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Microbial Assessment of Solid Waste and Bioaerosol Associated with Open Dumping Sites of the Kathmandu City, Nepal

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Abstract *— The study aims to isolate and identify bacteria and fungi (mold) present in solid waste and its associated bioaerosol in the Kathmandu city. A total of 10 samples; 5 different solid waste samples and 5 different bioaerosol samples, collected from 5 open dumping sites in the Kathmandu city, were transported to the microbiology laboratory of St. Xavier's College for processing. Standard microbiological procedures were followed for the identification of isolates. The Kirby-Bauer disk diffusion method was used to determine the antibiotic susceptibility of bacterial isolates following CLSI 2020 standards. In the collected solid waste samples, the bacterial colony count ranged from 1.27 × 10^8 to 2.8 × 10^8 CFU/ml, whereas the fungi colony count ranged from 1 × 10^5 to 4 × 10^5 CFU/ml. Bacterial colony counts from bioaerosol samples ranged from 116 to >300 CFU/90mm/15 minutes, whereas fungi colony counts were between 2 and 6 CFU/90mm/15 minutes. Out of 48 bacteria and 34 molds identified, Bacillus spp. (27%) and Aspergillus niger (29%) were found to be predominant than other isolates. Citrobacter spp., Salmonella spp., and Escherichia coli isolated from solid waste samples of dump site S3 showed maximum resistance to the different antibiotics used. The common microbial isolates from solid waste samples and bioaerosol samples included 7 different bacteria and 4 different molds. The presence of antibiotic-resistant bacteria and pathogenic fungi in waste dump sites pose public health-related risks.*

Keywords *— **Open dumping, Solid waste, Bioaerosol, Bacteria, Fungi, Antibiotic susceptibility***

I. INTRODUCTION

Solid waste can be either solid or semi-solid materials varying in physical and chemical characteristics based on their origin, usually generated as a result of anthropogenic activities, and comprises yard waste, food waste, plastics, wood, metals, papers, rubber, leather, batteries, inert materials, textiles, paint cans, and other sources that are difficult to categorize [1].

In many developing countries, such as Nepal, there is a widespread practice of open and unscientific disposal of waste [2], [3]. The existing practice of illegal dumping at unallotted locations, usually in streets, vacant spaces, and water streams has several environmental and public health-related implications [4], [5]. The healthcare, pharmaceutical, food and cosmetic industries, academic and industrial research laboratories, veterinary facilities, and household and animal discards are the largest generators of infectious waste products [6], [7]. The whole collection, processing, and disposal of solid waste is a labor-intensive operation with several chances of human exposure to microorganisms taking place at nearly every step along the way from the generation to disposal [6].

Bacteria and fungi are the most commonly identified organisms in solid waste [8]. The bacteria commonly isolated from the dumpsites include *Salmonella* spp., *Klebsiella* spp., *Pseudomonas* spp., *Bacillus* spp., *Lactobacillus* spp., *Streptococcus* spp., *Staphylococcus* spp., and *Micrococcus* spp., while fungal species include

Penicillium spp., *Mucor* spp., *Aspergillus* spp., *Fusarium* spp., *Saccharomyces* spp., and *Candida* spp., [9]–[11]. *Escherichia coli*, *Proteus mirabilis*, *Staphylococcus sciurii*, *Staphylococcus xylosus*, *Aspergillus fumigatus*, and *Aspergillus flavus* are involved in the degradation of solid waste [12].

Solid waste can release bioaerosols which are airborne entities that either contain microorganisms or biological materials derived from living organisms, mixed with solids or fluids [13], [14] with particle size ranging from 0.001 nm to 100 µm [15]. Due to their controlling influence on the growth of microorganisms, environmental factors like temperature and moisture content can significantly affect the amount of bioaerosol formation and dispersion [16]. Albeit good management and maintenance, landfills can emit and disperse bacterial and fungal aerosols up to a distance of 1000–1200 m, which implies that the vicinity may pose risks to its neighboring residents [17]. Because of their minimal size, bioaerosols can easily deposit in different parts of the body via the lungs and circulatory system [15]. Bacteria and fungi are the major microbial constituents along with their endotoxins, mycotoxins, and allergens [18].

