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Bio-Augmentation as an Emerging Strategy to Improve the Textile Compost Quality Using Identified Autochthonous Strains

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Abstract: The present investigation is devoted, for the first time, to the potential of autochthonous inoculums through bio-augmentation tests to improve the compost quality and to decrease the composting time during composting of textile waste. For this reason, three strains were isolated from a mixture of textile waste, green waste, paper, and cardboard waste, and therefore identified as *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, and *Serratia liquefaciens*, employed using bio-augmentation test. The organic matter decaying was assessed according to three different inoculums doses, separately and in consortium (4%, 6%, and 8%), to describe the effect of bio-augmentation process on the organic matter decaying. Indeed, these three strains and their consortium have shown a strong potential of organic matter degradation, equally the bacterial consortium showed a total organic carbon degradation of 20.3%, total Kjeldahl nitrogen of 1.52%, and a Carbon/Nitrogen ratio of 13.36. Compost maturity has been completed after only 12 weeks of treatment instead of 44 weeks using the classical treatment by composting. Ultimately, according to these results, bio-augmentation could be an emerging and promising strategy to accelerate the composting process of solid waste, especially in the case of industrial waste. Equally, it could be an effective tool to avoid the accumulation of industrial waste disposal in public landfills and/or nature while allowing their treatment.

Keywords: bio-augmentation; composting time; organic matter; textile solid waste; composting

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1. Introduction

The textile industry depicts a substantial economic sector worldwide, and it is considered one of the largest industrial sectors from the aspect of solid waste generation [1]. Despite their economic value, this industry is ranked among the most polluting industries, which generates huge amounts of solid waste. Its toxicity is based on the fact that these wastes contain various pollutants such as degradable organics, dyes, salts, sulfuric acid, toxicants, as well as refractory organics [2]. These pollutants depict a significant environmental and health issue, especially in the case of dyes such as azo dyes, anthraquinones, phthalocyanines, etc., which are toxic, persistent in nature, and affect the biotic species of the environment. Equally, they have a genotoxic and carcinogenic effect on the health public [1], in the whole world, particularly Fez city in Morocco. This problem is further aggravated in Fez city, because these wastes are disposed of directly into the environment without any treatment. Several chemical and physical methods are used in color removal, such as precipitation, flocculation, membrane filtration, adsorption, and wet oxidation.

These methods are quite expensive, could generate the production of toxic by-products, and have posed operational problems [2]. For this reason, it is mandatory to promote the stabilization of these wastes to avoid their innumerous environmental problems. On the contrary, textile wastes are a source of organic matter, and these wastes could be bio-converted into a nutrient source to the soil if they are treated properly [3,4].

For many years, composting has been considered as the most efficient technology for the stabilization of the solid waste generated [5]. Although composting has several advantages regarding processing cost and product quality, these do not preclude that there are equally some disadvantages, especially the presence of recalcitrant molecules, which are not easily dissipated by microorganisms, thus allowing a slowdown in biodegradation during composting was observed. According to a previous study, textile waste had only 31% of organic matter that may be degradable by microorganisms [6], so it is necessary to increase this percentage by adding other organic waste such as green waste. In this sense, the implementation of this process to improve some biological and physical–chemical parameters is widely recommended.

Bioaugmentation is defined as a technique for improvement of the degradative capacity of contaminated areas by the introduction of specific competent strains or consortia of microorganisms.

Otherwise, bio-augmentation is recognized as a cost-effective technology for improving the biodegradability of organic matter, even with the presence of recalcitrant molecules [7], by the introduction of specific competent strains or consortia of microorganisms [8]. This technology involves the inoculation of potential microorganisms to improve organic matter degradation, in which these microorganisms may be autochthonous or allochthonous, as well as potentially being a pure culture and/or a consortium [9–12]. The selection of appropriate strains for bio-augmentation should take into account the following characteristics of microorganisms: high degradation potential, rapid growth, and ease of culture [11]. Abed et al. [13] have revealed that bio-augmentation allows shortening the period required for the degradation of compounds relatively recalcitrant to degradation. Several studies are devoted to the effect of bio-augmentation on composting performance using commercial strains [5,8], but few of them are interested in the use of autochthonous strains during composting. For this reason, a deep understanding of the effect of autochthonous strains on composting is recommended.

