UJMR, Vol. 9 No. 2, December, 2024, pp. 80 - 90 *E-ISSN: 2814 – 1822; P-ISSN: 2616 – 0668*

https://doi.org/10.47430/ujmr.2492.009

Received: 14 June 2024 **Accepted:** 16 September 2024

Diversity and Enzymatic Activity Profile of Bacteria Isolated from Selected Organic Wastes in Owerri Imo State, Nigeria

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Abstract

Enzymes secreted by bacteria are bio-catalysts that play an important role in all stages of metabolism and biochemical reactions. This study was designed to unravel the activity profile of the enzymes produced by bacteria isolated from selected organic wastes. Using sterile sample vials, samples of Cow dung, Municipal Solid, Poultry, and Pig waste were taken from the Federal University of Technology, Owerri's Agricultural Research Farm, and delivered to the laboratory for examination. The Microbial isolates were identified and characterized following their cultural, microscopic, and biochemical characteristics on Nutrient agar, Salmonella Shigella agar, McConkey Agar, and Eosin Methylene Blue agar. There were 832 bacteria isolates identified in the organic waste samples, with Enterococcus faecalis having the highest reoccurrence rate, 167(20.1%). Staphylococcus spp was the second highest occurring organism across the sites with 124(14.9%), closely followed by Bacillus subtilis 107(12.9%), while Shigella spp had the least reoccurrence at 23(2.8%) among others. The Primary screening for enzyme production of the isolates revealed that Protease, Amylase, cellulase, pectinase, lipase, Lectinase, and oxidase enzymes were generated by Pseudomonas aeruginosa, but Shigella species produced none. Other bacterial isolates produced at least one enzyme. This study has demonstrated that a wide variety of bacterial species isolated from different organic wastes showed a high capacity to produce lipase, amylase, and protease enzymes. It underscored the ability of these isolates to produce these essential enzymes, which have found application in biodegradation of organic wastes which can help in biocontrol and environmental conservation and recycling.

Keywords: Enzymes, Bacteria, Organic Wastes, Soil.

INTRODUCTION

According to Adesemoye and Egamberdieva (2013), bacteria and other creatures that form intimate relationships and take part in creating food for people and animals call the soil home. One of the most crucial elements influencing field emergence, healthy plant development, and, ultimately, the caliber of the final agricultural product is crop protection throughout the early phases of plant growth (Adesemoye *et al.*, 2018). Microorganisms enhance plant health and productivity while protecting ecologically benign plants through biological management. Plant growth-promoting bacteria (PGPB) or plant growth-promoting rhizobacteria (PGPR) are bacteria that promote plant development and yield (Beneduzi *et al.*, 2012). PGPB positively impacts plant health and crop productivity and can be used in biological crop protection (Ahemad and Kibret, 2014). Organic wastes are by-products of decomposition. These by-products are useful to the soil because they enrich it with nutrients like nitrogen. Plants growing in areas where organic waste abounds are bound to blossom (Aloni *et al.*, 2016).

The whole activity of soil-dwelling microorganisms is reflected in the enzymatic activity of the soil. Enzyme activities represent crop production potential and can be utilized as markers of soil fertility and agrobiocenotic equilibrium (Çakmakçı *et al.*, 2017). Dehydrogenases, phosphatases, urease, catalase, proteases, and cellulases are the main enzymes that bacteria create. Nitrifying, ammonifying, and nitrogen-fixing bacteria are crucial for supplying nitrogen to plants and decreasing the need for external nitrogen sources (Compant *et al.*, 2015).

The balance of the soil is disturbed by crop protection agents, fertilizers, and cultivation techniques. Reduced resistance to pathogens, reduced nutrient uptake by roots, decreased enzyme activity, and decreased soil quality are all consequences of soil microbial community impoverishment.

Organic waste breaks down due to well-known extracellular enzymes released by bacteria, primarily *Pseudomonas* species (Cai *et al.*, 2023). These Gram-negative bacteria, which enter mostly as contaminants, are primarily responsible for the breakdown of organic waste, even though *Pseudomonas species* may be eradicated by sharply raising or lowering the temperature. Because *Pseudomonas spp*. release hydrolytic enzymes that are extremely heat resistant. After heating, they can still cause rancidity and proteolysis when decomposing organic waste is infected before heat processing (Anjaiah *et al.*, 2013). According to Bhattacharyya and Jha (2012), the lipases and proteases may withstand ultra-high temperature (UHT) treatment and high-temperature short-time pasteurization.

The amount of municipal waste generated is rising alarmingly due to the population tripling and residents' shifting living patterns. The eco-friendly treatment of trash is the biggest challenge to environmentalists, and the use of microorganisms in this context has proven more effective than other existing methods. Organic waste is no longer there to cause odors, sludge, pollution, or ugly mess since it is digested by bacteria and used as nutrients. Bacteria break down waste into safe byproducts during consumption. In the process, the bacteria release many metabolites that help break down complicated waste into simpler components. The hunt for industrially significant microorganisms is increasingly turning soil microbes into important molecules (Adomako *et al.*, 2020), and the amount of microbial variety in the natural world is still mainly unknown. Thus, it's possible that many more beneficial compounds derived from soil microbes are still to be discovered. The soil is a large reservoir of many economically important microorganisms whose biological activities are understood to be crucial to the upkeep of a healthy biosphere. As a result, there is a great chance to filter beneficial bacterial strains from waste disposal sites. There has been a continuous attempt to isolate novel bacteria from various environments to meet the need for new organisms with the ability to produce special enzymes or compounds for industrial use and waste degradation.

