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Research article

Characterization of physicochemical parameters and bacterial diversity of composted organic food wastes in Dubai

Carole Ayoub Moubareck [a,*], Buthaina Alawlaqi [a], Salama Alhajeri [b]

[a] College of Natural and Health Sciences, Zayed University, Dubai, United Arab Emirates
[b] Department of Corporate Environmental Health & Safety, Dubai Health Authority, Dubai, United Arab Emirates

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ABSTRACT

Composting favours recycling organic waste and producing an end product with high bioenergy potential and significant nutritional value for the soil. Analysing composted organic waste prepared in Dubai, a region with a desertic climate and a unique environment is essential since environmental conditions can greatly affect the physicochemical and biological soil properties and no studies in the Gulf region have been published yet on that process. This study analysed twelve different compost samples prepared in well ventilated wooden chambers, using home-generated organic wastes following the hot aerobic composting method for a duration of three months. The physicochemical parameters, measured at the end of the study, revealed that organic matter, electrical conductivity and pH were within the standard ranges while moisture content was low. Concerning macronutrients, most of the samples were within the standard range for carbon, potassium and sodium, while they were poor in phosphorous and nitrogen. Metagenomic analysis with Illumina MiSeq revealed the abundance of *Firmicutes* (30.35%), followed by *Bacteroidota* (26.69%), *Proteobacteria* (21.47%), and *Actinobacteriota* (11.17%). The phylum *Planctomycetota*, solely detected in compost and known to have a significant impact on soil ecosystem and decomposition of organic matter, was reported at a relatively significant level (2.35%). The Clostridia class, efficient in degrading cellulose, was described at high levels compared to other studies. The composting project succeeded in generating a healthy soil but lengthening the duration will allow the samples to fully decompose and therefore increase the total available nitrogen and phosphorus to meet the criteria of a typical mature compost. Various microbial consortia helped in the decomposition process. The qualitative information collected in this study will help in improving the composting technology to favour its utilization by a larger public in the Gulf region.

1. Introduction

Composting relies on the natural process of decomposition of organic wastes by microorganisms under controlled conditions to produce an end-product with significant bioenergy potential and nutritional value [1]. It is associated to multiple environmental, social, and economical benefits including sanitation, bioremediation and waste management. For years and still nowadays, organic waste is considered as a serious environmental issue especially with the exponential population growth and the increased rate of per

Abbreviations: EC, Electrical Conductivity; ASV, Amplicon Sequence Variants; OTUs, Outer Taxonomic Units; NA, Not Assigned.

* Corresponding author. P.O. Box 19282, Dubai, United Arab Emirates.
E-mail address: carole.ayoubmoubareck@zu.ac.ae (C.A. Moubareck).

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List of abbreviations

EC	Electrical Conductivity
ASV	Amplicon Sequence Variant
OTUs	Outer Taxonomic Units
NA	Not Assigned

capita food consumption that contributes directly to the increase generation of waste. Food waste are usually disposed in landfills or incinerators which are environmentally, socially, and economically undesirable techniques that require both energy and space. In addition, they liberate unpleasant odours, lead to greenhouse gas emissions and pollute surrounding soils, groundwater and water bodies [2,3]. The possibility to dispose organic waste by using them as materials for compost preparation is seen as a key solution to alleviate the burden on the environment. In addition, composting plays an important role in sustaining soil fertility. It improves soil aggregation, infiltration and aeration and increases water holding capacity allowing therefore the soil to become more resistant to drought, diseases and toxicity. Furthermore, it improves the nutrient content and microbial activity in soil and helps in the elimination of weed and pests [4,5]. These benefits manifest themselves in reducing cropping risks, higher crop yields and lowering outlays on inorganic fertilizers [6,7].

Different types of composting techniques, such as cold composting, vermicomposting, Bokashi composting, or hot aerated composting can be applied in small or large scales. Cold composting involves decomposition of organic materials in nature for example a fallen tree in the forest. Generally, the leaves are first decomposed by bacteria and the moist punky wood of the trunk is attacked by fungi and some bacteria and insects. In vermicomposting, worms attack the organic matter to break it down into a high value compost. Anaerobic degradation of organic waste, or Bokashi composting, is another process that uses a specific group of microorganisms to ferment organic matter in absence of oxygen in an acidic environment, resulting in a finished product that can be easily digested by the soil biota [8]. The hot aerated composting technique begins with the proper balance of organic material and appropriate amount of water and air in a pile of adequate size which goes through three phases: the heating up or mesophilic phase, the hot or thermophilic phase and the curing or maturation phase. The pile includes organic matter that may be classified as green and brown materials. The brown materials, such as wood chips or fallen leaves, are high in carbon and represent a source of energy for the composting microbes. Green materials such as grass clippings, fruit and vegetable peels are a source of nitrogen. Understanding the Carbon to Nitrogen ratio of the pile is very important because it is very effective in creating a hot compost pile with minimum odour. The ideal C: N ratio of a compost pile is 25:1 to 30:1. If the ratio is too low the pile may get excessively hot or the pile uses all the oxygen in it and turns into an anaerobic process. This technique is a common practice for large scale composting in which waste are formed into rows of long piles and aerated by turning the pile either by mechanical or manuals means. In-vessel aerobic composting is a method of composting in which waste are placed in a rotary drum. Rotating causes, the material to tumble and this provides good distribution of the organic matter [9]. The hot aerated composting technique is applied too in small scales at home or in schools, universities and hospitals where the composting process is used to treat aerobically small amount of biodegradable waste without referring to automation methods.

Decomposition of organic waste, following the hot aerated composting technique, starts with the breaking down of large organic materials in the compost bin by small insects and bugs like beetles, centipedes, mites, earthworms, ants. Then comes the role of bacteria and fungi for a further decomposition of the compost matter and liberation of nutrients. Microbial diversity is important at that step because each microorganism produces specific sets of enzymes to degrade certain organic molecules [10]. *Firmicutes* were found in the early stages of the composting. *Actinomycetes*, members of the Phylum *Actinobacteriota*, are characterized by their ability to decompose complex compounds such as proteins, cellulose, and lignin [11]. *Proteobacteria* are gram negative bacteria that include gamma-proteobacteria, reproducing in temperature ranging from −10 °C to 40 °C, beta-proteobacteria capable of increasing the availability of nitrogen in the soil and ammonia oxidizing bacteria helping in the oxidation of ammonia to nitrite [12,13].

