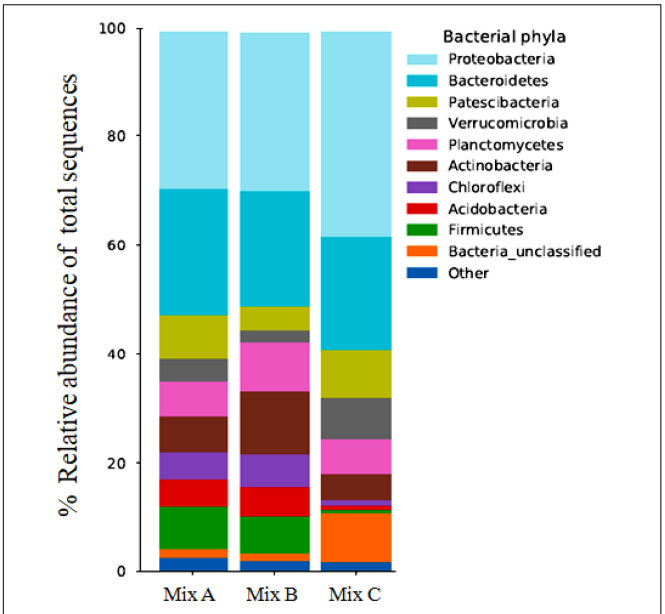

FIGURE 1 | Relative abundance of bacterial phyla in compost samples (Mix A, B, and C). "Uncultured" denotes sequences similar to bacteria that were reported in the database as uncultured bacteria. "Other" denotes bacterial sequences with similarity to classes other than the major bacterial phyla. "Unclassified" denotes bacterial sequences with no close similarity to sequences in the nucleotide database.

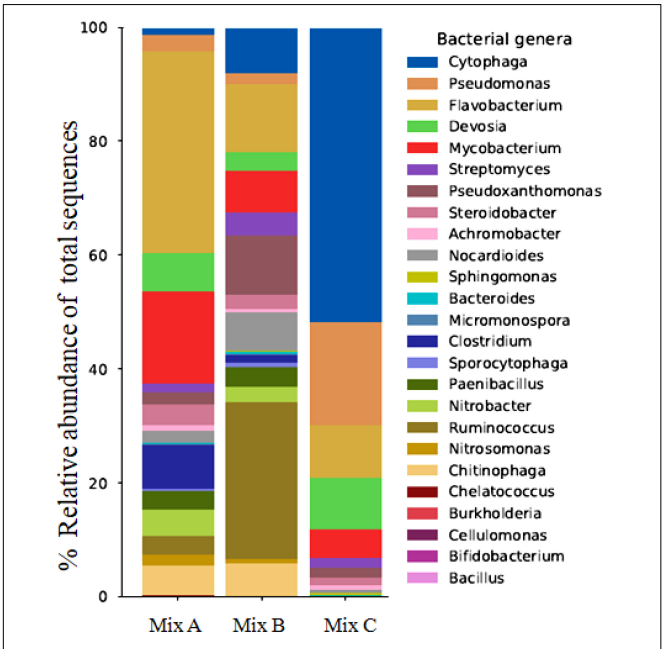

FIGURE 2 | Relative abundance of bacterial genera in compost samples (Mix A, B, and C).

abundant species in each mixture. It is noteworthy that there is a difference in the diversity within the samples from the three mixtures analyzed. The dominant genera within these mixtures were represented by *Cytophage, Steroidobacter,*

TABLE 6 | The most abundant bacterial species in each mixture (Mix A, B, and C).

