Eurasia Specialized Veterinary Publication

International Journal of Veterinary Research and Allied Science

2024, Volume 4, Issue 1, Page No: 1-6

Investigation of Bacterial Contamination in House Flies across Various Environments

G. Gioia[1]*, J. Freeman[2], A. Sipka[1], C. Santisteban[1], M. Wieland[1], V. Alanis Gallardo[1,3], V. Monistero[4], J.G. Scott[2], P. Moroni[1,4]

[1]Quality Milk Production Services, Animal Health Diagnostic Center, Cornell University, Ithaca, NY 14850.
[2]Department of Entomology, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY 14853.
[3]Departamento de Medicina Preventiva y Salud Pública, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, CDMX 04510, México.
[4]Dipartimento di Medicina Veterinaria, Università degli Studi di Milano, Via dell'Università, 6, 26900 Lodi LO, Italy.

***E-mail** ✉ gg363@cornell.edu

ABSTRACT

Musca domestica is a key vector for transferring harmful pathogens from contaminated surfaces to humans. Several studies have confirmed the critical role of houseflies in the spread of various infectious diseases. This research aimed to investigate the bacterial contamination present in *M. domestica* from diverse environments. Samples were collected from locations such as slaughterhouses, coastal regions, hospital premises, and both rural and urban waste sites. Once collected, the samples were placed in sterile glass containers, and bacterial isolation and identification were performed in the laboratory. The results showed that *Escherichia coli* was the predominant species. The majority of contamination was associated with *E. coli*, followed by *Staphylococcus aureus*, *Enterobacter aerogenes*, and *Staphylococcus epidermidis*. This study highlights the potential of houseflies to act as vectors of harmful pathogens in public spaces. To prevent the spread of infection and contamination in different environments, it is essential to implement and enhance sanitary measures aimed at controlling these insects.

Keywords: Transmission, *Musca domestica*, Diseases, Pathogenic organisms

Received: 20 December 2023
Revised: 22 February 2024
Accepted: 23 February 2024

How to Cite This Article: Gioia G, Freeman J, Sipka A, Santisteban C, Wieland M, Gallardo VA, et al. Investigation of Bacterial Contamination in House Flies across Various Environments. Int J Vet Res Allied Sci. 2024;4(1):1-6.

Introduction

Houseflies are frequently close to humans, coming into contact with food and human waste [1-3]. This constant interaction allows them to serve as vectors, transmitting harmful pathogens from contaminated surfaces to people. Studies have demonstrated the significant role of houseflies in spreading diseases, particularly intestinal infections caused by gram-negative bacteria such as Salmonella, Shigella, and Campylobacter [4-9]. Flies are also implicated in the transmission of gram-positive bacteria, including Streptococci and Staphylococci [10, 11]. Their ability to pick up pathogens from various environments is facilitated by the structure of their proboscis, which can easily become contaminated due to their fine hairs. Furthermore, the sticky secretion from the fly's hairy legs further enhances its capacity to spread pathogens. As a result, it isn't surprising that over 100 different species of pathogenic microorganisms have been isolated from the digestive tracts of houseflies [12, 13].

Pathogenic bacteria can persist on the surface of houseflies' bodies and within their digestive systems for extended periods. Houseflies are capable of ingesting liquid food and typically regurgitate it to dilute solids for easier digestion. Furthermore, during feeding, they may deposit fecal droplets. Wolff's research demonstrated a connection between enteric fever and houseflies, noting that *Salmonella typhi* and *Salmonella paratyphi* type A are carried by flies and can survive within their bodies for prolonged periods [14].

Other studies have suggested that houseflies could also serve as vectors for *Helicobacter pylori*, especially if they contaminate food that has been exposed to human waste. *H. pylori* infection is one of the most common chronic bacterial infections in humans worldwide, affecting a significant portion of the global population [15, 16]. Research by Cohen *et al*. [17], Metwally *et al*. [18], and Esrey *et al*. [19] highlighted a notable correlation between fly populations and outbreaks of diarrhea and shigellosis. Additionally, Emerson *et al*. [20] and Robinson *et al*. [21] demonstrated that controlling fly populations could reduce the incidence of trachoma and diarrhea, particularly in children in the Gambia. Prüss and Mariotti [22] further observed that flies are likely the primary mode of transmission for trachoma, a disease spread through direct contact between individuals.

