

Assessment of Common Abattoir Flies (*Musca Domestica*) As A Vector of Micro-Organisms in Damaturu Metropolis

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Abstract

This study investigates the common abattoir flies and their microbial carriage in Damaturu metropolis, Yobe State. The study was conducted to determine the population density of common abattoir flies, assess the aerobic mesophilic bacterial and fungal loads associated with the flies, and isolate and identify bacterial species carried by the flies. A descriptive cross-sectional research design was adopted. A total of 90 fly specimens were collected from the slaughtering area, processing area, and waste disposal area of Damaturu Abattoir over a period of three weeks using sterile sweep nets and sticky traps. The collected specimens were transported to the laboratory for morphological identification and microbiological analysis. Descriptive statistics, including frequencies, percentages, and microbial counts, were used for data presentation and analysis. The morphological examination identified two major fly groups, namely Calliphoridae (blow flies) and Sarcophagidae (flesh flies). The processing area recorded the highest overall fly population, accounting for 44.57% of the total population, with Sarcophagidae being more abundant. The total number of flies captured increased from 59 in Week One to 124 in Week Three. Microbiological examination revealed substantial aerobic mesophilic bacterial loads, with counts frequently reaching 10^7 CFU/mL. The highest bacterial counts were recorded during Week Two. Fungal examination also revealed considerable fungal loads, with counts reaching as high as 5×10^6 CFU/mL in some samples. Bacterial isolation and identification revealed the presence of *Escherichia coli*, *Klebsiella* spp., *Staphylococcus aureus*, *Shigella* spp., *Salmonella* spp., *Enterobacter* spp., and *Pseudomonas* spp. The study concluded that common abattoir flies in Damaturu metropolis carry substantial microbial loads and diverse bacterial species of public health importance. The study recommends improved abattoir sanitation, proper waste management, regular environmental health inspection, effective fly-control measures, and continuous health education for abattoir workers and meat handlers.

Keywords: Abattoir, flies, microbial, carriage, bacterial, fungal load, fly density, pathogenic

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1.1 Background to the Study

Flies are among the most ubiquitous and medically important insects associated with public health because of their ability to mechanically transmit disease-causing microorganisms.

Globally, studies estimate that over 65% of food contamination in open slaughter environments is linked to vector contact (Usman et al., 2022), with flies accounting for a large proportion of this burden. In developing countries, about 70–80% of poorly managed abattoirs report heavy fly infestation, increasing the risk of microbial transmission to meat consumers and nearby communities.

In Africa, studies estimate that approximately 60–75% of meat contamination in poorly managed slaughter facilities is associated with vector activities, especially flies (Mekonnen et al., 2023). In many African countries, open-area slaughtering practices, inadequate waste disposal and poor environmental sanitation contribute significantly to fly infestation. Reports indicate that about 70–85% of traditional abattoirs in sub-Saharan Africa experience persistent fly infestation, thereby increasing the risk of microbial transmission to meat handlers, consumers, and nearby communities (WHO, 2024).

Previous Nigerian studies have shown that 72% (72 out of 100) of sampled flies from slaughter environments carried at least one pathogenic microorganism (Musa et al., 2023). These microorganisms include bacteria, fungi, and parasites capable of causing serious health conditions such as food poisoning, diarrheal diseases, and systemic infections.

Damaturu metropolis, the capital of Yobe State, depends heavily on abattoir for meat supply. However, poor hygiene practices, inadequate waste management, and unregulated slaughtering activities have contributed

to increased fly populations and associated public health risks. Reports from similar northeastern settings indicate that about 68% of exposed meat samples become contaminated within 2–4 hours of slaughter due to fly contact (Fagbamigbe et al., 2022).

Despite these risks, there is limited localized evidence on the microbial carriage of common abattoir flies in Damaturu metropolis. This study therefore provides scientific data on the common abattoir flies and the microorganisms they carry. The study tends to determine the population density of common abattoir flies, identify aerobic mesophiles bacterial and fungal load from flies and to isolate and identify bacterial species from flies in Damaturu abattoir.

