



(RESEARCH ARTICLE)



MICROBIOLOGICAL EXAMINATION OF *MUSCA DOMESTICA* (HOUSEFLY) AS AN AGENT FOR THE SPREAD OF ANTIBIOTIC-RESISTANT BACTERIA IN CALABAR, CROSS RIVER STATE, NIGERIA

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ABSTRACT

This study investigated the role of *Musca domestica* (houseflies) in the carriage and potential dissemination of antibiotic-resistant bacteria in Calabar, Cross River State, Nigeria. Fifty adult houseflies were collected by random sampling from homes, markets, schools and hospitals and examined using conventional microbiological methods. Bacterial isolates were identified by Gram staining and biochemical tests, and antimicrobial susceptibility was assessed using the disc diffusion method. Five bacterial groups were recovered: *Staphylococcus aureus* (14/50; 28%), *Escherichia coli* (12/50; 24%), *Clostridium* spp. (10/50; 20%), *Salmonella* spp. (8/50; 16%) and *Shigella* spp. (6/50; 12%). Markets yielded the highest number of isolates (17/50; 34%), followed by hospitals (15/50; 30%), homes (10/50; 20%) and schools (8/50; 16%). Gram-negative isolates accounted for 26/50 (52%) and Gram-positive isolates for 24/50 (48%). The susceptibility profile showed substantial resistance to several commonly used antibiotics, particularly Septrin, Sparfloxacin and Amoxicillin, with resistance also observed to other agents. These findings support the public-health importance of houseflies as mechanical carriers of potentially resistant bacteria and underscore the need for improved sanitation, fly control, antimicrobial stewardship and routine surveillance. Because the study was based on phenotypic testing and a small, geographically limited sample, molecular confirmation of resistance genes is recommended in future work.

Keywords: Housefly (*Musca domestica*); Antimicrobial resistance; Antibiotic resistance; Bacterial pathogens; Calabar; Nigeria

1 INTRODUCTION

Antimicrobial resistance (AMR) is a major global health challenge because it reduces the effectiveness of medicines used to treat bacterial infections. AMR is also a One Health problem involving humans, animals and the shared environment [1]. The emergence and dissemination of resistance are accelerated by inappropriate antimicrobial use and by horizontal gene transfer through mechanisms such as conjugation, transformation and transduction [2,3].

Houseflies (*Musca domestica*) are cosmopolitan insects closely associated with human settlements, livestock facilities, markets, hospitals and waste sites. Their feeding and breeding behaviour exposes them to faeces, decaying organic matter, food waste and other contaminated substrates. They can subsequently transfer microorganisms to food, surfaces and humans through their legs, mouthparts, regurgitation and faeces [4,5]. More than 100 pathogens have been associated with houseflies, including bacterial pathogens such as *Escherichia coli*, *Salmonella* spp., *Shigella* spp. and *Staphylococcus aureus* [6].

Evidence also indicates that flies may carry antimicrobial-resistant bacteria and resistance determinants. Arthropods collected in healthcare environments have been reported to harbour clinically important resistance genes, while houseflies associated with farms and waste environments may facilitate movement of resistance traits between environmental reservoirs and human settings [7,8]. The public-health relevance is heightened where sanitation is inadequate and antibiotics are heavily used.

Despite the importance of environmental reservoirs in AMR transmission, local evidence on the bacterial and antimicrobial susceptibility profiles of houseflies in Calabar remains limited. This study therefore examined bacteria associated with *M. domestica* collected from selected environments in Calabar and assessed their antimicrobial susceptibility patterns.

2 METHODS

2.1 Study area

The study was conducted in Calabar, the capital of Cross River State, southeastern Nigeria. Calabar is located approximately at 4.98°N and 8.34°E and comprises Calabar Municipal and Calabar South Local Government Areas. The city contains residential areas, markets, schools and healthcare facilities that provide diverse environments for housefly activity.

2.2 Study design, subject and sample size

This was a descriptive laboratory-based study of adult houseflies (*Musca domestica*). A total of 50 flies were collected. Sampling was random and covered homes, markets, schools and hospitals/health facilities in Calabar.