To control fly populations, a variety of strategies are employed, such as environmental improvements (e.g., installing nets on windows and doors, ensuring proper garbage disposal, using poison-impregnated tapes, and performing spatial spraying), with proper waste collection and disposal being regarded as the most effective method [23]. Given the critical role of houseflies as mechanical vectors in disease transmission, this study aimed to assess the bacterial contamination of *Musca domestica* across different environments.

Materials and Methods

This observational study aimed to assess the contamination of houseflies across various seasons. A total of 10 locations were chosen from 5 different sources, which included rural and urban waste, coastal zones, hospital grounds, and slaughterhouses. Only adult flies were captured using an entomological net. Sampling occurred bi-monthly, with one collection per area during each sampling period. Following the Gantt chart schedule, continuous sampling took place over at least 1 year. In total, 384 houseflies were gathered for microbial analysis and transported to the laboratory in sterile glass containers.

Initially, the houseflies were identified using a stereomicroscope based on their morphological features such as antennae, wings, body surface hairs, and head furrow. Following this, their external body surfaces were rinsed with sterile physiological serum. They were then dissected using an entomological needle, and their digestive systems were carefully transferred to physiological serum. To prevent contamination between external and internal bacteria, each fly was first washed in a sterile cleaning solution and then rinsed in sterile serum. The intestines were then removed from the mouth to the anus, followed by washing and crushing. Both the solution from washing the external surface and the physiological serum containing the insect's digestive system were centrifuged for five minutes at two thousand rpm. The sediment obtained from the centrifuge was then analyzed. For bacterial identification, Blood Agar, Nutrient Agar, EMB Agar, Mannitol Salt Agar, and Nutrient Broth, all sourced from Merck Germany, were used in the study.

The culture media were prepared following the instructions provided and using standard techniques, then stored in the refrigerator. After inoculation, the samples were incubated at 37 °C for 24 hours. Following incubation, the samples were stained and examined under a microscope. To confirm the identity of the colonies, several standard diagnostic tests were conducted, including mannitol, lysine, Simon Citrate, urea (OF test), Methyl Red (MR test), Voges-Proskauer (VP test), Triple Sugar Iron Agar (TSI), and DNase, among others [24].

Results and Discussion

The findings of this study revealed that *Escherichia coli* was the most prevalent species identified. Among all the samples analyzed, the majority of contaminants were found to be *E. coli*, followed by *Staphylococcus aureus*, *Enterobacter aerogenes*, and *Staphylococcus epidermidis*, in that order.

The highest proportion of *E. coli* contamination was found in samples collected from hospital premises, while the lowest was from urban waste. Conversely, urban waste samples exhibited the highest contamination rate with *Staphylococcus aureus*, and the lowest was seen in coastal area samples. *Enterobacter aerogenes* and *Staphylococcus epidermidis* were more prevalent in both rural and urban waste samples.

Regarding *Staphylococcus aureus*, the study found that the percentage of isolates from the digestive tract of flies (10%) was higher than those from the body surface (8%). The highest infection rate of *Staphylococcus aureus* from the digestive tract of flies was observed in hospitals, while the highest infection rate from the body surface was in slaughterhouses. Similarly, *E. coli* was more commonly isolated from the digestive tract of flies (24%) compared to the body surface (22%). The highest contamination rates for *E. coli* in both the digestive tract (6%) and on the fly's body surface (6%) were also associated with hospitals.

The greatest contamination of *Staphylococcus epidermidis* in flies' digestive systems was linked to urban waste, while the highest contamination on their body surface was associated with rural waste. A higher percentage of *Staphylococcus epidermidis* was isolated from the body surface of flies (6%) compared to the digestive system (3%).

The most significant infection rate of *Enterobacter aerogenes* found in the digestive systems of flies was linked to urban waste, while the highest contamination on the body surface was found in both rural and urban waste. The isolation of *Enterobacter aerogenes* from the digestive tract of flies (9%) was more prevalent than from the body surface (5%).

Table 1. Microbial contamination of flies caught from different regions.