No published work was reported for the use of the bio-augmentation technique during textile waste composting as an additional technology to improve the composting performance and the final compost quality, or even for the isolation of autochthonous strains and their re-inoculation during textile waste composting. The main aim of the present work was to isolate and identify bacterial strains from a mixture of textile waste, green waste, and waste paper and cardboard intended for treatment by composting and re-inoculating them during the bio-augmentation test. More specifically, this study focuses on the use of different doses of autochthonous inoculum to show their effect on the composting process. The proposed method could be an effective tool to treat and recover solid textile waste in a short time and with surprising results from the aspect of organic matter decaying, therefore reducing the number of landfills built and their harmful impact on the environment.

2. Materials and Methods

2.1. Characterization of Feedstock

Preparation of the mixture was followed according to the procedure explained previously [14]. The composition of the feedstock was summarized in Table 1.

Table 1. Physical–chemical characterization of the feedstock.

Physical–Chemical Parameters	Textile Waste	Green Waste	Paper and Cardboard Waste	Norm NF U44-051/A2
Moisture%	51.28 ±1.03	61.49 ± 1.41	11.28 ±1.07	40–60
pH	7.4 ± 0.15	6.6 ± 0.53	7.2 ± 0.35	6.5–8.5
Total Organic Carbon (TOC%)	31.63 ± 1.48	45.67 ± 1.37	59.35 ± 0.90	>20
Total Nitrogen (TN%)	0.57 ± 0.04	1.23 ± 0.04	1.05 ± 0.05	-
C/N ratio	55.1	37.2	56.7	20–40

Values designate mean ± standard deviation based on 3 samples.

In a previous study [15], a mixture symbolized as Mix C of the three wastes was set up for composting using silo technique according to the following proportion ratio of 40%:30%:30%, respectively, for textile waste, green waste, and paper and cardboard waste. A total of 40 kg was used during composting at room temperature and turned at least three times per week for 44 weeks. Samples were collected according to the four cardinal positions (north, east, south, and west).

2.2. Isolation of Bacterial Strains from Compost Mixture

Isolation of the bacterial strains was carried out using a medium based on the mix of the initial substrate, prepared as follows: 35 g of initial substrate (textile waste, green waste, and paper and cardboard waste) in one liter of distilled water, macerated overnight, and subsequently the filtrate was supplemented with 15 g of agar. Isolates of bacteria morphologically distinct were selected and purified by successive preculture until the pure strains were obtained [16]. Pure cultures were stored on nutrient agar slants at 4 °C as working stock cultures.

2.3. Bio-Augmentation Test

In previously sterilized pots (with an effective size of 0.17 × 0.17 m), 1 kg of sterile waste from Mix C (textile waste, green waste and paper and cardboard waste) was inoculated on the surface using different inoculums doses. All the pots were mixed daily for aeration throughout 12 weeks of treatment at room temperature. Three inoculums' doses were studied, which were 4%, 6%, and 8% (v/w), as well as a consortium of the three isolates with the same concentrations. A negative test (T) was prepared under the same conditions and used without inoculum to reveal the bio-augmentation efficiency of our isolates.

2.4. Experimental Analysis

Physical–chemical parameters of the mixtures, such as total organic content (TOC%), was carried out by methods as described by [9]. The total Kjeldahl nitrogen (TKN%) content was determined using the standard method of nitrogen Kjeldahl analysis according to [17]. The C/N ratio was calculated from the percentage of total organic carbon (TOC%) and the total Kjeldahl nitrogen (TKN%). Measurement of the temperature was carried out according to the protocol described by the French Association for Standardization [18]. Microbial analysis was assessed using a standard serial dilution procedure. All assays were estimated in triplicate (in weeks 0, 2, 4, 6, 8, 10, and 12), and were then placed into polythene bags and stored at 4 °C until further analysis was conducted.

2.5. Molecular Identification of Isolated Strains

DNA extraction was carried out according to kit protocol using the Genomic DNA purification Kit of Thermo Fisher. Then, 16S rRNAs gene targeting was amplified by polymerase chain reaction (PCR) using the universal bacterial primers: FD1 (5′ AGA GTT TGA TCC TGG CTC AG 3′) and RP2 (5′ ACG GCT ACC TTG TTA CGA CTT 3′) and a thermal cycler (Verity ABI). Ultimately, the amplified fragments were sequenced using ABI 3130XL capillary sequencer. Obtained sequences were aligned using the BLASTn software.

