AKENTEN APPIAH- MENKA UNIVERSITY OF SKILLS TRAINING AND
ENTREPRENEURIAL DEVELOPMENT

MPHIL THESIS

MICROBIAL CARRIAGE AND ANTIBIOTIC RESISTANCE PROFILE OF BACTERIA IN COCKROACHES IN PUBLIC PLACES AND HOUSEHOLDS IN ASHANTI MAMPONG, GHANA

BY

ESTHER AYEMUGAH

2025

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BY

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A thesis submitted to the Department of Public Health Education of the Faculty of Environment and Health Education, Akenten Appiah-Menka University of Skills Training and Entrepreneurial Development, in partial fulfilment of the requirements for the award of a Master of Philosophy Degree in Public Health

SEPTEMBER, 2025

DECLARATION

I hereby declare that this thesis, with the exception of quotations and references contained in published works which have been duly acknowledged; is the result of my own original work and that no part of it has been presented for another degree at this university or elsewhere.

Candidate's Name: Esther Ayemugah

Signature: ……………………………… Date: ……………………..

Supervisors' Declaration

We hereby declare that the preparation and presentation of the thesis were supervised in accordance with the guidelines on supervision of thesis laid down by the Akenten Appiah-Menka University of Skills Training and Entrepreneurial Development.

Principal Supervisor's Name: Rev. Dr. Denis Dekugmen Yar (PhD)

Signature: …………………………. Date: ……………………......

Co-Supervisor's Name: Papa Kofi Amissah-Reynolds

Signature: ………………………….. Date: ………………………..

ABSTRACT

Cockroaches are common pests in human environments and important carriers of pathogenic microorganisms. This cross-sectional study was conducted to examine the microbial carriage and antibiotic resistance profiles of bacteria isolated from cockroaches collected from hospitals, eateries, and households in the Ashanti Mampong Municipality, Ghana. A total of 358 cockroaches were collected and examined for parasite and bacterial carriage, as well as antimicrobial resistance patterns of the bacteria isolated. The results showed that 242 (67.6%) of the cockroaches carried at least one parasite, with *Ascaris* being the most prevalent, found in 199 (55.6%) of the cockroaches, and *Toxoascaris* in 172 (48.0%) of the cockroaches. Co-carriage were common, with 66 (18.4%) carrying two parasites and 28 (7.8%) carrying three or more. Bacterial prevalence was also high, with 217 (74.6%) of samples testing positive. *Salmonella* 214 (73.5%) and *Enterococcus* 201 (69.1%) were the most frequently isolated, while *E. coli* 68 (23.4%) and *Proteus* 58 (19.9%) were relatively less common. Antibiotic susceptibility testing revealed high resistance to chloramphenicol, ampicillin, and clindamycin, ranging between 55% and 75%. Moderate resistance was observed for erythromycin and amoxicillin-clavulanate (45–67%), while ciprofloxacin and azithromycin showed the lowest resistance levels (below 27% and 11%, respectively). *Klebsiella* and *Salmonella* were the most resistant bacteria, while Proteus and Shigella exhibited moderate resistance. The findings confirm that cockroaches act as reservoirs and vectors of medically important and antibiotic-resistant microorganisms in different environments. This poses a significant threat to both community- and hospital-acquired infections. Effective cockroach control and improved sanitation practices are crucial for reducing the spread of resistant pathogens in both public and domestic settings.

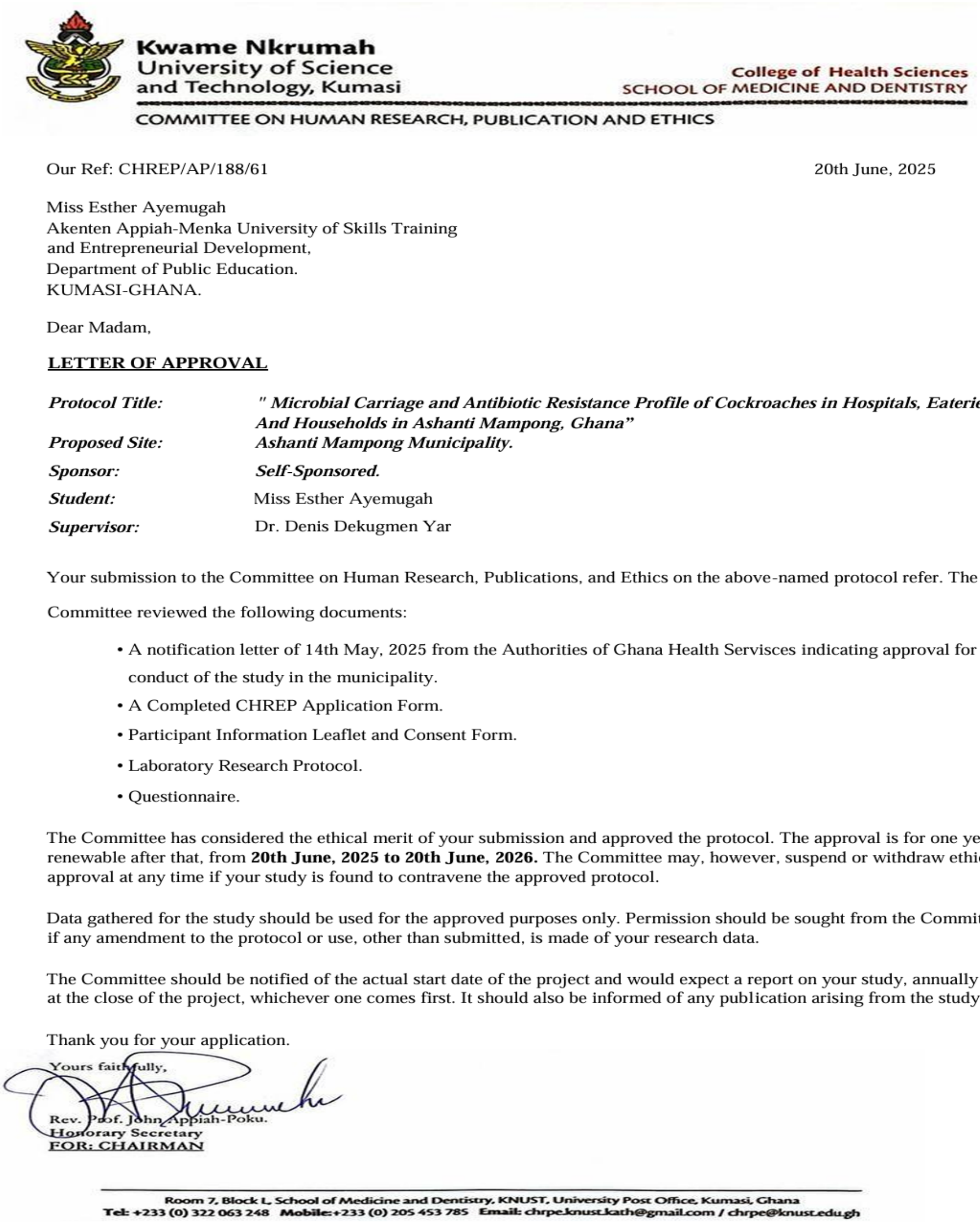
ACKNOWLEDGMENT

I am grateful to the Almighty God for His protection and guidance while pursuing this degree and for making it possible for me to complete this thesis successfully. I sincerely wish to express my heartfelt appreciation to my supervisors, Rev. Dr. Denis Dekugmen Yar and Papa Kofi Amissah-Reynolds, for their assistance, guidance, close, meticulous supervision, constructive scholastic criticism, moderation, and correction, which saw me through the successful completion of this thesis.

DEDICATION

I dedicate this work to my family for their support, advice, and encouragement throughout my education and research period. I further dedicate this work to all my loved ones, who have contributed to the success of this research piece in diverse ways.

ETHICAL CLEARANCE



Kwame Nkrumah
University of Science
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College of Health Sciences
SCHOOL OF MEDICINE AND DENTISTRY
COMMITTEE ON HUMAN RESEARCH, PUBLICATION AND ETHICS

Our Ref: CHREP/AP/188/61 20th June, 2025

Miss Esther Ayemugah
Akenten Appiah-Menka University of Skills Training
and Entrepreneurial Development,
Department of Public Education.
KUMASI-GHANA.

Dear Madam,

LETTER OF APPROVAL

Protocol Title:	***" Microbial Carriage and Antibiotic Resistance Profile of Cockroaches in Hospitals, Eateries, And Households in Ashanti Mampong, Ghana"***
Proposed Site:	***Ashanti Mampong Municipality.***
Sponsor:	***Self-Sponsored.***
Student:	Miss Esther Ayemugah
Supervisor:	Dr. Denis Dekugmen Yar

Your submission to the Committee on Human Research, Publications, and Ethics on the above-named protocol refer. The Committee reviewed the following documents:

- A notification letter of 14th May, 2025 from the Authorities of Ghana Health Servisces indicating approval for the conduct of the study in the municipality.
- A Completed CHREP Application Form.
- Participant Information Leaflet and Consent Form.
- Laboratory Research Protocol.
- Questionnaire.

The Committee has considered the ethical merit of your submission and approved the protocol. The approval is for one year, renewable after that, from **20th June, 2025 to 20th June, 2026.** The Committee may, however, suspend or withdraw ethical approval at any time if your study is found to contravene the approved protocol.

Data gathered for the study should be used for the approved purposes only. Permission should be sought from the Committee if any amendment to the protocol or use, other than submitted, is made of your research data.

The Committee should be notified of the actual start date of the project and would expect a report on your study, annually or at the close of the project, whichever one comes first. It should also be informed of any publication arising from the study.

Thank you for your application.

Yours faithfully,

Rev. Prof. John Appiah-Poku.
Honorary Secretary
FOR: CHAIRMAN

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CHAPTER ONE

INTRODUCTION

1.1 Background of the Study

Cockroaches are among the most widespread pests that thrive in human environments, particularly in areas where food, warmth, and shelter are readily available (Ramalho-Ortigao & Gubler, 2020;Brenner & Kramer, 2018). Beyond being a nuisance, their presence represents a significant public health concern, as they have been shown to harbor and transmit a wide range of pathogens (Chala & Hamde, 2021). Studies across various geographical regions have established that cockroaches harbor pathogenic bacteria, fungi, and parasites on their exoskeletons and within their digestive tracts (Bisetegn et al., 2024;Donkor, 2019). Cockroaches contaminate food, utensils, and hospital equipment through these organisms, thereby posing dire consequences to human health (Turki Jalil et al., 2023; Donkor, 2020; Donkor, 2019; Solomon et al., 2018).

Only about 30 species of cockroaches are directly associated with humans and regarded as pest despite the fact that most cockroach species inhabit natural environments. Their distribution is particularly centered in tropical and subtropical regions, where warm and humid conditions provide highly conducive environments for survival and breeding (Brenner & Kramer, 2019). The global spread of pest cockroach species has been largely affected by human activities, such as trade, migration, and urbanization (Ma et al., 2025). The German cockroach (*Blattella germanica*), though originating in Southeast Asia, is now a ubiquitous global species, found on every continent except Antarctica

(Marín-Miret et al., 2024; Hashemi-Aghdam & Oshaghi, 2015). Similarly, the American and Oriental cockroaches (*Periplaneta americana* and *Blatta orientalis*) are now synanthropic species that predominantly infest urban structures, such as sewer systems, food preparation areas, and other human-altered environments (Dokmaikaw & Suntaravitun, 2019). These man-made structures provide stable microclimates that enables them to thrive in temperate regions where outdoor conditions are otherwise unfavorable. (Ma et al., 2024). This significant adaptability facilitates their role as major global vectors for the transmission of microbial and parasitic pathogens (Abbasi, 2025; Chala & Hamde, 2021).

Cockroaches have been incriminated as vectors of intestinal parasites across Africa and Asia, with studies in Ethiopia, Nigeria, and Thailand reporting carriage rates of 36%, 93%, and 46%, respectively (Victor et al., 2024; Debash et al., 2022 & Dokmaikaw & Suntaravitun, 2019). Parasitic pathogens such as *Entamoeba* and *Giardia* species have been detected in both hospital and community environments (Adenusi et al., 2018; Rose, Chrispinus & Ngeiywa, 2018). Research from Ghana and northern Nigeria further ascertain that cockroaches act as both vectors for both external and internal parasitic organisms (Donkor, 2020; Nasirian, 2019; Adenusi et al., 2018).

Cockroaches have also been implicated in the transmission of bacterial pathogens including *Salmonella*, *Shigella*, and *Escherichia coli* (Donkor, 2020; Moges et al., 2016; Adejumo B-F et al., 2016). Previous research further establishes that many microbes obtained from cockroaches display resistance to conventional antibiotics, citing a justification for studies that assess resistance patterns in different environmental settings (Murray et al., 2022; Mostafa-Hosseini, 2020; Obeng-Nkrumah et al., 2019; Perlin et al., 2017). The presence of cockroaches in hospital areas, such as intensive care units and patient wards, contributes to an increased risk of hospital-acquired infections (HAIs), especially given the immune-compromised status of patients, who are more susceptible to opportunistic pathogens (Awere-Duodu & Donkor, 2024; Donkor, 2019; Adejumo B-F et al., 2016). Similarly within households and food establishments, they facilitate the transmission of foodborne pathogens (Liu et al., 2024; Donkor, 2020 & Obeng-Nkrumah et al., 2019). Alarmingly, studies show that most of the microorganisms carried by cockroaches have developed resistance to commonly used antibiotics, raising further concerns about their potential role in the growing crisis of antimicrobial resistance (Kakooza et al., 2025; Murray et al., 2022).

