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Research Article

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Comparative Assessment of Microbial Community in Compost Samples

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ABSTRACT

Soil, composed of inorganic and organic materials, supports diverse microbial communities, including bacteria, fungi, and yeasts, which play essential roles in compost formation. Composting is a controlled biodegradation process that converts organic waste into a nutrient-rich soil conditioner. This study aimed to compare the microbial diversity and density in two compost samples (S1 and S2) prepared on campus. Sample S1 consisted of poultry waste, vegetable waste, and fruit waste, whereas Sample S2 was composed of vegetable waste and cow dung. Microbial isolation was performed using serial dilution, spread plate, and streak plate techniques. A total of 23 microbial isolates were obtained, including 12 bacterial, 6 fungal, and 5 yeast isolates. Bacterial density was significantly higher in S1 compared to S2, suggesting a potential influence of compost composition on microbial proliferation. Identified bacterial genera included *Aeromonas*, *Staphylococcus aureus, Pseudomonas, Edwardsiella, Salmonella, Klebsiella, Shigella,* and *Streptococcus sp*. Fungal isolates comprised *Rhizopus sp., Aspergillus sp., Fusarium sp*., and *Helminthosporium sp.,* while *yeast* genera included *Saccharomyces, Candida,* and *Cryptococcus*. The comparative analysis highlights the impact of compost composition on microbial diversity and suggests that poultry and fruit waste may enhance bacterial density more than cow dung-based compost. These findings provide insights into microbial contributions to compost stability and potential applications in soil conditioning and nutrient solubilization.

Keywords: Microbial Isolation, Compost, Diversity

INTRODUCTION:

The earth's surface is covered by soil, which is made up of layers of materials with different levels of organization made up of both inorganic and organic substances. It is a natural medium in which microbes live and multiply. Sustainable agriculture depends on the soil's microbial communities and populations remaining healthy, diverse, and viable. Algae, bacteria, fungus, protists, and viruses are the five main taxonomic categories used to classify microorganisms. They are tightly linked to soil constituents, primarily clay-organic matter complexes (Giri *et al*., 2005). By decomposing organic matter, recycling nutrients, and exercising biological control, microbial composition and function impact the quality of the soil. Bacteria and fungus in the soil play important roles in promoting soil fertility and the health of plants (Kirk*et al*., 2004).

Fungi are important for soil ecosystem functioning. The soil microbiota includes fungi, which are significant. Because they control the biological activity of the soil, micro fungi are essential to the cycling of nutrients. Both organic and inorganic components in the soil directly influences its microbial population (Gaddeyya *et al*., 2012). Soil is an oligotrophic medium for the growth of fungi. Fungi also employs antagonism to lessen competition by creating antibodies that prevent the growth of other microbes. Numerous vitamins that they manufacture aid in the growth of plants. To protect, the host plants, beneficial fungi create nets and webs around the roots and leaves.Additionally, fungi shield plants from harm by delivering water and phosphate to the plant roots during dry spells (Raja *et al*., 2017). The presence of fungi changes with depth *Rhizopus* and *Aspergillus* are typically found on the top layer of soil, while *Penicillium* and *Alternaria* are found in the deep soil. Fungi are also used as biological pesticides to control weeds, plant diseases and insect pests (Saini *et al*., 2016).

Yeasts are single-celled microorganisms that are categorized as belonging to the Kingdom Fungi. In contrast to their single-celled relatives, bacteria, which lack a nucleus and are categorized as prokaryotes, they are categorized as eukaryotic organisms. Yeast inhabits a range of habitats and is extensively distributed in nature. They are frequently discovered in soil, as well as on the leaves, flowers, and fruits of plants. Yeast is also present on the skin's surface and in warm-blooded animals' intestinal tracts, where they may coexist harmoniously or as parasites. *Candida albicans* often causes the widespread "yeast

infection." Despite infections, yeast has many commercial applications. For the creation of alcoholic beverages, bread, and a wide range of industrial items, yeast has long been regarded as the ideal organism. The petrochemical sector uses yeasts, which have been modified to make biofuels including ethanol, diesel, and jet fuel precursor. They are also employed in the creation of detergents, lubricants, and enzymes. Yeast cells can also be used to create flavour enhancers, colorants, and antioxidants for use in food. In addition, it is utilised to make biomedicines like insulin, vaccines, and nutraceuticals as well as pharmaceuticals like antiparasitic, anticancer substances, and nutraceuticals. The rapid replication and ease of genetic manipulation of yeasts, which are employed as model organisms, are key characteristics as well. For yeast, the time it takes to double is roughly 90 minutes (Thapa *et al*., 2015).

The secret to recycling carbon and nitrogen is soil microbes. Bacteria typically range innumber from 100 million to one billion per teaspoon of productive soil. Per acre, a ton of microscopic bacteria may be active, and there may be more than a million different bacterial species. Bacteria are incredibly small, one-celled animals that range in size from 0.2 to 2 micrometers in width and 1 to 10 micrometers in length. In terms of size, bacteria are comparable to silt soil particles (2-50 m) and clay soil particles (2 m). They develop and dwell in a region known as rhizosphere, which is a thin aqueous film that surrounds soil particles and is close to roots. Compared to larger, complex organisms, bacteria can develop and adapt to changing environmental conditions more quickly because of their small size. In the soil, bacteria carry out important functions by breaking down organic wastes produced by enzymes secreted there. Several bacteria decomposers can break down pesticides and pollutants in soil (J. Hoorman 2011).