The quality of compost relies on its microbial population but also on several other factors including its water retention ability and its content in organic matter, a valuable component of the compost for the soil health improvement. Compost pH may also affect plant growth and should be preferably moderately acidic to moderately basic, that means between pH 6 to 8. Manure based composts, with a slightly basic pH, are unsuitable for acid loving plants such as Rhodhodendron and Blueberry [14]. Electrical Conductivity, an indicator of soluble salt content, must be preferably low. Macro-nutrients such as nitrogen, phosphorous and potassium are important for plant nutrition.

In this study we analysed twelve compost samples by investigating their physicochemical properties (Organic matter content, nitrogen, potassium, phosphorous, sodium, water retention, electrical conductivity, pH) and by studying their microbial composition using 16S rRNA metagenomics sequencing technique targeting v3-v4 regions with Illumina MiSeq. Learning more about these properties will help in understanding better the degradation process and in improving the composting technique.

2. Methods

This is an analytical experimental study that involved the assessment of the physicochemical properties and the microbiological composition of twelve different compost preparations performed by Zayed University students on Dubai Campus between September 2018 and January 2019.

2.1. Composting technique

All compost samples were prepared on Zayed University campus in Dubai, using the hot aerobic method, and were mainly composed of common organic wastes which fall into two categories green and brown materials in 1:3 ratios. The green materials used were grass clippings, green leaves, flowers, hair, herbs, fruit and vegetable peels. Brown materials consisted of fallen leaves, cardboard, paper, hey, corn cobs, pine needles, crushed egg shells, tea leaves, old herbs, spices and cereals. Coffee grounds were added as activators to accelerate the composting process to the samples 1, 2, 4, 6, 7, 8, and 11. Some of the food items like citrus peels, onion were excluded because of their acidic or antimicrobial properties. Dairy or meat products were not added to prevent bad odours and attraction of rodents. Heavily coated or printed paper and diseased plants were not used because of toxicity. All composts were prepared in wooden box chambers with the dimension of 1 m × 1 m × 1 m. Wooden boxes were not tightly sealed to facilitate aeration and compost preparations were mixed and watered once every week for 12 weeks.

2.2. Physicochemical characteristics

At the end of the 12 weeks, 2 kg of each compost preparation were dried in the laboratory oven at 60 °C for 12 h, slightly ground to finer particles using a large brass mortar and pestle, then sieved with a 2 mm equipment.

To check the presence of organic matter in each preparation, 10 g of compost was put in a crucible and kept in the furnace at 550 °C for 4 h and allowed to cool; then the final weight was noted.

Moisture content or water retention was measured using a soil moisture unit with a pressure of 0.1 Bar. Each sample was put in a dish filled with distilled water until the sample is moist, then the instrument was turned on. Once the pressure instrument stopped, the weight of the dish containing the fresh sample was recorded. Then, the sample was dried in the laboratory's oven at 100 °C for 12 h and cooled down. The weight of the dry sample was taken, and the water retention percentage of each sample was calculated using the average of replicates [15].

Electrical conductivity (EC) and pH values were measured using respectively an electrical conductivity meter and a pH meter. Each sample was diluted in a ratio of 1:5 with distilled water, stirred and allowed to settle overnight before getting the readings [15].

Kjeldahl total Nitrogen was calculated using the Kjeldahl method which consists of two main steps, digestion and distillation. A total of 0.5 g of dried sample was digested with half Kjeldahl tablet, 1 ml distilled water and 20 ml sulphuric acid in the digestion tube at 150 °C for 2 h. Later the sample was distilled with 25 ml boric acid. After complete distillation, the colour of the distillate changes from pink to different shades of green depending on the amount of nitrogen. This was titrated against 0.01 N sulphuric acid. Readings were noted to calculate the available nitrogen content in the samples [15].

To assess the assimilable concentrations of phosphorous (P), sodium (Na) and potassium (K), compost samples were digested using acid mixtures (H_2SO_4, HCl, and Ammonium) and subjected to colorimetric analysis after filtration. The standards for P, Na and K were prepared to design standard curves. A total of 5 ml of digested samples were added to volumetric flasks with 10 ml of 2 N Nitric Acid and treated with Molybdate-Vanadate for 20 min. Phosphorous content was measured using a UV-VIS Scanning spectrophotometer Spectro UV-2510TS. To measure the Na and K, the samples were diluted 10 times and the readings were taken using a flame photometer. The readings were then compared with standards and calculated the amount of sodium, potassium and phosphorous present in the sample [15]. The carbon content was calculated using the formula [Organic matter (%) = Total organic carbon (%) x 1.72]. The number 1.72 is the commonly used conversion factor which provides a reasonable estimate and is suitable for most of the soil type [16].

2.3. Microbial identification using 16S rRNA metagenomics study

2.3.1. Extraction of genomic DNA and 16S rRNA Illumina sequencing

Microbial DNA were extracted from samples using the ZymoBIOMICS™ DNA Miniprep Kit (Zymo Research Corporation, California, USA), following the manufacturer's instructions and assessed for quality using the DeNovix dsDNA High Sensitivity Fluorescent Assay Kit and measured on the DeNovix DS-11 FX spectrophotometer/fluorometer (DeNovix Inc., Delaware, USA). The DNA integrity was checked using agarose gel electrophoresis.

Amplicon libraries of the v3 and v4 regions were generated using two-step Polymerase Chain Reaction (PCR) process followed to generate barcoded amplicons from v3-v4 region of 16S rRNA genes. First round PCR has performed with 1 μM of 16S Amplicon PCR Forward Primer (5′ TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGGNGGCWGCAG) and Reverse Primer (5′ GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATCTAATCC). Later purified this using AMPure XP beads (Beckman Coulter, California, USA) and used for the second round PCR along with sample-specific barcodes (Nextera XT index kit, Illumina). Final libraries were quantified, using DeNovix dsDNA High Sensitivity Fluorescent Assay Kit. Subsequently, they were normalized, multiplexed and sequenced using Illumina MiSeq with a paired-end protocol (2 × 300 bp).