Species	Genbank code	Mix A	Mix B	Mix C
Pseudomonas putida	D84020	4.22	0.00	0.37
Pseudomonas stutzeri	AF094748	0.11	0.00	0.02
Bacillus horikoshii	AB043865	14.73	7.17	1.23
Bacillus megaterium	D16273	1.22	0.87	0.00
Bacillus cereus	AE016877	5.00	5.51	0.19
Opitutus terrae	AJ2292350	2.83	0.00	2.76
Ohtaekwangia koreensis	GU117702	0.25	3.16	0.00
Cytobacillus firmus	D78314	0.69	0.50	0.00
Paenibacillus koleovorans	AB041720	0.00	0.07	0.00
Nocardioides aquiterrae	AF529063	0.30	1.26	0.00
Nocardioides dilutus	EF466121	0.13	0.18	0.00
Nocardioides hwasunensis	AM295258	0.00	0.13	0.06
Nocardia neocaledoniensis	AY282603	0.02	0.00	0.00
Nocardia takedensis	AB158277	0.02	0.00	0.00
Nitrosomonas ureae	FR828472	1.11	0.87	0.00
Nitrosomonas communis	HE856821	0.02	0.05	0.00
Chitinophaga cymbidii	JN680880	3.14	0.84	0.00
Sphingopyxis alaskensis	Z73631	1.44	0.02	3.61
Steroidobacter agariperforans	AB174844	0.33	0.02	0.47
Lysobacter pocheonensis	EU273938	0.00	0.71	0.00
Bacteroides graminisolvens	AB363973	0.00	0.00	0.21
Xanthobacter autotrophicus	X94201	0.00	0.21	0.00
Chelatococcus asaccharovorans	AJ294349	0.08	0.11	0.00
Bifidobacterium longum	M58739	0.02	0.02	0.00
Ruminococcus bromii	L76600	0.00	0.05	0.00
Rhodococcus fascians	X79186	0.05	0.00	0.00
Devosia riboflavin	AJ549086	0.00	0.00	0.05
Parvibaculum lavamentivorans	AY387398	0.00	0.00	0.76

Pseudoxanthomonas, Cytophage, Devosia, Flavobacterium, Streptomyces, Paenibacillus, Pseudomonas, Chelatococcus, Achromobacter, Mycobacterium, Clostridium, *Nitrobacter,* and *Nocardioides*. In fact, it should be noted that *Mycobacterium*, *Clostridium, Nitrobacter*, and *Bifidobacterium* are highly present in mixture A. Mixture B was most abundantly colonized by *Flavobacterium, Pseudoxanthomonas, Paenibacillus, Pseudomonas, Chelatococcus, Nocardioides, Enterobacter, Chitinophaga,* and *Nitrosomonas,* whereas mixture C is characterized by a relatively higher abundance of *Steroidobacter, Devosia, Streptomyces, Achromobacter,* and *Cytophaga* (**Figure 2**). It should also be noted that many genera and species are present in mixtures A and B and absent in mixture C, and this is the case of *Nitrobacter*, *Chelatococcus* (*C. asaccharovorans*), *Chitinophaga* (*C. cymbidii*), *Bifidobacterium* (*B. longum*), and *Nitrosomonas* (*N. ureae* and *N. communis*) (**Figure 2** and **Table 6**).

The difference between the three mixtures was also detected using the UniProt database. Several enzymatic activities were identified using the UniProt database. It is well known that the absence of some species in mixture C compared with mixtures A and B correlated with the disappearance of some enzymatic activities in this mixture and the appearance of these enzyme activities in mixtures A and B (**Table 7**).

Composition of the Fungal Community in the Compost Identified by DADA2

Figure 3 depicts the most dominant fungal phyla detected in the different mixtures and were compared. Samples of

TABLE 7 | Enzymatic profile detected in some bacterial species involved in organic matter degradation throughout the composting using different concentrations of textile waste, according to the UniProt database.