The bio-catalysts that are essential to all phases of metabolism and biochemical processes are called enzymes. It is well known that microbial enzymes, which are derived from various microorganisms, are better enzymes that are used in commercial enterprises. Global research has been conducted on microorganisms such as bacteria, fungi, and yeasts to determine how to biosynthesize commercially viable preparations of different enzymes (Asghar *et al.*, 2014).

Although enzymes are considered to be substrate-specific, it has been shown that some bacteria release enzymes that can break down many substrates. However, nothing has been done about the enzymatic activity, profile, and potentials of bacteria isolated from certain organic wastes in Owerri, Imo State, Nigeria, despite many bacterial strains being isolated and identified from the soil throughout the years. This area has remained unexplored even though there is an urgent need to find new alternatives to supplement the use of chemicals in agriculture due to the increased use of chemical pesticides and fertilizers that have caused runoff through erosion and leaching that has contaminated surface and groundwater. It became essential to understand the enzyme activity profile of these bacteria to use bacteria isolated from specific organic wastes to boost plant growth and productivity and avert the persisting problem of pollution.

This study investigated the enzymatic activity profile of bacteria isolated from selected organic wastes.

MATERIALS AND METHODS

Collection of Samples

Samples of Cow dung, Municipal Solid, Poultry, and Pig waste were taken from the Federal University of Technology, Owerri's Agricultural Research Farm in sterile sample bottles and immediately transported to the laboratory for analysis.

Preparation of Samples and Inoculation

To achieve a 10^{-1} dilution, ten grams of the sample—which included cow dung, pig wastes, municipal wastes, and poultry wastes—were serially diluted in 90 milliliters of sterile physiological saline and well mixed.

Isolation and Identification of Microbial Isolates

After dilution, 100 µl of each dilution were inoculated into 20 ml of sterile Nutrient Agar (N.A.) plates *Salmonella Shigella* agar, McConkey Agar, and Eosin Methylene Blue agar for 18 to 24 hours. The overall bacterial count was recorded as CFU g-1 after incubation of Nutrient Agar (N.A.) plates at 48 ◦C for 48 h; subsequent bacterial colonies were selected based on colony morphology and pigmentation.

The isolated colonies were streaked on N.A. plates several times to isolate pure cultures. Finally, the pure colonies were placed on N.A. slants and stored in the refrigerator for further study.

After microscopic (Gram Staining Test, Motility Test and Spore Staining Test) and biochemical tests (Coagulase Test, Catalase Test, Oxidase Test, Sugar Fermentation/Oxidation, Urease Test, Indole Test and Citrate Utilization Test, Hydrogen Sulphide Production (H_2S) Test, IMViC Test) were performed as described by Cheesbrough (2000) to identify the Microbial isolates.

Screening for Extracellular Enzyme Production
To identify the bacterial communities that produce protease, cellulase, amylase, pectinases, and lipase, diluted samples (0.1 mL) were added to peptone gelatin agar (PG), carboxymethylcellulose agar (CMC), starch agar (SA), and tributyrin agar (TA). The synthesis and presence of extracellular enzymes released by the bacteria were determined using standard microbiological procedures, as Masi et al. (2023) reported.

Screening for microorganisms that produce Amylase
The amylase-producing bacteria were screened for using a starch hydrolysis assay. About 50 µL of the resulting culture was utilized for the hydrolysis zone in the well of the starch agar plate. Bacterial isolates were cultured in a broth medium containing the starch substrate. The starch agar medium plates were then incubated for 24 hours at 45 °C (Ullah et al., 2021). After incubation, a dropper poured the iodine solution onto the plates. After a few minutes of no disturbance, the plates were examined to look for the hydrolysis zone.

Screening for bacteria that produce Cellulase
To look for microorganisms that produce cellulase, a test for cellulose hydrolysis was conducted. First, a broth medium with cellulose substrate was used to cultivate the bacterial isolates. The hydrolysis zone in a CMC agar medium plate well was filled with approximately 50 µL of the resulting culture. Then, a carboxymethyl cellulose (CMC) agar medium was employed to increase bacterial activity. The agar medium plates containing carboxymethyl cellulose (CMC) were incubated at 48 ◦C for a whole day. After that, a dropper was used to fill the plates with iodine solution. After a few minutes of no disturbance, the plates were examined to look for the hydrolysis zone.

Screening for microorganisms that produce Lipase
To screen for microorganisms that produce lipids, a tween 80 hydrolysis test was conducted. In broth medium, bacterial isolates were cultured. After that, around 50 µL of the resulting culture was added to tween 80 agar medium, which included 10g of peptone, 5.0g of yeast extract, 5g of NaCl, 20g of agar, and 10.0 ml of tween 80. The pH was then adjusted to 7.5, and the mixture was incubated for 48 hours at 45 °C. An enzymatic test is not as practical for screening the degrading bacteria in high sample quantities as determining the hydrolysis capacity (H.C.) value. Extracellular enzyme-producing bacteria were subjected to qualitative testing using the clear zones on various media.