2.3.2. Bioinformatics and statistical analysis

The sequencing run was analysed with the QIIME 2 with demultiplexing. The raw sequence data in the *fastq* files were processed to remove Illumina adaptors, low-quality and chimeric regions. The processed sequence data were then assessed for the analysis. The DADA2 pipeline was used for detecting and correcting Illumina amplicon sequence data. Quality filtered reads were assigned to OTUs applying the open-reference OTU picking protocol using QIIME toolkit. Taxonomic analysis was performed using average taxonomic composition of the 12 samples. The *qiime2* feature-classifier trained on the SILVA 138 reference was used to classify ASVs at different

taxonomical levels (7 levels: Kingdom; Phylum; Class; Order; Family; Genus; Species).

3. Results

3.1. Physicochemical parameters

Prepared compost samples using the hot aerobic method were analysed for various physical and chemical properties. Organic matter, moisture content or water retention, EC and pH values of all compost samples are displayed in Table 1.

The content in organic matter of compost samples was between 38% and 50%. Concerning moisture content, samples 3 and 11 were within the range of 40–50%, sample 5 and 12 were above and the remaining eight samples were below 40%. Sample 12 had the highest moisture content with a percentage higher than 60% which made the compost clumpy and hard to spread. The average EC values for all the samples ranged between 1 and 5.1 mS/cm and pH values were around 8 with a slight increase in the pH of sample 1 equivalent to 8.5.

Macronutrients including potassium, sodium, nitrogen, phosphorous and carbon were measured and described in Table 2. The content in Carbon was found between 22.1 and 28.8%. Potassium was found between 0.32 and 0.95% followed by sodium between 0.11 and 0.45% and phosphorous between 0.05 mg/kg and 0.31 mg/kg. Nitrogen content was the lowest with quantities between 0.02% and 0.15%.

3.2. Microbial identification using 16S rRNA metagenomics study

3.2.1. Statistical analysis

Genomic DNA extracts of all twelve samples were subjected to Illumina MiSeq sequencing platform targeting v3-v4 variable region of the 16S rRNA genes. A total of 1.06 million reads was generated from the 12 samples, and 24778 (23.28%) reads were retained after removing the chimers; then OTUs (Operational Taxonomic Units) clustering allowed the detection of 1145 OTUs which were later assigned as ASVs (Amplicon Sequence Variants). Alpha diversity was calculated, and no significant differences in terms of diversity and richness were observed among the 12 samples. Shannon entropy and Pielou evenness were used to reflect on the variation in microbial diversity and bacterial richness in the samples. Based on the Shannon entropy, estimations of the total bacterial diversity for the twelve samples ranged from 5.66 to 6.73, which corresponded to close values. Pielou evenness was observed between 0.89 and 0.95, close to the value of 1, indicating also the absence of differences among the samples. Sample 8 showed the highest Shannon entropy (6.73), and a Pielou evenness value of 0.94, with 141 OTUs.

3.2.2. Microbial identification

After categorising the sequence variants to taxonomical units, a total of 20 different phyla of bacteria having 148 OTUs was found for all analysed samples. Fig. 1 shows the various microbes found in the 12 different samples based on the phylum level. The *Firmicutes* were the most abundant in the majority of samples and contributed to 30.35% of the total gene fragment abundance. *Firmicutes* were followed by the phylum *Bacteroidota* with 26.69%, *Proteobacteria* with 21.47%, *Actinobacteriota* with 11.17%, and *Planctomycetota* with 2.35%.

A total of 41 different classes having 254 OTUs was found. Fig. 2 shows the various microbes found in all 12 different samples at the class level and reveals that nearly 26.34% belongs to *Bacteroidia,* 20.16% to *Clostridia,* 12.58% to *Gamma-proteobacteria,* 8.89% to *Alpha-proteobacteria*, 8.51% to *Actinobacteria*. A total of 9.42% of bacterial classes was detected in very low number and referred as others.

Fig. 3 represents the taxonomic hits for the order level and reveals the detection of the top 10 orders out of the 97 found in all the samples with 638 OTUs. *Bacteriodales* are the most dominant with 15.87%, followed by *Lachnospirales* with 10.63%, *Oscillospirales* with 7.91%, *Rhizobiales* with 6.12%, *Flavobacteriales* with 4.88% and *Bacillales* with 4 0.41%. A total of 36.95% of bacterial orders was detected in low quantity and referred as others.

Table 1
Physico-chemical properties of the described compost samples.

Sample	Organic matter %	Moisture %	EC (mS/cm)	pH
1	49.6	27.7	3.2	8.5
2	49.1	20.8	1.2	8
3	39.5	44.8	5.1	7.8
4	41.9	28.1	2.1	7.8
5	38.1	53.6	3.1	8
6	39.3	21.5	2.3	8.2
7	41.1	12.6	1	8.1
8	48	24.2	3.4	7.8
9	42.9	14.9	1.7	8.3
10	40.4	19.9	2.3	8.3
11	39.9	50.5	4	8
12	42.1	73.8	2.6	8.1
Average ± SD	42.65 ± 4	32.75 ± 18.73	2.7 ± 1.17	8.1 ± 0.22

Table 2
Content in macronutrients of described compost samples.

Sample	Potassium (K) %	Sodium (Na) %	Phosphorous (P) mg/kg	Kjeldahl Nitrogen (N) %	Carbon (C) %
1	0.9	0.33	0.3	0.11	28.83
2	0.32	0.22	0.18	0.06	28.52
3	0.49	0.41	0.15	0.11	22.97
4	0.49	0.11	0.19	0.09	24.37
5	0.63	0.26	0.27	0.15	22.14
6	0.7	0.29	0.19	0.06	22.87
7	0.27	0.18	0.06	0.03	23.9
8	0.95	0.29	0.27	0.08	27.89
9	0.47	0.22	0.06	0.03	24.91
10	0.56	0.24	0.15	0.05	23.49
11	0.95	0.45	0.31	0.13	23.19
12	0.63	0.19	0.05	0.02	24.5
Average ± SD	0.61 ± 0.22	0.27 ± 0.09	0.18 ± 0.09	0.04 ± 0.04	24.80 ± 2.31