Additionally, the neighbor-joining tree was constructed using neighbor-joining (NJ) method MEGA_11-0.2 software. Molecular identification was performed at the laboratory of the National Center of Scientific and Technical Research (CNRST) at the Functional Genomics Platform in Rabat city, Morocco.

2.6. Statistical Analysis

The data are shown as the mean value ± standard deviation (SD) from three independent experiments. ANOVA two-way tests were performed to determine significant differences between the different strains, consortium, and organic matter degradation; the differences were additionally performed using Tukey's tests. A p-value of <0.05 was considered to be statistically significant. These tests were performed using Graph-Pad prism.

3. Results and Discussion

3.1. Morphological Appearance of the Isolated Strains

Three morphologically distinct isolates with opaque forms were isolated and purified. The isolates are symbolized as S1, S2, and S3.

3.2. Effect of the Bio-Augmentation on the Composting Process

3.2.1. Evolution of Bacterial Growth

Bacterial growth evolution is depicted in Figure 1. From the beginning, the three isolated strains (S1, S2, and S3) and their consortium experienced considerable growth. All of the isolates grew swiftly with a maximum value at a time corresponding to the 8th week (Figure 1a–d). Nevertheless, the bacterial growth was significantly higher with the consortium relative to the pure culture (p-value < 0.05). Equally, the bacterial growth was considerably higher using these selected strains, with maximum growth reached in 8 weeks compared to the basic composting without inoculation, with a maximum of growth in 28 weeks [6], which could be assigned to the antibiosis phenomenon between the different microbial strains existing during the classical composting, and consequently prevent the growth of the strains which allows organic matter degradation, including those isolated. No growth of bacteria was noticed with a negative test (T) without bacteria, thus proving that organic matter decaying has been accomplished by the strains isolated. Moreover, the increase in microbial activity using these strains could be explained on the one hand by the fact that these isolates have already been adapted to the compost environment and have the ability to resist toxic molecules of textile waste. On the other hand, it could be explained by the abundance of organic matter with nutrients such as carbon and nitrogen, which are indispensable for microorganism's growth and therefore stimulates their proliferation. The decrease in microbial growth towards the end of the test could be linked to the depletion of medium [19].

3.2.2. Evaluation of Temperature, Total Organic Carbon, (TOC) Total Kjeldahl Nitrogen (TKN), and C/N Ratio

The effects of inoculum doses on some physical–chemical parameters (Temperature, TOC, TKN, and C/N ratio) are depicted during this investigation. Measurement of temperature using different inoculums doses is presented in Figure 2. A noteworthy increase in temperature was noticed with the three strains and their consortium, depending on different inoculum concentrations (4%, 6%, and 8%). The highest temperature was recorded with strain S3 whatever the inoculum dose, and for strain S3 (42 °C) and the consortium (54.17 °C) at the inoculum dose of 8% (Figure 1). The increase in temperature could be mainly ascribed according to several authors to microbial metabolisms resulting from the decomposition of organic matter, particularly carbohydrates, thus releasing energy during their degradation [6,15,20]. Biyada et al. [21] have shown the presence of carbohydrates in composted waste like cellulose through FTIR analysis, thus confirming that this increase of the temperature could be explained by the break of these carbohydrates by the isolated strains used.