Screening for microorganisms that produce Proteases
A test for protease-producing bacteria was conducted using skim milk hydrolysis. The bacterial isolates were cultured in broth media containing casein substrate, and the resulting culture, containing approximately 50 µL, was utilized for the hydrolysis zone in the skim milk agar plate well. After that, the plates were incubated at 45 °C for 24 hours. Masi et al. (2014) examined and noted the zone of inhibition of bacterial proteolytic activity. The isolates' proteolytic, amylolytic, lipolytic, pectinolytic, and cellulolytic activities were identified based on colorimetric alterations. The symbols "-", "+", "++", and "+++" were randomly used to score the activity to record the data and indicate whether or not extracellular enzymes were present in each sample.

RESULTS

Numerous isolates were isolated based on colony morphological differences (cell shape, colour, opacity, and surface texture). Gram staining was performed, and many biochemical tests revealed various bacteria in the organic waste samples as shown in Tables 1 and 2. All the samples had *Bacillus cereus, Staphylococcus aureus, Pseudomonas aeruginosa, Bacillus subtilis, Enterococcus faecalis, Micrococcus luteus, Shigella* spp, *Enterobacter* spp, *Bacillus cereus,* and *Escherichia coli.*

Table 1: Colonial and Microscopic Characteristics of Bacteria Isolated from Wastes

Colonial characteristics	Spore formation	Motility	Gram morphology	Microbial Identity
Smooth, moist, and shiny low convex golden yellow colonies on NA	-	-	Gram-positive cocci predominantly in clusters, few in pairs	*Staphylococcus spp*
Dull and dry serrated flat cream colonies on NA	+	+	Large gram-positive rods in short chains with central spores	*Bacillus cereus*
Mucoid and slimy cream colonies on NA and BHIA	-	+	Gram-positive rods in chains	*Bacillus subtilis*
Small circular, moist, and shiny low convex cream colonies on NA	-	-	Gram-positive cocci in long chains, few in pairs and clusters	*Enterococcus spp*
Circular light pink colonies on MCA and EMBA	-	-	Gram-negative rods in short chains	*Enterobacter spp*
Small circular low convex moist and shiny yellow colonies on NA	-	-	Gram-positive cocci predominantly in tetrads, few in pairs	*Micrococcus spp*
Small smooth pink colonies on MCA and purple metallic sheen on EMBA	-	_	Gram-negative small rods predominantly in singles and short chains	*Escherichia coli*
Small circular fish eye colonies on SSA	-	+	Gram-negative small short rods in chains	*Salmonella spp*
Large, smooth, moist, and shiny light pink colonies on SSA	-	-	Gram-negative slender rods in short chains and few in singles	*Shigella spp*
Small smooth, moist, and shiny yellow colonies on NA	-	-	Gram positive cocci in tetrads	*Micrococcus spp*
Moist and shiny bluish-green colonies on NA and small smooth cream colonies on cetrimide agar	-	+	Short Gram-negative rods in singles and short chains	*Pseudomonas spp*

NA = Nutrient Agar; MCA = MacConkey Agar; SSA = Salmonella Shigella Agar; EMBA = Eosin Methylene Blue Agar. + = Positive/Present; - = Negative/Absent

The bacterial species in the different waste samples were isolated at Percentage distribution (%) (Figures 1, 2, 3 & 4). There were 832 bacteria isolates identified from the different sample sites. From the pig wastes, isolates showed a microbial distribution that had the presence of *Bacillus cereus 16; Staphylococcus aureus* 37(19%); *Pseudomonas aeruginosa 9; Bacillus subtilis 32(19%); Enterococcus faecalis 24 (14%); Micrococcus luteus 26 (16%); Micrococcus spp 18 (11%); Shigella* spp 02 (1%); *Enterobacter* spp 04 (2%) (Figure 1).

Table 2: Biochemical Characteristics of Bacteria isolated from organic Wastes

NO_3	H_2S	Ure	Oxi	Cat	Coag	In	MR	VP	S	L	G	M	Identity of isolates
+	-	-	-	+	-	+	-	+	+	+	+	-	*Escherichia coli*
+	-	-	-	+	-	-	+	-	-	+	+	-	*Enterobacter spp*
+	-	+	-	+	+	-	-	+	+	+	+	+	*Staphylococcus spp*
-	-	-	-	-	-	-	+	-	+	+	+	+	*E. faecalis*
-	-	+	-	+	-	-	+	-	-	-	-	-	*Micrococcus luteus*
+	-	-	-	-	-	-	+	-	-	-	-	+	*Shigella spp*
+	-	-	-	+	-	-	-	+	-	-	-	-	*Bacillus cereus*
+	-	-	-	+	-	-	-	+	-	-	-	+	*Bacillus subtilis*
+	+	-	-	+	-	-	+	-	-	-	+	+	*Salmonella spp*
+	-	-	-	+	-	-	+	-	+	-	+	-	*Micrococcus roseus*
+	-	+	+	+	-	-	+	-	-	-	+	+	*P. aeruginosa*

Cat = Catalase; MR = Methyl Red Test; M = Maltose; G = Glucose; S = Sucrose; Lac = Lactose; Ure = Urease Test; H_2S = Hydrogen sulphide production; NO_3, = Nitrate reduction Test; Oxi = Oxidase; Coag = Coagulase; In = Indole; VP = Voges Proskauer