Genera/Species		Genbank code	Protein type
Terrimicrobium	*Terrimicrobium sacchariphilum*	GU129926	Endoglucanase, beta-xylanase
Opitutus	*Opitutus terrae*	AJ229235	β-xylanase, endo-1,4-beta-xylanase, cytochrome D ubiquinol oxidase, subunit II,
Brevundimonas	*Brevundimonas vesicularis*	–	Endoglucanase, β -xylanase, acid phosphatase, alkaline phosphatase D and A, glucoamylase
Panacagrimonas	*Panacagrimonas perspica*	AB257720	Glucan 1,4-alpha-glucosidase, cellulase
Pseudomonas	*Pseudomonas putida*	D84020	Glucanase, putative phoD-like phosphatase, alkaline phosphatase, acid phosphatase, laccase-like multicopper oxidase, class B acid phosphatase, cellulase
Parvibaculum	*Parvibaculum lavamentivorans*	AY387398	Alkaline phosphatase
Sporocytophaga	*Sporocytophaga myxococcoides*	–	Endo-1,4- β -xylanase, endoglucanase
Cytobacillus	*Cytobacillus firmus*	D78314	Endo-1,4- β -xylanase, β -xylanase, phosphodiesterase/alkaline phosphatase D, alkaline phosphatase
Chitinophaga	*Chitinophaga cymbidii*	JN680880	Endoglucanase, β-xylanase
Parafilimonas	*Parafilimonas terrae*	KF934397	β-xylanase
Bacillus	*Bacillus cereus*	AE016877	Alkaline phosphatase, D, 3 and 4, Cellulase, Acid Phosphatase, β-xylanase, 5′-nucleotidase, lipoprotein e (P4) family (acid phosphatase), endoglucanase, S-layer protein,
	Bacillus megaterium	D16273	Alkaline phosphatase, D and 4, β-xylanase, endoglucanase
Ohtaekwangia	*Ohtaekwangia koreensis*	GU117702	β-xylanase, acid phosphatase and alkaline phosphatase
Parvibaculum	*Parvibaculum lavamentivorans*	AY387398	Alkaline phosphatase

different mixtures showed several fungal similarities. The fungal communities in compost samples were largely dominated by Rozellomycota (31, 4, and 0.1%), Basidiomycota (17, 25, and 93%), Ascomycota (19, 37, and 4%), Mucoromycota (11, 29, and 3%), Mortierellomycota (9, 5, and 0%), and Aphelidiomycota (9, 0, and 0%), respectively, for mixtures A, B, and C. In mixture A, the most dominated fungi identified belonged to Rozellomycota, Mortierellomycota, as well as Aphelidiomycota. For mixture B, the highest number of phyla presented in compost samples with species belonging to Ascomycota and Mucoromycota, whereas for mixture C, species belonging to Basidiomycota phylum were

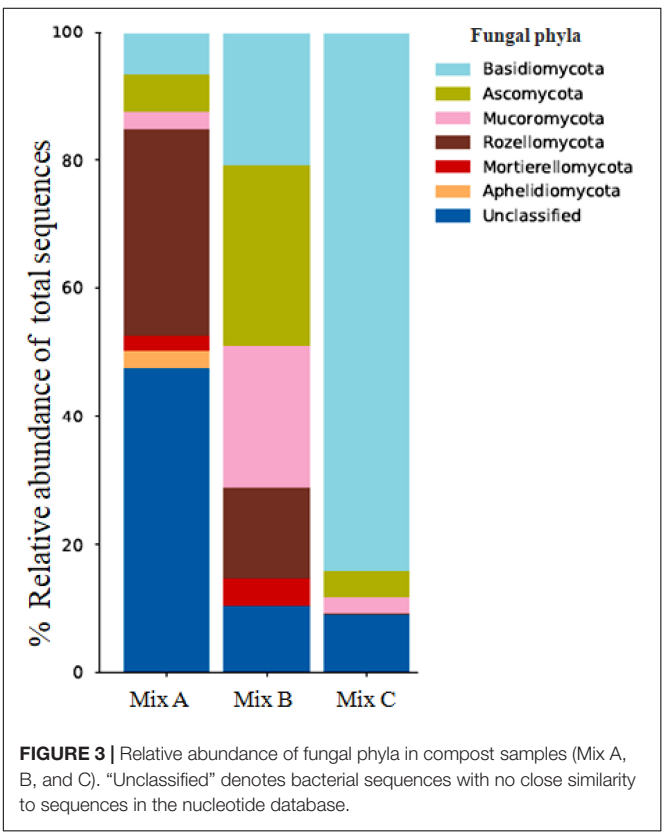

FIGURE 3 | Relative abundance of fungal phyla in compost samples (Mix A, B, and C). "Unclassified" denotes bacterial sequences with no close similarity to sequences in the nucleotide database.