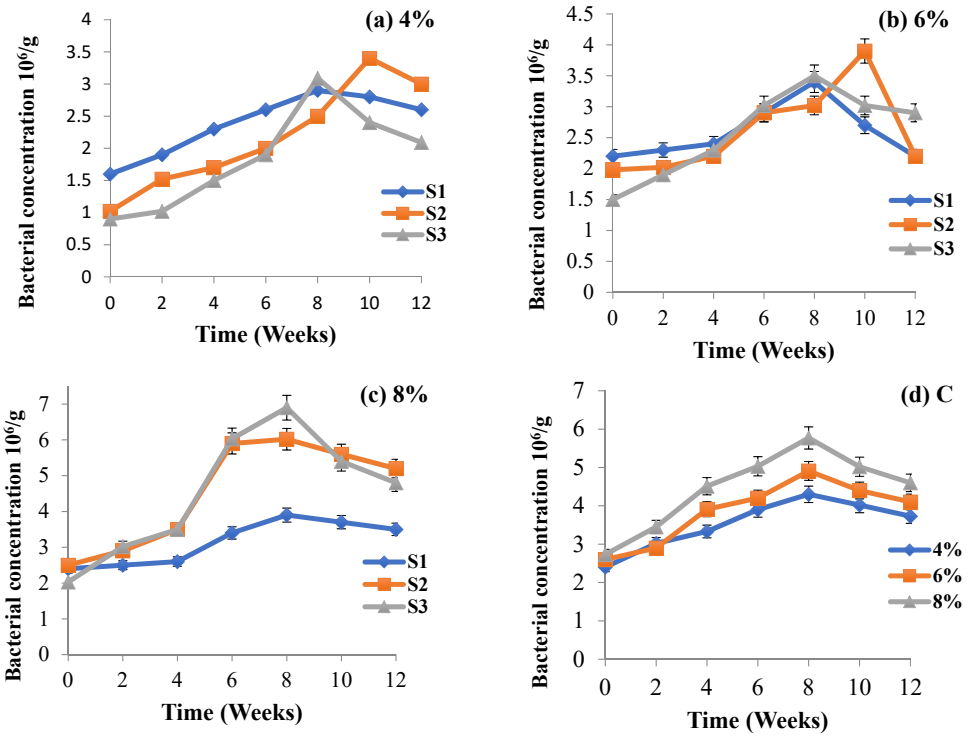

Figure 1. Evolution of bacterial growth of the three strains isolated and their consortium as function of the time at different inoculum doses (4% (**a**), 6% (**b**), and 8% (**c**)). S1: Strain 1; S2: Strain 2; S3: Strain 3; (**d**) C: Consortium.

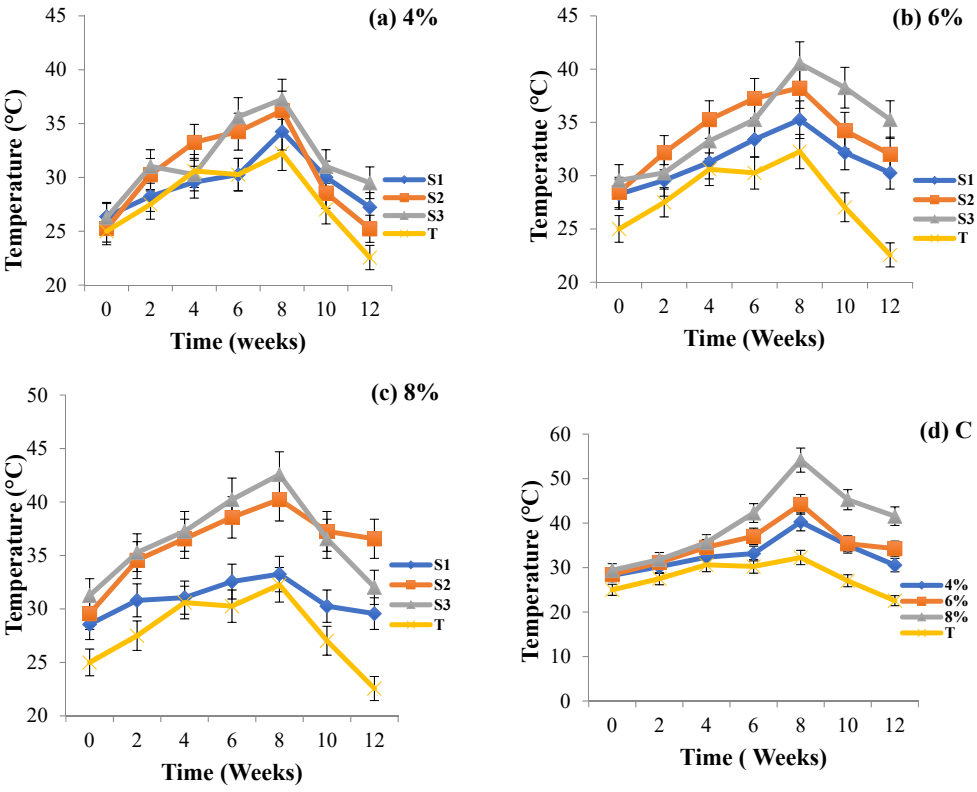

Figure 2. Evolution of temperature (°C) of the three strains isolated and their consortium as function of the time at different inoculum doses (4% (**a**), 6% (**b**), and 8% (**c**)), T; negative test. S1: Strain 1; S2: Strain 2; S3: Strain 3; (**d**) C: Consortium.