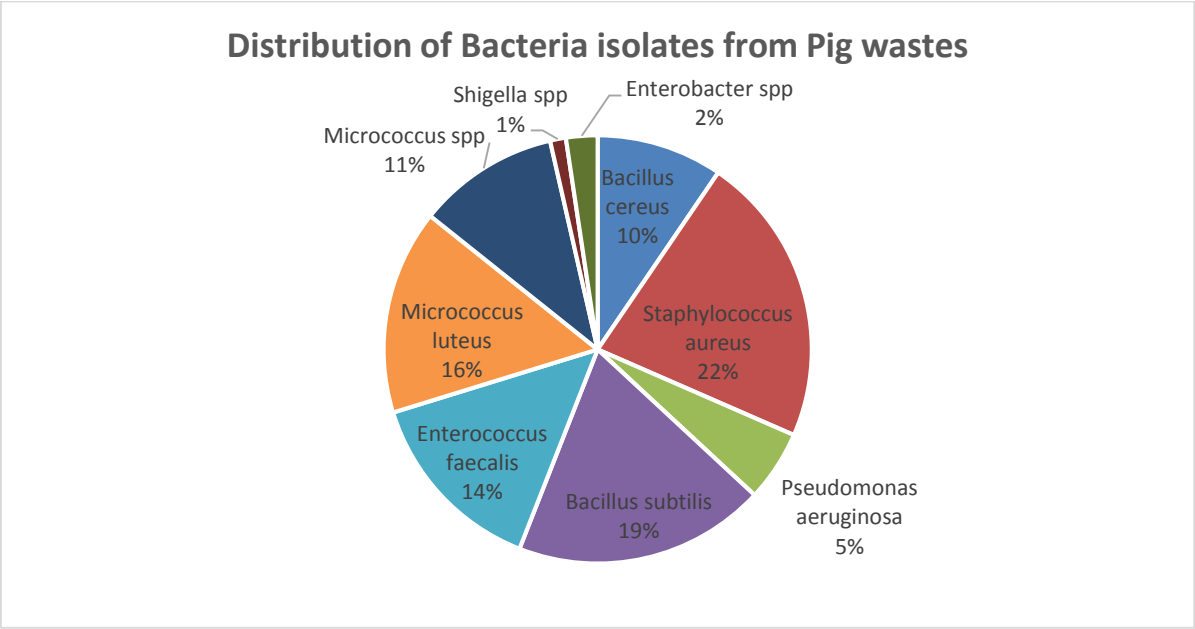

Figure 1: Distribution of Bacteria isolates in Pig wastes samples

The municipal waste samples showed varying bacterial species present at Percentage distribution (%), as shown in the Figure 2 below. The isolates showed a microbial distribution that had the presence of *Bacillus cereus* 41(13%); *Staphylococcus aureus 58* (19%); *Bacillus subtilis 28 (9%); Enterococcus faecalis 72 (24%); Micrococcus spp 21 (7%); Shigella* spp 14 (5%); *Escherichia coli 18 (6%); Enterobacter* spp 24 (8%); *Pseudomonas aeruginosa 28 (9%).*

Analysis of the Poultry waste samples showed varying bacterial species present at Percentage distribution (%), as shown in the Figure 3 below. The isolates showed a microbial distribution that had the presence of *Bacillus cereus 26* (13%); *Staphylococcus aureus 17 (12%); Bacillus subtilis 15* (8%); *Enterococcus faecalis 53* (26%); *Micrococcus luteus 11* (6%); *Micrococcus spp 9* (5%); *Salmonella* spp 36 (18%); *Shigella* spp 3 (2%); *Escherichia coli 9* (5%); *Enterobacter* spp 6 (3%); *Pseudomonas aeruginosa 15* (8%).