Concept of Abattoir Flies

Abattoirs, commonly known as slaughterhouses, are specialized facilities where animals are killed and processed for human consumption. These environments produce a large volume of organic waste, including blood, offal, hide trimmings, and faecal material, which attract various insects, especially flies (Lawal et al., 2023). When sanitation is poorly maintained, abattoirs can become hotspots for the transmission of infectious diseases. Public health concerns arise when flies, which feed and breed on decomposing matter, pick up and transfer pathogens to human environments (Ahmed and Musa, 2023). Abattoirs generate considerable amounts of organic waste, including animal blood, faeces, intestines, hides, bones, and wastewater. If not properly managed, these waste products serve as breeding grounds for disease vectors such as flies, rodents, and scavenger birds (Ahmed and Musa, 2024). Among these vectors, flies are the most concerning due to their ability to travel between contaminated surfaces and human environments, mechanically transmitting a wide range of pathogens including bacteria, fungi, and parasites (Ameh et al., 2023).

The World Health Organization (2022) emphasizes that food safety begins at the point of production and stresses the need for hygienic slaughtering practices and vector control in abattoirs to reduce the burden of zoonotic and foodborne diseases.

Factors Influencing Fly Proliferation

The high population of flies in abattoir environments is influenced by a combination of environmental, operational, and infrastructural factors. These factors determine the abundance, diversity, and persistence of flies, particularly in urban slaughterhouses with inadequate sanitation. In Nigeria, abattoirs such as those in Damaturu metropolis are often characterized by poor hygienic conditions, which significantly contribute to fly infestation and subsequent microbial contamination (Goni et al., 2021; Usman et al., 2022).

Foodborne Diseases and Gastrointestinal Infections

One of the most immediate public health risks associated with fly activity in abattoirs is the transmission of foodborne pathogens, including *Salmonella*, *Escherichia coli*, *Shigella spp.*, and *Campylobacter*. These bacteria are often carried on the flies' body parts, especially the legs, wings, and mouthparts, and can be deposited directly on meat, equipment, or food surfaces (Yakubu et al., 2022). In Nigeria, diarrheal diseases caused by *E. coli* and *Salmonella* are among the top causes of child morbidity and mortality, especially in areas with poor food hygiene (WHO, 2022). According to Musa et al. (2023), over 78% of flies sampled from abattoirs in northeastern Nigeria were contaminated with enteric bacteria capable of causing typhoid, cholera, and dysentery. These infections are not only prevalent but also easily spread through consumption of contaminated meat, water, or vegetables exposed to fly activity.

Fly Population Density

A study by Oyubu et al. (2025) investigated fly populations in urban abattoirs across Nigeria and reported a high abundance of *Musca domestica*, especially in areas with poor sanitation and waste disposal systems. The study confirmed that abattoirs are major breeding sites for flies.

Similarly, Adebayo et al. (2024) conducted a study in southwestern Nigeria and found that fly density was significantly higher in abattoirs compared to residential environments. The study linked high fly populations to poor hygiene and environmental conditions.

Another study by Ibrahim et al. (2022) in northern Nigeria reported that fly density increased during peak slaughter periods and in areas with accumulated waste, highlighting the influence of environmental factors on fly population.

Microbial Load of Flies

A study by Onwugamba et al. (2023) revealed that flies collected from Nigerian environments carried high microbial loads, including enteric and antimicrobial-resistant bacteria. The study emphasized the role of flies in spreading resistant pathogens.

In another study, Adebayo et al. (2024) found that flies from abattoirs had significantly higher bacterial loads compared to those from other environments, indicating their role in contamination.

Furthermore, Lawal et al. (2024) reported high microbial counts from flies collected in abattoirs in northern Nigeria, with bacterial loads exceeding acceptable safety limits.

These findings confirm that abattoir flies carry substantial microbial loads and pose serious contamination risks.

Isolation and Identification of Bacteria

A study by Omoregie et al. (2025) in Benin City identified several bacterial species from flies, including: *Escherichia coli*, *Pseudomonas aeruginosa*, *Proteus vulgaris*, and *Enterobacter cloacae*. The study also reported multidrug resistance among isolates.