Antimicrobial resistance (AMR) is a growing global threat, and cockroaches contribute by actively carrying and disseminating resistant bacteria (Murray et al., 2022). Studies have linked cockroaches to harbour vancomycin-resistant enterococci (VRE) and methicillin-resistant *Staphylococcus aureus* (MRSA) (Solomon et al., 2018). The emergence of AMR complicates treatment and increases the risk of recurring infections (Pattnaik et al., 2023; Muzny & Sobel, 2022). Antibiotic resistance, predominantly driven by the misuse and overuse of antibiotics, is increasingly aggravated in Africa by its fragile health infrastructure and inadequate diagnostic capabilities (Irfan et al., 2022; Guyader et al., 2019; Bengtsson-Palme et al., 2018 & Lim et al., 2016). Households can also unknowingly foster the development of drug-resistant bacteria, driven by inadequate hygiene routines, the overuse or misuse of antibiotics, and close proximity to pets that may harbor resistant organisms (Endale, Mathewos & Abdeta, 2023). Resistant strains in homes are dangerous for children, the elderly and immunocompromised individuals (Maillard et al., 2020). This study sought to examine parasite and bacterial carriage, identify microbial species, and assess the antibiotic resistance profiles of the microorganisms isolated.

1.2 Statement of the Problem

The abundance of cockroaches in many environments, and their role as carriers of infectious diseases has been well established (Geng et al., 2025). A major gap exists in fully understanding cockroach-associated microbial and antibiotic resistance patterns, despite their known role in carrying highly resistant pathogens that worsen infections (Awere-Duodu & Donkor, 2024 & Donkor, 2019). These insects can spread resistant bacteria between environments, increasing the transmission of infectious diseases (Pikkemaat et al., 2016).

Albeit these risks, there is little information available on cockroach-associated microbial contamination in the Ashanti Mampong Municipality. Although a few studies have examined cockroach populations, the extent of their role in harbouring pathogens remains unclear. This scarcity of data makes it difficult to assess the true scale of the public health problem. Furthermore, antimicrobial resistance is an increasing global concern, yet its connection with cockroach infestations in Ghana is poorly documented. The lack of local evidence poses a challenge for government and health professionals seeking to design appropriate interventions. The organisms they carry may not only be medically important but also resistant to conventional antibiotics. If unaddressed, the role of cockroaches in spreading resistant pathogens will remain underestimated, increasing infection risks in homes, food establishments, and healthcare facilities. This study investigated cockroach abundance in selected settings and examined the key pathogens they carry along with their antibiotic resistance patterns.

1.3 Study Objectives

This study assessed the microbial carriage and antibiotic resistance profile of cockroaches in hospitals, eateries, and households in Ashanti Mampong Municipality

1.3.1 Specific Objectives

Specifically, this study sought to:

1. Assess the prevalence of parasite carriage in cockroaches from hospitals, households, and eateries.
2. Assess the prevalence of bacterial carriage in cockroaches from hospitals, households, and eateries.
3. Investigate the antibiotic resistance profiles of microbes isolated from cockroaches in each setting.

1.4 Research Questions

1. What is the prevalence of parasite carriage in cockroaches from hospitals, households, and eateries?
2. What is the prevalence of bacterial carriage in cockroaches from hospitals, households, and eateries?
3. Which microbial species do cockroaches in different environments carry?
4. How do microbes isolated from cockroaches in hospitals, households, and eateries show antibiotic resistance?

1.5 Justification

Cockroaches are linked with the spread of diseases such as gastroenteritis, dysentery, and food poisoning (Ifeanyi & Olawumi 2015). Their ability to survive in diverse environments and their role in spreading microbes make them an important public health concern. In Ghana, pathogenic bacteria have been isolated from American cockroaches collected in urban areas of Accra (Donkor, 2020; Brown & Alhassan, 2015). The rapid growth and urbanization of this city have created overcrowded and poorly developed districts suitable for cockroach proliferation (Gondhalekar et al., 2021). *Periplaneta americana* is the most common cockroach species in Ghanaian hospitals, due to favourable environmental and climatic conditions (Bisetegn et al., 2024). Few studies have investigated the antibiotic susceptibility of human pathogenic bacteria hosted by cockroaches in Ghanaian hospitals, households, and eateries.

1.6 Significance

This study will contribute to better understanding of cockroaches as carriers of infectious diseases. The information will be important for developing effective strategies to prevent community outbreaks. The study will also provide data on the prevalence of antibiotic-resistant bacteria in cockroach populations. This is important because antibiotic resistance is a global challenge that reduces treatment effectiveness and increases disease risks. Results will provide evidence to guide cockroach control programs, improve healthcare facilities, and inform public health campaigns in Ashanti Mampong and similar regions.

1.7 Limitations of the study

This study also had limitations that should be considered when interpreting the findings. The first limitation is a geographically limited sample size for a single municipality, which may limit the generalizability of the findings to different ecological and socio-economic zones. Also, routine phenotypic protocols for bacterial identification and antimicrobial susceptibility testing were employed, molecular procedures such as the polymerase chain reaction (PCR) were not utilized, which likely resulted in an underestimate of the prevalence of antimicrobial resistance genes. Finally, the sampling was undertaken at a single point in time and therefore does not account for seasonal variations in the density of cockroach populations or pathogen burden.

1.8 Scope

The study will involve three healthcare facilities (one government and two private hospitals), food-catering centres, and households in Ashanti Mampong. Areas to be studied include kitchens, bathrooms, storerooms, dispensaries, wards, outpatient rooms, staff rest rooms, cafeterias, and food handling areas in hospitals. In restaurants, sites will include tea and coffee machines, food and drink cabinets, food processing units, drawers, and ceilings

1.8 Organization of the Study

This study is organized into five chapters. Chapter one presents the introduction, research problem, objectives, justification, significance, scope, and organization of the study. Chapter Two reviews related literature on cockroaches as vectors, microbial carriage, antibiotic resistance, and public health concerns. Chapter Three describes the study area, research design, sampling, data collection, and laboratory procedures. Chapter Four presents the results, accompanied by tables, figures, and a detailed analysis. Chapter Five discusses the findings, draws conclusions, and provides recommendations for public health interventions and future research.

CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

The literature review is organized into key themes. First, it presents the global burden of vector-borne diseases and the role of insect vectors. Next, it discusses the biology and ecology of cockroaches, focusing on their adaptability and habitats. The review then examines cockroaches as vectors of bacteria, parasites, and fungi. A section on antimicrobial resistance follows, indicating resistant microbes associated with cockroaches and their public health implications. Finally, the review identifies knowledge gaps and the Conceptual Framework, which justify the present study.

2.1 Overview of Antimicrobial Resistance (AMR)

Antimicrobial resistance (AMR) poses a major threat to human health worldwide. Previous studies have estimated the effect of AMR on incidence, deaths, hospital length of stay, and health-care costs for specific pathogen-drug combinations (Murray et al., 2022). Antimicrobial resistance (AMR) threatens to erode decades of medical progress in the 21st century (Fenollar & Mediannikov, 2018). Getahun (2023) warns that AMR undermines the effective treatment of a broad spectrum of infections, resulting in increased illness, mortality, and healthcare costs. AMR causes ~1.27 million deaths annually worldwide, with Gram-negative bacteria (*E. coli*, *Klebsiella*) as major contributors (Murray et al., 2022). Low/middle-income countries (LMICs) face higher AMR due to antibiotic misuse and weak surveillance (O'Neill, 2016). Africa has the highest AMR-associated mortality rates (99 deaths per 100,000 in West Africa). This is due to limited diagnostics and the unregulated use of antibiotics (Ranjbar, R., & Alam, M., 2023). Amid this global crisis, cockroaches (Order:

Blattodea) have garnered increasing attention as potential vectors in the transmission of antimicrobial-resistant microorganisms (Kakooza et al., 2025; Bisetegn et al., 2024). These insects live in close proximity with humans owing to their omnivorous diets and nocturnal activity (Rust et al., 2024). Their presence in kitchens, hospitals, and food-handling environments makes them suitable reservoir for carrying and transmitting a wide range of pathogenic organisms, (Kakooza et al., 2025).

Recent research by Kakooza et al., (2025), provides compelling evidence of this where more than 80% of cockroaches collected from Ugandan households carried multidrug-resistant bacteria, such as extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* and carbapenem-resistant strains. Similarly, experimental work in Denmark demonstrated that cockroaches have the tendency to exchange resistance genes via their gut microbiomes, facilitating the spread of AMR genes rapidly when resistant and non-resistant populations come into contact (Bogri et al., 2024). These findings demonstrate the role of cockroaches in both the mechanical and biological transfer of pathogens and amplifiers of resistance.

With resistance documented in pathogens such as *E. coli*, *Klebsiella pneumoniae*, and *Salmonella enterica* in Ghana, AMR is increasingly recognized as a major public health concern (Donkor et al., 2024). Owing to the fact that these pathogens have been identified in both clinical and environmental samples, cockroaches, presence in hospitals, markets, and other unsanitary areas, may serve as overlooked yet important carriers. Their established role positions them as vital factor in the epidemiology of AMR, necessitating a clearer understanding of their influence to resistance dynamics. Therefore, this review aimed to critically examine the intersection between cockroach ecology, their potential as vectors of antimicrobial-resistant pathogens, and the implications for public health in Ghana and globally. This review establishes a critical link between cockroaches and the broader AMR challenge, thereby providing a conceptual framework for risk assessment and a basis for practical intervention to curb AMR.

2.2 Antimicrobial Resistance: Global and Regional Overview

2.2.1 Global Burden and Drivers of AMR

Antimicrobial resistance (AMR) is a globally recognized and escalating public health emergency. In 2022, a landmark systematic analysis in *The Lancet* established the most comprehensive global estimates of AMR burden to date, synthesizing 471 million records across 204 countries and comprising 23 bacterial pathogens and 88 pathogen-drug combinations. According to 2019 estimates, AMR was directly responsible for 1.27 million deaths and contributed to approximately 4.95 million more, resulting in a total mortality burden that exceeded that of HIV/AIDS and malaria combined (Murray et al., 2022).

Figure 2.1 illustrates the global distribution of AMR-attributable mortality, highlighting stark regional disparities. According to this analysis, Western sub-Saharan Africa exhibited the highest mortality burden at approximately 115 deaths per 100,000 population, whereas Australasia reported the lowest at roughly 28 deaths per 100,000 (Murray et al., 2022). These findings underscore the disproportionate impact of AMR on low-resource regions.

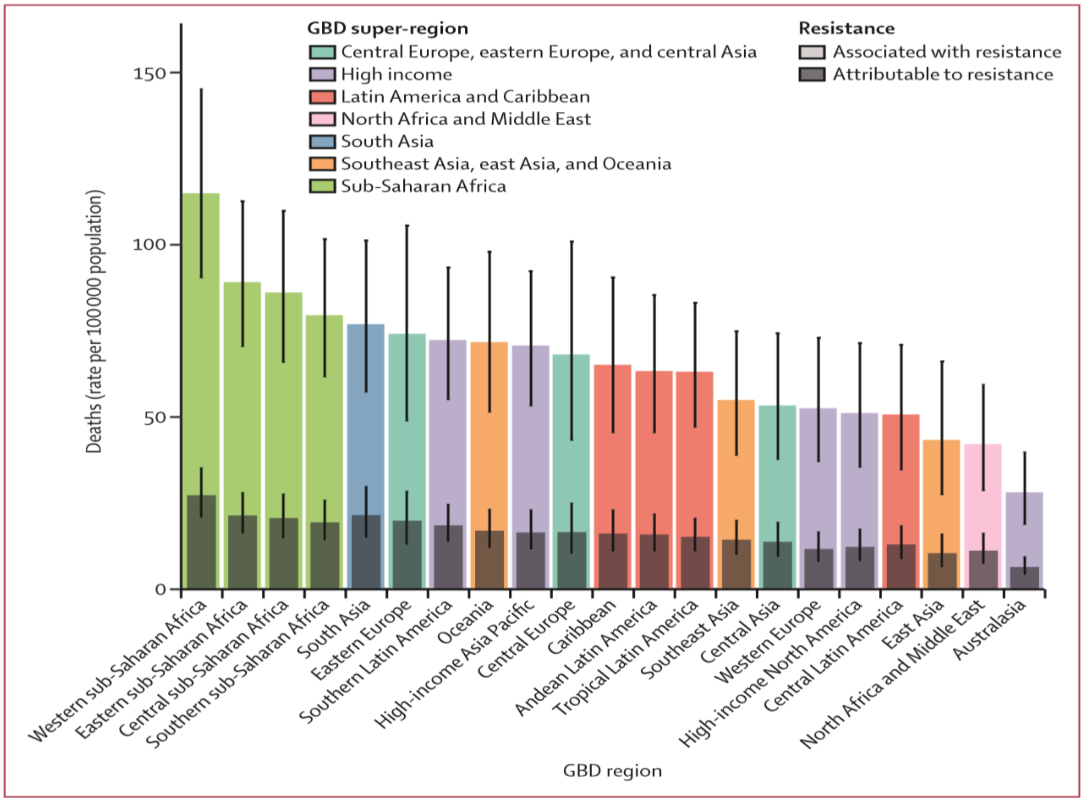


Figure 2. 1: All-age rate of deaths attributable to and associated with bacterial antimicrobial resistance by GBD region, 2019. Source: (Murray et al., 2022)

*Estimates were aggregated across drugs, accounting for the co-occurrence of resistance to multiple drugs. Error bars show 95% uncertainty intervals. GBD=Global Burden of Diseases, Injuries, and Risk Factors Study***.**

Projections suggest the critical need for intervention, with modeling studies indicating that integrated strategies such as enhanced clinical care and novel Gram-negative antibiotics, could avert up to 92 million deaths globally between 2025 and 2050 (Murray et al., 2022 & Naghavi et al, 2021). Notably, approximately 11.1 million of these preventable deaths are specifically associated with Gram-negative bacterial infections (Chilanga et al., 2025). Also, preventive public health measures including sanitation improvements, infection control, and expanded childhood vaccination programs could reduce annual AMR-linked mortality by an estimated 750,000 deaths, particularly in low- and middle-income countries (World Health Organization, 2023; Temkin et al., 2018)**.** Antimicrobial resistance (AMR) constitutes a critical global health threat, driven by multifaceted factors including overuse of antibiotics, inadequate infection control, and environmental contamination (Naghavi et al 2021). Recent estimates indicate that in low- and middle-income countries, especially, AMR contributes significantly to morbidity and mortality though precise global burden data remain elusive (O'Neill, 2016). Gwenzi et al (2021) emphasizes that insects, act as reservoirs and mechanical vectors for AMR, disseminating both antibiotic-resistant microorganisms and resistance genes via direct contact, contamination of human food, and horizontal gene transfer. This undermines the environmental dimension of AMR transmission, suggesting the need for integrative One Health frameworks (Donkor et al., 2024).