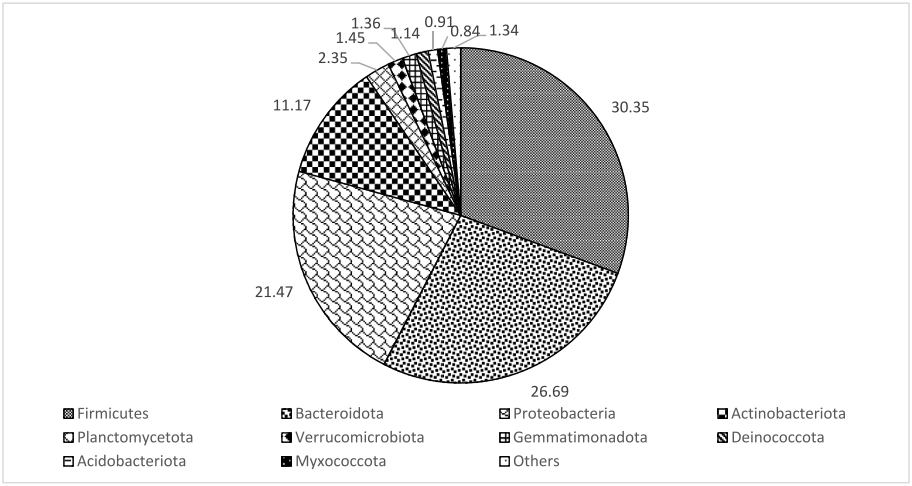

Fig. 1. Relative abundance of top 10 taxa at the phylum level classification.

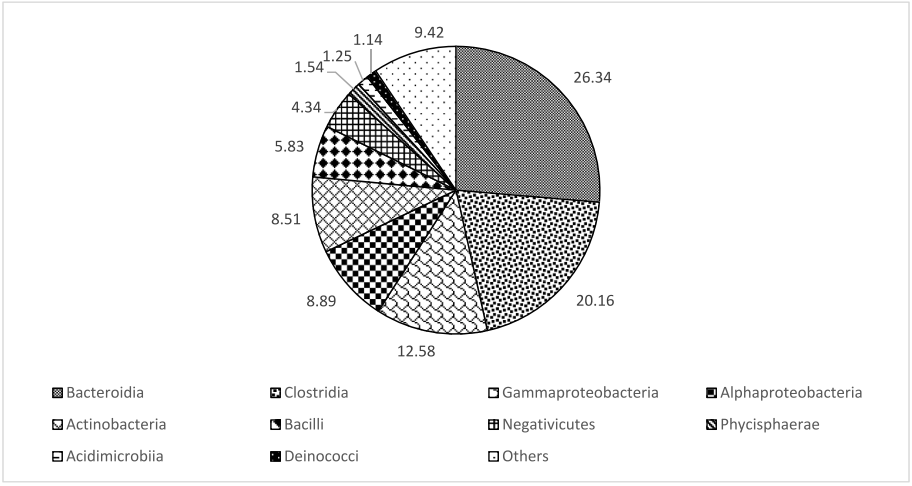

Fig. 2. Relative abundance of top 10 taxa at the class level classification.

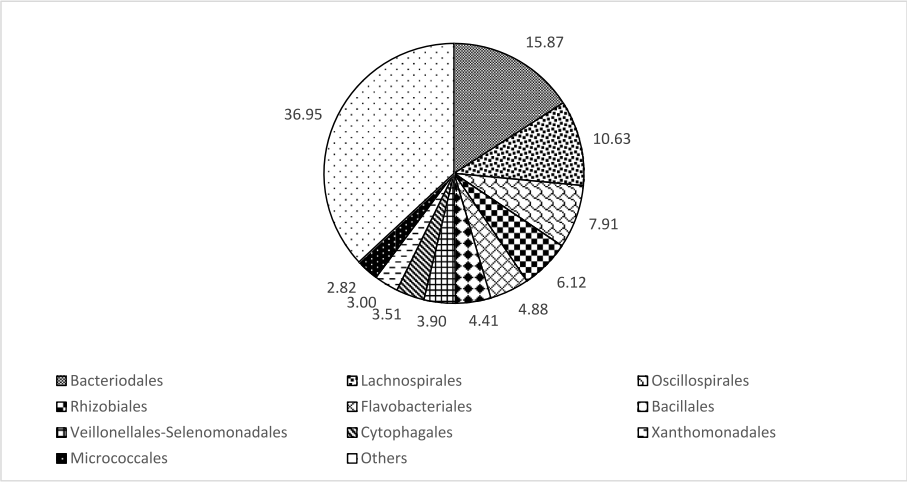

Fig. 3. Relative abundance of top 10 taxa at the order level classification.

From the twelve different samples, 179 unique genera were found with 820 OTUs. As shown in Fig. 4, 10.18% of genera were not assigned to any category. Genus *Prevotella* contributed to 9.67%, followed by the *Bacteroides* having 6.92%. *Mesorhizobium* was the next genus with 3.93% followed by *Bacillus* with 3.50%. *Faecalibacterium* made up to 3.38%, *Blautia* 2.32%, *Lysobacter* 2.19%, *Dialister* 2.18%, and UCG-002 2.17%. A total of 53.56% of the genus was detected in very low number and referred as others.

4. Discussion

In the present study, different house generated organic waste such as fruit and vegetable peels, coffee grounds, tea bags, grass clippings, woodchips, eggshells were used by Zayed University students to prepare on-campus compost using a hot aerobic method. In the presence of oxygen, aerobic microbes break down organic matter and the heat generated during this process accelerates the degradation of proteins, fats and complex carbohydrates such as cellulose and hemi-cellulose [17,18]. The produced 12 compost samples were subjected to different physicochemical experiments and to microbial identification.