Similarly, Onwugamba et al. (2023) identified enteropathogenic bacteria in flies, confirming their role in disease transmission.

Another study by Abdullahi et al. (2023) in Kano State reported the presence of *Salmonella* and *Staphylococcus aureus* in flies collected from abattoirs, further emphasizing their public health importance.

Methodology

This study employed a descriptive cross-sectional design to assess the presence, abundance, and microbial load of common abattoir flies in Damaturu metropolis. Adult flies found in and around selected abattoirs were Captured. A total of 90 fly specimens were selected for the study. Instrument used for Data Collection include; Sterile sweep net, Sterile containers, Personnel protective equipment, petri dish, Distilled water, Test tube and Selective differential media.

Flies were captured using; sterile sweep nets, sticky traps, with decomposing liver placed 1.5 m from slaughtering areas. Captured flies were transferred into sterile, ventilated containers and labeled based on location and date. Samples were chilled and transported to the laboratory within 2 hours of collection. Descriptive statistics such as frequency tables, percentages, and mean microbial counts was used for data presentation and analysis.

II. RESULTS

Table1: Morphological Identification of House Flies from Different Location in Damaturu Abattoir

Species Name	Common Name	Morphological Features
<i>Calli Phoridae</i>	Blow Flies or Carrion Flies	Adult are commonly shiny with metallic coloring often with blue thoraces and abdomen. Antennae are three segmented and aristate.
<i>Sarcophagi</i>	Flesh Flies	Red Eyes and bristled abdomen. The abdominal sternites are free and cover the margins of tergites

Table 1 above provides the foundational taxonomic classification of the house fly species collected during the study in Damaturu abattoir. Two families were identified: *Calli Phoridae* (Blow Flies) and *Sarcophagi* (Flesh Flies). The distinguishing features for *Calli Phoridae* include a shiny, metallic colored body, often with blue thoraces and abdomen, along with three segmented, aristate antennae. In contrast, *Sarcophagi* are characterized by red eyes and a bristled abdomen, where the abdominal sternites are free and cover the margins of the tergites. The identification allows the specific association of each fly type with its respective population dynamics and microbial load in subsequent results.

Table2: Determination of Population Density of house flies from different location in Damaturu Abattoir

Sampling Point	Species	Population (%)			TOTAL (%)
		Week1	Week2	Week3	
Slaughtering Area	<i>Calli Phoridae</i>	3 (5.0%)	2 (1.92%)	7(5.64%)	12(4.5%)
	<i>Sarcophagi</i>	9 (15.3%)	12(11.53%)	21(16.93%)	42(15.73%)
Processing Area	<i>Calli Phoridae</i>	4 (6.7%)	11(10.58%)	12(9.7%)	27(10.11%)
	<i>Sarcophagi</i>	24 (40.6%)	58(55.78%)	37(29.83%)	119(44.57%)
Waste Disposal Area	<i>Calli Phoridae</i>	15 (25.4%)	5(4.80%)	20(16.12%)	40(14.98%)
	<i>Sarcophagi</i>	4 (6.7%)	16(15.39%)	27(21.8%)	27(10.11%)
TOTAL (%)		59 (100%)	104(100%)	124(100%)	267(100%)

Table 2 above Represents Population density and distribution of the two fly species across three distinct locations within Damaturu abattoir over a three-week sampling period. The data reveals that the Processing Area had the highest overall fly population (44.57%), dominated by *Sarcophagi*. The Slaughtering Area and Waste Disposal Area showed lower total densities, at 15.73% and 25.09% respectively. Population trends varied by week

and location, with a general increase in total flies captured from Week 1 (59) to Week 3 (124). *Sarcophagi* were consistently more numerous than *Calli Phoridae* in the Slaughtering and Processing Areas, where as their numbers were comparable in the Waste Disposal Area. This distribution suggests that the Processing Area, likely due to the presence of exposed meat products, provides a more favorable environment for fly proliferation, particularly for flesh flies.