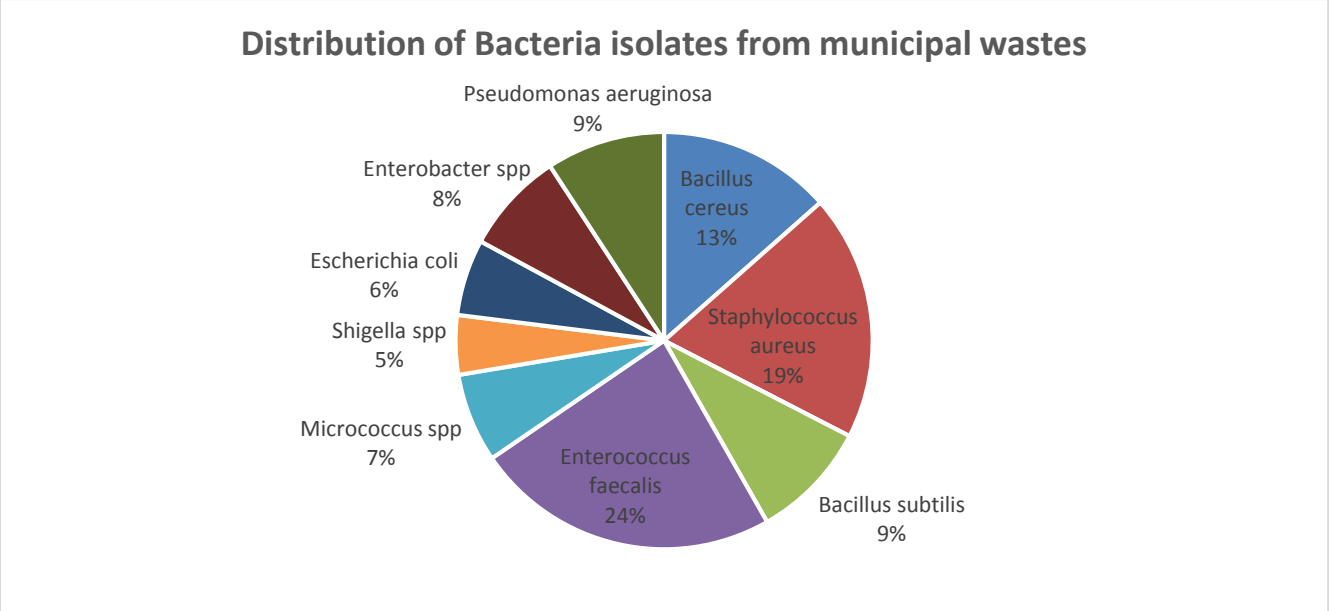

Figure 2: Distribution of Bacteria isolates from municipal waste samples

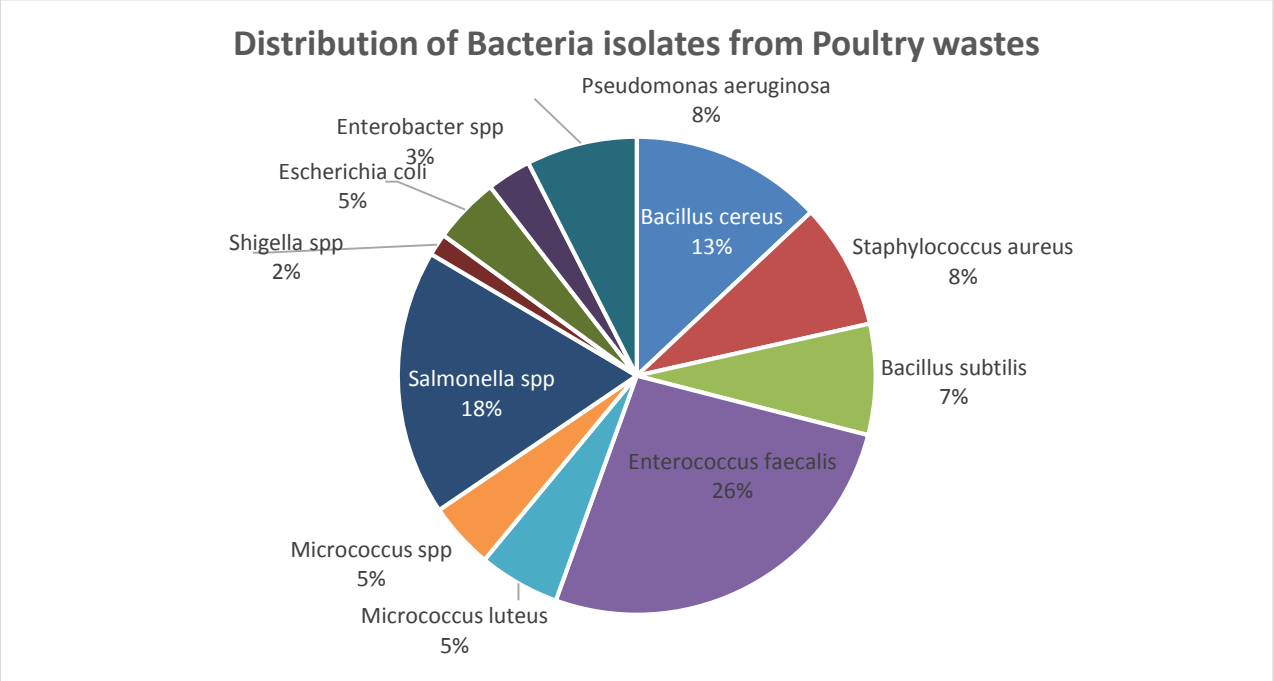

Figure 3: Distribution of Bacteria isolates from Poultry waste samples

Analysis of the cow dung samples showed varying bacterial species present in the waste sample at Percentage distribution (%), as shown in the Figure 4 below. The isolates showed a microbial distribution that had the presence of *Bacillus cereus 13* (9%); *Staphylococcus aureus 12 (8%); Bacillus subtilis 19* (13%); *Enterococcus faecalis 18 (12%); Micrococcus luteus 12 (8%); Micrococcus spp 17* (11%); *Salmonella* spp 19 (13%); *Shigella* spp 4 (3%); *Escherichia coli 7 (5%); Enterobacter* spp 7 (5%); *Pseudomonas aeruginosa 19*(13%).

Figure 5 below shows the overall distribution and prevalence across the sample sites, with *Enterococcus faecalis* having the highest reoccurrence rate, 167(20.1%). *Staphylococcus* spp was the second highest occurring organism across the sites, with 124(14.9%), closely followed by *Bacillus subtilis* 107(12.9%), while *Shigella* spp had the least reoccurrence at 23(2.8%). Others include *Bacillus cereus* 96(11.5%), *Pseudomonas aeruginosa* 71(8.5%), *Micrococcus* spp 65(7.8%), *Salmonella* spp 55(6.6%), *Micrococcus luteus* 49(5.9%), *Enterobacter* spp 41(4.9%), and *Escherichia coli* 34(4.1%).