Table 2 depicts the total organic carbon (TOC%) evolution using isolated strains and their consortium. In fact, a significant decrease in TOC was recorded ($p < 0.05$) towards the end for the three strains and their consortium depending on different inoculums doses (4%, 6%, and 8%). The decrease in TOC was together with the increase in bacterial growth, which confirms the capacity of these strains to degrade carbonaceous compounds during their growth [20,22]. This was confirmed in a previous study using infrared spectroscopy analysis, thus showing that the wastes used in this study are rich in carbohydrates and polysaccharide compounds, which is considered as a source of carbon and energy for the bacterial growth as mentioned above [21]. Through this investigation, a decrease attributed to these compounds (carbohydrates and polysaccharide, which are rich in carbon) depending on the composting time was recorded, which could be assigned to the degradation and/or the assimilation of these compounds by the microorganisms of the compost, especially as TOC in negative test remains stable during the composting process (Table 2). Indeed, this decrease of TOC could explain the increase of the temperature and confirm our previous hypothesis.

Similarly, for TKN from the beginning, a significant increase was recorded ($p < 0.05$) (Table 3), which could be attributed to the organic matter decaying (proteins and peptides) to ammoniacal compounds, which are assimilated forms by bacterial isolates and their consortium [23,24]. Together with a decrease of TOC and the increase of TKN, a significant decrease in the C/N ratio was noticed, but it still remains above the maturity standard (15–20), with values of 20.00, 19.87, and 19.30 for 4%, 6%, and 8%, respectively, in the case of pure strains, and below the maturity standard in the case of bacterial consortium 18.69, 15.70, and 13.36 for 4%, 6%, and 8%, respectively (Table 4). Nevertheless, whether for TOC, TKN, or even C/N ratios, the content remained stable over time within the negative Test (T). This could confirm that the organic matter degradation was carried out by the three strains used. Additionally, the decrease in C/N ratios was higher using the consortium compared to that using pure culture.

Using these strains, whether on pure culture or their consortium, the results obtained are significantly higher and swiftly compared to the results obtained during classic composting without selected inoculums [6].

In this respect, Tukey's multiple comparison test, revealed that the use of the inoculum affected positively the quality of the final compost produced. Equally, by increasing the inoculums concentration (from 4%, 6%, to 8%), the TOC content and C/N ratios were decreased; at the same time, the temperature and TKN were increased. For the consortium of the three strains (S1, S2, and S3), there is a significant effect (p-value < 0.05) between the consortium concentration and the degradation of organic matter.

3.3. Molecular Identification of Isolated Strains

The FASTA formats were analyzed using the database of BLASTn software. The identification was based on the score, the percentage of identity, and Query covers, which must be greater than 96%, thus identifying these isolates as: *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, and *Serratia liquefaciens* for S1, S2, and S3, respectively (similarity more than 98%). Briefly, a sequence from these strains was submitted to GenBank with their accession numbers KC429648, JX050258, and CP033893, respectively, for *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, and *Serratia liquefaciens*. Based on the 16S RNA gene sequence of the strains isolated, three neighbor-joining trees were formed during this investigation and some other phylogenetically related taxa (Figure 3). These phylogenetic trees indicated that S1, S2, and S3 were closely related to *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, and *Serratia liquefaciens*, respectively, thus revealing that the strains isolated were identified as *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, and *Serratia liquefaciens*, respectively.

Table 2. Evolution of TOC degradation of the three isolated strains (S1: Strain 1; S2: Strain 2; S3: Strain 3) and their consortium as function of the time at different inoculum doses (4%, 6%, and 8%).