Composting is a method that can be used to produce soil conditioners and fertilizers while reducing the quantity of organic waste that is generated. Because compost has a high organic content (90–95%) but often low amounts of nitrogen, phosphorous, and potassium as well as macro- and micronutrients compared to commercial fertilizers, it is largely utilised as a soil conditioner rather than a fertilizer. Additionally, if done properly, the composting process turns foul-smelling, moist organic waste into a decomposed, appealing, and reusable product. Along with numerous off-farm leftovers and wastes, co-compost cover materials can include crop residues, unused bedding materials, silage, manures, and similar on-farm items. During compost production, quality control should be used to guarantee that the material has the required chemical and physical characteristics, as well as stability and maturity levels (Sayed & Khater, 2015). When added to the soil, the degraded materials and mobile nutrients in compost can be utilised to enrich the soil, increase its fertility, improve its structure, and modify some of its physical properties, which can change the quality of the goods produced. Compost is made up of all the minerals that are not volatile or that have not been in any manner absorbed or exported during the composting process. The ratios of these components match those of the raw materials utilised in the process. The composts could occasionally contain heavy metals and other toxic compounds in amounts that could cause subsequent soil pollution (Mladenov 2018). The process of composting involves the controlled breakdown of organic material to produce stabilized, sanitized organic material that can be utilised as a soil conditioner in farming. There are many ways to compost, from small, homemade reactors used byindividual families to relatively basic, on-site reactors used by farmers to huge, simple to complicated reactors used by professional composters to which the biowaste must becarried (Termorshuizen *et al*., 2004).

Traditional applications of composted materials to agricultural and horticultural soils have improved soil fertility and crop growth, primarily through strengthening the physical and chemical characteristics of the soil. The biological features of the soil are also improved by these organic additions, which frequently effectively manage diseases that are transmitted through the soil. The potential of compost to control soil-borne plant diseases has gained interest as a method of minimizing the unfavorable environmental effects of extensive fungicide use. Many theories have been put up to explain how compost can manage plant diseases, including competition, hyper parasitism, activation of disease-resistance genes, or the manufacture of antibiotics by helpful bacteria (Cuesta *et al*., 2012). The primary objective of this study was to compare the microbial diversity and density in two different compost samples, sample S1 (poultry, vegetables and fruits) and sample S2 (vegetable and cow remains). This research focuses on to analyze the influence of compost composition on bacterial, fungal, and yeast population to understand the role of microbial diversity in improving soil fertility and nutrient solubilization. This research was conducted to determine variations in dominant microbial genera between the compost samples.

This research expands the knowledge on the microbial diversity of compost derived from different organic waste. By characterizing bacterial, fungal and yeast populations, it provides information on how specific microbial communities differ based on the type of organic materials used, such as poultry waste versus cow dung. This brings valuable data in the field of soil microbiology and sustainable agriculture, where the quality of the compost is crucial. Through isolation and detailed identification, the study identifies beneficial microbial strains (e.g., *Pseudomonas, Rhizopus,* and *Saccharomyces*) that support nutrient cycling, organic matter

decomposition, and plant growth. These results provide potential candidates for the development of biofertilizers and soil amendments, which promote soil health and sustainability in agriculture. By analyzing the microbial density and diversity affected by different compost materials, the research plays an important role in optimizing compost formulations for specific agricultural applications. This results in improvements in composting mixtures aimed at soil conditioning, reducing reliance on chemical fertilizers, and contributing to environmentally friendly agricultural practices. Unlike most studies that focus on the microbial diversity of compost in general, this research provides a comparative analysis of microbial communities in two specific types of compost: one derived from poultry, vegetable and fruit waste, and the other from cow manure and plant residues. This distinction highlights how different organic materials affect microbial composition, providing valuable information about the suitability of compost for optimal soil health.

While bacterial communities in compost are often well documented, this study involved a targeted characterization of fungal and yeast populations. The specific identified genera of fungi *(Rhizopus, Aspergillus)* and yeasts *(Saccharomyces, Cryptococcus)* adds new insights about the role of these organisms in compost, such as nutrient recycling and organic matter decomposition, which have critical implications for soil fertility and plant growth. By comparing the microbial density of nitrogen-rich poultry compost with carbon-rich cow manure, the research provides information about how different nutrient sources affect microbial density and diversity. These results can guide the selection of compost materials to support specific microbial communities that improve soil conditioning, thus contributing to more effective and sustainable composting practices.

MATERIALS AND METHODS

Sample Collection: To evaluate the microbial diversity two compost samples S1 and S2 were analyzed. These compost samples were prepared at AIOU, Islamabad. S1 was composed of vegetable waste, poultry waste, and fruit waste whereas, the S2 was made up of vegetable waste and Cow dung.

Sample Processing

Each compost sample was serially diluted up to dilution factor 10^{-4}. A total number of 8 dilutions were prepared from 2 compost samples. Compost samples were serially diluted by making suspension of compost in eppendorf by adding 1000 microliter of distilled water and a pinch of S1 and S2 sample in separate eppendorf and mixed by vortex.