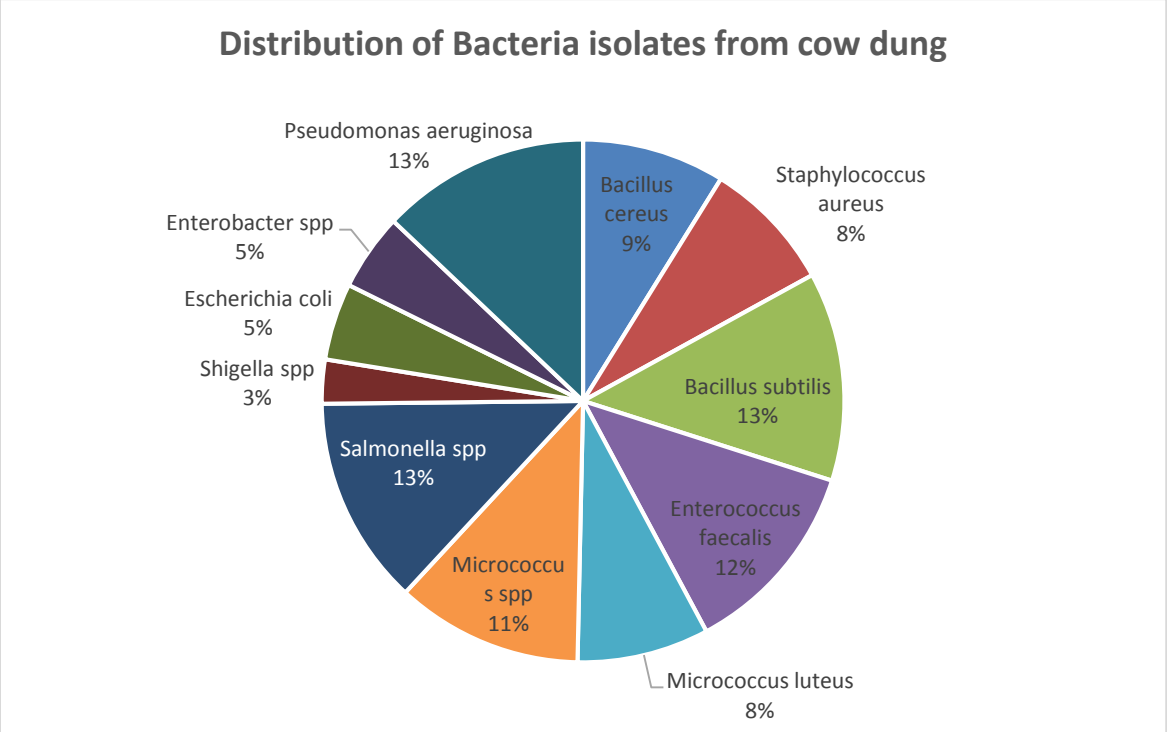

Figure 4: Distribution of Bacteria isolates from Cow Dung samples

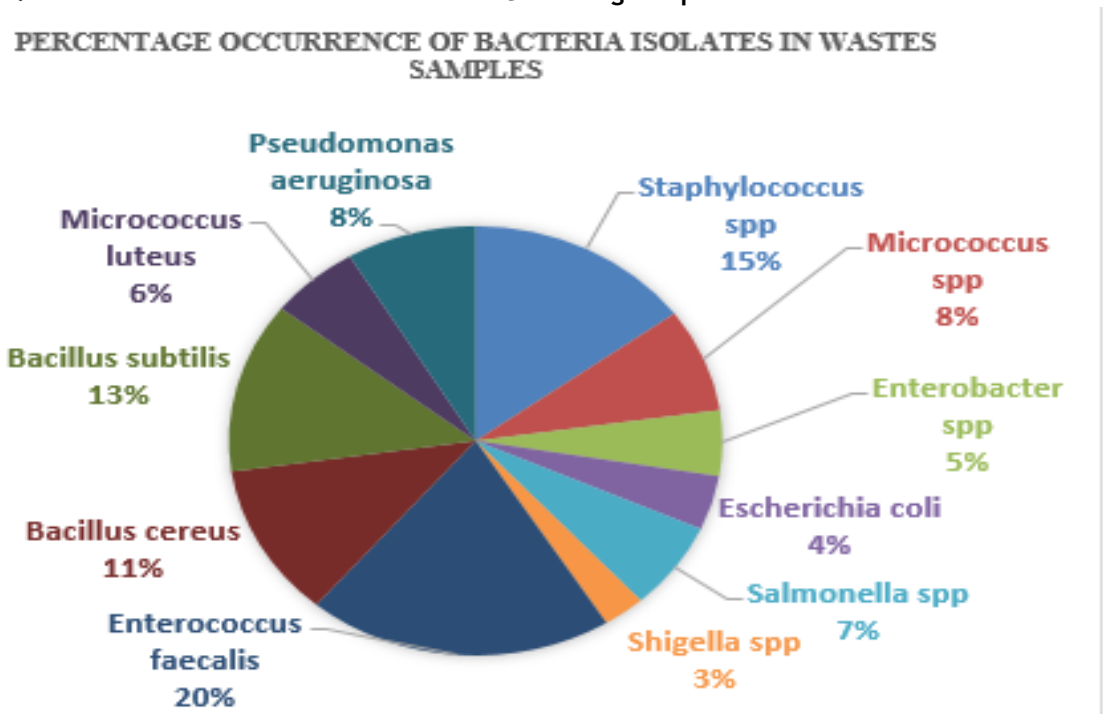

Figure 5: Percentage occurrence of Bacteria isolates in wastes samples

Total bacteria colony-forming units (CFU) were counted, then multiplied by the dilution factor and expressed in CFU/g, as shown in Table 3 below. Pig Wastes had MCA values of 2.8×10^6 to 1.66×10^8, NA values of 5.4×10^8 to 2.32×10^{10}, SSA values of 1.8×10^5 to 1.43×10^6, and EMBA values of 1.4×10^5 to 6.6×10^5. The colony-forming units derived from the municipal wastes, poultry wastes, and cow dung yielded the following results: Pig Wastes showed 2.8×10^6 - 1.66×10^8 on MCA, 5.4×10^8 - 2.32×10^{10} on NA, 1.8×10^5- 1.43×10^6 on SSA, and 1.4×10^5 - 6.6×10^5 on EMBA.

Table 3: Total counts of Bacteria isolated from Organic Wastes

Sample codes	Total counts on MCA (Cfu/g)	Total counts on NA (Cfu/g)	Total counts on SSA (Cfu/g)	Total counts on EMBA (Cfu/g)
Pig Wastes (PG)	2.8×10^6 - 1.66×10^8	5.4×10^8 - 2.32×10^{10}	1.8×10^5- 1.43×10^6	1.4×10^5 - 6.6×10^5
Municipal Wastes (MW)	1.7×10^6- $9.1 \times 5.4 \times 10^6$	6.4×10^8 - 1.99×10^{10}	2.1×10^5- 1.22×10^6	2.7×10^5 - 1.06×10^6
Poultry Wastes (PW)	8.8×10^6- 1.55×10^7	8.4×10^8- 2.56×10^{10}	8.0×10^5 - 9.6×10^5	1.00×10^6 - 1.69×10^6
Cow Dung (CD)	6.9×10^6- 1.64×10^6	7.7×10^8 - 2.53×10^{10}	2.0×10^5 - 1.66×10^6	4.8×10^5 - 5.1×10^5

Key: CFU/g = Colony Forming Unit Per Gram; MCA =McConkey Agar; NA= Nutrient Agar; SSA = *Salmonella Shigella* Agar; EMBA =Eosin Methylene Blue Agar

The Primary screening for enzyme production of the isolates revealed that Protease, Amylase, cellulase, pectinase, lipase, Lectinase, and oxidase enzymes were generated by *Pseudomonas aeruginosa*, but Shigella species produced none. Other bacterial isolates produced at least one enzyme (Table 4).

Table 4: Extracellular Enzyme Production by the Bacterial isolates

Bacterial isolates	Prot	Amy	Cell	Pect	Lip	Lec	Oxi
Staphylococcus spp	++	+	+	-	+	+	-