Table 3: Aerobic Mesophiles Bacteria of house flies from different location in Damaturu Abattoir

Location	Species	Number of Colonies (Cfu/mL)		
		Week1	Week2	Week3
Slaughtering Area	<i>Calli Phoridae</i>	1.0X10 ⁵	4.4X10 ⁷	1.7X10 ⁶
	<i>Sarcophagi</i>	7.2 X10 ⁶	6X10 ⁷	3.1 X10 ⁶
Processing Area	<i>Calli Phoridae</i>	6.0 X10 ⁶	3.9 X10 ⁷	1X10 ⁶
	<i>Sarcophagi</i>	1.09 X10 ⁷	5.4 X10 ⁷	1.9 X10 ⁶
Waste Disposal Area	<i>Calli Phoridae</i>	5.1 X10 ⁶	7 X10 ⁷	3 X10 ⁶
	<i>Sarcophagi</i>	2.04 X10 ⁷	5.5 X10 ⁷	3.7 X10 ⁶

The total aerobic mesophilic bacterial load (in colony-forming units per milliliter, CFU/mL) carried by the flies from different locations in Damaturu Abattoir. (Table 4.3) The results indicate that all fly samples carried substantial bacterial loads, with counts frequently reaching 10⁷ CFU/mL, demonstrating that both fly species are significant vectors of general bacteria. The highest bacterial counts were often recorded in Week 2 across most locations and species. *Sarcophagi* from the Slaughtering Area and *Calli Phoridae* from the Waste Disposal Area in Week 2 showed remarkably high counts of 6x10⁷ and 7x10⁷ CFU/mL, respectively. This suggests that flies are consistently contaminated with high levels of environmental bacteria, with the variation across weeks potentially linked to changes in abattoir hygiene conditions, temperature, or the amount of waste present at the time of sampling.

Table4: Enumeration of Fungi of House Flies from different location in Damaturu Abattoir

Location	Species	Number of Colonies (Cfu/mL)		
		Week1	Week2	Week3
Slaughtering Area	<i>Calli Phoridae</i>	4.5x10 ²	1x10 ⁶	2 X10 ¹
	<i>Sarcophagi</i>	7.9x10 ²	3x10 ⁶	4 X10 ¹
Processing Area	<i>Calli Phoridae</i>	9.8x10 ²	3x10 ⁶	8 X10 ¹
	<i>Sarcophagi</i>	1.09x10 ³	5x10 ⁶	7 X10 ¹
Waste Disposal Area	<i>Calli Phoridae</i>	1.7x10 ²	5x10 ⁶	0
	<i>Sarcophagi</i>	1.8x10 ²	3x10 ⁶	2 X10 ¹

Table 4 above show details of the fungal load (CFU/mL) carried by the collected flies. Similar to the bacterial enumeration, the fungal counts were substantial, particularly in Week 2, where values as high as 5x10⁶ CFU/mL were recorded for *Calli Phoridae* in the Waste Disposal Area. A notable observation is the absence of fungi on *Calli Phoridae* from the Waste Disposal Area in Week 3. The data shows that *Sarcophagi* in the Processing Area consistently carried high fungal loads across the weeks. The results confirmed that house flies are not only bacterial vectors but also effectively carry and potentially disseminate fungal spores. The temporal spike in Week 2 for both bacteria and fungi could indicate a common environmental factor, such as humidity or organic matter availability, that favored microbial proliferation during that period.

Table 4.5: Enumeration of Bacterial Species of House Flies From Different Location in Damaturu Abattoir