Microorganism isolation zone	**Source of microorganism isolation**	**Total number of samples**	**The percentage of contamination with *E. coli* (%)**	**The percentage of contamination with *Staphylococcus aureus* (%)**	**The percentage of contamination with *Staphylococcus epidermidis* (%)**	**The percentage of contamination with *Enterobacter aerogenes* (%)**
Urban	Northern urban waste	48	5.2	2.60	2.08	2.34
	Southern urban waste	48	5.7	3.13	2.60	2.86
	Eastern hospital campus	48	6.25	2.08	0	1.56
	Western hospital campus	48	6.25	1.82	0.2	1.56
Rural	Rural waste	48	5.7	2.60	2.08	2.60
	North coastal areas	48	5.46	2.08	1.56	1.82
	Southern coastal areas	48	5.7	1.82	1.04	1.82
	Slaughterhouse	48	5.7	2.34	0.2	2.08
Total	All regions	384	46	19.01	9.89	16.66

The samples obtained from rural and urban waste showed a higher level of contamination with *E. coli* while being less contaminated with *Staphylococcus epidermidis*. Hospital samples were predominantly infected with E. coli, with a lower presence of *Staphylococcus epidermidis*. Coastal area samples showed a higher prevalence of E. coli infections, with lower rates *of Staphylococcus epidermidis* and *Enterobacter aerogenes*. Slaughterhouse samples were primarily infected with *E. coli* and had a lower incidence of *Staphylococcus epidermidis*. In general, urban waste samples exhibited the highest levels of E. coli contamination and lower levels of *Staphylococcus epidermidis* **(Table 1)**.

It is well-established that high levels of fly contamination with harmful pathogens pose a significant risk for bacterial diseases within communities. The presence and abundance of infected flies in public areas, such as urban and rural waste, represent a serious threat to public health. Studies have confirmed that houseflies, which frequently come into contact with various sources like garbage containing pathogenic microorganisms, act as vectors for the transmission of these harmful agents [3, 25, 26]. Given their unique behavior, houseflies are recognized as one of the most significant mechanical vectors of disease, and their presence has been noted in diverse locations where pathogens have been isolated. Environments such as slaughterhouses, hospital waste, and rural and urban waste are among those frequented by flies. In the current study, species such as *Enterobacter aerogenes*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *E. coli* were identified in flies. The findings align with those from studies conducted globally, particularly regarding the presence of *Streptococcus*, *Staphylococcus*, and *Escherichia coli* bacteria [10, 27].

Houseflies are known to transmit a variety of bacterial diseases, with some of the most harmful being cholera, dengue fever, and food poisoning caused by *Staphylococcus aureus* [28]. Due to their feeding habits and behavioral traits, these flies contribute to the spread of intestinal pathogens to humans. Serving as reservoirs for numerous digestive pathogens, houseflies play a significant role in the transmission of gastrointestinal diseases, including colitis, diarrhea, and gastroenteritis [28].

In this study, *E. coli* was the most commonly isolated bacterium from the digestive tract of houseflies. As a gram-negative bacterium that naturally resides in the intestines and warm-blooded animals, the higher infection rate of E. coli in the digestive tract compared to the body surface of the flies is likely due to its specific habitat. *E. coli* is frequently found in feces and has been isolated from flies in the Musidae and Caliphoridae families in various studies [29, 30].

The study also revealed that *Staphylococcus epidermidis* was the most prevalent bacterium on the body surface of the flies. The findings showed a higher incidence of bacterial isolation from the intestines than from the body surface, which aligns with the results of previous research [30]. Several factors could contribute to this, including the type of microorganism, its ability to adhere to the fly's body, and the level of contamination in the environment. The presence of these insects in public spaces and various environments is a significant concern as they serve as carriers of harmful pathogens, drawing attention from health engineers. Hospitals, rural and urban waste, and landfills are key sources of contamination, offering ideal conditions for flies to transmit infectious agents and contribute to outbreaks of diseases like summer diarrhea. To prevent the spread of pollution and infection, public areas must be maintained as clean and safe spaces to protect the health of individuals, communities, and the environment. Thus, improving environmental health through engineering measures, along with controlling fly populations, is essential to achieving the primary goals of public health and ensuring a healthy and secure environment. In combating fly infestations, it is crucial to implement effective methods carried out by trained professionals to minimize environmental contamination. Ultimately, the presence of flies is often an indication of poor sanitation and unhygienic conditions. Effective fly control remains a vital public health strategy, particularly in developing countries, to mitigate the transmission of diseases.