4.1. Physicochemical characterization

The content in organic matter of all analysed samples was within the standard range of 25–70% reported previously by Crohn in 2016 [18], and linked to a mature compost. A good content in organic matter plays a major role in establishing and maintaining both soil structure and fertility. Total organic carbon is another important criterium to consider in studying compost. Ideal carbon to nitrogen ratio for a healthy compost should be between 25 and 30:1. Microorganisms use carbon as a source of energy and nitrogen for building cell structure. According to the Washington State University, Whatcom county extension, accessed on 12th, October 2022

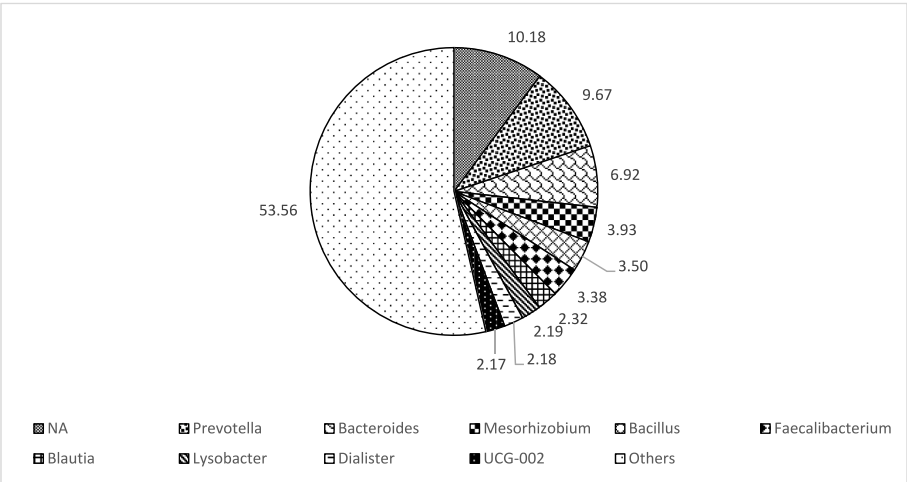

Fig. 4. Relative abundance of the top 10 taxa at the genus level classification.

[19], presence of high carbon content slows down the decomposition process. A C: N ratio of 20:1 causes no danger of robbing soil and nitrogen [20]. The carbon content values of all our samples were between 22.1 and 28.8% which is within the recommended range.

Soluble Salts (EC) are mineral ions that are naturally present in compost. In 2017, Agricultural Analytical Services Laboratory [21] set standard values for EC in compost ranging between 1 and 10 mS/cm, and all analysed samples were within this range. Salinity in this range does not affect most of the crops and soil microbial processes. EC below 1 may even be used as a planting media directly, but it requires some additional nutrients for plant growth. The pH of standard composts normally ranges between 6 and 8 and our samples were reported with pH values were within this range. The slightly basic pH of 8.5 of sample 1 may help in controlling odours because of preventing the formation of organic acid intermediate [22].

Concerning macronutrients found in compost, U.S. Composting council in 2018, has established standard ranges for these macronutrients [23]. Potassium standard range is between 0.5 and 1.5% and most of our samples were within the range. Standard range for sodium is below 0.6%. Compost containing more than 1% sodium is considered to be quite high in sodium [18]. All our samples were below 1%. Excess sodium can lead to sodicity and phytotoxicity problems. Phosphorous standard range is within 0.3–0.9% [24]. Only three samples were within the range and the majority scored low. Phosphorous encourages the development of root, improves the flower formation and seed production and strengthen the plant by making it resistant to diseases. Kjeldahl nitrogen results, with percentages ranging from 0.02 to 0.15%, were lower than the standard range of 0.5–2.5% in mature composts. Nitrogen present in compost is in its complex organic condition and it is not readily available for plants. During mineralization, microbes, naturally present in the soil, break down the complex N molecules releasing a simpler form of nitrogen easily available for plants. The low availability of nitrogen and phoshorus is strongly related to the immaturity of the compost. One of the cause of immaturity of compost could be the low content in water, an important factor for the growth of microbial decomposers. Indeed, the majority of our samples scored below 40% while the standard compost values range between 40 and 50%. Comparing the results of moisture content with phosphorous and nitrogen levels reveals that samples 5 and 11, associated with the highest levels of moisture, exhibit also the highest levels of phosphorus and nitrogen. The values for the same is depicted in Tables 1 and 2 Moisture content of compost is proportional to the frequency of watering. Even though water was added at a regular frequency during the experiments, it seems that the quantity was not sufficient to allow the optimal growth of microorganisms needed to promote the decomposition process; or compost samples which were in direct contact with the desert sand of Dubai could not retain the needed quantity of water for an optimal process [25].

Analysing the studied physicochemical properties of the compost preparations allowed to improve the composting technique on Zayed University campus and has helped other teams to reach better composting results [26,27]. All samples met the standards for the organic matter, pH and EC as well as for the carbon, sodium and potassium content. Challenges were encountered concerning water retention, phosphorus and nitrogen concentrations. The moisture content of the majority of samples was low, probably due to mixing of compost with sand [25]. Increasing the watering volume and extending the duration of the composting process to sixteen weeks in order to complete the degradation of raw materials and increase the nutrient value of compost samples is essential to meet the criteria of the typical mature compost. Phosphorous content can be increased also by enriching the compost with the rock-phosphate or by inoculating *Aspergillus awamori,* or by adding manure [28–30]. Inoculating *Azotobacter* into already decomposed material can increase nitrogen content. Besides, adding zerolite to compost increases the adsorption of ammonium ions, reduces ammonia loss and leads to a higher total nitrogen content in the final compost [17].

4.2. Microbial identification using 16S rRNA metagenomics study

The microbial diversity of the 12 compost samples was investigated since it is considered as an indicator of the quality of the soil. In this study, the phylum *Firmicutes* was the most predominant in most of the samples followed by the phylum *Bacteroidota*. These findings are similar to the ones described by authors [17,31]. Bacteria belonging to the phylum *Firmicutes* plays a role mainly in the early stages of the composting process, and degrades cellulose, hemicellulose; a major constituents of coffee grounds [32]; while the ones belonging to the phylum *Bacteroidota* interfere at the initial and final stages of composting. Both hydrolyze the complex carbohydrates and degrades organic matter through decomposition and fermentation process, and influence denitrification [17]. Also they form endospores which make them to survive on unfavourable conditions or under environmental stress [33]. *Proteobacteria* is the third most abundant phylum usually found dominant after the thermophilic phase. In general, bacteria belonging to *Proteobacteria* play an important role in the degradation of glucose, propionate, butyrate [34] and they are mainly responsible of nitrogen fixation. Concerning *Actinobacteriota,* this study has detected this phylum at an abundance of 11.17% while [35] Partanem et al., 2010 have detected that phylum at levels reaching 42%. It has been reported that more acidic soil with high carbon content favours the growth of *Actinobacteria* [36]. These bacteria have the ability to grow in mesophilic and thermophilic conditions; they produce extracellular enzymes and bioactive metabolites which play a crucial role in the degradation of proteins, complex macromolecules like chitin, lignin, cellulose and hemicellulose that releases inorganic nutrients helping in the formation of humus [37–39]. Liu et al. in 2018 [40] described that phyla Proteobacteria, Bacteriotoidetes, Firmicutes, Actinobacteria and Chloroflexi were found associated with degrading the organic carbon and nitrogen, thus play a major role in the decomposition of the raw materials. This study is among the few ones that highlight the presence of the phylum *Planctomycetota* in compost. Members of the *Planctomycetota* phylum have a significant impact on soil ecosystem and decomposition of organic matter. They grow slowly, but their number increases during the maturation stage of the composting [41]. Increased richness of the *Planctomycetes* was correlated with the spatial heterogenicity of the nitrate [42].