Isolation and Identification of Bacteria: Bacterial isolation was carried out by spread plate method, 10 microliters of 10^{-2} and 10^{-3} dilution factors was used for S1 and S2, respectively ("Spread plate method of the bacterial cells", 2023). These plates were then incubated at 37°C for 24-48 hours, allowing the growth of distinct bacterial colonies. Bacterial density was quantified by calculating colony forming units ("Microbial techniques and methods: basic techniques and microscopy", 2022). Colonies with distinctive morphology were classified based on their morphological characteristics. Colony morphology was done on the basis of shape, colour, texture, size, elevation and edge of the colony (Patra *et al*., 2020). An identity number was assigned to each bacterial colony, and each colony was then streaked over solidified nutrient agar to get pure culture (Fröhlich & König, 2006). Gram staining was initially used to distinguish gram-negative and gram-positive bacteria after purification, followed by microscopic examination at 100X to observe the cellular arrangement and shape (cocci or rods) (Patra *et al*., 2020). Selective and differential media include MacConkey agar and blood agar were used for further characterization. To identify the bacterial isolates biochemically, several tests were conducted. Biochemical tests carried out for identification included catalase test, coagulase test, indole test, triple sugar iron test (TSI), citrate utilization test, motility test (Chamberlain, 2009; Vashist *et al*., 2013; Chauhan & Jindal, 2020; Shoaib *et al*., 2020). Hemolysis pattern was studied on blood agar.

Isolation and Identification of Fungi: Fungal isolation was carried out by inoculating 10µl of 10^{-3} dilution sample suspension (S1 and S2) on Potato Dextrose Agar (Witfeld *et al*., 2021; Temporiti *et al*., 2022). The plates were incubated at 25°C to 28°C for three to seven days. Plates were observed under stereo microscope to assess morphology of developing colonies. Fungal colonies were purified on Potato dextrose agar, followed by lacto-phenol staining (Istifadah *et al*., 2021). The identification of fungi was done by macroscopic and microscopic identification. Macroscopically, the colour and texture of the colony were evaluated at 4X magnification by using stereo microscope. The morphological characteristics evaluated included colony growth (length and width), presence or absence of aerial mycelium, colony colour, presence of wrinkles and furrows, pigment production (Istifadah *et al*., 2021). Microscopically, the conidia, conidiophores, and spore arrangement was examined using a compound microscope after being stained with lacto-phenol cotton blue (Nariyampet *et al*., 2022).

Isolation and Identification of Yeasts: For isolation of Yeast, 10µl from dilution 10^{-3} were spread on Potato Dextrose Agar, and incubated at 25℃ for 72 hours in an aerobic environment. Colonies that appeared on plates were recorded and were analyzed for their morphology based on colony colour, size, and microbiological examination under a compound microscope in an oil immersion lens. For microscopic examination of isolates, lacto-phenol cotton blue staining was used. In addition, catalase test, sucrose utilization test, lactose fermentation test was done. (Oda & Mohammed., 2024).

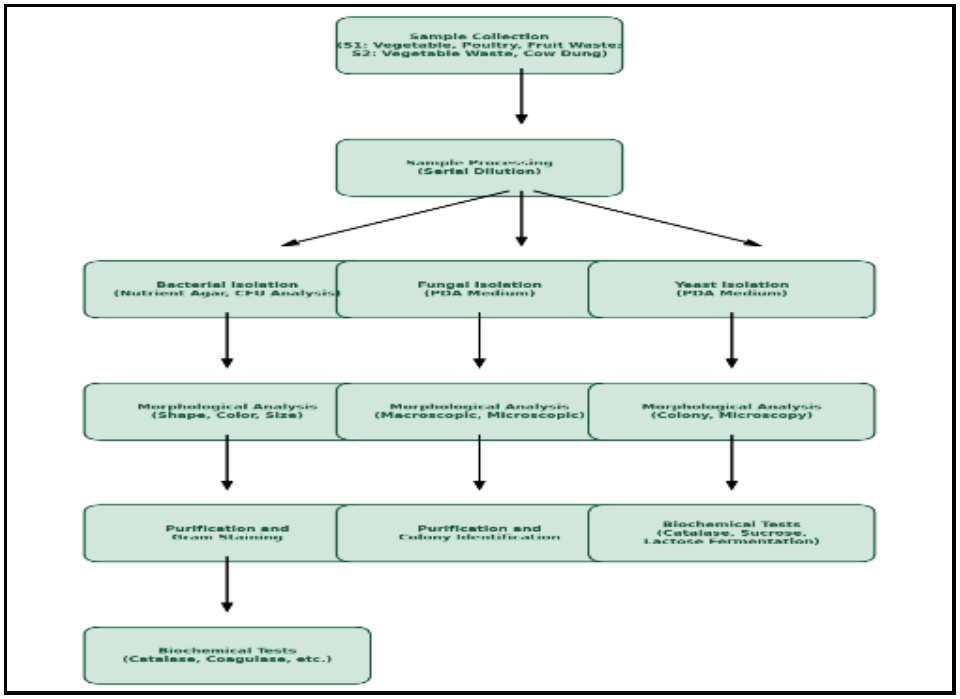

Figure 1. Research methodology for the isolation and identification of Bacteria, Fungi and Yeasts Isolates.

RESULTS

Bacterial Isolation and Identification: A total of twelve distinct bacterial colonies were isolated from the two compost samples, Sample 1 (S1) and Sample 2 (S2). S1, consisting of poultry waste, vegetable waste, and fruit waste, yielded eight distinct bacterial colonies, while S2, containing vegetable waste and cow dung, produced four distinct bacterial colonies.

Colony Forming Unit (CFU) Calculation: The bacterial density was quantified by calculating the colony-forming units (CFU) per milliliter of the compost sample. The CFU for S1 was 2.64×10^3 CFU/mL, while S2 had 1.86×10^3 CFU/mL, indicating that S1 had a higher bacterial density compared to S2, as shown in figure 2.