Micrococcus spp	+	+	-	-	+	-	-
Enterobacter spp	++	-	-	-		-	-
Escherichia coli	+++	-	+	+	+	-	-
Salmonella spp	+	+	-	-		-	-
Shigella spp	-	-		-		-	-
Enterococcus faecalis	-	-	-	-	+	-	-
Bacillus cereus	+	+	+	+	+	+	-
Bacillus subtilis	+++	+	+	+	+	+	-
Micrococcus spp	+	_	-	-	+	-	-

Key: +++ = Present; ++ = Present; += Present; - =Not present, Prot = Protease, Amy = Amylase, Cell = Cellulase, Pect = Pectinase, Lip = Lipase, Leci= Lecithinase, Oxi = Oxidase

DISCUSSION

Our screening for the diversity and enzymatic profile of bacteria isolated from organic wastes in Owerri Imo state revealed that microorganisms of different genera can be found in the organic wastes. The result showed that these wastes contain a significant number of microbes belonging to the *Bacillus cereus, Staphylococcus aureus, Bacillus subtilis, Enterococcus faecalis, Shigella* spp, *Escherichia coli, Enterobacter* spp, *Pseudomonas aeruginosa* which has the potential to help in bioremediation, bio-control of pollution, preventing the proliferation of wastes, and even preventing the development of resistant strains in the environment. Some of these Soil microbial communities have been widely established to be essential in the regulators and recycling of carbon processes in the soil, according to (Shamshitov *et al*. 2023; Gougoulias *et al.*, 2014; Jacoby *et al.*, 2017) and (Emmanuel *et al.*, 2017). A previous study by López-Mondéjar *et al. (*2016) suggests that these organisms are known to make an essential impact in the decomposition processes of organic wastes since they are the main producers of enzymes that participate in the degradation processes of plant cell wall polymers, including cellulose, hemicellulose and lignin in soils.

Per distribution, there were 832 bacteria isolates identified from the different sample sites (Figures 1, 2, 3, 4 & 5). The isolates showed an overall prevalence across the samples with *Enterococcus faecalis* having the highest rate of reoccurrence of 167(20.1%).