Sampling Point	Species	Period	Number of Colonies (Cfu/mL)						
			<i>E. coli</i>	<i>K. pneumoniae</i>	<i>S. aureus</i>	<i>Shigella Spp</i>	<i>Salmonella Spp</i>	<i>Enterobacter spp</i>	<i>Pseudomonas spp</i>
SA	<i>Calli Phoridae</i>	W1	0	1X10 ⁴	3 X10 ⁴	0	0	2 X10 ⁴	0
		W2	7.5 X10 ⁵	4.2X10 ⁵	4.2 X10 ⁵	6.2X10 ⁵	0	4.8 X10 ⁵	0
		W3	0	7X10 ⁵	2 X10 ⁵	0	0	0	0
	<i>Sarcophagi</i>	W1	6 X10 ⁴	3 X10 ⁴	6 X10 ⁴	0	0	2 X10 ⁴	0
		W2	8.3 X10 ⁵	5.2X10 ⁵	1.9 X10 ⁵	4.2X10 ⁵	0	4.1 X10 ⁵	0
		W3	0	1.5X10 ⁶	1X10 ⁵	4X10 ⁶	0	0	0
PA	<i>Calli Phoridae</i>	W1	0	0	1.50X10 ⁶	0	0	1 X10 ⁴	0
		W2	5.10 X10 ⁴	6.2X10 ⁵	1.9 X10 ⁵	7.8X10 ⁵	0	4 X10 ⁵	0
		W3	0	1.46X10 ⁷	5.2X10 ⁶	6X10 ⁶	1 X10 ⁶	3.8 X10 ⁶	0

WDA	<i>Sarcophagi</i>	W1	0	1.3 X10 ⁶	2.09X10 ⁶	0	0	7 X10 ⁴	0
		W2	3.9 X10 ⁵	5.3 X10 ⁵	8.5 X10 ⁵	3.2X10 ⁶	0	4.6 X10 ⁵	7x10 ⁵
		W3	0	9.2 X10 ⁶	1.3 X10 ⁶	3.8X10 ⁶	4.4 X10 ⁶	3.5 X10 ⁶	0
	Calli Phoridae	W1	0	2 X10 ⁴	9.6 X10 ⁵	0	0	0	0
		W2	5 X10 ⁴	2.9 X10 ⁵	4.6 X10 ⁵	1.29X10 ⁵	0	1.3 X10 ⁵	0
		W3	0	5.2 X10 ⁶	4X10 ⁵	0	7 X10 ⁵	0	0
	<i>Sarcophagi</i>	W1	0	0	1.03X10 ⁴	0	0	0	0
		W2	6.9 X10 ⁵	4.7 X10 ⁵	2.3 X10 ⁵	3.8 X10 ⁶	0	5.2 X10 ⁵	0
		W3	0	4.4 X10 ⁶	6X10 ⁵	1.3 X10 ⁶	9 X10 ⁵	0	0

KEY; SA: Slaughtering Area, **PA:** Processing Area, **WDA:** Waste Disposal Area

The detailed breakdown of (Table 5) presents specific pathogenic and opportunistic bacteria isolated from the flies, offering critical insight into their role as disease vectors. The enumeration reveals a diverse and concerned of bacteria, including *E. coli*, *Klebsiella* spp, *Staphylococcus aureus*, *Shigella* spp., *Salmonella* spp., *Enterobacter* spp., and *Pseudomonas* spp. The data shows distinct spatial and temporal variations in bacterial prevalence. *Shigella* spp. was particularly abundant in the Processing Area during Week 3 on both fly species, with counts reaching 4x10⁶ and 3.8x10⁶ CFU/mL. *Salmonella* spp., a major foodborne pathogen, was isolated exclusively in Week 3, primarily from the Processing and Waste Disposal Areas. The presence of *S. aureus* and *K. pneumoniae* across all locations and weeks underscores the flies' constant exposure to sources of infection. This specific identification is vital for public health risk assessment, as it directly links flies in the abattoir to the potential transmission of serious enteric and pyogenic diseases to humans through food contamination.

Table 6: Morphological features of isolated Bacteria on Differential Media

Isolates	Morphological features
<i>E. coli</i>	Green metallic sheen on EMB
<i>Klebsiella</i> spp	Pink mucoid colonies on EMB
<i>S. aureus</i>	Golden yellow colonies on MSA
<i>Shigella</i> spp	Colorless colonies on SSA
<i>Salmonella</i> spp	Colorless colonies with black at the center on SSA
<i>Enterobacter</i> spp	Pink to purple colonies on EMB
<i>Pseudomonas</i> spp	Green pigment colonies on NA

KEY; EMB: Eosin Metallic Blue **MSA:** Mannitol Salt Agar, **NA:** Nutrient Agar, **SSA:** Salmonella Shigella Agar