At the class level classification, *Bacteroidia* was found to be the most dominant class in the majority of the samples, followed by the class *Clostridia*. In our study the abundance of *Clostridia* (26%) was much higher than the one observed by Varma et al., 2018 (13.9%) [17]. Members of *Clostridia* include pathogens as well as free living anaerobic species and they play a major role in the decomposition

of cellulose [1]. *Gamma-proteobacteria* represent the third most detected class and are specifically known to degrade protein, starch and cellulose [40]. It is interesting to highlight the detection of both *Bacteroidia* and *Gamma-proteobacteria* in compost, bacteria known to have the ability to remove total petroleum hydrocarbon from soil [43]. *Alpha-proteobacteria,* the fourth most dominant class, plays a major role in nitrogen fixation, mineralization and denitrification [41].

At the order level classification, *Bacteriodales* was the most dominant order with a similar abundance level observed by Varma et al., 2018 [17], followed by *Lachnospirales* and *Oscillospirales. Lachnospiraceae* includes anaerobic, fermentative, and chemoorganotrophic organisms that can process a wide range of substrates including proteins, oligopeptides, dietary polysaccharides, endogenous mucins, and glycoproteins. *Rhizobiales,* the fourth most represented order in this study, contains nitrogen fixing, legume nodulating, micro-symbiotic bacteria [44]. The order *Bacillales* was detected at an abundance of 4.4%, a level close to the one reported in the study of Khalid et al., in 2019 [31] while a much higher level was observed by Lemos et al. in 2017 [45] reaching 72%. Members of this order are known to synthesize enzymes involved in the degradation of cellulose and hemicellulose.

At the genus level classification, *Prevotella* (9.67%) and *Bacteroides* (6.92%) were the most abundant, both belonging to the phylum *Bacteroidota. Prevotella* is one of the major fecal coliform mostly present in the thermophilic stage of the composting process [46]. *Mesorhizobium* (3.93%), a *Proteobacteria*, is the third most abundant genus followed by *Bacillus* (3.5%), a genus capable of inhibiting the soil-borne pathogen through the production of antifungal compounds and degrading pectin, a complex polysaccharide of plant cell wall. Other genera found in our samples include *Lactobacillus* known to produce organic acids that lower the pH of the compost which helps the growth of other bacteria [47].

5. Conclusion

Composting in Dubai was a challenging but successful project that generated a healthy soil in a region highly in demand. Our findings revealed that the use of the hot aerated technique is efficient in leading to valuable compost, rich in organic matter, carbon and potassium, exhibiting adequate pH and electrical conductivity and including a diverse microbial community capable of undergoing waste degradation. *Planctomyceota,* known to improve soil carbon sequestration, and *Clostridia*, key microorganisms for cellulose degradation, were detected at high levels. To improve the composting process in Dubai, it is recommended to extend the duration of the composting experiments to sixteen weeks to allow the samples to fully decompose and therefore increase the total available nitrogen and phosphorus and meet the criteria of a typical mature compost. This study revealed also that composting strongly depends on the microbial community and favouring the growth of this community by an appropriate watering process is essential. Mastering the composting technique in Dubai will not only improve the soil properties but it will also limit the use of chemical fertilizers in that part of the world and it will help in reducing the waste heading to the landfills. To achieve a sustainable future, it is important for communities to develop similar projects that involve environment-friendly skills, values, and attitudes.

Author contribution statement

Carole Ayoubmoubareck: Conceived and designed the experiments; Contributed reagents, materials, analysis tools or data; Wrote the paper.

Buthaina Alawlaqi: Performed the experiments.

Salama Alhajri: Analysed and interpreted the data.

Data availability statement

Data included in article/supplementary material/referenced in article.

Additional information

No additional information is available for this paper.

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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.

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References

[1] P. Galitskaya, L. Biktasheva, A. Saveliev, T. Grigoryeva, E. Boulygina, S. Selivanovskaya, 'Fungal and bacterial successions in the process of co-composting of organic wastes as revealed by 454 pyrosequencing', PLoS One 12 (No. 10) (2017) 1–20, https://doi.org/10.1371/journal.pone.0186051.

[2] M.A. Gladchenko, D.A. Kovalev, A.A. Kovalev, Y.V. Litti, A.N. Nozhevnikova, 'Methane production by anaerobic digestion of organic waste from vegetable processing facilities', Appl. Biochem. Microbiol. 53 (No. 2) (2017) 225–233, https://doi.org/10.1134/S0003683817020090.

[3] J. Jara-Samaniego, M.D. Pérez-Murcia, M.A. Bustamante, C. Paredes, A. Pérez-Espinosa, I. Gavilanes-Terán, 'Moral, R. Development of organic fertilizers from food market waste and urban gardening by composting in Ecuador', PLoS One 12 (No. 7) (2017) 1–17, https://doi.org/10.1371/journal.pone.0181621.

[4] R. Barrena, X. Font, X. Gabarrell, A. Sanchez, 'Home composting versus industrial composting: influence of composting system on compost quality with focus on compost stability', Waste Manag. 34 (No. 7) (2014) 1109–1116, https://doi.org/10.1016/j.wasman.2014.02.008.