Quantifying the complex global burden of AMR is challenging, yet the role of non-clinical reservoirs, such as household insects, must be accounted for. Gwenzi et al, (2021) further suggests that while current evidence remains largely qualitative, there is an urgent need for quantitative microbial risk assessment (QMRA) to understand the health risks posed by these environmental vectors. Moreover, emerging experimental studies bolster the theoretical understanding: for example, (Bogri et al., 2024) employed cockroaches as in vivo models to demonstrate horizontal transmission of tetracycline resistance genes through microbiome interaction, illustrating how resistance can spread even among untreated individuals in close-contact populations. An accompanying press release (American Society for Microbiology, 2023) summarizes this finding, confirming real-world implications for AMR dynamics.

Together, these studies illuminate a global landscape where AMR extends beyond hospitals and farms, permeating domestic and urban environments via synanthropic vectors. Understanding the breadth of AMR spread thus demands cross-sectoral attention, from clinical surveillance to ecological health.

2.2.2 Regional Trends in Sub-Saharan Africa (Emphasis on Ghana)

In Sub-Saharan Africa, antimicrobial resistance (AMR) poses acute challenges in both community and clinical settings. A recent systematic review surveying 34 studies across Africa, including human and livestock samples, emphasized methodological limitations in quantifying transmission events, directionality, and transmission dynamics (Chilanga et al., 2025). The authors stress that despite increasing AMR prevalence, robust data on interspecies transmission and molecular epidemiology remain scarce (Sarkodie-Addo et al., 2025; Chilanga et al., 2025). Focusing on Ghana, multiple systematic reviews under a One Health framework underscore alarmingly high AMR prevalence across human, animal, and environmental sectors. A meta-analysis of 48 pathogens revealed high resistance rates to common antibiotics such as ampicillin and tetracycline (over 80%) and multidrug resistance (MDR) ranging from 17.6% in *Shigella* spp. to 100% in *Acinetobacter* spp. (Donkor et al., 2024).

Genetic studies further highlight the circulation of key antibiotic-resistance genes, *bla_{CTX-M-15}, bla_{NDM-1}, bla_{OXA-48}, sul1, gyrA, ermB, qnrS, and mecA* across human, animal, and environmental sources, signifying extensive inter-domain gene sharing (Donkor et al., 2024). Insights into specific pathogens augment this bleak picture. A 2025 meta-analysis on typhoid fever in Ghana reported a pooled prevalence of 4.14% (CI: 2.78–5.75%), with Multi Drug Resistance rates of 20–66%, and comparatively lower ciprofloxacin resistance (0–17%) (Awere-Duodu & Donkor, 2024). Additionally, ready-to-eat street food in Africa (Ghana inclusive), displayed high resistance levels: ceftazidime (85%), ceftriaxone (78%), sulfamethoxazole-trimethoprim (73%), and ampicillin (58%) (Onohuean et al., 2025). Historical data indicate widespread resistance in clinical isolates to tetracycline (82%), cotrimoxazole (73%), ampicillin (76%), and chloramphenicol (75%), with lower resistance to ceftriaxone (6.3%) and ciprofloxacin (11%) (Donkor et al., 2024).

Collectively, these findings portray a landscape in which AMR in Ghana is ubiquitous and deeply entrenched across environments. The One Health nexus is evident, as resistance genes and multidrug-resistant organisms permeate human, animal, food, and environmental interfaces (Sarkodie-Addo et al., 2025). The prevalence of high-priority genes such as *bla_{NDM-1} and bla_{CTX-M-15}* signals the urgent need for integrated surveillance, molecular epidemiology, and coordinated interventions in both regional and national contexts (Onohuean et al., 2025).

The regional review highlights a pervasive and escalating AMR burden in Sub-Saharan Africa, and particularly in Ghana, grounded in contemporary evidence. Despite methodological gaps in transmission quantification across sectors (Chilanga et al., 2025), the widespread presence of multidrug-resistant organisms and antibiotic-resistance genes in clinical, food, and environmental contexts underscores systemic vulnerabilities (Donkor et al., 2024). The detection of high-level resistance in food sources not only reflects misuse in clinical and agricultural sectors but also highlights public exposure risks (Onohuean et al., 2025).

Also, pathogen-specific data, such as the typhoid fever prevalence and resistance trends, add practical significance. A percentage of 4.14% pooled prevalence with MDR rates up to 66% indicates both endemic disease burden and evolving drug resistance, although relative ciprofloxacin susceptibility may offer interim clinical leverage (Sarkodie-Addo et al., 2025).

The implications are multifold:

Surveillance Enhancement: There is an imperative for comprehensive surveillance systems integrating clinical, environmental, and food chain data, with molecular diagnostics to monitor ARG dissemination.

One Health Interventions: Policies must traverse across human, veterinary, agricultural, and environmental sectors to control antibiotic use, improve hygiene, and reduce selective pressures.

Antibiotic Stewardship: Clinical treatment guidelines must adapt to reflect resistance patterns, with preference for antibiotics showing retained efficacy, including cautious use of ciprofloxacin where indicated.

Research and Capacity Building: Investments in local laboratory capacity, epidemiological research, and risk modeling (including quantitative microbial risk assessments) are critical to understand AMR dynamics and inform policy.

Public Engagement: Effective community education, supported by insights into street-food contamination and diagnostic limitations (Typhidot RDT underperformance; see section 2.2.1), remains central to combating misuse and transmission.

In summary, the evidence coalesces to emphasize that antimicrobial resistance in Ghana is not merely a clinical concern, it is an ecological and societal challenge requiring interdisciplinary response frameworks. The trajectory suggests that without urgent, integrated, and sustained action, AMR will continue to erode gains in infectious disease control across the region.

2.3 Biology and Ecology of Cockroaches.

2.3.1 Taxonomy and medically important species (*Periplaneta americana, Blattella germanica, Blatta orientalis*).

Cockroaches belong to the order Blattodea, with medically important synanthropic species concentrated in a few genera that thrive in human-made environments. Among these, Blattella germanica (German cockroach; family Ectobiidae), *Periplaneta americana* (American cockroach; family Blattidae), and *Blatta orientalis* (Oriental cockroach; family Blattidae) are the most consequential for public health due to their global distribution, infestation intensity, and proximity to food-handling areas and health-care premises (Crespo et al., 2025).

Contemporary faunistic updates continue to document the spread and establishment of these species, and closely related congeners, across new urban settings, reinforcing their invasive potential and medical relevance (de Luna et al., 2025). Urban entomology syntheses further underscore that structural pests such as cockroaches impose substantial health and economic burdens, linking infestations to allergen exposure, asthma exacerbations, and carriage of pathogens (Rust et al., 2024). In hospital environments, systematic evidence mapping 2000–2024 indicates that *E. coli* and *P. aeruginosa* are the most frequently reported bacteria associated with hospital-collected cockroaches, often exhibiting antimicrobial resistance, thus elevating their significance beyond nuisance status (Crespo et al., 2025). In sum, the core triad, *B. germanica, P. americana, and B. orientalis*, constitute the primary medically important taxa in most regions, with additional public-health importance from *Supella longipalpa* and other peridomestic species where they are established.

2.3.2 Life cycle and reproduction

Cockroaches undergo hemimetabolous development (egg–nymph–adult), with reproduction centered on the ootheca, an egg case that is formed, tanned, and hardened shortly after oviposition. Comparative developmental studies show that ootheca formation and sclerotization are conserved adaptations that protect embryos from desiccation and microbial insult, supporting successful colonization of warm, xeric indoor niches (Wang, 2022). Species differ in maternal investment and ootheca carriage: *B. germanica* typically carries the ootheca until close to hatching, increasing offspring survival in unstable microhabitats, whereas *P. americana* and *B. orientalis* deposit oothecae in sheltered crevices earlier in embryogenesis (Du et al., 2022; Lin et al., 2022). Recent life-table work on *P. americana* provides updated parameters for embryonic duration, nymphal instars, and fecundity under stable laboratory conditions, clarifying baseline demography that underpins the species' population growth potential in buildings (Lin et al., 2022). These reproductive strategies, high fecundity, rapid nymphal development under optimal temperature and humidity, and flexible ootheca management, help explain the explosive resurgence of infestations after incomplete control. Collectively, the reproductive ecology of synanthropic cockroaches is finely tuned to anthropogenic habitats, enabling persistence despite sanitation measures and promoting rapid rebound following partial suppression.

2.3.3 Feeding habits and behavior

Synanthropic cockroaches are omnivorous, opportunistic scavengers with strong preferences for carbohydrate- and lipid-rich foods commonly found in domestic kitchens, restaurants, and hospital food-prep areas. Their behavioral ecology, nocturnal foraging, thigmotaxis (preference for tight spaces), aggregation in warm and humid harborages, and reliance on water as a limiting resource, promotes frequent contact with human food and fomites (Rust et al., 2024; Wang & Cooper, 2025). These traits interact with evolving behavioral resistance: glucose-aversion in *B. germanica*, a heritable change that renders glucose-containing baits unpalatable, compromises bait efficacy and reshapes foraging decisions, illustrating rapid adaptation under control pressures (Wada-katsumata & Schal, 2024). Reviews of management tactics describe how such behavioral shifts compound traditional insecticide resistance, necessitating diversified baits, improved sanitation to remove competing food, and precise monitoring(Gondhalekar et al., 2021). Recent work in Journal of Economic Entomology highlights that water availability and age influence gel-bait performance, reinforcing that resource ecology (especially moisture) governs both cockroach survival and control outcomes indoors (Wang & Cooper, 2025). In aggregate, feeding plasticity, social aggregation, and microhabitat selection explain why cockroaches effectively exploit urban resource networks, and why interventions must address both biology (resistance/aversion) and behavior (harborage, foraging routes).

2.3.4 Adaptation to human environments

Cockroaches' success in human environments is a product of evolutionary robustness (e.g., ootheca-mediated reproductive protection) and contemporary selection from urban ecosystems (temperature buffering, abundant micro-refugia, and predictable food/water inputs). Urban entomology syntheses emphasize that infestations persist where sanitation gaps, structural defects (cracks, voids, utility chases), and moisture sources converge, creating stable metapopulations across apartments, restaurants, and hospitals (Rust et al., 2024). Modern monitoring reviews and IPM studies show that traps, crack-and-crevice targeting, and moisture management are central to surveillance and suppression, while resistance and bait aversion demand rotational chemistries and non-insecticidal tactics (Appel et al., 2022; Gondhalekar et al., 2021; Wang & Cooper, 2025). From a public-health angle, ecological fit to food-related premises increases opportunities for mechanical transmission of enteric pathogens; recent field work in China documented viruses, bacteria (including STEC), and protozoa recovered from cockroaches captured in kitchens and catering areas, underscoring risk at the food safety interface (Liu et al., 2024). Complementary hospital-based evidence indicates frequent recovery of clinically important, often drug-resistant bacteria from cockroaches, strengthening the case for zero-tolerance infestation policies in health-care settings (Crespo et al., 2025; Molewa et al., 2022). Altogether, adaptation to buildings is not merely survival in proximity to people; it is optimization of life history, behaviour, and resource use that sustains high-density populations and elevates public-health risk.

2.4 Cockroaches as Vectors of Pathogens

2.4.1 Mechanical transmission routes

Cockroaches' frequent microhabitats are rich in organic debris (drains, refuse areas, kitchen crevices, hospital utility spaces), where they acquire microbes on leg spines, mouthparts, and the cuticle before dispersing them across food-contact surfaces and medical environments. High-quality evidence shows that species captured in food-service areas and hospital premises carry enteric bacteria (e.g., *Escherichia coli, Salmonella enterica*), non-fermenters (e.g., *Pseudomonas aeruginosa*), and other clinically relevant taxa, including extended-spectrum β-lactamase (ESBL) and metallo-β-lactamase (MBL) producers (Bisetegn et al., 2024; Crespo et al., 2025). Field investigations in catering settings demonstrate plausible mechanical pathways, physical displacement, regurgitation, and faecal deposition onto ready-to-eat foods or inadequately cooked items, linking cockroach activity to exposure risks in kitchens (Liu et al., 2024). In healthcare settings, systematic evidence mapping (2000–2024) documents repeated recovery of medically important bacteria from hospital-collected cockroaches, highlighting their vectorial potential where susceptible patients, invasive devices, and antimicrobial selection pressures converge (Crespo et al., 2025).

Beyond direct contact, indoor environmental studies employing metagenomics indicate cockroaches measurably contribute to the microbial load of settled dust and airborne particulates, including potential pathogens and antibiotic resistance genes (ARGs). This supports an indirect mechanical route wherein insects augment the background bioburden that can re-aerosolize or settle onto food and fomites (Ma et al., 2025). Taken together, contemporary data suggest that cockroaches are efficient mechanical disseminators across hospitals, markets, and domestic kitchens. For infection prevention, the implication is straightforward: entomological control and environmental hygiene are integral to interrupting faecal–oral transmission cycles and reducing AMR dissemination risks in both clinical and community settings.