TOC%	[4%]				[6%]				[8%]				Negative Test
	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	
S1	32.90 ± 0.44	31.00 ± 0.09	30.50 ± 0.96	26.4 ± 0.30	34.00 ± 0.20	31.20 ± 0.26	25.20 ± 1.02	24.20 ± 0.95	33.70 ± 0.02	29.10 ± 0.56	26.70 ± 0.52	24.60 ± 0.30	32.90 ± 0.10
S2	32.74 ± 0.13	30.27 ± 0.36	26.67 ± 0.30	25.04 ± 1.01	31.23 ± 0.10	29.37 ± 0.95	26.25 ± 0.26	24.15 ± 0.12	31.60 ± 0.10	27.55 ± 1.02	24.30 ± 0.10	23.45 ± 0.20	32.90 ± 0.12
S3	33.01 ± 0.23	30.72 ± 0.40	29.35 ± 0.50	28.11 ± 1.05	31.46 ± 0.50	29.49 ± 0.86	26.16 ± 0.15	24.46 ± 0.50	31.50 ± 0.23	26.50 ± 0.20	23.50 ± 0.20	22.20 ± 0.15	32.90 ± 0.20
Consortium	32.10 ± 0.01	30.10 ± 0.04	28.50 ± 0.30	24.30 ± 0.12	31.70 ± 0.40	29.40 ± 0.20	26.50 ± 0.13	22.30 ± 0.30	30.30 ± 0.15	26.90 ± 0.15	23.60 ± 0.01	20.30 ± 0.12	32.90 ± 0.60

Values designate mean ± standard deviation based on 3 samples.

Table 3. Evolution of TKN degradation of the three strains isolated (Strain 1; S2: Strain 2; S3: Strain 3) and their consortium as function of the time at different inoculum doses (4%, 6%, and 8%).

TKN%	[4%]				[6%]				[8%]				Negative Test
	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	
S1	0.89 ± 0.02	0.98 ± 0.01	1.03 ± 0.03	1.13 ± 0.01	0.75 ± 0.03	0.90 ± 0.01	1.01 ± 0.03	1.10 ± 0.02	0.76 ± 0.01	1.00 ± 0.01	1.09 ± 0.02	1.23 ± 0.02	0.50 ± 0.01
S2	0.50 ± 0.01	0.86 ± 0.02	1.02 ± 0.12	1.09 ± 0.03	0.59 ± 0.04	1.01 ± 0.02	1.09 ± 0.02	1.12 ± 0.02	0.65 ± 0.01	1.09 ± 0.03	1.13 ± 0.03	1.18 ± 0.01	0.50 ± 0.02
S3	0.7 ± 00.10	0.84 ± 0.01	1.00 ± 0.01	1.20 ± 0.01	0.75 ± 0.05	1.01 ± 0.01	1.12 ± 0.05	1.15 ± 0.02	0.69 ± 0.01	1.09 ± 0.02	1.14 ± 0.01	1.15 ± 0.02	0.50 ± 0.01
Consortium	0.68 ± 0.03	0.77 ± 0.04	0.98 ± 0.01	1.30 ± 0.02	0.70 ± 0.01	0.92 ± 0.02	1.09 ± 0.04	1.42 ± 0.01	0.69 ± 0.02	1.03 ± 0.04	1.19 ± 0.02	1.52 ± 0.01	0.50 ± 0.02

Values designate mean ± standard deviation based on 3 samples.

Table 4. Evolution of C/N ratio of the three strains isolated (S1: Strain 1; S2: Strain 2; S3: Strain 3) and their consortium as function of the time at different inoculum doses (4%, 6%, and 8%).