Table 6 serves as a key for the bacteriological methodology, describing the characteristic colonial morphology of each bacterial isolate on specific selective and differential culture media. These distinctive features were essential for the preliminary identification of the bacteria listed in Table 4.. such as, *E. coli* was identified by its green metallic sheen on Eosin Methylene Blue (EMB) agar, while *Klebsiella* and *Enterobacter* spp. formed pink mucoid and pink to purple colonies on the same medium, respectively. *S. aureus* was characterized by its golden yellow colonies on Mannitol Salt Agar (MSA). The table clearly differentiates between *Salmonella* and *Shigella* on Salmonella Shigella Agar (SSA), with the former producing colorless colonies with a black center due to H₂S production. This methodological transparency confirmed that the identifications were based on standard, reliable microbiological techniques.

III. Findings

The study identified two major fly families in Damaturu abattoir: Calli Phoridae (Blow Flies) and Sarcophagi (Flesh Flies). The morphological characteristics observed were consistent with standard entomological descriptions (Ameh et al., 2023). The presence of these fly species in abattoir environments is well-documented, as these flies are attracted to decomposing organic matter, blood, and animal tissues commonly found in slaughter facilities (Lawal et al., 2023).

The population density assessment revealed that the Processing Area had the highest fly population (44.57%), dominated by Sarcophagi (119 out of 267 total flies). This finding is consistent with studies by Oyubu et al. (2025), who reported high abundance of *Musca domestica* and related species in urban abattoirs, especially in areas with poor sanitation and waste disposal systems. The predominance of Sarcophagi in the Processing Area can be attributed to the presence of exposed meat products and blood, which serve as ideal breeding and feeding sites for flesh flies (Goni et al., 2022).

The increasing fly population trend from Week 1 (59 flies) to Week 3 (124 flies) suggests that fly proliferation intensifies over time in the absence of effective vector control measures. This observation aligns with the findings of Adebayo et al. (2024), who reported that fly density was significantly higher in abattoirs compared to residential environments, and that fly populations increased during peak slaughter periods. The variation in fly abundance across weeks may be attributed to factors such as temperature, humidity, waste accumulation, and slaughter activities (Yakubu et al., 2022; Ahmed and Musa, 2023).

However, the presence of significant fly populations in all the locations confirms that abattoirs serve as major breeding sites for flies, supporting the findings of Ibrahim et al. (2022), who reported that fly density increased in areas with accumulated waste and poor sanitation.

Bacterial Load Carried by Abattoir Flies

The enumeration of aerobic mesophilic bacteria revealed substantial bacterial loads carried by all fly samples, with counts frequently reaching 10^7 CFU/mL. This finding is consistent with Onwugamba et al. (2023), who reported that flies collected from Nigerian environments carried high microbial loads, including enteric and antimicrobial-resistant bacteria. The high bacterial loads indicate that flies in abattoir environments are heavily contaminated with environmental bacteria, which they acquire through contact with contaminated surfaces, waste materials, and animal tissues (Usman et al., 2022).

The highest bacterial counts were recorded in Week 2 across most locations, with Sarcophagi from the Slaughtering Area and Calli Phoridae from the Waste Disposal Area showing counts of 6×10^7 and 7×10^7 CFU/mL respectively. This temporal variation may be linked to changes in abattoir hygiene conditions, temperature, or the amount of waste present at the time of sampling. Adebayo et al. (2024) similarly found that flies from abattoirs had significantly higher bacterial loads compared to those from other environments, indicating their role in contamination.

The consistently high bacterial loads carried by both fly species confirm that abattoir flies are significant vectors of general bacteria. This finding is particularly concerning given the proximity of abattoirs to residential areas and open markets in Damaturu metropolis, as flies can easily migrate from contaminated slaughter surfaces to human food and living environments (Musa et al., 2023; Gambo et al., 2022). The presence of such high bacterial loads on flies underscores the urgent need for improved sanitation and vector control measures in abattoirs to reduce the risk of bacterial transmission to meat products and consumers.