2.4.2 Biological transmission potential.

Although cockroaches are primarily regarded as mechanical vectors, recent experimental work reveals biologically meaningful interactions between their gut microbiota and transmissible resistance. A controlled in vivo study in Systems demonstrated that when one socially interacting cockroach population was exposed to tetracycline, tetracycline-resistance genes increased not only in treated insects but also in untreated cockroaches after intergroup contact; resistance also rose in the shared soil substrate. The magnitude of transfer scaled with interaction frequency, evidencing microbe-to-microbe gene flow across hosts (Bogri et al., 2024). This indicates that dense aggregations, coprophagy, and trophallaxis-like behaviours can facilitate horizontal gene transfer (HGT) within and between cockroach groups, sustaining a mobile resistome that is subsequently available for environmental dissemination. Complementary studies demonstrate that the cockroach gut community is resilient and adapts after antibiotic perturbations, with recovery dynamics influenced by repeated exposure pulses (Marín-Miret et al., 2024).

Biological relevance extends beyond AMR: A study showed the cockroach gut microbiota confers colonization resistance against *Salmonella typhimurium*, implying that microbial community structure modulates pathogen carriage and shedding (Turner et al., 2024). Together, these findings position cockroaches as living reservoirs in which ARGs can amplify and spread through social interactions, while community composition influences the establishment of pathogens. From a One Health standpoint, this elevates cockroaches from passive carriers to active participants in the ecology of resistance, justifying surveillance that integrates metagenomics, resistome tracking, and behaviour-aware control strategies.

2.5 Diversity of microorganisms carried by cockroaches

The microbial cargo of synanthropic cockroaches comprises bacteria, fungi, viruses, and enteric parasites, with its composition shaped by species, habitat (hospital, household, or food premises), and sanitation gradients. Contemporary systematic mapping of hospital-collected cockroaches (2000–2024) reports frequent isolation of *Enterobacter ales* (E. *coli*, *Klebsiella spp*., *Salmonella*), non-fermenting Gram-negatives (*P. aeruginosa*, *Acinetobacter spp*.), and staphylococci, with many isolates exhibiting ESBL, carbapenemase, or MBL phenotypes (Crespo et al., 2025; Bisetegn et al., 2024). In food-related environments, recent surveillance in Shanghai documented intestinal pathogens in *Blattella germanica* and *Periplaneta fuliginosa*, reinforcing the food safety relevance of cockroach contamination pathways (Liu et al., 2024).

Fungal communities are also common: a prospective hospital study identified *Candida spp., Aspergillus spp*., and other opportunists on cockroaches, underscoring potential transfer into patient care areas (Merad et al., 2023). Beyond microbes, modern reviews consolidate evidence of helminths (e.g., *Ascaris, Trichuris, Taenia*) and protozoa (*Entamoeba, Giardia, Cryptosporidium*) recovered from or on cockroaches across multiple geographies, supporting their role as carriers in faecal–oral transmission cycles (Patel et al., 2022). Finally, indoor metagenomic work indicates cockroaches contribute to the household resistome by adding ARG-harbouring bacteria to floor dust and, to a lesser extent, indoor air, creating additional exposure interfaces (Ma et al., 2025). Overall, current evidence substantiates a broad and clinically significant spectrum of cockroach-associated microorganisms that intersect with public health through food hygiene, hospital IPC, and environmental AMR stewardship.

2.5.1 Bacteria

2.5.1.1 *Escherichia coli*

Escherichia coli (*E. coli*) is one of the most frequently isolated bacteria from cockroaches collected in both hospital and community settings. As an enteric commensal that can harbour pathogenic strains causing diarrheal illness, urinary tract infections, and sepsis, its detection in cockroaches raises significant public health concerns. A systematic review of 24 years of literature confirmed that *E. coli* was the single most reported bacterium from hospital-collected cockroaches, appearing in over 50% of studies (Crespo et al., 2025). Beyond presence, resistance phenotypes are highly prevalent: extended-spectrum β-lactamase (ESBL) producing E. coli are frequently recovered, particularly in low- and middle-income countries where hospital sanitation and pest control are inconsistent (Bisetegn et al., 2024).

Experimental and field studies reinforce the relevance of cockroach-borne *E. coli*. In Ethiopia, nearly 40% of hospital-isolated *E. coli* from cockroaches were resistant to third-generation cephalosporins, with 34.7% identified as ESBL producers (Bisetegn et al., 2024). In food-related premises in China, enterotoxigenic and Shiga-toxin-producing E. coli strains were isolated from cockroaches, highlighting their significance to food safety (Liu et al., 2024). Resistance genes such as *bla_{CTX-M}, bla_{TEM}, and bla_{NDM}* have been documented in cockroach-associated *E. coli*, signalling their contribution to the environmental resistome and underscoring horizontal transfer risk to human pathogens (Donkor et al., 2024). Collectively, the evidence indicates cockroaches are consistent carriers of resistant E. coli strains in clinical and food environments, making them important in AMR surveillance.

2.5.1.2 *Salmonella* spp.

Salmonella enterica has been repeatedly recovered from cockroaches in food-preparation areas, markets, and hospital kitchens, reinforcing its significance as a vector-borne pathogen. In Shanghai, Salmonella spp. was isolated from cockroaches in catering facilities, with genotyping confirming strains identical to those recovered from contaminated food sources, suggesting a mechanical link in transmission (Liu et al., 2024). Salmonella carriage in cockroaches has also been documented in African hospitals, where multidrug resistance, including resistance to ampicillin, cotrimoxazole, and tetracycline, was common (Bisetegn et al., 2024).

Recent molecular epidemiology has further highlighted cockroaches as potential reservoirs for plasmid-mediated resistance genes in Salmonella. Genes encoding ESBLs, carbapenemases, and quinolone resistance determinants have been found in cockroach-borne isolates, consistent with findings from clinical strains in Ghana and Nigeria (Donkor et al., 2024). The public health significance is compounded by the persistent burden of typhoid and non-typhoidal salmonellosis in Sub-Saharan Africa, where food- and water-borne exposure remains high. In Ghana, systematic reviews report multidrug-resistant Salmonella prevalence ranging from 20% to 66% in clinical settings, mirroring resistance profiles found in cockroach-borne isolates (Sarkodie-Addo et al., 2025)

These data collectively suggest that cockroaches may act as environmental amplifiers of resistant Salmonella strains, sustaining transmission pathways in both food safety and hospital IPC contexts. Their role as mechanical vectors is well established, but growing evidence of biological persistence in the gut suggests they may also serve as transient reservoirs of viable, virulent Salmonella.

2.5.1.3 *Klebsiella* spp.

Klebsiella pneumoniae is an opportunistic pathogen of increasing concern, frequently associated with hospital-acquired infections, including pneumonia, bloodstream infections, and urinary tract infections (Temkin et al., 2018). Hospital-based cockroach surveys consistently recover *K. pneumoniae*, with a significant fraction exhibiting multidrug resistance (Moges et al., 2016). In Ethiopia, isolates from cockroaches were resistant to carbapenems and cephalosporins, with 23.1% identified as metallo-β-lactamase (MBL) producers (Bisetegn et al., 2024). This aligns with the global trend of carbapenem-resistant *K. pneumoniae* (CRKP), which the WHO has designated as a critical-priority pathogen (Fuller et al., 2022).

Systematic evidence confirms that *K. pneumoniae* is one of the most frequently reported bacteria from cockroaches in hospital environments, alongside *E. coli* and *Pseudomonas spp*. (Crespo et al., 2025). Genomic investigations have revealed that cockroach-borne Klebsiella carry clinically relevant resistance genes such as *bla_{KPC}, bla_{NDM}, and bla_{OXA-48},* which are also prevalent in Ghanaian clinical isolates (Donkor et al., 2024). This overlap underscores the ecological continuum between hospital vectors and clinical pathogens.

The implications are profound: cockroach infestations in hospitals create potential reservoirs for CRKP, compromising IPC efforts. As carbapenem resistance severely limits treatment options, the detection of these strains in cockroaches amplifies concerns about indirect patient exposure via contaminated surfaces, medical equipment, or food items. Integrated surveillance targeting cockroaches in healthcare settings could thus provide an early-warning system for high-priority resistance threats.

2.5.1.4 *Pseudomonas* spp.

Pseudomonas aeruginosa is a non-fermenting Gram-negative bacterium frequently associated with nosocomial infections, particularly in immunocompromised patients (Fuller et al., 2022). Notably, it exhibits intrinsic resistance to multiple antibiotic classes and easily acquires further resistance mechanisms, including carbapenemases and efflux pump overexpression. Cockroach-borne Pseudomonas isolates have been repeatedly reported, particularly from hospital wards, kitchens, and ICUs (Crespo et al., 2025).

Recent Ethiopian studies documented *P. aeruginosa* among the most common cockroach-associated pathogens, with a substantial subset displaying resistance to β-lactams and fluoroquinolones (Bisetegn et al., 2024). Metagenomic assessments confirm cockroaches harbour non-fermenters with diverse ARGs, indicating their role in expanding the environmental resistome (Ma et al., 2025). The significance of cockroach-carried P. aeruginosa lies not only in its prevalence but also in its ability to persist in hospital environments characterized by high moisture, biofilms, and frequent exposure to antimicrobial agents. Given its capacity for multidrug resistance, the presence of *P. aeruginosa* in cockroaches complicates the prevention and control of infections. Importantly, ESBL and carbapenem-resistant strains carried by cockroaches mirror those reported in clinical isolates in Ghana, suggesting potential vector-mediated bridging between environmental reservoirs and human infections (Donkor et al., 2024). The convergence of evidence positions cockroaches as critical, though often neglected, contributors to the nosocomial ecology of Pseudomonas resistance. Mitigation requires stringent pest management alongside antimicrobial stewardship.

2.5.1.5 *Shigella* spp.

Shigella species are Gram-negative bacteria that cause shigellosis, a leading cause of diarrheal disease worldwide. These pathogens are highly infectious, with an inoculum as low as 10–100 organisms, and are transmitted via the faecal-oral route (Khalil et al 2018). Clinical symptoms range from mild watery diarrhoea to severe dysentery with fever and abdominal pain. In recent years, antimicrobial resistance (AMR) has become a significant concern. Extensively drug-resistant (XDR) Shigella strains, resistant to multiple oral agents, have been increasingly reported in the United States and globally (CDC 2019). Between 2015 and 2022, the proportion of XDR Shigella infections in the U.S. rose to approximately 5%, significantly limiting oral treatment options (CDC 2019). Traditionally, azithromycin and ciprofloxacin have been recommended, but resistance trends necessitate susceptibility-guided therapy. Global efforts are focusing on vaccine development, with promising candidates in late-stage trials; however, none are licensed yet (Lu et al., 2024). These trends underscore the need for surveillance, stewardship, and accelerated vaccine availability.

2.5.1.6 *Enterococci*

Enterococci, mainly *Enterococcus faecalis* and *Enterococcus faecium*, are commensals of the human gut but have become significant nosocomial pathogens (Hammerum et al., 2024). They cause urinary tract infections, bacteremia, and endocarditis, especially in hospitalized patients with invasive devices. Since 2015, the emergence of vancomycin-resistant enterococci (VRE) has complicated treatment strategies. *E. faecium* exhibits higher resistance rates compared to *E. faecalis*, and cases of linezolid-resistant isolates have also been documented (Mullally et al., 2024). Treatment for VRE infections typically involves linezolid or high-dose daptomycin, sometimes in combination therapy for severe cases. Infection prevention measures and antimicrobial stewardship remain critical because colonized patients can serve as reservoirs, spreading VRE within healthcare facilities (Navarra et al., 2025). Surveillance reports highlight the continued global rise in VRE prevalence, emphasizing the need for molecular detection of resistance genes (vanA, vanB) and tailored antibiotic therapy (Hammerum et al., 2024).

2.5.1.7 *Proteus* spp.

Proteus mirabilis is a Gram-negative bacterium commonly associated with complicated urinary tract infections, especially in patients with long-term catheterization (Chakkour et al., 2024). Its ability to produce urease leads to urine alkalinization, facilitating struvite stone formation and catheter encrustation (Werneburg & Werneburg, 2022). The organism exhibits swarming motility and biofilm formation, increasing its persistence on indwelling devices and resistance to host defences. Infections may ascend to the kidneys and occasionally cause bacteremia, particularly in vulnerable populations. Although Proteus is generally susceptible to many antibiotics, resistance to fluoroquinolones and third-generation cephalosporins has been observed (Yang et al., 2024). Management involves prompt removal or replacement of the catheter, targeted antimicrobial therapy, and addressing underlying risk factors. Research efforts in 2023–2025 have focused on anti-biofilm coatings and urease inhibitors to prevent recurrent infections and catheter blockage, though these remain experimental (Slate et al., 2023).

2.5.1.8 *Enterobacter* spp.

The Enterobacter cloacae complex (ECC) includes species frequently implicated in healthcare-associated infections, such as bacteremia, pneumonia, and urinary tract infections (Davin-Regli et al., 2019). These organisms harbour inducible AmpC β-lactamases, which can be upregulated during therapy, causing treatment failure with third-generation cephalosporins (Tamma et al., 2024). The global spread of carbapenemase-producing Enterobacter strains, including KPC and NDM producers, further complicates therapy (Prinzi & Moore, n.d.). Current clinical guidance recommends cefepime, carbapenems, or novel β-lactam/β-lactamase inhibitor combinations based on susceptibility and infection severity (Hassan et al., 2021). Accurate species-level identification is essential because taxonomic changes, such as reclassifying Enterobacter aerogenes as *Klebsiella aerogenes*, affect antimicrobial interpretation (Wesevich et al., 2020). Increasing multidrug resistance among ECC underscores the urgent need for stewardship, surveillance, and infection prevention measures.