3 MATERIALS

Materials included sterile fly traps, sterile containers, sterile swab sticks, sterile pins, Petri dishes, culture media/agar, inoculating wire loops, incubator and antibiotic susceptibility testing materials. Sample collection and laboratory processing

Live houseflies were collected into sterile containers and transported to the laboratory. Individual flies were secured on sterile cardboard with a sterile pin and sampled using a sterile swab. The swab was inoculated onto prepared culture media and streaked with a sterile wire loop to obtain discrete colonies. Plates were incubated at 37°C for 24–48 h. Representative colonies were subjected to Gram staining and biochemical identification, including catalase, oxidase, indole, Salmonella-Shigella agar (SSA), hydrogen sulphide production and Kligler's Iron Agar (KIA) reactions.

3.1 Antimicrobial susceptibility testing

Antimicrobial susceptibility was assessed by the disc diffusion method. The antibiotics reported in the source dataset were Septrin (SXT), Cephalexin (CH), Sparfloxacin (SP), Ampiclox (APX), Gentamicin (CN), Pefloxacin (PEF), Streptomycin (S), Erythromycin (E), Zinnacef (Z), Amoxicillin (AM), Rocephin (R), Ciprofloxacin (CPX) and Augmentin (AU). Results were recorded as resistant (R) or sensitive (S).

3.2 Data analysis

Frequencies and percentages were used to summarize bacterial isolates and their distribution across collection sites. The analysis was descriptive; no inferential statistical testing was reported in the original dataset.

4 RESULTS

Table 1: Bacterial isolates recovered

Bacterial isolate	Number	Percentage (%)
Staphylococcus aureus	14	28
Clostridium spp.	10	20
Escherichia coli	12	24
Salmonella spp.	8	16
Shigella spp.	6	12
Total	50	100

Table 2: Distribution by collection area

Isolate	Home	Market	School	Hospital	Total
Staphylococcus aureus	3	5	2	4	14
Clostridium spp.	2	3	1	4	10
Escherichia coli	2	4	3	3	12
Salmonella spp.	1	3	1	3	8
Shigella spp.	2	2	1	1	6
Total	10	17	8	15	50

Markets accounted for 34% of all isolates, hospitals 30%, homes 20% and schools 16%.

Table 3: Biochemical reactions

Isolate	Catalase	Oxidase	Indole	SSA	H ₂ S	KIA
Staphylococcus aureus	+	–	–	No growth	–	+/-
Escherichia coli	+	–	+	Moderate growth	–	+/-
Clostridium spp.	–	–	Variable	Poor growth	+	+/-
Salmonella spp.	–	–	–	Good growth	+	+
Shigella spp.	–	–	–	Good growth	–	+

The biochemical profile was used together with Gram staining and culture characteristics for phenotypic identification.

Table 4: Gram reaction

Gram reaction	Bacterial species	Number	Percentage
Gram-positive	<i>S. aureus</i> and <i>Clostridium</i> spp.	24	48%
Gram-negative	<i>E. coli</i> , <i>Salmonella</i> spp. and <i>Shigella</i> spp.	26	52%
Total		50	100%

Table 5: Antibiotic susceptibility pattern

Isolate	SXT	CH	SP	APX	CN	PEF	S	E	Z	AM	R	CPX	AU
<i>S. aureus</i>	R	R	R	S	S	S	S	R	S	R	S	R	R
<i>E. coli</i>	R	S	R	S	S	S	S	S	S	R	R	S	R
<i>Clostridium spp.</i>	S	R	R	R	S	S	R	R	S	R	S	S	S
<i>Salmonella spp.</i>	R	S	S	S	R	R	R	S	R	R	S	R	R
<i>Shigella spp.</i>	R	R	R	S	S	R	R	S	R	S	S	R	—

R = resistant; S = sensitive. The source manuscript contained a formatting ambiguity in the *Shigella* row and did not clearly provide a value for Augmentin; this is retained as missing (—) rather than inferred.