The commonly isolated bacteria during bioaerosol testing of samples collected from municipal solid waste were mostly from *Enterobacteriaceae* family which included *Escherichia coli*, *Salmonella*, *Enterobacter*, *Klebsiella*, *Serratia*, and *Proteus* species [17], [19]. Similarly, *Bacillus*, *Streptococcus*, *Staphylococcus aureus*, and *Clostridium perfringens* are also reported [20], [21]. *Aspergillus fumigatus* is the most identified fungus [22]–[24]. Other reported fungi include *Penicillium*, *Alternaria*, *Cladosporium*, *Mucor*, *Rhizopus*, and *Fusarium* [17], [19].

Solid wastes and their bioaerosols have a comparative relationship leading to various diseases in humans caused by various microorganisms, especially bacteria and fungi [21]. This study intends to account for different bacteria and fungi present in solid waste and bioaerosol samples isolated from open solid waste dumping sites in the Kathmandu city.

II. MATERIALS AND METHODS

Study design, study area, and sample size

A random sampling method was employed comprising field visit for sample collection followed by laboratory-based procedures for processing. Kathmandu city was selected the study area. Solid waste samples and bioaerosol samples were collected from various open solid waste dumping sites. Samples were collected from *Kupondole*, *Balkumari*, *Seto pul*, *Shova Bhagwati*, and *Teku* Transfer Station. A total of 10 samples; 5 different solid waste samples and 5 different bioaerosol samples, were collected from 5 different open waste dumping sites.

Sample collection and transportation

For solid waste samples, surface waste was carefully removed using sterile forceps. A sterile spatula was used to scoop the subsurface at the depth of 10 cm. About 10 grams of solid waste sample was transferred to a sterile plastic container [11].

Bioaerosol samples were collected by exposing culture media plates to the same open dumping site's air for 15 minutes, where solid waste samples were collected [25]. The plates were then sealed with parafilm tape.

The selectively used culture media plates included Plate Count Agar (PCA), Xylose Lysine Deoxycholate Agar (XLD), MacConkey Agar (MA), Cetrimide Agar (CA), Mannitol Salt Agar (MSA), and Sabouraud Dextrose Agar (SDA).

Samples were labeled properly, kept inside the ice box maintaining a temperature of 4ºC and then transported to the Microbiology Laboratory of St. Xavier's College, Kathmandu. The collected samples were processed within 2 hours of collection.

Sample processing

One gram of solid waste sample was weighed and transferred to 9 ml sterile saline. Serial dilution was performed up to 10^{-6} dilutions. Then, 0.1 ml sample, from 10^{-2}, 10^{-4}, and 10^{-6} dilutions, was inoculated into different respective culture media plates (PCA, XLD, MA, CA, MSA, and SDA) [11].

Bioaerosol samples collected in culture media plates were incubated directly.

Isolation of bacteria and fungi (mold)

For isolation of bacteria in solid waste samples, the respective culture media were incubated at 37°C for 24 hours. Bacterial counts were made from plates with 30-300 colonies. The calculation of the total number of bacteria was done by multiplying the number of colonies and dilution by the volume of sample used. Colony morphologies of similar-looking, selective bacterial colonies were recorded and subcultured on Nutrient Agar (NA) plates and incubated at 37°C for 24 hours [26].

For isolation of fungi (mold) from solid waste samples, SDA plate was incubated at 28°C for 120 hours. The total number of fungi (mold) was calculated by multiplying the number of colonies and dilution by the volume of sample used. Each distinct fungus (mold) was subcultured on SDA plates using the point-inoculation technique and incubated at 28°C for 72 hours [26].

The exact protocol was followed for the isolation of bacteria and fungi (molds) from bioaerosol samples, while only the microbial enumeration was performed by calculating the total number of colonies as a colony forming unit (CFU)/90 mm plate/exposure time [25].

Identification of bacteria and fungi (mold)

The isolated bacterial colonies were identified using standard microbiological techniques which comprised colony morphology, Gram-staining reactions, and various biochemical properties while fungi (mold) were identified based on colony morphology and lactophenol cotton blue (LPCB) staining [26]–[28].