2.5.2 Fungi

2.5.2.1 *Candida* spp.

Cockroaches are increasingly recognized as carriers of opportunistic fungi such as *Candida* spp (Mloka et al., 2020)., which are a major cause of nosocomial bloodstream infections and mucosal disease. Recent hospital-based surveys have demonstrated the carriage of *Candida albicans* and non-*albicans* species *(C. glabrata*, *C. tropicalis, C. parapsilosis*) on cockroach cuticles and in gut contents (Merad et al., 2023). These isolates often mirror those circulating in the clinical environment, suggesting cross-contamination pathways. Importantly, non-*Candida albicans* species are notable for their reduced susceptibility to azoles and echinocandins, which complicates treatment (Perlin et al., 2017).

From an ecological standpoint, cockroaches provide a moist, nutrient-rich environment that supports the persistence and dispersal of fungi. *Candida* species may be disseminated mechanically via body surfaces or through faecal deposition after transient gut colonisation. Their survival on fomites and food surfaces enhances the likelihood of human exposure, particularly in hospital kitchens and patient wards (Donkor, 2019; Perlin et al., 2017). A prospective Algerian study found *Candida* species on 36% of hospital-collected cockroaches, underscoring their vector potential in clinical spaces (Merad et al., 2023).

Public health implications are significant as cockroach infestation in health facilities may contribute to nosocomial *Candida* burden, particularly among immunocompromised patients. As invasive candidiasis remains a leading cause of hospital mortality, vector control becomes a crucial adjunct to antifungal stewardship and infection prevention.

2.5.2.2 *Aspergillus* spp.

Aspergillus species, particularly *A. fumigatus* and *A. flavus*, are ubiquitous moulds implicated in allergic bronchopulmonary disease, invasive aspergillosis, and keratitis (Donkor, 2020). Recent entomological surveys highlight cockroaches as carriers of *Aspergillus* spores in hospitals and food premises (Merad et al., 2023). Recovery of *Aspergillus* from cockroach integuments suggests insects may disseminate conidia through movement across surfaces and air currents. This finding has significant clinical relevance in immunocompromised populations, where invasive aspergillosis is associated with a high mortality rate.

Moreover, azole-resistant *A. fumigatus*, driven by the use of agricultural fungicides, has emerged globally, raising concerns about additional environmental reservoirs (Perlin et al., 2017). Although direct resistance profiling from cockroach-borne Aspergillus is limited, the potential role of insects in dispersing resistant spores cannot be discounted. In hospital ecology, *Aspergillus* contamination is associated with construction dust, poor ventilation, and bioaerosols; the presence of cockroach vectors adds another layer to this risk, particularly in wards with high patient vulnerability. By harbouring spores externally or internally, cockroaches may exacerbate indoor fungal loads, contributing to nosocomial outbreaks. Preventive strategies must therefore integrate pest control with environmental air quality monitoring and surveillance of antifungal resistance.

2.5.3 Parasites

2.5.3.1 *Ascaris lumbricoides*

Ascaris lumbricoides, the most prevalent soil-transmitted helminth globally, has been identified on or within cockroaches in endemic regions. A systematic review by Tamma et al., (2024) consolidates evidence from multiple countries, confirming the detection of *Ascaris* ova on cockroach cuticles and in faeces. The transmission mechanism is mechanical: cockroaches foraging in latrine pits or contaminated soil acquire ova, which remain viable when transferred to food, water, or kitchen surfaces. Ingestion of embryonated eggs by humans perpetuates infection, leading to intestinal obstruction, malnutrition, and impaired growth in children. Given that Ghana and other sub-Saharan African countries continue to report high prevalence of soil-transmitted helminths, cockroach vectors represent an overlooked but plausible exposure route. The resilience of *Ascaris* ova, able to survive harsh environmental conditions, amplifies this risk. The implication is that vector management should complement mass drug administration campaigns. Controlling cockroach infestations in kitchens, schools, and hospitals can reduce indirect exposure to helminth eggs, particularly in areas where sanitation infrastructure remains inadequate.

2.5.3.2 *Trichuris trichiura*

Like Ascaris, *Trichuris trichiura* (whipworm) eggs have been recovered from cockroaches in environments with faecal contamination. (Patel et al., 2022) highlight consistent findings across Africa and Asia, demonstrating carriage of Trichuris ova by domestic cockroach species. Mechanical transmission is the likely route, with ova adhering to cockroach cuticles and being deposited onto food or fomites.

The public health burden of Trichuris is considerable: chronic infections in children result in anaemia, growth retardation, and impaired cognitive development. Where open defecation and poor waste management coincide with cockroach infestations, the risk of indirect transmission is elevated. Unlike direct faecal–oral transmission, cockroach-mediated spread allows helminth ova to bypass sanitation barriers by contaminating food in supposedly protected settings (kitchens, schools, hospitals). Given that *Trichuris* ova are resistant to environmental degradation, cockroaches may extend their persistence in human habitats.

2.5.3.3 *Strongyloides stercoralis*

Strongyloides stercoralis is an intestinal nematode capable of autoinfection, allowing for lifelong carriage in humans. Although traditionally linked to soil exposure, cockroaches have been implicated as incidental carriers of infective larvae. (Patel et al., 2022) reviewed entomological studies showing *Strongyloides* larvae recovered from cockroach intestines, suggesting potential survival during transit. Clinical significance lies in the severe, sometimes fatal, hyperinfection syndrome observed in immunocompromised individuals. In endemic regions, where both cockroach infestation and immunosuppressive therapy (for HIV, transplantation) are common, the intersection magnifies risk. The exact role of cockroaches in transmission is less studied than that of *Ascaris* or *Trichuris*, but mechanical transport from contaminated soil or faeces into households remains a plausible mechanism.

This pathway underscores the broader ecological role of cockroaches as carriers of diverse helminths, not merely bacterial or fungal pathogens. Research gaps remain regarding larval viability post-carriage; however, the evidence supports including *Strongyloides* in the portfolio of parasites relevant to cockroach-mediated exposure.

2.5.3.4 *Taenia* spp.

Taenia spp. (notably *T. saginata* and *T. solium*) cause taeniasis and cysticercosis, with major public health impact in endemic regions. Evidence compiled by (Patel et al., 2022) shows *Taenia* eggs attached to cockroach surfaces and in gut contents, particularly in regions where sanitation is poor and pork is consumed undercooked. The mechanical role of cockroaches is analogous to that of flies: they transport eggs from faecal matter to food sources. While direct epidemiological linkage is difficult to prove, detection of viable Taenia ova on cockroaches provides strong circumstantial evidence for their contribution to exposure pathways. For *T. solium*, this is particularly concerning, as cysticercosis is a leading cause of acquired epilepsy in Sub-Saharan Africa (Dokmaikaw & Suntaravitun, 2019). Control strategies must therefore consider cockroaches as adjunct vectors. Improving kitchen hygiene, ensuring thorough cooking of meat, and strengthening pest management in rural and peri-urban areas are critical. As *Taenia* eggs are highly resilient, cockroach-mediated spread represents an under-appreciated risk in endemic zones.

2.5.3.5 *Entamoeba histolytica*.

Entamoeba histolytica is the protozoan responsible for amoebic dysentery and liver abscesses. (Patel et al., 2022) confirm that cockroaches can mechanically carry *E. histolytica* cysts, particularly when collected from latrines and hospital kitchens. The cysts' resilience enables their survival on cockroach surfaces and within the gut contents. Ingestion of contaminated food or water remains the primary transmission route, but cockroach-mediated spread can bypass sanitation safeguards, especially in institutions where food hygiene is compromised. Outbreak investigations in endemic regions often implicate foodborne routes; cockroaches may represent a hidden contributing factor.

Given the global burden of amoebiasis, which affects up to 50 million people annually, the potential role of cockroaches in sustaining transmission cycles warrants greater attention (Dokmaikaw & Suntaravitun, 2019). Integration of pest management into diarrheal disease control programs is warranted, particularly in urban slums and healthcare facilities.

2.5.3.6 *Giardia lamblia*.

Giardia lamblia is a protozoan parasite causing giardiasis, a diarrheal disease associated with malabsorption and growth impairment. (Patel et al., 2022) reviewed studies documenting cysts of *Giardia* on cockroach exoskeletons and in digestive tracts. Like *Entamoeba*, mechanical dissemination is the most plausible pathway for transmission. Children are most affected by giardiasis, and the contamination of school food programs or household meals with cockroaches could constitute a significant transmission vector. Importantly, cysts of *Giardia* are resistant to chlorination, meaning even treated water supplies can become re-contaminated via insect vectors. From a One Health perspective, cockroach-mediated *Giardia* spread links environmental contamination, animal reservoirs, and human infection. Vector control in food handling environments thus has added importance for reducing protozoan transmission in endemic regions.

2.5.3.7 *Cryptosporidium* spp.

Cryptosporidium spp. are protozoan parasites causing cryptosporidiosis, a diarrheal illness notable for severe disease in immunocompromised individuals (e.g., HIV/AIDS patients). (Patel et al., 2022) highlight detection of oocysts on cockroach bodies and within guts, confirming their role as mechanical carriers. The oocysts' resistance to environmental stressors and chlorine treatment renders cockroach-mediated dissemination especially problematic. In healthcare facilities, cockroach carriage could contribute to outbreaks among vulnerable populations, while in households, they may exacerbate endemic transmission cycles. Recent global health alerts emphasize *Cryptosporidium* as a leading cause of waterborne outbreaks, but cockroach-mediated dissemination offers a parallel pathway that is less visible yet epidemiologically significant (Dokmaikaw & Suntaravitun, 2019). Integrated control measures must therefore consider cockroaches in conjunction with water and sanitation improvements.

2.5.3.8 Hookworm

Hookworm infection, primarily caused by *Necator americanus* and *Ancylostoma duodenale*, remains a significant public health concern in tropical and subtropical regions. These parasites attach to the intestinal mucosa, leading to chronic blood loss, iron-deficiency anaemia, and impaired physical and cognitive development in children (World Health Organization, 2023). Transmission occurs when infective larvae in contaminated soil penetrate the skin, initiating a lifecycle that includes pulmonary migration before establishing in the small intestine (Chen et al., 2024). The cornerstone of control is mass drug administration (MDA) with benzimidazoles such as albendazole or mebendazole. However, variable cure rates and rapid reinfection limit program effectiveness ((Patel et al 2021; Colella et al., 2021). Recent studies highlight that albendazole remains more effective than mebendazole against hookworm, achieving higher egg reduction rates (Patel et al., 2022). Additionally, molecular diagnostic techniques have revealed lower clearance rates than previously estimated by microscopy, signalling the need for improved monitoring (Colella et al., 2021). Advances in vaccine development offer promise, with Na-GST-1 and Na-APR-1 (M74) candidates demonstrating safety and immunogenicity in Phase 1 trials in both non-endemic and endemic populations

(Adegnika et al., 2021). These candidates elicited robust IgG and T-cell responses, indicating potential as complementary interventions to MDA (Mouwenda et al., 2021). Furthermore, integrated WASH (water, sanitation, and hygiene) strategies have been shown to significantly reduce reinfection rates when combined with MDA, supporting the need for multi-component approaches (Nery et al., 2019).

2.5.3.9 *Oxydurid* spp.

Oxydurid nematodes, also referred to as pinworms in veterinary contexts, primarily infect herbivorous mammals such as horses, rabbits, and rodents. Infections in these animals are generally associated with irritation of the intestinal mucosa, weight loss, and reduced productivity in livestock (Patel et al., 2022)Reports of zoonotic transmission to humans are exceedingly rare and poorly documented in the scientific literature, suggesting minimal public health importance (Zajac et al 2021). Diagnosis in animals relies on faecal flotation for egg detection, while recent molecular approaches, including ITS-based PCR assays, have enhanced species identification and epidemiological studies (Patel et al., 2022). Control of oxyurid infections primarily relies on benzimidazole anthelmintics; however, confirmed cases of drug resistance in this group are scarce (Nielsen, 2022). Further research is necessary to clarify species diversity, pathogenic potential, and the potential for cross-species transmission.

2.5.3.10 *Toxoascaris leonina.*

Toxoascaris leonina is a parasitic roundworm that infects dogs, cats, and other carnivores. Its lifecycle is direct, involving ingestion of infective eggs from contaminated environments, and does not include the extensive tissue migration observed in *Toxocara* species (Zajac et al

2021). Clinical signs in definitive hosts, particularly young animals, include diarrhoea, vomiting, and stunted growth, although infections are often subclinical (Waindok et al 2020). Human infections are rare and typically occur in individuals with close contact with domestic animals. While occasional serological evidence of exposure has been reported, confirmed cases of clinical disease in humans remain exceptional (Eslahi et al., 2020). Diagnostic methods include faecal flotation for eggs, while treatment relies on broad-spectrum anthelmintics such as pyrantel and fenbendazole (Eslahi et al., 2020). No vaccines are currently available, and reports on drug resistance in this species are lacking.

2.6 Transmission Significance: Role in Faecal–Oral Transmission in Hospitals, Kitchens, and Food Stores

Cockroaches are strongly implicated in the faecal–oral transmission cycle, bridging environmental contamination and human exposure. Their scavenging behaviour brings them into contact with human waste, sewage, refuse, and hospital effluent, after which they traverse food preparation areas and wards, mechanically transferring pathogens on their exoskeletons and in faecal deposits (Crespo et al., 2025; Liu et al., 2024). Modern surveillance confirms that Escherichia coli, *Salmonella enterica*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* isolated from cockroaches are often identical in resistance profiles to clinical isolates, demonstrating overlap between insect-carried and patient-derived pathogens (Bisetegn et al., 2024; Donkor et al., 2024).