Colony Morphology: In S1, the colonies exhibited diverse morphologies: Colonies C1 large, yellowish, opaque and circular, C2 appeared circular, medium-sized, glistening, and moist with different elevations; C3 and C5 were medium size, creamy white with entire margins, C4, C6 and C7 were large, mucoid, raised, C8 medium, convex colonies. In S2, C9 appeared as small, circular, slightly raised, moist, C10 was large, convex with irregular margins, C11 was yellowish medium size, and C12 appeared as pinpoint, small moist colonies.as shown in figure 3.

Selective and differential media were used for further characterization and different biochemical tests were done. Blood agar was used to assess hemolysis pattern of selected colonies as shown in figure 4 and 5.

Gram Staining and Microscopic Examination: The results from Gram staining revealed that the bacterial isolates from both samples included both gram-positive and gram-negative organisms. In Sample 1, seven colonies were gram-negative rods, while one colony (C1) was gram-positive cocci. In Sample 2, two isolates were gram-negative rods, and two were gram-positive cocci, both staphylococci and streptococci under the microscope.

Biochemical Test Results: The biochemical tests provided valuable insights into the identity and characteristics of the bacterial isolates. In the catalase test, ten isolates (eight from S1 and two from S2) were catalase-positive, producing bubbles upon the addition of hydrogen peroxide, indicating the presence of catalase enzymes, while two isolates were catalase-negative. The coagulase test identified two isolates (one from each sample) as coagulase-positive, suggesting the presence of *Staphylococcus aureus*, which is known to coagulate plasma; the remaining isolates were coagulase-negative. The oxidase test showed that only one isolate was oxidase-positive, developing a dark purple colour, while eleven isolates were oxidase-negative. Among nine gram-negative bacterial isolates, three were positive for indole test upon addition of Kovac's reagent and six were for indole production. In the Triple Sugar Iron (TSI) test, eight out of nine gram-negative isolates were positive for sugar fermentation, while one isolate showed no reaction. The citrate utilization test revealed that five of the gram-negative isolates were citrate-positive, as indicated by a colour change to blue, whereas three isolates were citrate-negative. Lastly, the motility test showed that five of the gram-negative isolates were motile, displaying diffuse growth from the stab line, while four were non-motile shown in table 1 and 2.

Identified Bacterial Genera: Based on the

morphological, gram staining, and biochemical test results, the bacterial genera were identified. The gram-positive cocci isolate from Sample 1 was identified as *Staphylococcus aureus*, and the gram-negative rods included *Salmonella*, *Klebsiella*, *Aeromonas* and *Shigella*. In Sample 2, isolates were identified as *S. aureus*, *Streptococcus*, *Pseudomonas* and *Edwardsiella*, as shown in table 3.

Figure 2. Bacterial isolation from compost using spread plate method

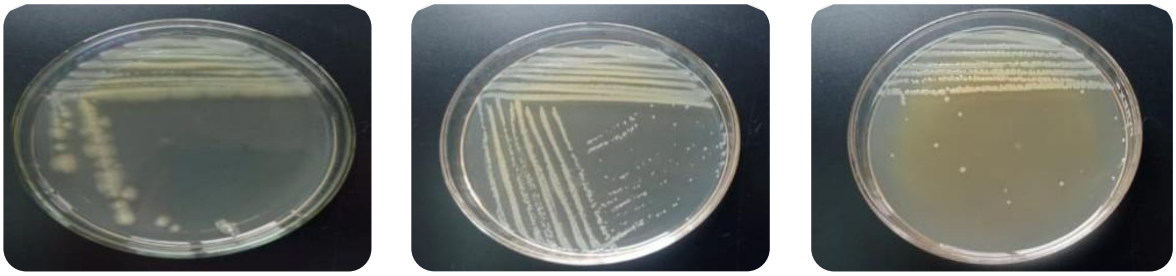

Figure 3: Pure bacterial culture by streak plate method.

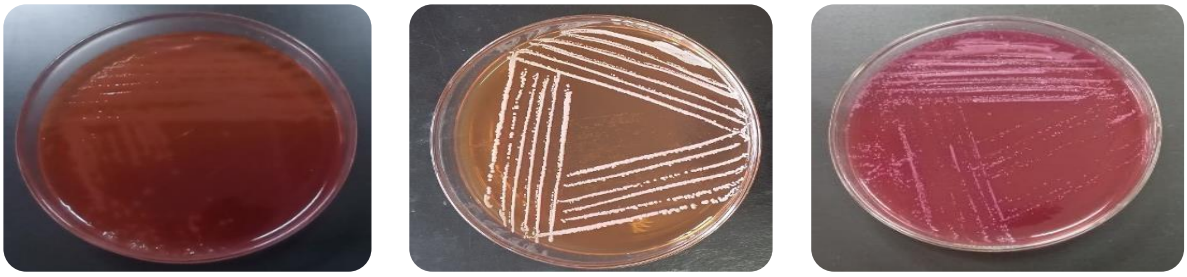

Figure 4: Representative isolated colonies on MacConkey agar.

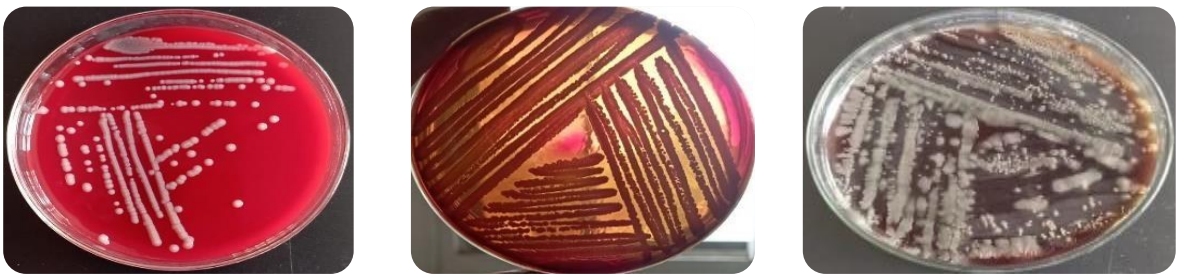

Figure 5: Hemolysis pattern on blood agar.