C/N	[4%]				[6%]				[8%]				Negative Test
	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	Week (0)	Weeks (4)	Weeks (8)	Weeks (12)	
S1	36.97	31.63	29.61	23.36	45.33	34.67	24.95	22.00	44.34	29.10	24.50	20.00	65.80
S2	65.48	35.20	26.15	22.97	52.93	29.08	24.08	21.56	48.62	25.23	21.50	19.87	65.80
S3	47.16	36.57	29.35	23.43	41.95	29.20	23.36	21.27	45.65	24.31	20.61	19.30	65.80
Consortium	47.21	39.06	29.08	18.69	45.29	31.96	24.31	15.70	43.91	26.12	19.83	13.36	65.80

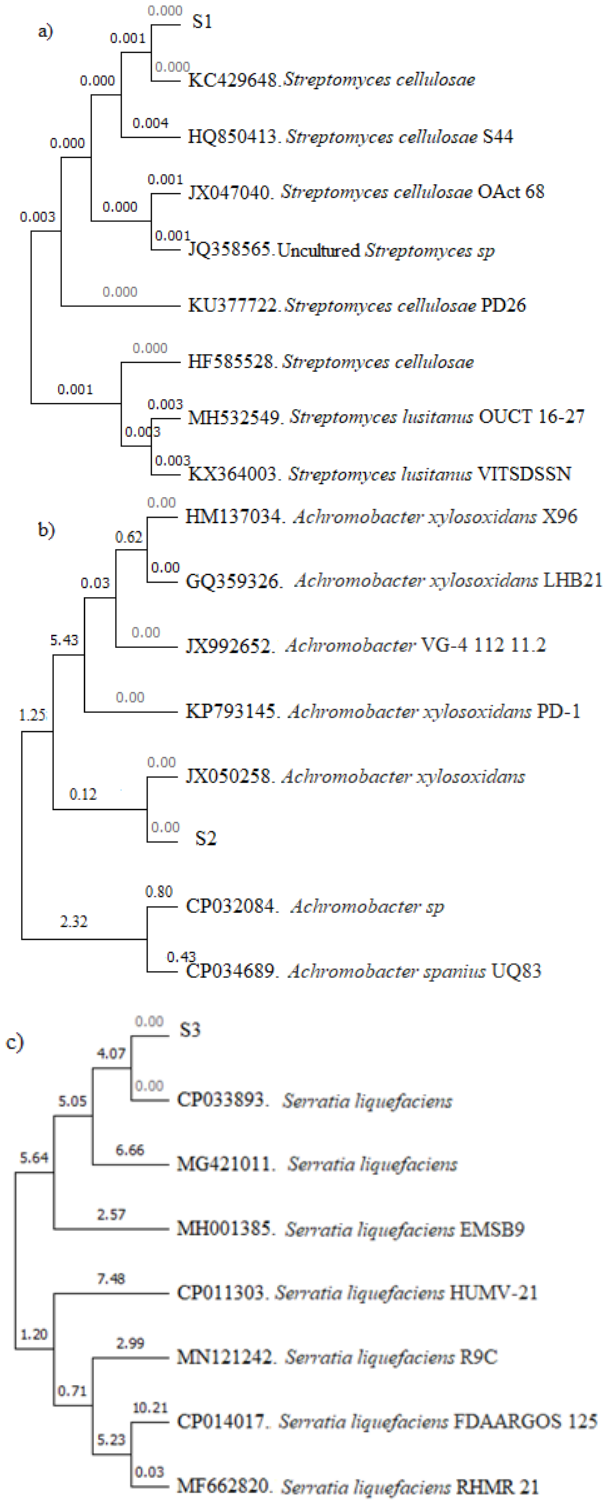

Figure 3. Neighbor-joining phylogenetic tree based on the 16S rRNA gene sequence of the isolates and other reference sequences ((**a**) S1, (**b**) S2, and (**c**) S3) (Numbers in figures show branch lengths).

Several authors reveal the effects of bio augmentation on the composting process using a wide range of microorganisms as well as different types of solid waste [5,7,11]. Regarding the literature, it was demonstrated that species belonging to *Streptomyces*, *Achromobacter*, and *Serratia* are able to use a wide range of organic matter, particularly in ligno-cellulosic compounds, as a fountainhead of carbon and energy and consequently use it for their growth [25]. Several authors revealed that *Streptomycetes cellulosae* was studied among