The significance of this pathway is amplified in hospitals where patients are vulnerable and invasive devices increase the risk of infection. (Bisetegn et al., 2024) reported that more than one-third of hospital cockroach isolates were ESBL producers, while nearly a quarter carried metallo-β-lactamases. This finding mirrors those in Ghana, where carbapenemase-encoding genes have been detected in both clinical and environmental isolates, suggesting that vectors may facilitate cross-compartmental dissemination (Donkor et al., 2024).

In kitchens and food stores, cockroaches facilitate direct contamination of raw and ready-to-eat food. A Shanghai-based study detected enteropathogenic *E. coli*, *Salmonella*, and protozoan cysts in cockroaches collected from restaurants and catering facilities (Liu et al., 2024). In Ghana, resistance documented in ready-to-eat street food for cephalosporins and sulfamethoxazole-trimethoprim echoes the AMR phenotypes reported in cockroach isolates (Onohuean et al., 2025). Overall, the transmission significance of cockroaches lies not only in their mechanical mobility but also in their ecological bridging capacity. They connect sewage, refuse, kitchens, and hospitals into a single epidemiological network, enabling faecal–oral transmission of resistant pathogens and undermining food safety and infection prevention programs.

2.7 Mechanisms of Antimicrobial Resistance

2.7.1 Intrinsic Resistance

Intrinsic resistance in cockroach-associated bacteria refers to the naturally encoded mechanisms that confer baseline insensitivity to antimicrobial agents. Non-fermenting Gram-negative bacteria such as *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, both frequently recovered from cockroaches, inherently possess efflux pumps, reduced outer membrane permeability, and chromosomally encoded β-lactamases (Bisetegn et al., 2024). These features render them less susceptible to β-lactams and many other antibiotic classes even before acquisition of mobile resistance determinants. Similarly, fungal organisms such as *Candida glabrata* exhibit intrinsic reduced susceptibility to fluconazole, raising challenges when carried into clinical environments (Merad et al., 2023).

Intrinsic resistance is clinically significant because it limits empiric therapy options and provides a background against which acquired resistance can accumulate. For example, cockroach-associated P. aeruginosa isolates resistant to cephalosporins and carbapenems may reflect amplification of both intrinsic (efflux pump activity) and acquired (plasmid-mediated carbapenemases) mechanisms (Donkor et al., 2024). Thus, cockroach-borne organisms often present multi-layered resistance challenges from the outset, compounding infection control risks.

2.7.2 Acquired Resistance

Acquired resistance arises through horizontal gene transfer (HGT) of mobile genetic elements (plasmids, integrons, transposons) or spontaneous mutations under selective pressure. Cockroach microbiomes, shaped by coprophagy, aggregation, and repeated contact with contaminated environments, provide fertile grounds for ARG acquisition and exchange. Experimental work by (Bogri et al., 2024) demonstrated that tetracycline resistance genes spread from antibiotic-exposed cockroaches to untreated cohorts and to their shared soil environment, evidencing inter-individual and environmental HGT (Bogri et al., 2024).

Molecular surveillance confirms carriage of acquired resistance determinants in cockroach-borne pathogens, including *bla_{CTX-M}, bla_{TEM}, bla_{NDM}, qnrS, and sul1* (Donkor et al., 2024). These genes encode ESBLs, carbapenemases, and resistance to fluoroquinolones and sulfonamides, antibiotics critical in both human and veterinary medicine. In Ethiopian hospitals, 34.7% of cockroach E. coli isolates were ESBL producers, while 23.1% of Klebsiella carried MBLs (Bisetegn et al., 2024). Such high proportions indicate that cockroaches serve as active reservoirs where acquired resistance develops under antibiotic selection pressures.

The importance of acquired resistance mechanisms in cockroach-associated bacteria is twofold: they complicate treatment of infections potentially linked to vectors, and they expand the environmental resistome available for transfer into human pathogens. This positions cockroaches not merely as carriers, but as amplifiers of AMR in the built environment.

2.7.3 Resistance Genes in Cockroach-Associated Bacteria.

Modern molecular studies have directly identified resistance genes in cockroach-derived isolates. In Ghana, Donkor et al. (2024) reported detection of bla, mecA, sul1, and ermB in isolates spanning *E. coli*, *K. pneumoniae*, *Staphylococcus aureus*, and others. Such genes correspond to ESBLs, carbapenemases, methicillin resistance, sulfonamide resistance, and macrolide resistance. Their presence in cockroach-associated organisms highlights the insects' role as reservoirs of environmental genes. Beyond Ghana, Ethiopian hospital isolates from cockroaches carried ESBL and MBL genes, while food-premise cockroaches in China yielded E. coli with shiga-toxin genes in addition to classical AMR determinants (Bisetegn et al., 2024; Liu et al., 2024). Metagenomic analysis further confirms ARG enrichment in cockroach-associated microbiomes, including tetracycline, aminoglycoside, and sulfonamide resistance genes (Ma et al., 2025).

This gene-level evidence is critical for surveillance: it links cockroach carriage to global resistance trends, including carbapenemase spread and the persistence of ESBLs. The overlap between cockroach-borne ARGs and those found in clinical isolates highlights the insects' bridging role in the ecology of resistance. Routine molecular surveillance of cockroach populations, particularly in hospitals and food chains, could thus serve as a sentinel strategy for early detection of emergent resistance threats.

2.8 AMR in Cockroach-Borne Pathogens

Cockroach-borne pathogens frequently display multidrug resistance (MDR), with consistent evidence across hospital, food, and household environments. Systematic mapping of hospital-collected cockroaches (2000–2024) found that *Escherichia coli, Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most frequently isolated species, and in many studies, over 50% of these isolates exhibited antimicrobial resistance, particularly to β-lactams, fluoroquinolones, and aminoglycosides (Crespo et al., 2025). Ethiopian surveillance identified ESBL-producing *E. coli* (34.7%) and metallo-β-lactamase (MBL)–producing *Klebsiella* (23.1%) in cockroaches collected from wards, reflecting phenotypes found in patient isolates (Bisetegn et al., 2024). Metagenomic analyses further reveal enrichment of resistance determinants in cockroach microbiomes, including *bla, qnrS, sul1, and ermB,* confirming carriage of genes conferring resistance to cephalosporins, carbapenems, quinolones, sulfonamides, and macrolides (Donkor et al., 2024; Ma et al., 2025). Notably, cockroach-borne Salmonella and shiga-toxin–producing *E. coli* strains have been detected in food-preparation environments in China, with resistance profiles matching those in human infections, raising food safety alarms (Liu et al., 2024).

The public health significance of AMR in cockroach-borne pathogens lies in their potential to act as mobile environmental reservoirs and amplifiers of clinically relevant resistance. By bridging contaminated habitats, kitchens, and hospitals, cockroaches disseminate pathogens that are not only infectious but also difficult to treat, undermining infection prevention and antimicrobial stewardship. Their role in maintaining and transmitting MDR organisms highlights the urgency of integrating entomological surveillance into AMR monitoring frameworks.

2.9 Environmental and Human Factors Promoting AMR in Cockroaches

The acquisition and persistence of antimicrobial resistance in cockroach-associated microorganisms are driven by intersecting environmental and human factors. Antibiotic misuse in human medicine and agriculture creates pervasive selective pressures. In Ghana, high rates of self-medication, over-the-counter antibiotic sales, and unregulated veterinary use contribute to widespread environmental contamination (Donkor et al., 2024). This aligns with broader Sub-Saharan African trends, where poor antibiotic stewardship fosters resistome enrichment in both clinical and environmental niches (Chilanga et al., 2025). Environmental contamination also plays a central role. Cockroaches thrive in sewage systems, refuse dumps, kitchens, and hospital wards, all of which harbour antibiotic residues and resistant microorganisms. Ready-to-eat foods in Ghana reported resistance prevalence exceeding 70% for several antibiotics, reflecting food-chain exposure points (Onohuean et al., 2025). Cockroaches feeding in these environments acquire and disseminate resistant bacteria.

Behavioural and biological traits of cockroaches amplify this process. Coprophagy, aggregation, and high reproductive rates facilitate horizontal gene transfer (HGT) among microbial populations within their guts (Bogri et al., 2024). Metagenomic evidence confirms that cockroach microbiomes contain transferable ARGs that can seed environmental microbial communities (Ma et al., 2025).

Structural and social determinants compound these risks: poor sanitation, weak infrastructure, and inadequate pest control in hospitals and households create favourable conditions for infestations. In low-resource healthcare settings, the convergence of high antimicrobial use and uncontrolled cockroach populations creates “hotspots” for resistance amplification (Bisetegn et al., 2024).

Thus, AMR in cockroaches is not an isolated entomological concern but a product of systemic antibiotic misuse, environmental contamination, and vector biology. Effective interventions must combine antimicrobial stewardship with robust sanitation, waste management, and pest control, particularly in healthcare and food-handling environments.

2.10 Methods of Detection of AMR in Cockroach Isolates

The detection of antimicrobial resistance (AMR) in cockroach-associated microorganisms requires a combination of classical microbiological approaches and modern molecular tools. Initial steps typically involve isolation and culture of bacteria from cockroach body surfaces, gut contents, or faecal pellets using selective and differential media such as MacConkey agar, blood agar, and chromogenic media (Crespo et al., 2025). Following isolation, antimicrobial susceptibility testing (AST) is performed using standardized protocols, including the Kirby–Bauer disk diffusion method, broth microdilution, and automated systems such as VITEK 2, with interpretation guided by the Clinical and Laboratory Standards Institute (CLSI) or

EUCAST breakpoints (Bisetegn et al., 2024). These assays allow identification of multidrug resistance, extended-spectrum β-lactamase (ESBL) production, and carbapenem resistance.

Advanced phenotypic methods, such as the combined disk synergy test (CDST) for ESBLs and the modified Hodge test or Carba NP test for carbapenemases, are increasingly applied in cockroach-related studies. However, the gold standard for confirming AMR determinants is molecular analysis, including polymerase chain reaction (PCR), multiplex PCR, and whole-genome sequencing (WGS). These techniques enable detection of resistance genes such as bla, mecA, and qnrS (Donkor et al., 2024). Metagenomic sequencing has further advanced the field, revealing the resistome structure of cockroach gut microbiota and environmental dust impacted by cockroaches (Ma et al., 2025).

Recent innovations emphasize integrative approaches: coupling high-throughput sequencing with quantitative microbial risk assessment (QMRA) to evaluate public health risks of cockroach-borne AMR (Gwenzi et al., 2021). Overall, detection methods range from culture-based phenotyping to gene-level characterization, reflecting the need for sensitive, rapid, and scalable tools to understand cockroach-associated AMR ecology.

2.11 Methods of Detection of Parasites in Cockroaches

Detection of parasites carried by cockroaches requires tailored methods depending on the life stage and species of the parasite. The most common approach is microscopic identification of eggs, cysts, and oocysts from homogenized cockroach gut contents or surface washes. Standard concentration methods, such as formalin ether sedimentation, flotation techniques, and staining methods (e.g., iodine wet mount, trichrome stain, modified Ziehl–Neelsen for

Cryptosporidium) enhance visualization (Patel et al., 2022). These techniques remain widely used in epidemiological surveys due to their cost-effectiveness and applicability in resource-limited settings.

For helminths such as *Ascaris lumbricoides* and *Trichuris trichiura*, ova are identified based on morphological features under light microscopy. Protozoan cysts (*Giardia lamblia*, *Entamoeba histolytica*) and oocysts (*Cryptosporidium spp*.) are also detectable by microscopy, though sensitivity varies with operator expertise. Recent parasitological studies recommend combining microscopy with immunofluorescence assays (IFA) or enzyme-linked immunosorbent assays (ELISA) for higher diagnostic accuracy, particularly for protozoa.

Molecular diagnostics are increasingly incorporated into cockroach-parasite research. Polymerase chain reaction (PCR) and real-time PCR enable the detection of species-specific genetic markers, offering greater sensitivity and specificity than microscopy. These methods are beneficial for differentiating morphologically similar organisms, such as *E. histolytica* from the nonpathogenic *E. dispar*. In some studies, sequencing of 18S rRNA or ITS regions has been used to confirm parasite identity and track genetic diversity (Patel et al., 2022).

Overall, detection strategies for cockroach-associated parasites have evolved from purely morphological identification toward molecular confirmation. The integrated use of microscopy, immunoassays, and PCR provides a comprehensive framework for the accurate surveillance of helminths and protozoa transmitted by cockroaches.

2.12 Public Health Significance

The public health significance of cockroach infestations extends far beyond nuisance. Cockroaches are now recognized as epidemiologically relevant vectors of antimicrobial-resistant (AMR) pathogens, fungi, and parasites. In hospitals, their role is particularly concerning: systematic reviews confirm that *E. coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* recovered from cockroaches often display resistance profiles identical to patient isolates (Bisetegn et al., 2024; Crespo et al., 2025). This alignment suggests insects may serve as reservoirs and bridging vectors, undermining infection prevention and control (IPC) measures.

Food safety is equally impacted. Surveillance in catering and food markets has revealed cockroach carriage of enteropathogenic bacteria and protozoa, highlighting risks of faecal–oral transmission through contamination of ready-to-eat foods (Liu et al., 2024). In Ghana, street food studies reporting resistance to cephalosporins, tetracyclines, and sulfonamides align with resistance phenotypes detected in cockroach-borne bacteria (Onohuean et al., 2025). Beyond infectious disease, cockroach allergens, such as Bla g 1 and Bla g 2, are established triggers of asthma exacerbations, disproportionately affecting children in urban slums and low-resource communities (Rust et al., 2024). Thus, the presence of cockroaches in households contributes simultaneously to the chronic non-communicable disease burden and infectious disease risk.