Conclusion

Flies play a significant role in the spread of diseases and the transmission of bacterial agents. Their presence indicates inadequate sanitation and a lack of proper health monitoring in the environment. To prevent the spread of infections, it is crucial to eliminate all fly breeding grounds and restrict their access to waste and food scraps. Additionally, practicing good hygiene, such as covering food, reheating leftovers before consumption, thoroughly cleaning containers, and using insecticides, will help minimize exposure to environmental vectors.

Acknowledgments: None

Conflict of Interest: None

Financial Support: None

Ethics Statement: None

References

1. Gupta SR, Rao CK, Biswas H, Krishnaswami AK, Wattal BL, Raghavan NG. Role of the house-fly in the transmission of intestinal parasitic cysts-ova. Indian J Med Res. 1972;60(8):1120-5.
2. Otu-Bassey IB, Efretuei GK, Mbah M. Gut Parasites of medical importance harboured by Musca domestica in Calabar, Nigeria. Trop Parasitol. 2022;12(2):99-104. doi:10.4103/tp.tp_51_21
3. Khamesipour F, Lankarani KB, Honarvar B, Kwenti TE. A systematic review of human pathogens carried by the housefly (Musca domestica L.). BMC Public Health. 2018;18(1):1049.
4. Cervelin V, Fongaro G, Pastore JB, Engel F, Reimers MA, Viancelli A. Enterobacteria associated with houseflies (Musca domestica) as an infection risk indicator in swine production farms. Acta Trop. 2018;185(6):13-7.