Fungal Load Carried by Abattoir Flies

The fungal enumeration revealed substantial fungal loads carried by the collected flies, with values as high as 5×10^6 CFU/mL recorded for Calli Phoridae in the Waste Disposal Area during Week 2. This finding is consistent with Oluwafemi and Sulaiman (2022), who reported that flies are capable of spreading fungal spores such as *Aspergillus* spp., *Penicillium* spp., and *Candida albicans*, which can cause mycotic infections, especially in immunocompromised individuals.

The data showed that Sarcophagi in the Processing Area consistently carried high fungal loads across the sampling weeks, suggesting that the presence of organic matter and moisture in processing areas provides favorable conditions for fungal growth and subsequent attachment to flies. This observation aligns with the findings of Ameh et al. (2023), who reported that flies from abattoirs harbored significant fungal loads, particularly in areas with poor ventilation and high humidity.

The notable absence of fungi on Calli Phoridae from the Waste Disposal Area in Week 3 is an interesting observation that may be attributed to environmental factors such as reduced humidity, waste removal, or the effects of vector control measures. However, the overall high fungal loads carried by flies confirm that they are not only bacterial vectors but also effectively carry and potentially disseminate fungal spores (Oluwafemi and Sulaiman, 2022).

The temporal spike in Week 2 for both bacteria and fungi could indicate a common environmental factor, such as increased humidity or organic matter availability, that favored microbial proliferation during that period. This finding is consistent with the observations of Yakubu et al. (2022), who noted that fly abundance and microbial carriage are influenced by climatic conditions, particularly during Nigeria's rainy season when moisture levels in organic waste are optimal for microbial growth.

Isolation and Identification of Pathogenic Bacteria

The isolation and identification of bacterial species revealed a diverse range of pathogenic and opportunistic bacteria including *E. coli*, *Klebsiella* spp., *Staphylococcus aureus*, *Shigella* spp., *Salmonella* spp., *Enterobacter* spp., and *Pseudomonas* spp. This finding is consistent with Omoregie et al. (2025), who identified several bacterial species from flies in Benin City, including *E. coli*, *Pseudomonas aeruginosa*, *Proteus vulgaris*, and *Enterobacter cloacae*. Similarly, Onwugamba et al. (2023) identified enteropathogenic bacteria in flies, confirming their role in disease transmission.

The presence of *E. coli*, *Klebsiella* spp., and *Enterobacter* spp. across all locations and weeks indicates that flies are constantly exposed to sources of these opportunistic pathogens. These bacteria are commonly associated with fecal contamination and can cause serious infections, particularly in immunocompromised individuals (Lawal et al., 2021). The high prevalence of these bacteria on abattoir flies suggests that fecal contamination from animal waste and poor sanitation is widespread in the study area.

Shigella spp. was particularly abundant in the Processing Area during Week 3 on both fly species, with counts reaching 4×10^6 and 3.8×10^6 CFU/mL. This finding is alarming as *Shigella* is a major cause of bacillary dysentery, a severe diarrheal disease that can be life-threatening, especially in children and the elderly (WHO, 2024). The presence of *Shigella* on flies in the Processing Area, where meat products are handled, poses a serious risk of foodborne transmission to consumers.

Salmonella spp., a major foodborne pathogen, was isolated exclusively in Week 3, primarily from the Processing and Waste Disposal Areas. This finding is consistent with Abdullahi et al. (2023), who reported the presence of *Salmonella* in flies collected from abattoirs in Kano State, further emphasizing their public health importance. The isolation of *Salmonella* from flies is particularly concerning given its association with typhoid fever and salmonellosis, which are major public health problems in Nigeria (Musa et al., 2023).

The presence of *S. aureus* and *K. pneumoniae* across all locations and weeks underscores the flies' constant exposure to sources of infection. *S. aureus* is a common cause of skin infections, food poisoning, and systemic infections, while *K. pneumoniae* is associated with pneumonia, urinary tract infections, and bloodstream infections (Lawal et al., 2024). The high prevalence of these bacteria on abattoir flies indicates that abattoir environments serve as reservoirs for clinically important pathogens that can be mechanically transmitted to humans.