Overall, cockroaches pose a multifaceted health hazard: they propagate resistant bacteria, disseminate intestinal parasites, exacerbate allergies, and compromise food hygiene.

Recognizing their significance elevates pest management from a matter of sanitation to a cornerstone of AMR containment and urban health policy.

2.13 Control and Prevention Strategies

Effective control of cockroaches, particularly in hospitals and food environments, is central to reducing their vectorial role in AMR transmission. Integrated Pest Management (IPM) has emerged as the gold-standard strategy, combining sanitation, structural repair, monitoring, and judicious insecticide use (Wang & Cooper, 2025). Sanitation measures, such as eliminating food residues, sealing cracks, and controlling moisture, directly disrupt cockroach survival and breeding. Monitoring tools such as sticky traps provide early detection and population estimates, supporting targeted interventions (Wang & Cooper, 2025).

Chemical control remains a key component, but widespread insecticide resistance complicates reliance on traditional sprays. Gel baits are preferred due to their targeted delivery and reduced environmental impact. However, behavioural resistance, such as glucose aversion in *Blattella germanica* has reduced bait effectiveness, necessitating rotation of bait matrices and incorporation of novel active ingredients (Wada-katsumata & Schal, 2024). Biological control strategies, including entomopathogenic fungi (*Metarhizium anisopliae*, *Beauveria bassiana*), are under evaluation for sustainable suppression (Appel et al., 2022).

In healthcare facilities, zero-tolerance infestation policies are recommended, integrating pest control with routine IPC programs. Structural audits and regular fumigation must be combined with strict food-handling protocols. In communities, public education on sanitation and safe food storage is equally essential. Importantly, pest control should be linked with antimicrobial stewardship and One Health surveillance, recognizing cockroaches as AMR reservoirs (Donkor et al., 2024).

In sum, sustainable prevention requires a multi-pronged approach: IPM, resistance-aware chemical use, biological alternatives, and systemic improvements in sanitation. When embedded within AMR policies, such strategies can substantially reduce the risks of cockroach-mediated diseases.

2.14 Conceptual Framework

The conceptual framework for this study is anchored in the One Health approach, which recognizes the interconnectedness of humans, animals, and the environment in the emergence and dissemination of antimicrobial resistance (AMR). Cockroaches occupy a unique ecological niche within this triad, functioning simultaneously as mechanical carriers, biological reservoirs, and amplifiers of resistant microorganisms.

Cockroach Biology and Ecology:

Synanthropic species (*Blattella germanica*, *Periplaneta americana*, *Blatta orientalis*) thrive in environments shared with humans due to their omnivorous diet, nocturnal foraging, aggregation behaviour, and high reproductive potential (Rust et al., 2024). These traits enhance opportunities for microbial acquisition and persistence.

Acquisition of Microorganisms:

Cockroaches pick up bacteria, fungi, and parasites from contaminated sources (sewage, refuse, hospital effluent, food debris). Empirical studies confirm carriage of ESBL-producing

E. coli, carbapenem-resistant K. *pneumoniae*, *Candida spp*., *Aspergillus spp*., and protozoan cysts (Crespo et al., 2025; Patel et al., 2022).

Transmission Pathways:

Transmission occurs via mechanical transfer (exoskeleton, faecal deposition), indirect environmental contamination (settled dust, air), and, in some cases, biological persistence within the gut microbiome (Bogri et al., 2024; Liu et al., 2024). These pathways facilitate faecal–oral transmission in hospitals, kitchens, and food stores.

Mechanisms of Resistance:

Isolates from cockroaches carry intrinsic and acquired resistance mechanisms. Genes such as bla, mecA have been detected, confirming that cockroaches harbour globally significant AMR determinants (Donkor et al., 2024). Experimental studies also demonstrate horizontal gene transfer within cockroach populations (Bogri et al., 2024).

Human and Environmental Drivers:

Factors such as antibiotic misuse, poor sanitation, food contamination, and inadequate pest control amplify the role of cockroaches as vectors. Weak infrastructure in hospitals and markets creates hotspots for resistance propagation (Bisetegn et al., 2024; Onohuean et al., 2025).

Public Health Outcomes:

The convergence of these dynamics results in increased risk of nosocomial infections, foodborne disease, and parasitic transmission. Vulnerable populations, children, immunocompromised patients, and slum dwellers are disproportionately affected.

This framework emphasizes that cockroach-mediated AMR transmission is not an isolated entomological issue but a systemic challenge at the human–environment interface. It justifies integrated interventions combining AMR surveillance, IPC, pest management, and public education within a One Health context.

2.14.1 Conceptual Framework of Cockroach-Mediated AMR Transmission.

The diagram below illustrates the conceptual framework of cockroach-mediated antimicrobial resistance (AMR) transmission. It presents the flow of microbial acquisition, carriage, transmission, and outcomes, with human and environmental drivers, and highlights intervention strategies.

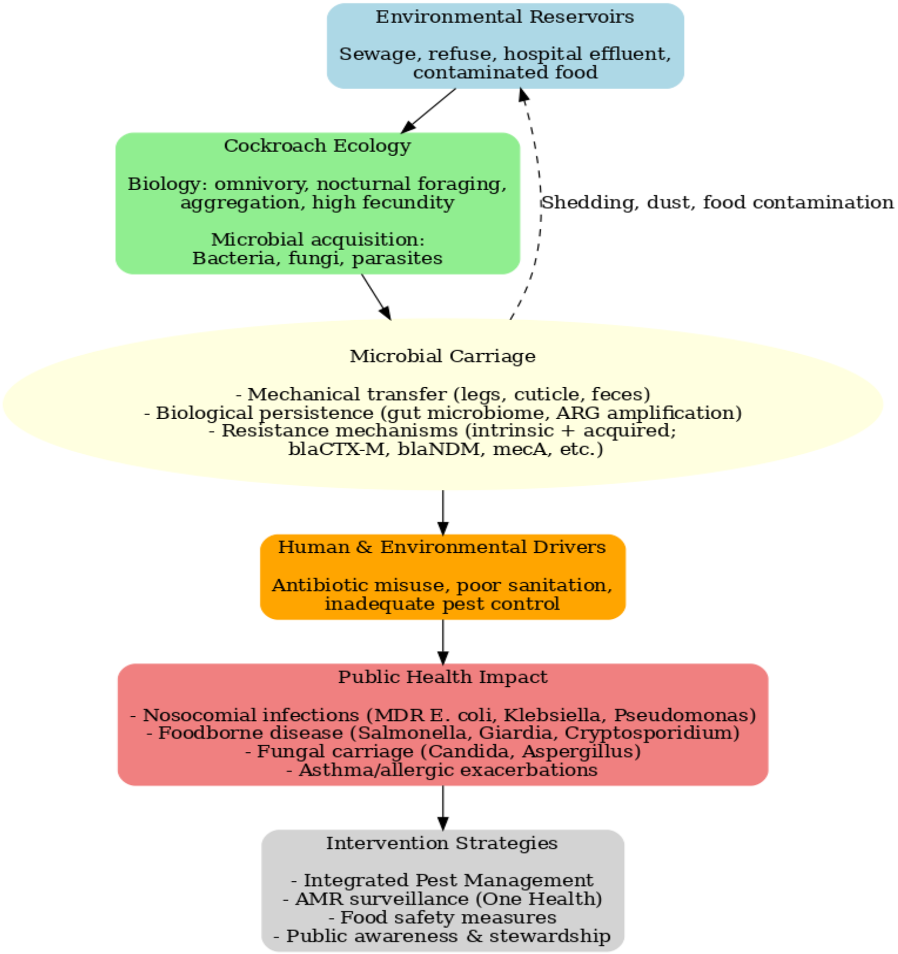


Figure 2. 2: Conceptual framework

(Source: Author’s own construct)

CHAPTER THREE

MATERIALS AND METHODS

3.1 Introduction

Several analytical tools and methodologies were employed to achieve the study's objectives regarding the prevalence, identification, and antibiotic resistance profiles of microbial carriage in cockroaches from different environments.

3.2 Study Area

The study was carried out at the Ashanti Mampong Municipality. Mampong is the capital of the Mampong Municipal Assembly in the Ashanti region of Ghana. Situated roughly 60 kilometers northeast of Kumasi, the regional capital, it is located at latitude 7°05′42″N and longitude 1°24′49″W. Its population is estimated to be 40,000, making up roughly half of the municipality's total population. The town features picturesque rolling land shapes that vary from low-lying tropical regions to hills and scarps, all within a moist semi-equatorial forest zone. Because of the rich soil, farming is the main industry in the municipality. Ashanti Mampong's warm and humid climates are ideal for cockroach breeding and survival. Tropical and subtropical regions often face higher infestation rates. Educational institutions bring together large numbers of students, faculty, and staff. Higher population densities increase the likelihood of food waste and spillage, providing ample feeding opportunities for cockroaches.

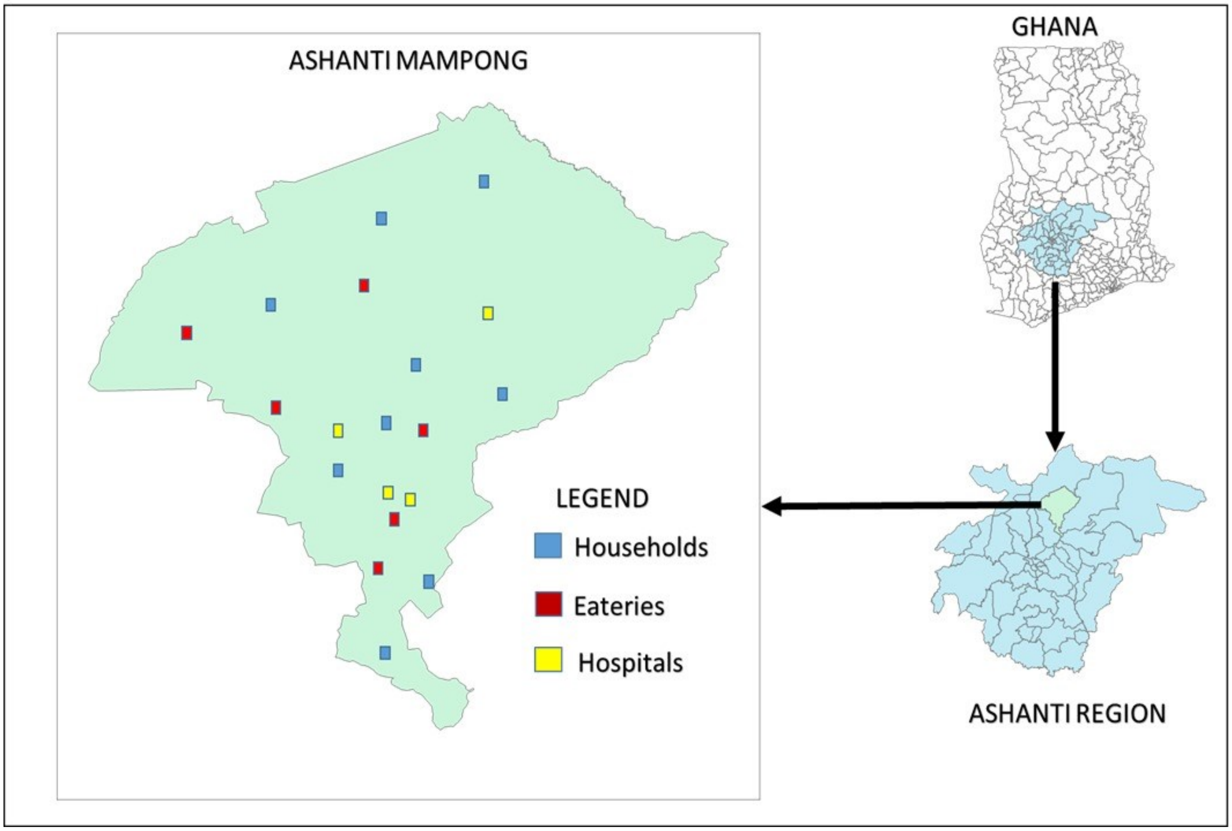


Figure 3. 1:Map of Mampong showing the study sites

3.3 Study Design

This study employed a cross-sectional design to assess the prevalence of microbial carriage and the antibiotic resistance profile in bacteria carried by cockroaches in Ashanti Mampong. This approach was suitable for comparing cockroaches from multiple sites and identifying potential public health risks.

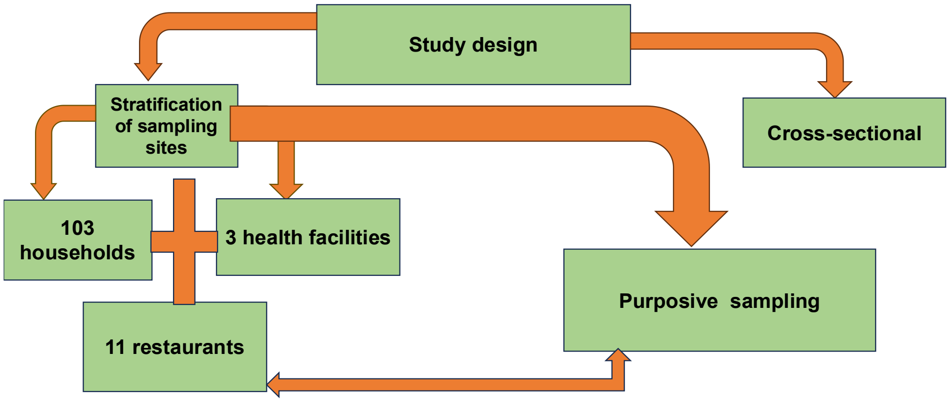


Figure 3. 2:Flow chart of study design

3.4 Study population

The study population included cockroaches found in human dwellings and food handling areas across the three study sites (households, hospitals, and eateries). These cockroaches were chosen because they are common carriers of microorganisms and may be important for understanding public health risks.