Antibiotic susceptibility test (AST)

The selection of culture media (Mueller Hinton Agar) and antibiotic discs were as per the Clinical and Laboratory Standard Institute (CLSI) guidelines 2020 [29]. AST was performed by the Kirby-Bauer disk diffusion method [30].

Isolated colonies from NA plates were taken and incubated in nutrient broth at 37º C for 6 hours and the turbidity of the broth was matched with 0.5 McFarland standard. A sterile cotton swab was used to evenly inoculate the Mueller Hinton Agar (MHA) surface three times while rotating the plate containing the culture. At room temperature, the plates were allowed to dry for 20 minutes. Upon incubation of the plates at 37ºC for 24 hours, the zone of inhibition around the antibiotic discs was observed. The diameter of the inhibition zone was measured and reported as susceptible, intermediate, and resistant according to the CLSI guidelines 2020.

The antibiotics used were Cefotaxime (30µg), Meropenem (10µg), Gentamycin (10µg), Ofloxacin (5µg), Imipenem (10µg) and Nalidixic Acid (30µg), Chloramphenicol (30µg), Ampicillin (10µg), Azithromycin (15µg), and Amoxicillin (10µg).

III. RESULTS

A total of 90 bacteria and 34 molds were isolated from 5 different solid waste samples and 5 different bioaerosol samples, where 54 bacteria and 15 molds were from solid waste samples, and 36 bacteria and 19 molds were from bioaerosol samples.

The results obtained are expressed as follows:

Microbial load of bacteria and fungi (mold)

The average bacterial load (CFU/ml) was enumerated from PCA plates and the average fungal load (CFU/ml) was enumerated from SDA plates collected from different dump sites (S1, S2, S3, S4, and S5).

In solid waste samples, the bacterial colony count ranged from 1.2×10^8 to 2.8×10^8 CFU/ml, whereas the fungi colony count ranged from 1×10^5 to 4×10^5 CFU/ml. In bioaerosol samples, the bacterial colony count ranged from 116 to >300 CFU/90mm/15 minutes, whereas fungi colony counts were between 2 and 6 CFU/90mm/15 minutes.

Table 1: Microbial load from solid waste samples

Dumpsite	Solid waste		Bioaerosol	
	Bacterial (CFU/ml)	Fungal (CFU/ml)	Bacterial (CFU/90mm/15 min)	Fungal (CFU/90mm/15 min)
S1	1.2×10^8	1×10^5	TMTC	2
S2	1.9×10^8	4×10^5	TMTC	2
S3	1.3×10^8	2×10^5	116	4
S4	2.4×10^8	4×10^5	217	5
S5	2.8×10^8	4×10^5	245	6

Distribution of identified bacteria

Out of 90 isolates, 48 isolates were identified; 29 isolates from solid waste samples and 19 isolates from bioaerosol samples, and included 9 different bacterial species.

Table 2: Distribution of identified bacteria

Organism	Solid waste					Bioaerosol				
	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5
Escherichia coli	1	1	1	1	1	-	-	-	1	-
Klebsiella spp.	1	-	-	1	1	-	-	-	-	1
Citrobacter spp.	1	-	1	-	-	-	-	1	-	-
Enterobacter spp.	-	1	-	-	-	1	1	-	1	-
Proteus spp.	-	-	-	1	1	-	-	-	-	-
Salmonella spp.	-	-	1	-	-	-	-	-	-	-
Staphylococcus aureus	-	1	-	1	1	1	-	1	-	-
Micrococcus spp.	1	1	1	1	1	1	1	1	1	1
Bacillus spp.	1	1	1	2	2	2	1	1	1	1
Total	**5**	**5**	**5**	**7**	**7**	**5**	**3**	**4**	**4**	**3**

Distribution of identified fungi (molds)

A total of 34 molds were isolated and identified, which included 9 different types of molds.