Table 1. Gram staining and biochemical tests results of gram-negative bacteria.

Sample no.	Colonies identified	Gram staining	Catalase	Oxidase test	Indole test	TSI	Citrate Utilization	Motility test	Haemolytic patterns
S1	C2. S1	Gram negative, rods	Positive	Positive	Positive	K/ A	Positive	Motile	*β*-hemolysis
	C3. S1	Gram negative, rods	Positive	Negative	Negative	K / A	Negative	Motile	*β*-hemolysis
	C4. S1	Gram negative, rods	Positive	Negative	Negative	A / A	Positive	Non-motile	*γ*-hemolysis
	C5. S1	Gram negative, rods	Positive	Negative	Negative	K / A	Positive	Motile	*β*-hemolysis
	C6. S1	Gram negative, rods	Positive	Negative	Negative	A / A	Positive	Non-motile	*γ*-hemolysis

	C7. S1	Gram negative, rods	Positive	Negative	Negative	A / A	Positive	Non-motile	*γ*-hemolysis
	C8. S1	Gram negative, rods	Positive	Negative	Positive	A / NC	Negative	Non-motile	*γ*-hemolysis
S2	C9. S2	Gram negative, rods	Negative	Negative	Positive	K / A	Negative	Motile	*B*-hemolysis
	C10. S2	Gram negative rods	Positive	Negative	Negative	Negative	Negative	Motile	*B*-hemolysis

Table 2. Gram staining and biochemical tests results of gram-positive bacteria.

Sample no.	Colonies identified	Gram staining	Morphology	Catalase test	Coagulase test	Haemolytic patterns
S1	C1. S1	Gram positive cocci	Clusters	Positive	Positive	*B*-hemolysis
S2	C11. S2	Gram positive cocci	Clusters	Positive	Positive	*B*-hemolysis
	C12. S2	Gram positive cocci	Chain	Negative	Negative	*B*-hemolysis

Table 3: Identified bacterial genera.

Sr. No	Sample	Isolate number	Identified Genera
1.	S1	C1. S1	*S. aureus*
2.		C2. S1	*Aeromonas*
3.		C3. S1	*Salmonella*
4.		C4. S1	*Klebsiella*
5.		C5. S1	*Salmonella*
6.		C6. S1	*Klebsiella*
7.		C7. S1	*Klebsiella*
8.		C8. S1	*Shigella*
9.	S2	C9. S2	*Edwardsiella*
10.		C10. S2	*Psuedomonas*
11.		C11. S2	*S. aureus*
12.		C12. S2	*Streptococci*

Fungal Isolation and Identification: Four different fungal genera were isolated from both compost samples. From S1, 4 isolations were made whereas S2 yielded 2 fungal isolates.

Macroscopic Identification of Fungi: The fungal isolates exhibited distinctive colony morphologies on Potato Dextrose Agar. In S1, fungal isolates displayed macroscopic features such as cottony white mycelium, velvety surfaces, and wrinkled or powdery textures. Similarly, S2 fungal isolates showed velvety, raised colonies with black or greenish pigmentation, common features in fungal species as shown in table 4.

Table 4: Macroscopic identification of fungi.

Sample	Isolate number	Colour	Shape	Appearance	Identified Genera
S1	F1. S1	Greyish	Flat and compact		*Rhizopus sp.*
	F2. S1	Black	Circular, raised, dry and powdery		*Aspergillus sp.*
	F3. S1	Light brown	Irregular, dry and powdery		*Fusarium. sp.*

	F4. S1	White	Loose and fluffy		*Rhizopus. Sp*
S2	F5. S2	Olive- green	Irregular, dry, and fluffy		*Helminthosporium. Sp*
	F6. S2	Mild green	Circular, loose and dry		*Aspergillus sp.*

Microscopic Identification of Fungi: Using Lactophenol Cotton Blue (LPCB) staining, fungal structures were observed under a microscope at 40X magnification, revealing hyphae, sporangia, conidia, and other reproductive structures that facilitated the identification of fungal genera. In S1, the identified fungal genera included *Rhizopus sp.*, *Aspergillus sp.*, and *Fusarium sp.*; *Rhizopus* displayed characteristic sporangia, while *Aspergillus* showed conidial heads with chains of spores. In Sample 2, the fungal isolates were identified as *Helminthosporium sp.* and *Aspergillus sp.*, both exhibiting distinct reproductive structures under the microscope.

Yeast Isolation and Identification: Five yeast colonies were isolated from the two compost samples, 02 from S1 and 03 from S2. Yeast Y1 and Y2 were opaque with large rough or mucoid textures, while colonies Y3 and Y4 were translucent, creamy, with glistening and textures. Colony Y5 showed a small slimy appearance as shown in table 5.

Table 5. Colony morphology and CFU of Yeast isolates.