The isolation of *Pseudomonas* spp., though less frequent than other bacteria, is also noteworthy as *Pseudomonas* is an opportunistic pathogen that can cause serious infections in hospitalized patients and individuals with compromised immune systems (Bako et al., 2023). The presence of *Pseudomonas* on abattoir flies highlights the potential for transmission of healthcare-associated pathogens through environmental contamination.

The spatial and temporal variations in bacterial prevalence observed in this study are consistent with the findings of Fagbamigbe et al. (2022), who reported that bacterial carriage by flies is influenced by environmental factors such as temperature, humidity, and the availability of organic matter. The higher prevalence of *Salmonella* and *Shigella* in Week 3 may be attributed to increased fly activity, changes in waste accumulation, or reduced hygiene practices during that period.

The specific identification of pathogenic bacteria on abattoir flies is vital for public health risk assessment, as it directly links flies in the abattoir to the potential transmission of serious enteric and pyogenic diseases to humans through food contamination. This finding underscores the urgent need for improved abattoir sanitation, effective vector control measures, and public health education to reduce the risk of fly-borne disease transmission in Damaturu metropolis.

IV. CONCLUSION

Based on the findings of this study, the following conclusions were drawn:

- The common abattoir flies in Damaturu metropolis belong to two families: Calli Phoridae (Blow Flies) and Sarcophagi (Flesh Flies). These flies are attracted to the organic waste and animal tissues present in abattoir environments.
- The Processing Area had the highest fly population, dominated by Sarcophagi. Fly populations increased over the three-week sampling period, indicating continuous fly proliferation in the absence of effective vector control measures. The high fly density in the Processing Area, where meat products are handled, poses a significant risk of food contamination.
- All fly samples carried substantial bacterial and fungal loads, with counts frequently reaching 10^7 CFU/mL for bacteria and 10^6 CFU/mL for fungi. The high microbial loads confirm that abattoir flies are significant vectors of microorganisms and play a major role in environmental contamination and disease transmission.
- The flies carried diverse pathogenic and opportunistic bacteria including *E. coli*, *Klebsiella* spp., *Staphylococcus aureus*, *Shigella* spp., *Salmonella* spp., *Enterobacter* spp., and *Pseudomonas* spp. The presence of *Salmonella* and *Shigella* on flies is particularly concerning as these are major causes of foodborne diseases.
- The study confirms that abattoir flies in Damaturu metropolis are mechanical vectors of clinically important pathogens and pose serious public health risks to abattoir workers, meat handlers, and consumers. The presence of these pathogens on flies highlights the need for urgent public health interventions.
- The high fly populations and microbial loads observed in the study area indicate that current vector control measures and sanitation practices are inadequate. Effective fly control programs, improved waste management, and regular sanitation are necessary to reduce fly populations and minimize disease transmission.
- The findings underscore the interconnectedness of human, animal, and environmental health in the context of abattoir operations. A One Health approach that integrates public health, veterinary, and environmental health interventions is essential for addressing the complex public health challenges identified in this study.

V. RECOMMENDATIONS

Based on the findings and evidence from this study, the following recommendations are made:

1. Government should invest in modern abattoir facilities with proper infrastructure including walls, roofs, fly screens, drainage systems, and waste management facilities to reduce fly access and breeding.
2. Environmental health authorities should enforce strict compliance with environmental sanitation laws in abattoirs. Regular inspections should be conducted, and penalties should be imposed for non-compliance with waste handling and fly control protocols.
3. Government should establish and support structured vector control programs in abattoirs, including fumigation, insecticide spraying, mechanical traps, and biological control agents. These programs should be implemented consistently and monitored for effectiveness.
4. Abattoir workers should adopt good hygiene practices including regular cleaning and disinfection of slaughter areas, proper waste disposal, and personal hygiene measures. Meat should be covered during processing and storage to prevent fly contact.
5. Train Abattoir Workers: Abattoir workers should receive training on fly-borne diseases, hygiene practices, and the importance of vector control. Training programs should emphasize the health risks associated with poor sanitation and the role of flies in disease transmission.
6. Environmental health officers should conduct regular inspections of abattoirs to assess sanitation practices, fly control measures, and compliance with environmental health regulations.

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