Table 3: Distribution of identified fungi (molds)

Organism	Solid waste					Bioaerosol				
	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5
Aspergillus niger	1	1	1	1	1	1	1	1	1	1
Aspergillus flavus	-	-	-	1	1	1	1	1	1	1
Aspergillus fumigatus	-	-	-	-	-	-	-	1	1	1
Aspergillus nidulans	-	-	-	-	-	-	-	-	-	1
Aspergillus tamarii	-	1	-	-	-	-	-	-	-	-
Trichoderma spp.	-	1	-	-	-	-	-	-	-	-
Neurospora spp.	-	1	-	-	-	-	-	-	-	-

Mucor spp.	-	-	1	1	1	-	-	1	1	1
Rhizopus spp.	-	-	-	1	1	-	-	-	1	1
Total	**1**	**4**	**2**	**4**	**4**	**2**	**2**	**4**	**5**	**6**

Antibiotic susceptibility test of identified bacteria from solid waste samples

A total of 10 different antibiotic discs of various concentrations were used against 7 different bacteria as per CLSI guidelines 2020. S represents Sensitive, I represents Intermediate, and R represents Resistant results.

Table 4: Antibiotic susceptibility test of identified bacteria from solid waste samples

Sample	Organisms	CTX	MRP	GEN	OF	NA	IPM	CPL	AMP	AZM	AMX
S1	*Escherichia coli*	S(31)	S(24)	S(25)	S(15)	S(31)	-	-	-	-	-
S1	*Citrobacter* spp.	I(24)	S(31)	S(18)	S(22)	S(22)	-	-	-	-	-
S1	*Klebsiella* spp.	S(27)	-	S(17)	S(26)	S(24)	S(27)	-	-	-	-
S2	*Escherichia coli*	S(29)	S(32)	S(22)	S(15)	S(30)	-	-	-	-	-
S2	*Enterobacter* spp.	S(28)	S(34)	S(28)	S(25)	-	S(29)	-	-	-	-
S2	*Staphylococcus aureus*	-	S(39)	S(25)	S(24)	-	-	S(30)	S(31)	-	-
S3	*Escherichia coli*	**R(9)**	**R(19)**	I(13)	S(19)	I(17)	-	-	-	-	-
S3	*Citrobacter* spp.	**R(11)**	**R(18)**	**R(12)**	**R(-)**	**R(-)**	-	-	-	-	-
S3	*Salmonella* spp.	S(27)	-	-	**R(15)**	**R(13)**	-	-	-	**R(9)**	**R(11)**
S4	*Escherichia coli*	S(28)	S(35)	S(16)	S(23)	S(29)	-	-	-	-	-
S4	*Klebsiella* spp.	S(30)	-	S(19)	S(30)	S(26)	S(32)	-	-	-	-
S4	*Proteus* spp.	S(31)	S(31)	S(15)	S(24)	**R(-)**	-	-	-	-	-
S4	*Staphylococcus aureus*	-	S(40)	S(27)	S(27)	-	-	S(29)	S(32)	-	-
S5	*Escherichia coli*	S(27)	S(30)	S(16)	S(26)	S(24)	-	-	-	-	-
S5	*Klebsiella* spp.	S(34)	-	S(18)	S(27)	S(24)	S(35)	-	-	-	-
S5	*Proteus* spp.	S(32)	S(30)	S(16)	S(22)	**R(-)**	-	-	-	-	-
S5	*Staphylococcus aureus*	-	S(39)	S(27)	S(24)	-	-	S(30)	S(32)	-	-

Antibiotic susceptibility test of identified bacteria from bioaerosol samples

A total of 10 different antibiotic discs of various concentrations were used against 5 different bacteria as per CLSI guidelines 2020. S represents Sensitive, I represents Intermediate, and R represents Resistant results.

Table 5: Antibiotic susceptibility test of identified bacteria from bioaerosol samples

Sample	Organisms	CTX	MRP	GEN	OF	NA	IPM	CPL	AMP	AZM	AMX
S1	*Enterobacter* spp.	S(29)	S(31)	S(28)	S(21)	-	S(42)	-	-	-	-
S1	*Staphylococcus aureus*	-	S(39)	S(25)	S(24)	-	-	S(30)	S(31)	-	-
S2	*Enterobacter* spp.	S(28)	S(34)	S(28)	S(25)	-	S(36)	-	-	-	-
S3	*Citrobacter* spp.	S(28)	S(34)	**R(12)**	S(26)	S(26)	-	-	-	-	-
S3	*Staphylococcus aureus*	-	S(30)	S(20)	S(21)	-	-	S(25)	S(25)	-	-

S4	*Escherichia coli*	S(35)	S(36)	S(17)	S(26)	S(27)	-	-	-	-	-
S4	*Enterobacter* spp.	S(32)	S(35)	S(17)	S(28)	-	S(25)	-	-	-	-
S5	*Klebsiella* spp.	S(31)	-	S(17)	S(24)	S(22)	S(32)	-	-	-	-

Common identified bacteria and molds between solid waste and bioaerosol

Out of 9 different bacteria identified and 9 different molds identified from solid waste samples and bioaerosol samples, 7 bacteria and 4 molds were common.