5. Bertelloni F, Bresciani F, Cagnoli G, Scotti B, Lazzerini L, Marcucci M, et al. House flies (Musca domestica) from swine and poultry farms carrying antimicrobial resistant enterobacteriaceae and Salmonella. Vet Sci. 2023;10(2):118. doi:10.3390/vetsci10020118
6. Junqueira ACM, Ratan A, Acerbi E, Drautz-Moses DI, Premkrishnan BNV, Costea PI, et al. The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. Sci Rep. 2017;7(1):16324.
7. Monyama MC, Taioe OM, Nkhebenyane JS, van Wyk D, Ramatla T, Thekisoe OMM. Bacterial communities associated with houseflies (Musca domestica L.) inhabiting hospices in South Africa. Microorganisms. 2023;11(6):1440. doi:10.3390/microorganisms11061440
8. Olsen AR, Hammack TS. Isolation of Salmonella spp. from the housefly, Musca domestica L., and the dump fly, Hydrotaea aenescens (Wiedemann) (Diptera: Muscidae), at caged-layer houses. J Food Prot. 2000;63(7):958-60.
9. Songe MM, Hang'ombe BM, Knight-Jones TJ, Grace D. Antimicrobial resistant enteropathogenic escherichia coli and salmonella spp. in houseflies infesting fish in food markets in Zambia. Int J Environ Res Public Health. 2016;14(1):21. doi:10.3390/ijerph14010021
10. Sukontason K, Bunchoo M, Khantawa B, Sukontason K, Piangjai S, Choochote W. Musca domestica as a mechanical carrier of bacteria in Chiang Mai, north Thailand. J Vector Ecol. 2000;25(1):114-7.
11. Issa R. Musca domestica acts as transport vector hosts. Bull Natl Res Cent. 2019;43(1):1-5. doi:10.1186/s42269-019-0111-0
12. Harwood RF. Muscoid flies and louse flies. Entomology in human and animal health. 1979:248-95.
13. Hornok S, Cini Bruno AM, Takács N, Keve G, Sándor AD, Kontschán J. An update on the occurrence of flies (Diptera: Muscidae, Calliphoridae) and sucking lice (Phthiraptera: Anoplura) of veterinary importance in Malta: first record of Lucilia cuprina and Linognathus africanus. Front Vet Sci. 2023;10:1143800. doi:10.3389/fvets.2023.1143800
14. Wolff HL, van Zijl WJ. Houseflies, the availability of water, and diarrhoeal diseases. Bull World Health Organ. 1969;41(6):952-9.
15. Grübel P, Hoffman JS, Chong FK, Burstein NA, Mepani C, Cave DR. Vector potential of houseflies (Musca domestica) for Helicobacter pylori. J Clin Microbiol. 1997;35(6):1300-3.
16. Magdy H, Rady MH, Salama MS, Sayed HAE, Hamza D, Azzam M, et al. Isolation of multidrug-resistant Helicobacter pylori from wild houseflies Musca domestica with a new perspective for the treatment. Vector Borne Zoonotic Dis. 2023;23(2):63-74. doi:10.1089/vbz.2022.0033
17. Cohen D, Green M, Block C, Slepon R, Ambar R, Wasserman SS, et al. Reduction of transmission of shigellosis by control of houseflies (Musca domestica). Lancet. 1991;337(8748):993-7.
18. Metwally AM, Salem SS, Hammad KM, Metwaly KH, Awad MA. Novel control of house fly Musca domestica and bacterial isolates by ozone gas. Int J Trop Insect Sci. 2023;43(2):761-7. doi:10.1007/s42690-023-00984-x
19. Esrey SA, Potash JB, Roberts L, Shiff C. Effects of improved water supply and sanitation on ascariasis, diarrhoea, dracunculiasis, hookworm infection, schistosomiasis, and trachoma. Bull World Health Organ. 1991;69(5):609-21.
20. Emerson PM, Bailey RL, Mahdi OS, Walraven GE, Lindsay SW. Transmission ecology of the fly Musca sorbens, a putative vector of trachoma. Trans R Soc Trop Med Hyg. 2000;94(1):28-32.
21. Robinson A, Bristow J, Holl MV, Makalo P, Alemayehu W, Bailey RL, et al. Responses of the putative trachoma vector, Musca sorbens, to volatile semiochemicals from human faeces. PLoS Negl Trop Dis. 2020;14(3):e0007719.
22. Prüss A, Mariotti SP. Preventing trachoma through environmental sanitation: a review of the evidence base. Bull World Health Organ. 2000;78(2):258-66.
23. Malik A, Singh N, Satya S. House fly (Musca domestica): a review of control strategies for a challenging pest. J Environ Sci Health B. 2007;42(4):453-69.
24. Turki Jalil A, Abdulhadi MA, Al-Ameer LR, Jaafar Naser S, Merza M, Alsandook T, et al. Bacterial contamination of cockroaches in different wards of hospital, restaurant and home. Heliyon. 2023;9(11):e22103. doi:10.1016/j.heliyon.2023.e22103
25. Butler JF, Garcia-Maruniak A, Meek F, Maruniak JE. Wild Florida house flies (Musca domestica) as carriers of pathogenic bacteria. Fla Entomol. 2010;93(2):218-23.

26. Umeche N, Mandah LE. Musca domestica as a carrier of intestinal helminths in Calabar, Nigeria. East Afr Med J. 1989;66(5):349-52.
27. De Jesús AJ, Olsen AR, Bryce JR, Whiting RC. Quantitative contamination and transfer of Escherichia coli from foods by houseflies, Musca domestica L. (Diptera: Muscidae). Int J Food Microbiol. 2004;93(2):259-62.
28. Ysquierdo CA, Olafson PU, Thomas DB. Fungi isolated from house flies (Diptera: Muscidae) on penned cattle in south Texas. J Med Entomol. 2017;54(3):705-11. doi:10.1093/jme/tjw214
29. Monyama MC, Onyiche ET, Taioe MO, Nkhebenyane JS, Thekisoe OMM. Bacterial pathogens identified from houseflies in different human and animal settings: a systematic review and meta-analysis. Vet Med Sci. 2022;8(2):827-44. doi:10.1002/vms3.496
30. Pava-Ripoll M, Pearson RE, Miller AK, Ziobro GC. Prevalence and relative risk of Cronobacter spp., Salmonella spp., and Listeria monocytogenes associated with the body surfaces and guts of individual filth flies. Appl Environ Microbiol. 2012;78(22):7891-902.