Sample	Colony number	Colour	Texture	Appearance	Colony forming unit
S1	Y1. S1	Opaque	Buttery	Large, rough, irregular	$1.26x10^3$
	Y2. S1	Opaque	Mucoid	Medium, dull, circular	$1.26x10^3$
S3	Y3. S2	Creamy	Slimy/Moist	Small, glistening,circular	$2.86 x10^3$
	Y4. S2	Creamy white	Slimy/Moist	Medium, regular	$2.86 x10^3$
	Y5. S2	Cloudy	Slimy/Moist	Small, glistening,circular	$2.86 x10^3$

Microscopy of Yeast Isolates: When LPCB staining of all colonies were done 4 isolates showed round shape cell while one show ovoid, morphology under 40X magnification. All cells were stained purple and showed budding in their cell as shown in figure 6.

Biochemical Characterization of Yeast

The biochemical tests provided insights into the metabolic capabilities of the yeast isolates. For catalase activity, four isolates were catalase-positive, indicating the presence of the enzyme, while one isolate was catalase-negative. In terms of lactose fermentation, two isolates were positive for lactose fermentation. For sucrose utilization, two isolates from S1 were positive, as indicated by a colour change to yellow upon the addition of phenol red indicator, while the remaining three isolates showed no colour change, indicating negative sucrose utilization as shown in table 6. While table 7 shows the identified genera of yeast.

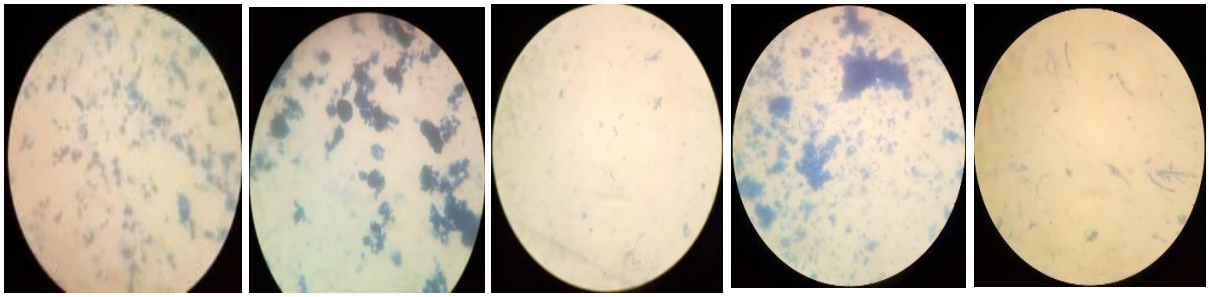

Figure 6: Microscopic observation of Yeast isolates.

Table 6: Biochemical test results of yeast isolates.

Sample	Colonynumber	Catalase activity	Lactose fermentation	Sucrose utilization
S1	Y1. S1	+	+	+
	Y2. S1	-	+	+
S2	Y3. S2	+	-	-
	Y4. S2	+	-	-
	Y5. S2	+	-	-

Table 7. Identified genera of yeast isolates.

Sr. no	Sample	Isolate number	Identified Genera
1.	S1	Y1. S1	*Saccharomyces*
2.		Y2. S1	*Candida spp.*
3.	S2	Y3. S2	*Cryptococcus*
4.		Y4. S2	*Cryptococcus*
5.		Y5. S2	*Cryptococcus*

Comparative assessment of Bacterial, Fungal and Yeast Diversity in Compost Samples: A total of 12 bacterial isolates were identified from both compost samples. S1 exhibited a greater bacterial diversity compared to S2. The most frequently isolated genera from S1 were *Klebsiella* and *Salmonella*. In contrast, S2 contained fewer bacterial genera, with much frequency of gram-positive genera including *Streptococci* and *Staphylococci* along with *Edwardsiella* and *Psuedomonas*. Comparative analysis showed that S1 had a higher bacterial density due to the presence of poultry waste, which is rich in proteins and organic matter, favoring bacterial growth. The bar chart (Figure 7) illustrates the distribution of bacterial genera in two compost samples.

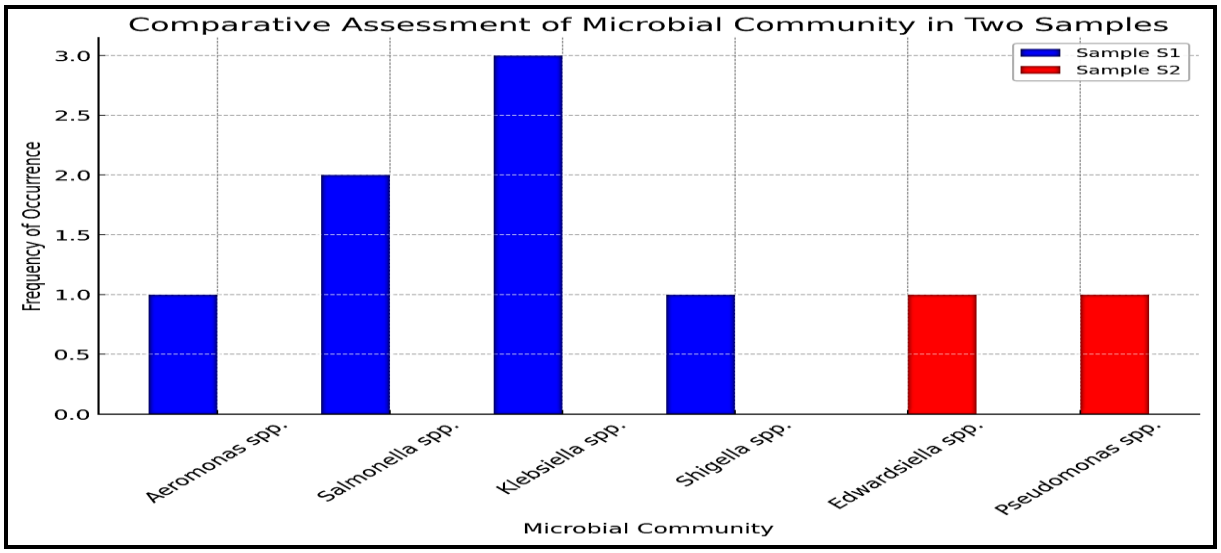

Figure 7. Comparative Bacterial Diversity in S1 vs. S2: Shows the number of isolates for each bacterial genus in both compost samples. S1 has a higher bacterial diversity overall.