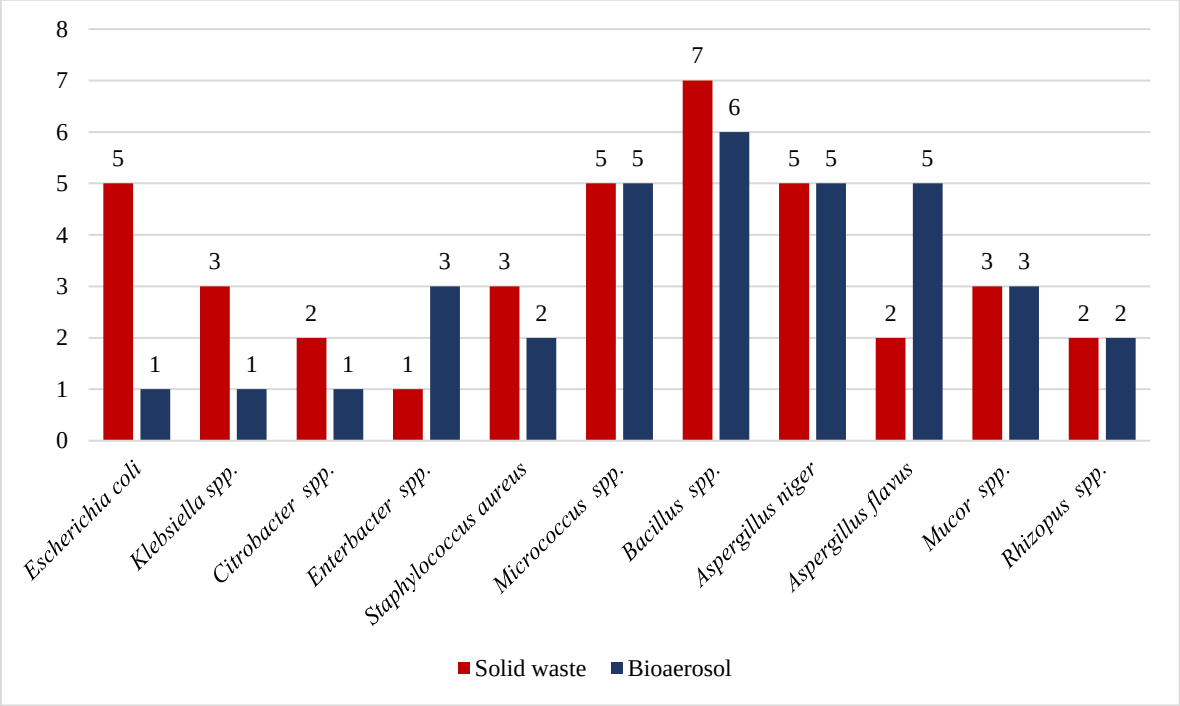
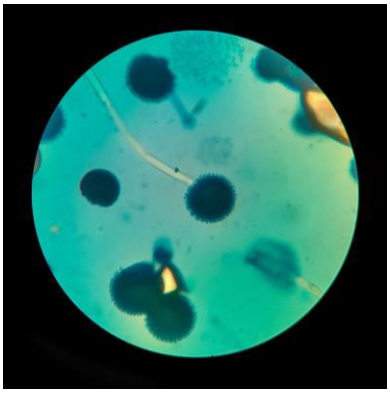


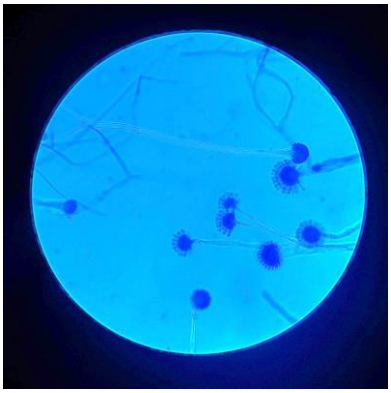
Fig.1: Common identified bacteria and molds between solid waste and bioaerosols