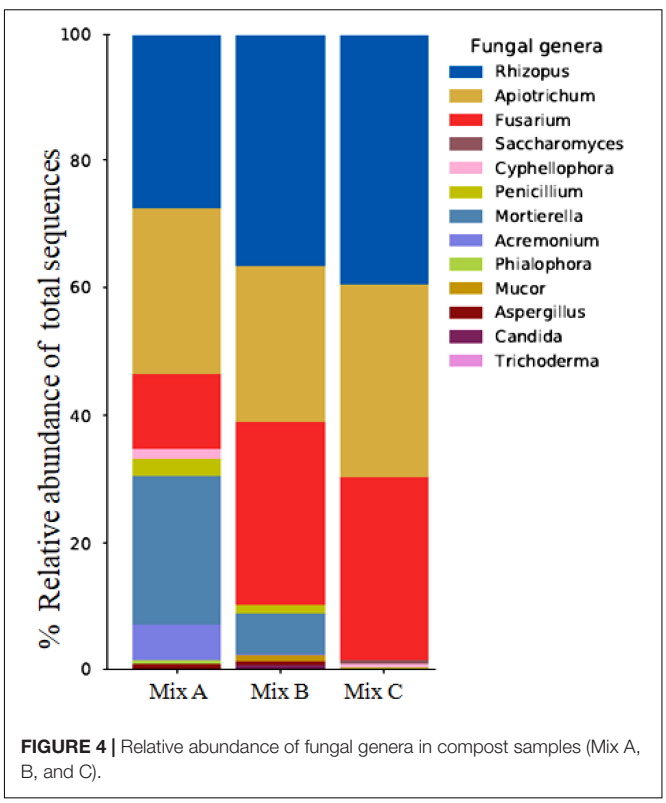

FIGURE 4 | Relative abundance of fungal genera in compost samples (Mix A, B, and C).

TABLE 8 | The most abundant fungi species in each mixture (Mix A, B, and C).

Species	Genbank code	Mix A	Mix B	Mix C
Acremonium persicinum	MF977728	1.34	0.00	0.00
Aspergillus flavus	MT270472	0.03	0.15	0.00
Aspergillus fumigatus	MN602899	0.00	0.89	0.00
Aspergillus heterocaryoticus	MH858642	0.40	0.00	0.00
Aspergillus penicillioides	MN210327	0.06	0.00	0.00
Candida picinguabensis	AJ876898	6.00	7.66	9.40
Cyphellophora fusarioides	HQ631022	0.85	0.00	0.00
Cyphellophora suttonii	GU225946	0.00	0.00	0.86
Mortierella alpine	MK927058	6.18	3.86	0.00
Penicillium aurantiogriseum	MH856348	1.25	0.15	0.37
Penicillium brevicompactum	AY484912	0.26	0.52	0.00
Penicillium roseopurpureum	GU944605	0.00	0.96	0.00
Phialophora cyclaminis	HQ713776	1.39	0.00	0.00
Phialophora geniculata	AB190395	1.90	0.00	0.00
Rhizopus arrhizus	HQ435097	16.11	65.00	57.31
Rhododendron molle	UDB0666128	41.00	0.00	0.00
Trichothecium crotocinigenum	AJ621773	0.00	0.40	0.00

identified as the most dominant in compost samples. It is noteworthy that there is disappearance in genera belonging to Mortierellomycota and Aphelidiomycota in mixture C. In the taxonomic distribution at the class level, members belonging to Tremellomycetes (11, 22, and 2%), Sordariomycetes (10, 26, and 2%), Saccharomycetes (1, 4, and 0.6%), Agaricomycetes (2, 2, and 90%), and Eurotiomycetes (4, 2, and 0.09%), respectively, for mixtures A, B, and C were present in majority.

As for bacteria, a difference was observed from one mixture to another. The most dominant fungal were identified as *Fusarium*, *Aspergillus*, *Penicillium*, *Rhizopus*, and *Apiotrichum,* which is especially found in mixture B. For mixture A, *Acremonium, Cyphellophora*, and *Phialophora* were dominated (**Figure 4**). In contrast, *Saccharomyces* was highly dominant in mixture C, with the total disappearance of species belonging to *Aspergillus* (**Table 8**).

As for bacterial communities, the UniProt database was used to identify different enzymatic activities; it was noted that many species are present in mixtures A and B but absent in mixture C; leading to the absence of their enzymatic activities (**Table 9**).