A total of 6 fungal isolates were recovered during study. S1 exhibited a higher diversity of fungal

species with *Rhizopus sp.*, *Aspergillus sp.*, and *Fusarium sp.* In contrast, S2 had only two fungal isolates, *Helminthosporium sp.* and *Aspergillus sp.* The presence of *Rhizopus sp.* and *Fusarium sp.* in S1 suggests a more active decomposition process, possibly due to the presence of fruit and vegetable waste. *Helminthosporium sp.*, found exclusively in S2, indicates a distinct fungal community influenced by cow dung content as shown in figure 8.

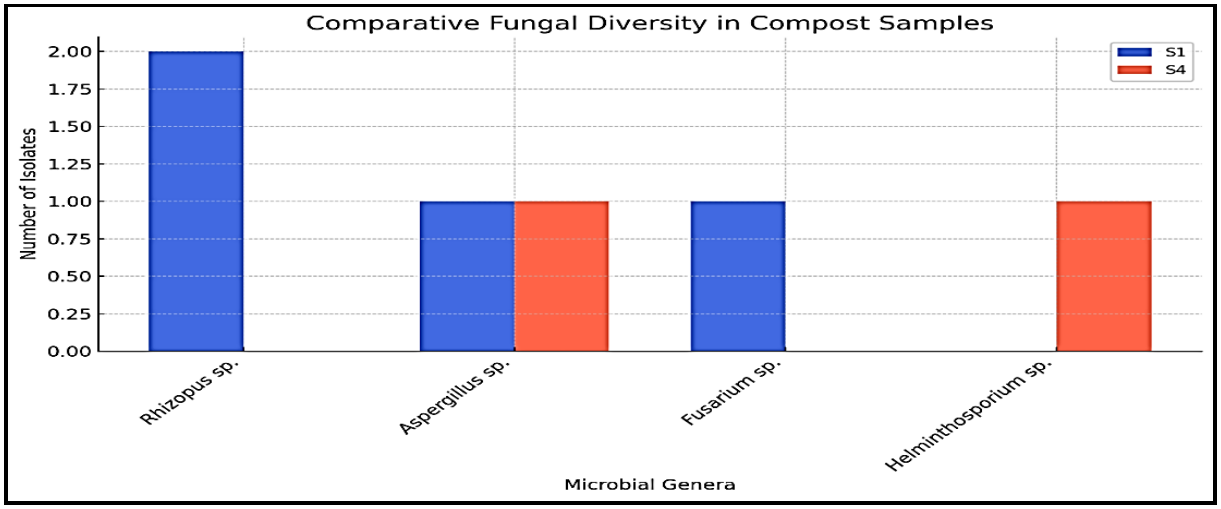

Figure 8. Comparative Fungal Diversity in S1 vs. S4: Highlights differences in fungal isolates, with *Rhizopus* and *Fusarium* found in S1, while *Helminthosporium* is only present in S4.

Yeast analysis revealed 5 isolates, with S1 containing *Saccharomyces* and *Candida spp.*, while S2 exclusively harbored *Cryptococcus* spp. The dominance of *Cryptococcus spp.* in S2 suggests that cow dung-based compost provides favorable conditions for its growth, whereas *Saccharomyces* and *Candida* were found in S1, likely influenced by the fermentation of fruit and vegetable waste as shown in figure 9.

DISCUSSION

The study of microbial diversity in compost reveals significant differences in microbial populations based on the organic materials used. Compost samples S1 and S2, derived from poultry waste and cow dung respectively, exhibit distinct microbial communities, particularly in bacterial abundance. Sample S1, enriched with nitrogen from poultry waste, supports a higher bacterial count compared to S2, which contains cow dung and vegetable waste. This nitrogen-rich environment fosters bacteria that thrive on such substrates. A total of 23 different microbes were identified, including 12 bacteria, 6 fungi, and 5 yeasts, highlighting the complexity of compost ecosystems. Bacteria initiate decomposition, while fungi break down complex materials like lignin and cellulose, and yeasts facilitate fermentation. The presence of specific microbial inoculants can enhance composting efficiency, as seen in studies where microbial formulations improved degradation rates and nutrient retention (Sarwari *et al*., 2024). While the findings emphasize the importance of nitrogen-rich materials in promoting bacterial growth, it is also crucial to consider that diverse microbial communities can be beneficial for composting efficiency, regardless of the organic waste type used.