Staphylococcus spp was the second highest occurring organism across the sites, with 124(14.9%), closely followed by *Bacillus subtilis* 107(12.9%), while *Shigella* spp had the least reoccurrence at 23(2.8%). Others include *Bacillus cereus* 96(11.5%), *Pseudomonas aeruginosa* 71(8.5%), *Micrococcus* spp 65(7.8%), *Salmonella* spp 55(6.6%), *Micrococcus luteus* 49(5.9%), *Enterobacter* spp 41(4.9%), and *Escherichia coli* 34(4.1%) (Figure 5). These results are consistent with those of Shamshitov *et al.* (2023) in their work on Characterizing Cellulolytic Bacteria Isolated from Agricultural Soil in Central Lithuania and Anene *et al.* (2021), which described the isolation of related organisms from organic wastes derived from animal dung. Additionally, it supports the findings of Mazzucotelli *et al.* (2015), who isolated and characterized comparable bacteria with a hydrolytic capacity that might be used in the bioconversion of waste and byproducts from the agro-industrial sector, and Robledo-Mahón *et al.,* (2020) reported on the enzymatic potential of bacteria and fungi isolates from the composting process of sewage sludge.

When the organic wastes were cultured in various mediums for microbial isolation, they displayed varied bacterial counts (cfu/g). Those isolated from Pig Wastes (PG) had MCA values of 2.8 x 106 to 1.66 x 10^8, NA values of 5.4 x 10^8 to 2.32 x 10^{10}, SSA values of 1.8 x 10^5 to 1.43 x 10^6, and EMBA values of 1.4 x 10^5 to 6.6 x 10^5. The colony-forming units derived from municipal wastes (MW), poultry wastes (PW), and cow dung (CD) have yielded the following results. Those isolated from Pig Wastes (PG) showed 2.8 x 10^6 – 1.66 x 10^8 on MCA, 5.4 x 10^8 – 2.32 x 10^{10} on NA, 1.8 x 10^5– 1.43 x 10^6 on SSA, and 1.4 x 10^5 – 6.6 x 10^5 on EMBA. The colony-forming units derived from municipal wastes (MW), poultry wastes (PW), and cow dung (CD) have yielded the results shown in Table 4, which corroborates (Emmanuel *et al.*, 2017).

Ten (10) bacterial strains from four distinct wastes (Table 4) were examined on particular growth media to ascertain their capacity to produce enzymes. The bacterial isolates can secrete enzymes that play specific roles in the biodegradation process. This is in line with the reports of Fenice *et al.* (2007). The organisms all had a high capacity for lipase, amylase, and protease enzymes. However, none of the other isolates could secrete the oxidase enzyme, except for the *Pseudomonas aeruginosa*. In the same vein, all but the *enterococcus faecalis* secreted the Protease enzyme. This is consistent with earlier findings by (Mazzucotelli *et al.*, 2015; Chukwuma *et al.*, 2023 and Gaspar *et al.*, 2023), where each isolated strain's presence of these hydrolytic enzymes is intimately related to the organic wastes from which it was recovered. Muthulakshmi *et al.* (2011) and Vishwanatha *et al.* (2010) reported that the chance of isolating an organism capable of producing the desired enzyme increases when a waste rich in that substrate is used.

Currently, there is a trend toward deploying cutting-edge technology for recycling and the effective usage of organic wastes, which are mostly centered on biological processes. This study has presented an immense report of the potential that abounds within these organic wastes as starter cultures with degradative abilities due to the ability of these isolates to produce/secrete these essential enzymes while using these organic leftovers as a source of energy by metabolizing them. The organic waste bacteria were characterized to find the strongest strains that contribute to cellulose degradation under favorable conditions. The cellulolytic activity of bacteria in organic wastes was assessed by measuring bacterial growth on selective media and other qualitative experiments.

The results showed that the strain isolates had great potential for application in the bioconversion of organic waste, both as a pure culture and a microbial consortium, because they produce enzymes with bio-control capabilities. The findings of this study demonstrate that a variety of bacterial genera that may be crucial in the decomposition of cellulose in the soil were identified and may be used as bio-fertilizers or in the bio-control of polluted environments. Several bacterial genera were discovered by analyzing cultured bacterial strains obtained from organic wastes. At that point, they may actively participate in the cycle of biological matter.

Any of the bacterial strains could not demonstrate the greatest activity for all the necessary enzymes. Because of this, we assume that employing bacterial pools that contain the top strains for each unique enzymatic activity could be more successful. To comprehend the impact of the active cellulolytic bacterial population on the breakdown of organic waste, future research will concentrate on the physiology of the most promising bacterial strains and trials under controlled settings. Further research is required to determine the efficiency of these enzymes in degrading resistant substances and quantify, characterize, and purify these enzymes for additional commercial uses.

CONCLUSION

This study, designed to screen and understand the diversity and enzyme activity profile of bacteria isolates in organic wastes, demonstrated that many bacterial species are present in very high numbers in these organic wastes. These bacteria isolated from different organic wastes also have them and showed a high capacity to produce lipase, amylase, and protease enzymes.

Although only *Pseudomonas aeruginosa* could secrete the oxidase enzyme among the isolates, the results indicated that extracellular enzyme-producing bacteria isolated from a different organic waste in Owerri Imo State offer useful features for environmental sustainability in a wide range of industrial applications due to their biodegradability and specialized stability under extreme conditions, increased raw material utilization, and decreased waste. The ability of the isolates to produce these essential enzymes, which have found application in the biodegradation of organic wastes from Owerri, Imo State, which can help in biocontrol and environmental conservation and recycling, is a refreshing relief in our continued search and efforts for environmental sustainability.

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