Photograph 1: Isolated colony of Aspergillus niger on SDA plate after incubation



Photograph 2: Aspergillus niger LPCB Staining (40X)

Photograph 3: Isolated colony of Aspergillus flavus on SDA plate after incubation



Photograph 4: Aspergillus flavus LPCB Staining (40X)

Photograph 5: Dumpsite 5 - Teku Transfer Station

IV. DISCUSSION

Isolation of microbes is an essential step in the microbiological studies performed to obtain pure cultures [31]. Depending on environmental conditions and stresses, microorganisms exist in different metabolic states and growth phases, whereas active replication of cells is not included in all the states [32].

In both the samples of solid waste and bioaerosol, the bacterial load is higher than the fungal load (Table 1). When compared to the other habitats, the soil environment is recognized to be heterogeneous, rich in substrates, and supports the highest bacterial species [33], while air harbors less diverse and more homogenized bacterial communities [34]. The growth rates of prokaryotes vary widely, with doubling times ranging from under 10 minutes to several days for laboratory-reared organisms. However, the majority of prokaryotic organisms' optimum or even adequate culture conditions are unknown, making it challenging to determine the true diversity of microbial maximal growth rates [35].

In solid waste samples (Table 2), *Bacillus* spp. constituted the higher percentage (27%) followed by *Micrococcus* spp. (17%), *Escherichia coli* (17%), *Klebsiella* spp. (10%), *Staphylococcus aureus* (10%), *Citrobacter* spp. (7%), *Proteus* spp., (7%) and, *Enterobacter* spp. and *Salmonella* spp. (4% each) which were similar to the finding of Sitotaw et al., (2021) [36]. A study by DM et al., (2017) and Emmanuel et al., (2017) isolated *Bacillus* spp., *Streptococcus* spp., *Staphylococcus* spp., and *Micrococcus* spp. from solid waste [8], [11].

Bioaerosol samples (Table 2) also resulted in the highest percentage of *Bacillus* spp. (32%) while *Escherichia coli*, *Klebsiella* spp., and *Citrobacter* spp. constituted the least; 5% which was similar to the findings of Kaźmierczuk and

Bojanowicz-Bablok (2014), Agarwal et al., (2016), and Frączek and Kozdrój (2016) who performed research on bioaerosol concentration in the air surrounding the municipal solid waste landfill [12], [17], [20].

The wide range of physiological abilities such as extracellular enzymes, formation of extremely resistant endospores to harsh physical and chemical conditions, and production of metabolites with antagonistic effects on other microorganisms are likely to be the causes of *Bacillus* spp. relatively higher percentage [37]. The presence of microorganisms in solid waste as well as in bioaerosol, particularly pathogenic organisms such as *Escherichia coli*, *Klebsiella* spp., *Citrobacter* spp., and *Aspergillus flavus* can trigger respiratory symptoms and gastrointestinal diseases which is discussed by Nair (2021) [21]. This can corroborate the fact that open dumping sites can be the source for the emission and dispersal of pathogenic bacteria as bioaerosols.

From solid waste samples (Table 3), the identified molds included *Aspergillus niger* (33%) which was predominant followed by *Mucor* spp. (20%), *Aspergillus flavus* (13%), *Rhizopus* spp. (13%), and *Aspergillus tamarii*, *Trichoderma* spp., and *Neurospora* spp. (7% each). A study by Ashraf et al., (2017) reported the presence of *Aspergillus niger*, *Aspergillus flavus*, *Penicillium expansum*, and *Trichoderma harzianum* in kitchen waste [38]. Similarly, *Aspergillus* spp. and *Mucor* spp. were reported by Janet and Kelechi (2016), and Emmanuel et al., (2017) from municipal solid waste [10], [11].

From bioaerosol samples (Table 3), *Aspergillus niger* and *Aspergillus flavus* constituted 26% of the total mold identified followed by *Aspergillus fumigatus* (16%), *Mucor* spp. (16%), *Rhizopus* spp. (11%), and *Aspergillus nidulans* constituted 5% which was similar to the findings of Breza-Boruta (2012), and Patil and Kakde (2017) [19], [40].