potential microorganisms in nitrogen biodegradation systems using their enzymatic complex [26,27], which is in concordance with the results obtained by *Streptomycetes cellulosae* mentioned overhead regarding TKN. Additionally, Li, et al. [28] identified species belonging to *Achromobacter* genera as cellulolytic strains with high ability of polysaccharides compounds decaying, especially those in paper waste, which is owing to its enzymatic system of mainly carbohydrate hydrolases, endoglucanase, and endoxylanase [29]. These findings could explain the results obtained by *A. xylosoxidans* regarding the decrease in TOC, and therefore, C/N ratio. The ability of *Achromobacter* to degrade the lignocellulosic compounds in solid waste is identified by several authors that worked on household waste discharged in landfills as well as in paper waste [28,30]. Indeed, Haq et al. [31] identified *S. liquefaciens* as a ligninolytic strain, which is due to their ability to degrade lignin from solid waste and based on its detoxification and reduction of pollutants activity, as well as the azo dyes containing in paper waste, which is the case for the present study. In fact, the abundance of textile waste, paper and cardboard waste, and green waste in ligno-cellulosic compounds and azo dyes, which is confirmed beforehand [14,21], allows to induce lignin peroxidase enzymes (LiP) in *S. liquefaciens*. Biyada et al. [14] depicted using FTIR and XRD analysis, which the intensities of pics attributed to lignin, carbohydrates, hemicelluloses, and/or cellulosic in compost samples appeared, thus proving the decaying of polysaccharides, aliphatic, and carbohydrates from the compost samples, which could be a good indication of compost stability and maturity. These findings could explain the high effectiveness of *S. liquefaciens* in the degradation of the organic matter represented by TOC, TKN, and C/N compared to the other strains tested, equally to their effect on the time of composting, which is significantly much less than that during classical composting. It can be noted that the use of *S. liquefaciens* allows the dyes present in textile waste to decay.

Nevertheless, when a consortium of isolates was used, the organic matter degradation was considerably more intense, relative, and swift compared to the use of these isolates separately, which could be due to their ability to coexist with each other. The results recorded during this investigation could be explained by the fact that different metabolism pathways of the bacteria within this consortium are involved to degrade organic matter [10]. Several studies indicate that there might be a synergistic cooperation between bio-augmented bacterial species into consortia, which has strengthening their ability to accelerate the conversion of organic matter, especially recalcitrant substances [10,20]. These findings are consistent with the results obtained in this investigation. Other studies deduced that recalcitrant compounds, such as lingo-cellulosic, are degraded by microbial consortia in which each strain has specialized roles: some of them attack the complex substrate, others provide essential nutrients [32,33]. Li et al. and Ariffin et al. [28,34] have demonstrated that *S. liquefaciens* and *A. xylosoxidans* could fulfill the role of a degrading agent for lignocellulosic compounds owing to their enzyme system. Indeed, [35] investigated that *Streptomycetes cellulosae* have the ability to use cellulose and other lignin byproducts as a source of carbon and energy.

Ultimately, as demonstrated during this study, the bioaugmentation could be a useful tool to improve the performance of composting process and the quality of final compost either with industrials wastes, which is the case in the present study or even with other kind of wastes, which has been confirmed previously by several authors [5,7,11]. For this reason, the choice of microorganisms is crucial, and should be based on the nature of waste used, particularly their composition.

4. Conclusions

The degradation of the organic matter during composting was reinforced by bioaugmentation tests with three well isolated strains: *Streptomyces cellulosae*, *Achromobacter xylosoxidans*, *Serratia liquefaciens*, and their consortium. *Serratia liquefaciens* recorded an intense and prompt degradation of organic matter compared to other strains and to the classical composting without selected inoculum. In addition, with an inoculum dose of 8%, a value of total organic carbon degradation of 22.2%, total Kjeldahl nitrogen of 1.15%, and a C/N ratio of 19.30, the degradation was considerably more intense compared to 4%

and 6% doses, either by testing the strains separately or in consortium with a value of total organic carbon degradation of 20.3%, total Kjeldahl nitrogen of 1.52%, and a C/N ratio of 13.36, which is statistically confirmed. The present study revealed for the first time that the bio-augmentation with isolated strains can be a useful tool to reduce organic matter degradation time of textile waste during composting from 44 weeks to only 12 weeks, thus proving the effectiveness of the bio-augmentation on the composting process and the quality of the compost from textile waste. This investigation proves that the coupling of bio-augmentation with composting could be an effective tool to reduce the cost of building landfills, and equally to adopt a sustainable alternative to protect the environment from the side effects of waste disposal in landfills and/or directly in the nature.

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