DISCUSSION

Composting cannot be understood without studying the microbial communities and their role in organic matter biotransformations. Recently, the microbial community changes during the composting process have attracted the attention of researchers. In this respect, this study provides insight into microbial changes across different textile waste concentrations through composting using the next-generation sequencing approaches. The level of bacteria and fungi diversity was considerably different from one mixture to another, and also the bacterial diversity was higher than the fungal diversity, which could be assigned to their small size and their ability to proliferate on a wide range of substrate even with high concentrations of heavy metals such as *Bacillus*, *Pseudomonas*, etc. (Barje et al., 2013; El Fels et al., 2014; Sharma et al., 2015; Łaba et al., 2019; Iravani and Varma, 2020), which is the case in this study. The comparison of the three study mixtures (A, B, and C) showed similarities at the phylum level for bacterial communities with a slight difference in the relative abundance of each phylum for each mixture. In contrast, the major difference was recorded with fungal communities, and the results obtained depicted that the diversity was higher for mixtures A and B, and lower for mixture C. Also, at the genus and species level, big differences in the distribution of the dominant species whether for bacterial or even fungal were noticed from one mixture to another, with a greater abundance in mixtures A and B compared with mixture C. This difference is probably owing to the better adaptation of these phyla to the initial feedstock concentration used in mixtures A and B compared with that in mixture C since the latter contains a high concentration of textile waste, thus explaining the difference in the physical-chemical results (C/N and concentration of heavy metals) and also the difference regarding the enzymatic activities (cellulase) recorded (Biyada et al., 2020b).

Furthermore, it is not wise to assume the presence of a standard composting microbiota in different composting samples since the concentration of feedstock determines the composition of microorganisms inside the compost mixture that nevertheless does not prevent that some of them might be primarily active agents in different kinds of composting processes, thus sharing similar characteristics during organic matter decaying. This is the case of *Aspergillus*, *Fusarium*, or even *Penicillium,* which are usually associated with lignocellulose material as feedstock during composting, and described as prevalent fungi, and *Flavobacterium, Streptomyces, Paenibacillus,* and *Pseudomonas*, for bacterial communities, as described in this study. These microorganisms have a tremendous metabolic ability during composting with lignocellulosic material as feedstock, and this was corroborated by the bioinformatic analysis using the UniPro database, thus proving the ability of these genera to produce a wide range of enzymatic activities. These findings are in agreement with those proved in previous studies (Chin et al., 2001; Yoon et al., 2011; Kim et al., 2013; Neher et al., 2013; Antunes et al., 2016; De Corato et al., 2018). At the same time, the predominance of these genera depends on their adaptation to the compost environment and subsequently their capacity to create specific combinations between nutrients and composting conditions, which could be explaining the variation in the abundance of microorganisms during textile waste composting. Additionally, this difference could be also linked to the microorganisms that play a decisive role during composting and which could determine the path of lignocellulosic compound degradation; these findings are in agreement with those elicited by Neher et al. (2013).

Otherwise, it should be noted that the temporal shifts in microbial communities (bacterial and fungal) during the composting were influenced chiefly by environmental conditions (temperature, humidity, pH, and electrical conductivity) and concentration of the feedstock used, which is confirmed previously (Vargas-garcía et al., 2014; Biyada et al., 2020b). It

TABLE 9 | Enzymatic profile detected in fungal communities involved in organic matter degradation throughout composting using different concentrations of textile waste, according to the UniProt database.

Genera/ Species		Genbank code	Protein type
Rhizopus	*Rhizopus oryzae*	HQ435097	Endo-1,4-β-xylanase 1,2 (xylanase 1, 2), glucan 1,4-α-glucosidase, glucoamylase 1 (Gluc 1), cellulase
	Rhizopus delemar	GCA_000149305.1	Glucoamylase amyD, alkaline phosphatase, cellulase, glucan 1,4-α-glucosidase, endoglucanase, alkaline phosphatase, purple acid phosphatase
Aspergillus	*Aspergillus flavus*	MT270472	Endopolygalacturonase A and B, endo-1,4-β-xylanase, carboxymethylcellulase D, alkaline phosphatase, purple acid phosphatase, and Glucoamylase
	Aspergillus fumigatus	MN602899	Endo-1,4-β -xylanase, purple acid phosphatase, Carboxymethylcellulase D, glucoamylase, alkaline phosphatase, endoglucanase celB