[5] R. Quiros, G. Villalba, P. Munoz, J. Colon, X. Font, X. Gabarrell, 'Environmental assessment of two home composts with high and low gaseous emissions of the composting process', Resour. Conserv. Recycl. 90 (2014) 9–20.

[6] A.C. Oluchukwu, A.G. Nebechukwu, S.O. Egbuna, 'Enrichment of nutritional contents of sawdust by composting with other nitrogen rich argo-wastes for bio-fertilizer synthesis', J. Chem. Technol Metall 53 (No. 3) (2018) 430–436.

[7] V. Stan, A. Virsta, E.M. Dusa, A.M. Glavan, 'Waste recycling and compost benefits', Not. Bot. Horti Agrobot. Cluj-Napoca 37 (No.2) (2009) 9–13, https://doi.org/10.15835/nbha3723461.

[8] A. Footer, 'Bokashi Composting Scraps to Soil in Weeks', New society publishers, Canada, 2013.

[9] R. Hareen, 'Large Scale Aerobic Composting of Source –Separated Organic Wastes: A Comparative Study of Environmental Impacts, Costs and Contextual Effects', MS Thesis, Columbia University, USA, 2009.

[10] K. Baumann, M.F. Dignac, C. Rumpel, G. Bardoux, A. Sarr, M. Steffens, P.A. Maron, 'Soil microbial diversity affects soil organic matter decomposition in a silty grassland soil', Biogeochemistry 114 (1–3) (2012) 1–12, https://doi.org/10.1007/s10533-012-9800-6.

[11] P. Golinska, H. Dahm, 'Occurrence of actinomycetes in forest soil', Dendrobiology 66 (1) (2011) 3–13. https://bibliotekanauki.pl/articles/41633.

[12] K.P. Williams, J.J. Gillespie, B.W.S. Sobral, E.K. Nordberg, E.E. Snyder, J.M. Shallom, 'Dickerman, A.W. Phylogeny of gamma-proteobacteria', J. Bacteriol. 192 (9) (2010) 2305–2314, https://doi.org/10.1128/JB.01480-09.

[13] G.A. Kowalchuk, S.Z. Naoumenko, P.L. Derikx, A. Felske, J.R. Stephen, I.A. Arkhipchenko, Molecular analysis of ammonia-oxidizing bacteria of the beta subdivision of the class *proteobacteria* in compost and composted materials, Appl. Environ. Microbiol. 65 (2) (1999) 396–403, https://doi.org/10.1128/AEM.65.2.396-403.1999.

[14] D.M. Sullivan, A.I. Bary, R.O. Miller, L.J. Brewer, Interpreting compost analyses, Oregon State University (2018), EM9217.

[15] T. Tadesse, I. Haque, E.A. Aduayi, 'WORKING DOCUMENT: soil, plant, water, fertilizer, animal manure & compost analysis manual', plant science division working document No.13, ILCA, Ethiopia, Addis Ababa, 1991, https://cgspace.cgiar.org/handle/10568/4448.

[16] H. Khatoon, P. Solanki, M. Narayan, L. Tewari, J.P.N. Rai, 'Role of microbes in organic carbon decomposition and maintenance of soil ecosystem', Int. J. Chem. Stud. 5 (6) (2017) 1648–1656. https://www.chemijournal.com/archives/?year=2017&vol=5&issue=6&ArticleId=1509.

[17] V.S. Varma, K. Dhamodharan, A.S. Kalamdhad, 'Characterization of bacterial community structure during in-vessel composting of agricultural waste by 16S rRNA sequencing', 3 Biotech 8 (301) (2018) https://doi.org/10.1007/s13205-018-1319-7.

[18] D.M. Crohn, 'Assessing compost quality for agriculture', ANR Publication (2016), 8514.

[19] Washington state university, Whatcom county extenstion, Compost fundamentals, Compost needs http://whatcom.wsu.edu/ag/compost/fundamentals/needs_carbon_nitrogen.htm (Accessed on 12 October, 2022) .

[20] L. Antunes, L. Martins, R. Pereira, et al., 'Microbial community structure and dynamics in thermophilic composting viewed through metagenomics and meta transcriptomics', Sci. Rep. 6 (38915) (2016) https://doi.org/10.1038/srep38915.

[21] Agricultural Analytical Services Laboratory. Compost Analysis Report. http://www.ucrra.org/wp-content/uploads/2017/08/June-2017-Compost-Test-Results.pdf. (Accessed April 15, 2020).

[22] N. Soobhany, Assessing the physicochemical properties and quality parameters during composting of different organic constituents of municipal solid waste, J. Environ. Chem. Eng. 6 (2) (2018) 1979–1988, https://doi.org/10.1016/j.jece.2018.02.049.

[23] U.S. Composting Council. Composting testing programs. https://compostingcouncil.org/programs/(Accessed May 6, 2018).

[24] E. Bazrafshan, A. Zarei, F.K. Mostafapour, N. Poormollae, S. Mahmoodi, M.A. Zazouli, 'Maturity and stability evaluation of composted municipal solid wastes', Health Scope 5 (1) (2016), e33202 https://doi.org/10.17795/jhealthscope-33202.

[25] S. Dolit, U. Asli, A. Khamis, N. Baharulrazi, N. Azman, N. Yunus, Improving the water retention characteristics of sandy soil using food waste compost amendment and indigenous microorganisms, Chem. Eng. Trans. 97 (2022) 211–216, https://doi.org/10.3303/CET2297036.

[26] A. Sahu, M.C. Manna, S. Bhattacharjya, M.M. Rahman, A. Mandal, J.K. Thakur, K. sahu, V.K. Bhargav, U.B. singh, K.P. sahu, A.K. Patra, S.K. Chaudhari, S. S. Khanna, Thermophilic ligno-cellulolytic fungi: the future of efficient and rapid bio-waste management, J. Environ. Manage 244 (2019) 144–153, https://doi.org/10.1016/j.jenvman.2019.04.015.

[27] A. Ditta, J. Muhammad, M. Imtiaz, S. Mehmood, Z. Qian, S. Tu, 'Application of rock phosphate enriched composts increases nodulation, growth and yield of chickpea', Int. J. Recycl. Org. Waste Agric. 7 (2018) 33–40, https://doi.org/10.1007/s40093-017-0187-1.