5 DISCUSSION

The recovery of five bacterial groups from houseflies demonstrates that *M. domestica* can carry a diverse bacterial burden in the environments sampled. *S. aureus* was the most frequent isolate (28%), followed by *E. coli* (24%), *Clostridium spp.* (20%), *Salmonella spp.* (16%) and *Shigella spp.* (12%). The predominance of *S. aureus* is consistent with reports of substantial bacterial contamination of houseflies collected from hospitals and waste sites [9]. The recovery of *E. coli*, *Salmonella* and *Shigella* is particularly relevant because these organisms are associated with faecal and food contamination and can be mechanically transferred by flies [8].

The highest number of isolates was associated with market and hospital collections. These settings may provide abundant food residues, organic waste, human activity and other contaminated substrates that favour fly contact with microorganisms. Similar observations have linked flies from waste-rich or healthcare environments with substantial bacterial carriage [10,5]. The lower number of isolates from schools and homes may reflect differences in sanitation, waste exposure and fly density, although the present study cannot establish causal relationships.

Gram-negative organisms accounted for 52% of isolates, compared with 48% Gram-positive organisms. Gram-negative bacteria possess an outer membrane that can contribute to intrinsic or acquired resistance to antimicrobial agents, making their presence in environmental vectors of potential concern [11]. However, Gram reaction alone does not establish antibiotic resistance and should not be interpreted as a surrogate for a resistance phenotype.

The susceptibility results showed resistance across several commonly used antibiotics, including Septrin, Sparfloxacin and Amoxicillin, with resistance also observed to other agents. This pattern is consistent with the broader concern that environmental and animal-associated bacteria can participate in the maintenance and movement of antimicrobial resistance traits [1,80]. Nevertheless, the present study used phenotypic susceptibility testing and did not identify specific resistance genes; therefore, the findings demonstrate phenotypic resistance rather than molecularly confirmed AMR determinants.

Overall, the findings support the public-health relevance of houseflies as mechanical carriers of bacteria in Calabar. Their movement between contaminated sites and human-associated environments provides a plausible route for dissemination. Improved sanitation, waste management, fly control and responsible antimicrobial use are therefore important components of AMR prevention.

6 CONCLUSION

Houseflies collected from selected environments in Calabar carried potentially pathogenic bacteria, including *S. aureus*, *E. coli*, *Clostridium spp.*, *Salmonella spp.* and *Shigella spp.* Markets and hospitals yielded the largest numbers of isolates. Phenotypic antimicrobial testing demonstrated resistance to multiple commonly used antibiotics among the recovered bacteria. The findings indicate that *M. domestica* may contribute to the environmental dissemination of antibiotic-resistant bacteria and reinforce the need for integrated sanitation, vector-control and antimicrobial-stewardship measures.

Recommendations

- Implement sustained community education on fly control, food hygiene, hand hygiene and safe waste disposal.
- Strengthen sanitation and waste-management practices in markets, hospitals, homes and other fly-prone environments.

- Adopt integrated fly-control measures, including removal of breeding sites, covered waste containers, environmental cleaning and appropriate traps or insect-control measures.
- Strengthen antimicrobial stewardship in healthcare facilities to promote appropriate antibiotic selection, dosing and duration and to reduce unnecessary antibiotic use.
- Establish routine environmental surveillance of bacterial contamination and antimicrobial susceptibility in high-risk settings.
- Future studies should use larger, stratified samples across seasons and should confirm fly species identification.
- Future research should employ PCR or sequencing to identify specific resistance genes and investigate the potential for horizontal transfer of AMR determinants.
- Future studies should quantify bacterial load and include appropriate quality-control and statistical procedures to improve comparability and inference.

6.1 Study limitations

The study was limited by its sample size of 50 flies, restricted collection sites and single sampling period. Species identification of the collected flies was not independently confirmed, total bacterial load was not quantified, and some culture plates were reportedly affected by irregular electricity supply. The antimicrobial panel was also limited. Finally, resistance genes were not characterized molecularly, so the study cannot determine the specific genetic mechanisms underlying the observed resistance.

STATEMENTS ON COMPLIANCE WITH ETHICAL STANDARDS

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Disclosure of conflict of interest

The authors declare that they have no competing interests, financial or otherwise, that could have influenced the work reported in this manuscript.

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