is notoriously shown that the bioavailability of the substrate stimulates microbial growth and consequently the degradation of organic matter. In fact, the presence of recalcitrant molecules with a high concentration which is the case of textile waste could be a limiting factor in microbial growth owing to their non-bioavailability because they are not easily dissipated by microorganisms, which is probably the case of mixture C. Actually, the high level of C/N in mixture C (59.29) at the beginning of composting, which is high compared with mixtures A and B, could be assigned to the poor humification of organic matter and/or low distribution of microbial activity inside of the silos (Biyada et al., 2020a). This is confirmed by microorganism diversity in this study, which is lower for mixture C than that present in mixtures A and B.

Furthermore, the low abundance of microbial communities in mixture C could be referred to the high concentration of heavy metals recorded with mixture C (Biyada et al., 2020b), which mainly results from the high concentration of textile waste in this mixture compared with the other ones (A and B). Despite their richness in lignocellulosic fiber, textile waste is considered as a fountainhead of heavy metals, owing to the use of chemicals and dyes produce in the production chain of textiles, such as sodium carbonate, sulfuric acid, acetic acid, copper sulfate sodium sulfate, ammonium chloride, and the pigments (Talouizte et al., 2017). The use of these products could preclude microorganism proliferation and consequently the degradation of organic matter. It is noticeable that mixture C presents a high concentration of heavy metals (especially of Zn) compared with mixtures A and B, which is considered one of the most toxic metals. The effect of Zn on the microbial enzyme activities (acid phosphatase, alkaline phosphatase, cellulase, *b*-D-glucosidase, and *b*-D-fructofuranosidase) was recorded (Kunito et al., 2001). These findings could also explain the variation of microorganism abundance in the three mixtures tested.

By analyzing carefully the results obtained, it can be noticed that the major difference between the three mixtures was observed for the actinomycete and fungal communities, which are less abundant and/or not found at all in mixture C compared with the other mixtures. According to several authors, a wide range of species belonging to actinomycete and fungal phyla have participated in the degradation of organic matter in general and cellulosic and lignocellulosic substrates in particular through their enzymatic systems (Tuomela et al., 2000; Verlag et al., 2000; Lynd et al., 2002; Tiquia, 2005; Raut et al., 2008; Vargas-garcía et al., 2014). Their presence indicates a more efficient and faster composting process, which is the case of mixtures A and B. The low abundance of these phyla could affect the rate of organic matter degradation, which is the case for mixture C in this study.

Eventually, it can be concluded that the nutritional value of initial feedstock and the concentration of heavy metals in different mixtures are probably the major factors affecting the microbial communities during textile waste composting. At the same time, the composition of the microbial communities throughout the composting of lignocellulosic materials is depending on the greater or lesser degree of the bioavailability of the nutrients.

Microorganisms are abundant and diverse in compost. Microbial communities are organized and affected by the feedstock concentration, which is demonstrated during this study. By increasing the concentration of textile waste in the mixtures used and therefore the concentration of heavy metals especially Zn, the abundance of species belonging to fungal and actinomycete communities decreased and consequently the rate of organic matter degradation. By analyzing the composition of microbiota associated with different concentrations of the feedstock used, the most effective control of the composting process can be achieved. Ultimately, it can be concluded that mixtures A and B, containing either 40 or 60% of textile waste, could be the best combination for the valorization of such waste using composting.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

AUTHOR CONTRIBUTIONS

SB, MM, and JU: conceptualization. SB, DV, JU, EM, and SV: methodology. SB and TD: software. MM and JU: validation. SB: formal analysis, investigation, data curation, and writing – original draft. JU, SV, and SB: resources. SB, MM, JU, and SV: writing, review, and editing. SB and JU: visualization. MM, JU, and SV: supervision. MM: project administration. JU: funding acquisition. All authors have read and agreed to the published version of the manuscript.

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