[28] K.K. Kapoor, K.S. Yadav, D.P. Singh, M.M. Mishra, P. Tauro, 'Enrichment of compost by *Azotobacter* and phosphate solubilizing microorganisms', Agric. Wastes 5 (3) (1983) 125–133.

[29] Y. Wei, Y. Zhao, B. Xi, Z. Wei, X. Li, Z. Cao, 'Changes in phosphorous fractions during organic wastes composting from different sources', Bioresour. Technol. 189 (2015) 349–356, https://doi.org/10.1016/j.biortech.2015.04.031.

[30] M.T. Chan, A. Selvam, J.W.C. Wong, 'Reducing nitrogen loss and salinity during struvite food waste composting by zerolite amendment', Bioresour. Technol. 200 (2016) 838–844, https://doi.org/10.1016/j.biortech.2015.10.093.

[31] N.A. Khalid, H. Rajandas, S. Parimannan, L.J. Croft, S. Loke, C.S. Chong, N.C. Bruce, A. Yahya, 'Insights into microbial community structure and diversity in oil palm waste compost', 3Biotech 9 (364) (2019) https://doi.org/10.1007/s13205-019-1892-4.

[32] J. Niu, X. Li, 'Effects of microbial inoculation with different indigenous Bacillus species on physicochemical characteristics and bacterial succession during short-Term composting', Fermentation 8 (152) (2022). https://www.mdpi.com/2311-5637/8/4/152.

[33] Q. Meng, W. Yang, M. Men, A. Bello, X. Xu, B. Xu, L. Deng, X. Jiang, S. Sheng, X. Wu, Y. Han, H. Zhu, 'Microbial community succession and response to environmental variables during Cow manure and corn straw composting' *front*, Microbiol. 10 (529) (2019), https://doi.org/10.3389/fmicb.2019.00529.

[34] M. Ventura, C. Canchaya, A. Tauch, G. Chandra, G.F. Fitzgerald, K.F. Chater, D. Van Sinderen, 'Genomics of Actinobacteria: tracing the evolutionary history of an ancient phylum', Microbiol. Mol. Biol. Rev. 71 (No. 3) (2007) 495–548, https://doi.org/10.1128/MMBR.00005-07.

[35] P. Partanen, J. Hultman, L. Paulin, P. Auvinen, M. Romantschuk, 'Bacterial diversity at different stages of the composting process', BMC Microbiol. 10 (94) (2010) https://doi.org/10.1186/1471-2180-10-94.

[36] K. Simek, V. Kasalicky, J. Jezbera, J. Jezberová, J. Hejzlar, M.W. Hahn, Broad habitat range of the phylogenetically narrow R-BT065 cluster, representing a core group of the *Betaproteobac*terial genus Limnohabitans, Appl. Environ. Microbiol. 76 (3) (2010) 631–639, https://doi.org/10.1128/AEM.02203-09.

[37] K. Gondek, M. Kopec, M. Mierzwa, M. Tabak, M. Chmiel, 'Chemical and biological properties of composts produced from organic waste', J. Elem. 19 (2) (2014) 377–390, https://doi.org/10.5601/jelem.2014.19.2.670.

[38] M.S. Gandhi, C. Udayasooriyan, Physico-chemical and biological dynamics of waterhyacinth biocompost: a compost maturity assessment scenario, J. Pure Appl. Microbiol. 8 (40) (2014) 2935–2944.

[39] J. Barta, K. Tahovska, H. Santruckova, F. Oulehle, 'Microbial communities with distinct denitrification potential in spruce and beech soils differing in nitrate leaching', Sci. Rep. 7 (9738) (2017) https://doi.org/10.1038/s41598-017-08554-1.

[40] L. Liu, S. Wang, X. Guo, T. Zhao, B. Zhang, 'Succession and diversity of microorganisms and their association with physicochemical properties during green waste thermophilic composting', Waste Manage. (Tucson, Ariz.) 73 (2018) 101–112, https://doi.org/10.1016/j.wasman.2017.12.026.

[41] M.N. Londhe, S.K. Sethy, S.K. Shettigar, S.B. Ghosh, 'Metagenomics and Physico-chemical analysis of the active mesophilic and mature phases of a fast composting system', Curr. Sci. 117 (11) (2019) 1842–1854, https://doi.org/10.18520/cs/v117/i11/1842-1854.
[42] D.H. Buckley, V. Huangyutitham, T.A. Nelson, A. Rumberger, J.E. Thies, 'Diversity of *Planctomycetes* in soil in relation to soil history and environmental heterogeneity', Appl. Environ. Microbiol. 72 (7) (2006) 4522–4531, https://doi.org/10.1128/aem.00149-06.
[43] J.A. Siles, R. Margesin, 'Insights into microbial communities mediating the bioremediation of hydrocarbon-contaminated soil from an Alpine former military site', Appl. Microbiol. Biotechnol. 102 (2018) 4409–4421, https://doi.org/10.1007/s00253-018-8932-6.
[44] L. Blomstrom, A1w, A.J. Komakech, S. Boqvist, A metagenomic analysis displays the diverse microbial community of a vermicomposting system in Uganda, Infect. Ecol. Epidemiol. 6 (32453) (2016), https://doi.org/10.3402/iee.v6.32453.
[45] L.N. Lemos, R.V. Pereira, R.B. Quaggio, L.F. Martins, L.M.S. Moura, A.R. da Silva, L.P. Antunes, A.M. da Silva, J.C. Setubal, 'Genome-centric analysis of a thermophilic and cellulolytic bacterial consortium derived from composting', Front. Microbiol. 8 (2017) 644, https://doi.org/10.3389/fmicb.2017.00644.
[46] Y.M. Piceno, G. Pecora-Black, S. Kramer, M. Roy, F.C. Reid, E.A. Dubinsky, G.L. Andersen, 'Bacterial community structure transformed after thermophilically composting human waste in Haiti', PLoS One 12 (No. 6) (2017), e0177626 https://doi.org/10.1371/journal.pone.0177626.
[47] C. Sundberg, I.H. Franke-Whittle, S. Kauppi, D. Yu, M. Romantschuk, H. Insam, H. Jönsson, 'Characterisation of source-separated household waste intended for composting', Bioresour. Technol. 102 (2011) 2859–2867, https://doi.org/10.1016/j.biortech.2010.10.075.