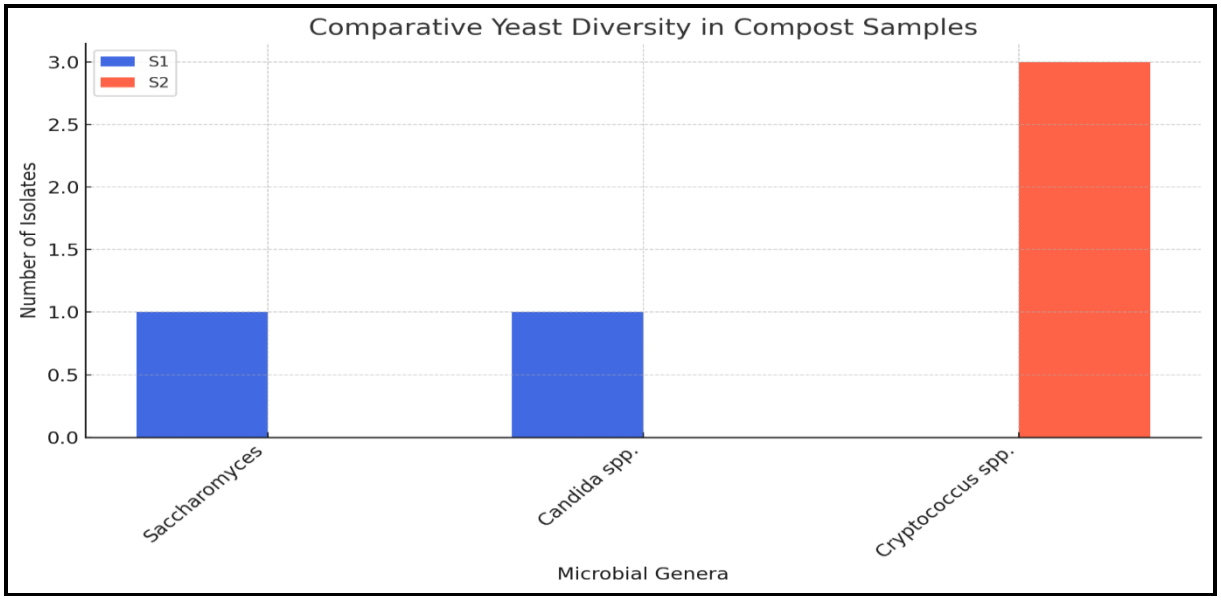

Figure 9. Comparative Yeast Diversity in S1 vs. S2: Illustrates the dominance of *Cryptococcus* in S2, while *Saccharomyces* and *Candida* are found in S1.

The presence of pathogenic bacteria such as *Staphylococcus aureus, Pseudomonas, Salmonella, Klebsiella,* and *Streptococcus* in compost raises significant concerns regarding agricultural safety. While these pathogens can pose risks to human health, particularly for immunocompromised individuals, the composting process can also yield beneficial microorganisms that enhance soil fertility and plant growth (Wan *et al*., 2021). Certain compost-derived bacteria, like *Pseudomonas* species, can suppress plant pathogens and promote growth, demonstrating the dual nature of compost. Compost enhances soil fertility by providing essential nutrients and improving soil structure, which is crucial for sustainable agriculture. Despite the risks associated with pathogenic bacteria, the potential benefits of compost as a natural fertilizer and biocontrol agent highlight the importance of effective compost management to ensure safety and sustainability in agricultural practices.

The role of fungal isolates such as *Rhizopus, Aspergillus, Fusarium,* and *Helminthosporium* in composting is multifaceted, contributing to organic matter breakdown while also posing potential risks. These fungi are essential for decomposing complex materials like lignin and cellulose, with *Aspergillus* species producing critical enzymes for this process. However, the presence of plant pathogens like *Fusarium* and *Helminthosporium* in immature compost can threaten crop health if not managed properly. Fungi, particularly *Aspergillus*, produce cellulases and ligninases, facilitating the breakdown of plant materials (Zhu *et al*., 2024) (Ezeagu *et al*., 2024). Fungal activity enhances soil nutrient availability, improving overall soil health and fertility (Roy *et al*., 2022) (Miao *et al*., 2022). *Fusarium* and *Helminthosporium* can introduce diseases if compost is not fully matured (Taneja *et al*., 2023). Effective monitoring and temperature control during composting are crucial to mitigate these risks. While composting is a valuable method for recycling organic waste, careful management of microbial communities is essential to prevent the introduction of harmful pathogens into agricultural systems (Zhu *et al*., 2024). The role of yeast isolates, including *Saccharomyces, Candida spp., and Cryptococcus spp.*, in composting is crucial for enhancing microbial diversity and promoting soil health. These yeasts contribute to the breakdown of organic matter, facilitating the production of beneficial compounds for plant growth. *Saccharomyces:* known for its fermentation capabilities, it rapidly consumes sugars during the early composting stages, aiding in organic matter breakdown (Nimsi *et al*., 2022). *Candida* and *Cryptococcus spp*. enhances the microbial diversity of compost, which is essential for a balanced ecosystem that supports nutrient (Sarwari *et al*., 2024) (Nimsi *et al*., 2022). Diverse microbial communities improve soil fertility by decomposing organic materials into simpler forms that plants can absorb (Sarwari *et al*., 2024). While the benefits of microbial diversity in composting are significant, the presence of potentially harmful microbes necessitates careful management to prevent risks to crops and human health.

CONCLUSION

Extensive diversity of bacteria, fungus, and yeast were revealed by the study through the successful isolation and identification of a variety of microbial species from compost samples. Because sample S1's organic substrates were more diversified than sample S2, the microbial community makeup differed between the two samples. These results underscore the significance of microbial diversity in composting and point to possible uses of these microorganisms in agriculture to enhance soil fertility and health. The

functions of these bacteria in composting and how they combine to maximize the quality and effectiveness of the compost should be the main topics of future study.

AUTHORS' CONTRIBUTION

All Authors are equal Contribution

AUTHORS' CONFLICT OF INTEREST

The authors have no conflict of interest to declare.

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