Most of the molds isolated from solid waste and bioaerosol samples were similar, whereas some were unique particular to the sample site and nature of the sample. Fungi's ability to grow and reproduce for prolonged periods of time, their capacity for branching and bifurcation, as in the case of *Aspergillus* species, and their ability to excrete goloco-protein, as in the case of *Mucor* species, may all contribute to their presence [39]. *Aspergillus* spp. is widespread and makes use of a variety of nutrients and can grow on the majority of organic and inorganic nutrients and does not require any particular nutrients [41] which may be the reason for the higher percentage of *Aspergillus* spp. found in both samples. *Aspergillus fumigatus* and *Aspergillus flavus* are the most potent fungi known for causing respiratory illness in humans, such as allergic bronchopulmonary aspergillosis, chronic pulmonary aspergillosis and invasive aspergillosis [42], especially in immunocompromised people. Prolonged exposure to the air around these dumping sites leading to the inhalation of sufficient spores of fungi can give rise to several fungal-related diseases.

Bacteria like *Pseudomonas*, *Streptococcus*, *Serratia*, *Acinetobacter*, and *Clostridium* species and fungi like *Penicillium*, *Fusarium*, *Alternaria*, and *Cladosporium* species were not detected [10], [17], [21]. Numerous factors, including variations in the complexity of the disposed waste and physicochemical characteristics of the dump site, may be responsible for the difference in microorganisms found in this study and earlier studies. A diverse community of microorganisms may exist at the dumpsite due to the environment's variability [36].

Bacterial pathogens, mainly Gram-negative than Gram-positive, are among the leading pathogenic microorganisms and have been posing serious public health problems globally by developing antibiotic resistance (ABR) [36], [43]. ABR was highly observed in bacteria *Citrobacter* spp., *Salmonella* spp., and *Escherichia coli* isolated from dump site S3 with the antibiotics used while *Klebsiella* spp., *Enterobacter* spp., and *Staphylococcus aureus* were found to be sensitive (Table 4). A study by Emmanuel-akerele and Peter (2020), and Bashir et al., (2021) reported similar findings [44], [45]. *Salmonella* spp. and *Escherichia coli* are listed in Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report [46] because of their extensive resistance to different classes of antibiotics. Increased antibiotic resistance of *Citrobacter* spp. has been reported worldwide, with some strains harboring extended-spectrum β-lactamase (ESBL) [47]–[49]. The antibiotic resistance observed in *Proteus* spp. to Nalidixic Acid has also been reported in studies conducted by Pathirana et al., (2018) and Bashir et al., (2021) [44], [50]. Ventola (2015) describes excessive use, inappropriate prescribing, extensive agricultural use, lack of new antibiotics, and regulatory barriers are the major reasons for ABR [51]. The occurrence of a high level of antibiotic resistance to commonly used antibiotics could pose a risk of spreading the ABR to opportunistic pathogens, ultimately giving rise to different public health-related hazards. This demands a proper waste management system, as well as research programs to monitor for antimicrobial resistance determinants in municipal solid wastes [36].

Bacillus spp. and *Micrococcus* spp. were the most common among the identified bacteria in both solid waste and bioaerosol samples while *Aspergillus niger* and *Mucor* spp. were the most common among identified molds (Figure 1). Occurrence of the same organism in two different samples can imply that bacteria and molds present in solid waste of open dumping sites can be aerosolized.

V. CONCLUSION

Open dumping of solid waste is a common practice in Kathmandu city where dumping sites are mostly located in close proximity to the human settlement areas. This solid waste harbors different bacteria and molds and can be aerosolized. Due to the presence and distribution of antibiotic-resistant bacteria in waste dump sites there is a risk of spreading antibiotic resistance to opportunistic pathogens. *Aspergillus fumigatus* and *Aspergillus flavus* observed in bioaerosol samples are known for their pathogenic effects. The occurrence of these pathogenic organisms present the possibility of public health hazards. Development of proper waste disposal sites far away from residential areas of Kathmandu city and periodic monitoring of antibiotic resistance is imperative.

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