3.5 Sampling

3.5.1 Sampling technique

A purposive sampling technique was used to select locations where cockroaches were more likely to be found, such as Bedroom, Kitchen, living room, Storeroom, Toilet, Washroom, and refuse collection points. Within each location, cockroaches were captured using sticky traps and manual collection during both day and night times to improve representativeness. This approach ensured that samples reflected different habitats and activity periods of cockroaches across the sites.

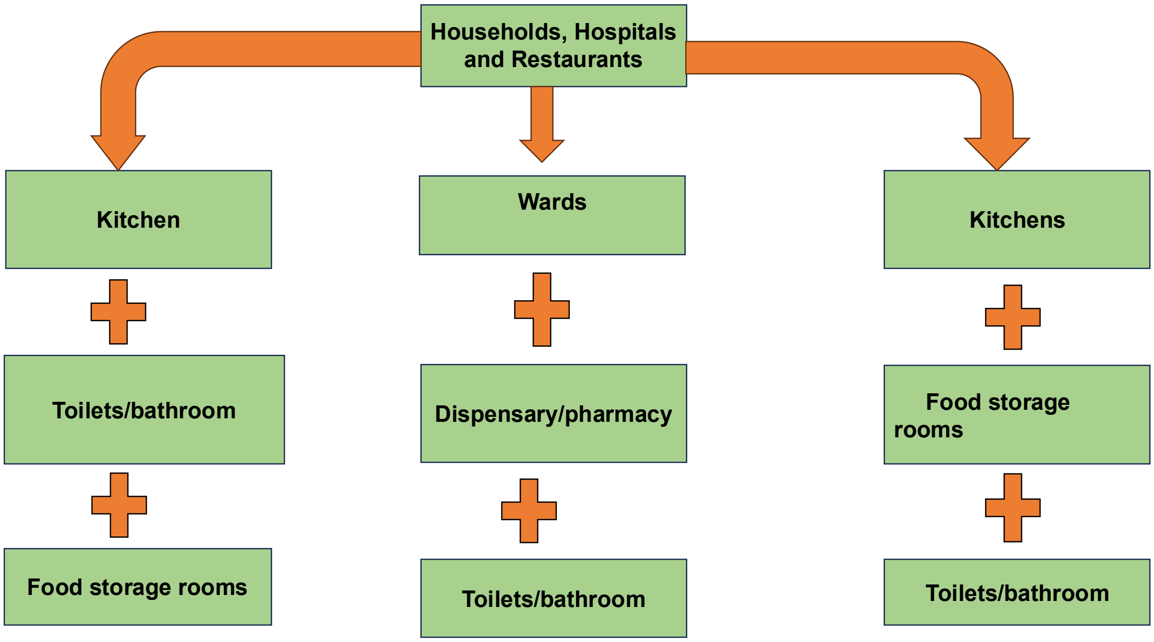


Figure 3. 3:Flow chart of sampling techniques

3.5.2 Sample size

The sample size was calculated using Cochran's formula: $n = \frac{Z^2 \times P(1-P)}{e^2}$, where n is the sample size, Z is the standard normal value at 95% confidence (1.96), P is the estimated proportion, and e is the margin of error. From this calculation, a total of 358 cockroaches were collected from the sites

3.5.3 Study Sites Selection

The study was conducted across three main categories of sites within Ashanti Mampong to represent varying human environments and activities. Three (3) hospitals were selected, varying in size and patient load, to capture differences in healthcare settings. Fifteen (15) eateries, including restaurants, fast food outlets, and cafeterias, were chosen to reflect a range of food service environments. Also, one hundred and three (103) households from different socio-economic backgrounds were included.

3.5.4 Data collection

Sampling was carried out during periods of cockroach activity, mostly at night when they are most active. The duration of sampling varied according to the size and accessibility of the sites but generally spanned several days to allow for the collection of sufficient specimens. Both passive and active methods were used. The passive method involved placing sugar-baited traps and sticky traps overnight in areas such as kitchens, bathrooms, toilets, wards, and drug dispensaries. These traps were retrieved the following morning in line with standard procedures for sampling nocturnal insects (Zha 2017). The active method involved directly collecting cockroaches by hand using sterile gloves and forceps, especially in areas where cockroach presence was observed during the daytime. This combination of passive and active techniques ensured that a representative sample of cockroaches was collected from different environments and activity periods. Each collected sample was labeled with relevant information, including location, date and time of collection

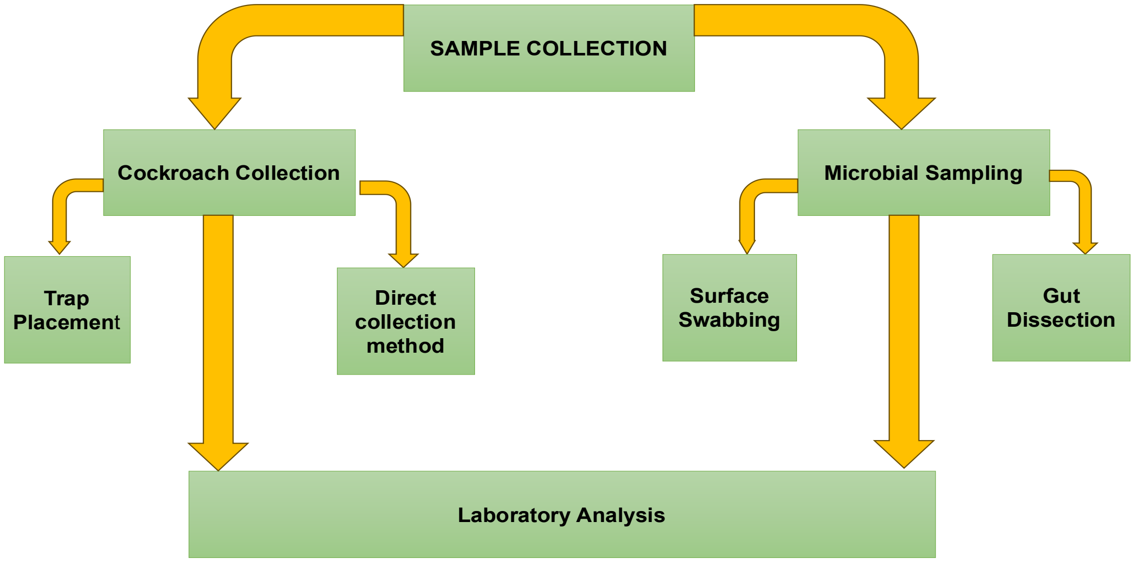


Figure 3. 4:Flow chart of sample collection methods

3.5.6 Transport of Specimens

After collection, cockroaches were transferred into well-labeled and sterile containers to avoid cross-contamination between samples. The containers were punctured with small holes to allow air circulation and maintain the viability of the specimens. All samples were placed in cold boxes and transported to the parasitological and microbiology laboratory within the same day of collection. During transportation, care was taken to maintain hygienic conditions and minimize stress or damage to the specimens. This ensured that they remained suitable for subsequent parasitological and microbiological analysis.

3.5.7 Cockroach Identification

In the laboratory, cockroaches were handled with sterile gloves to avoid direct contact and reduce the risk of contamination. Live specimens were kept in clean, ventilated containers until identification. During examination, each cockroach was immobilized carefully using sterile forceps to allow observation without causing damage. Standard entomological keys were followed to identify cockroaches based on external morphological features such as body size, shape, coloration, and the structure of the pronotum, wings, and antennae.

All instruments and surfaces used during identification were disinfected before and after handling each specimen to maintain sterile conditions. Identification was carried out to the species level to distinguish the most common household and hospital cockroach species. A hand lens was also used to improve visual observation of small morphological details.

3.6 Parasitological Examination

Cockroaches were examined for parasites. For this, each cockroach was placed in a 15mL tube containing 10 mL of normal saline (specific gravity 1.2) and vortexed for 1–2 minutes using a vortex machine (Batch No: GP/100/CLAD/100/HYD, China) to dislodge external contaminants. The cockroach was then removed, and the saline suspension was topped up with flotation fluid to a convex meniscus. As part of the flotation procedure, a clean cover slip was gently placed on top of the tube to allow parasitic stages to adhere by surface tension. After 10–15 minutes, the cover slip was removed and placed on a glass slide for microscopic examination. Direct wet mount preparations were also made and observed under a light microscope at ×10 and ×40 magnifications to identify parasitic stages.

3.7 Microbiological Analysis

For microbiological investigations, each cockroach was processed under sterile conditions. Individual specimens were placed in sterile zip lock bags with a 10mls volume of buffered peptone water. The samples were then homogenized using a Laboratory paddle blender machine (Batch No.88391, Weston-super-Mare England) for 30 seconds to ensure thorough release of microorganisms from both external and internal surfaces. The resulting homogenate was used for serial dilution and inoculation onto culture media (Bouamama et al., 2010).

3.7.1 Culture on Selective and Differential Media

3.7.1.1 MacConkey Agar

MacConkey agar (Batch No. CM0007 UK) was used as a selective and differential medium for the isolation and differentiation of *Enterobacteriaceae*. The dehydrated medium was suspended in distilled water and sterilized by autoclaving at 121 °C for 15 minutes. The molten medium was allowed to cool to about 45–50 °C. It was then poured into sterile Petri dishes (90 × 15 mm, Ice Medical, Ghana). The pouring was done inside a Class II Biosafety Cabinet (Esco Airstream, Singapore). Approximately 20 ml of medium was used for each plate.

After solidification, plates were dried and stored at 4 °C until use. For inoculation, 0.1 ml of prepared sample suspension was spread evenly on the agar surface using a sterile glass spreader. The medium contained bile salts and crystal violet, which inhibited Gram-positive bacteria, allowing the selective growth of Gram-negative organisms. Lactose fermentation was indicated by neutral red dye as shown in **Plate 2**. Lactose-fermenting organisms such as *Escherichia coli* produced pink to red colonies. *E. coli*, *Proteus*, and *Klebsiella* species were successfully isolated from MacConkey agar. Identification was based on colony morphology and Gram staining. Following incubation, growth appeared as distinct colonies, and pure cultures were achieved through sub-culturing.

3.7.1.2 *Salmonella-Shigella* (SS) Agar

Salmonella-Shigella agar (Batch No. CM0099 OXOID, UK) was used for the isolation of *Salmonella* and *Shigella* species. The medium was prepared according to the manufacturer's instructions, boiled to dissolve completely, but not autoclaved, as overheating can reduce selectivity. Approximately 20 ml of the molten medium was poured aseptically into sterile Petri dishes and allowed to solidify. Inoculation was performed using the quadrant streaking method with sterile disposable inoculating loops (Batch No. LP-020323, Copan Diagnostics, Italy). Plates were incubated at 43–44 °C for 18-24 hours in a calibrated incubator (Model GP 100 CLAD 100 HYD, Wagtech, UK). Lactose fermentation was indicated by neutral red. *Salmonella* appeared as colorless colonies with black centers due to hydrogen sulfide (H_2S) production, whereas *Shigella* produced colorless colonies without black centers. Colonies were further sub-cultured for confirmation. Growth was assessed by visible discrete colonies along streak lines, which were then purified.

3.7.1.3 Slanetz and Bartley Medium

Slanetz and Bartley medium (Batch No. CM0337, OXOID UK) was used for the isolation and enumeration of enterococci. The medium was prepared according to the manufacturer's guidelines, sterilized by autoclaving at 121 °C for 15 minutes, and poured aseptically into sterile Petri dishes using about 20 ml per plate. After solidification, plates were used immediately or stored at 4 °C until inoculation. For inoculation, 0.1 ml of prepared sample suspension was spread evenly across the agar surface with a sterile spreader. Plates were incubated at 43–44 °C for 24-48 hours. The medium contained sodium azide to inhibit Gram-negative organisms, while triphenyltetrazolium chloride (TTC) was reduced by enterococci to produce red to maroon colonies. Growth was assessed by visible red or maroon colonies as shown in Plate 4, and pure isolates were obtained through sub-culturing.

3.7.2 Bacterial Identification and Pure culture

Bacterial isolates obtained from the different media were identified primarily based on colony morphology and Gram staining. Colony morphology was assessed by observing characteristics such as shape, size, margin, elevation, opacity, and pigmentation on the culture plates. Distinctive colony appearances, for example pink-red colonies on MacConkey agar for lactose fermenters, guided the preliminary identification. Gram staining was carried out on representative colonies using standard procedures. Smears were prepared on clean glass slides and air-dried, then heat-fixed by passing briefly through a Bunsen burner flame. The primary stain, crystal violet solution (Batch No. CV-040323, Sigma-Aldrich, USA), was applied for 1 minute and rinsed with distilled water. Gram's iodine (Batch No. GI-030223, Merck, Germany) was added for 1 minute to fix the dye, followed by decolorization with 95% ethanol for 15–20 seconds. Immediately after decolorization, the slides were rinsed with water and counterstained with safranin (Batch No. SF-050423, Oxoid, UK) for 1 minute. After a final rinse and blotting dry, the slides were examined under a light microscope (Olympus CX23, Japan). Gram-positive organisms retained the crystal violet and appeared purple, while Gram-negative organisms took up the counterstain and appeared pink-red as shown in figure 3.8. Pure cultures were obtained by sub-culturing single, well-isolated colonies onto fresh plates of the same medium under aseptic conditions. This ensured that only one bacterial species was maintained for subsequent analyses.

3.8 Antimicrobial Susceptibility Testing (AST)

Antimicrobial susceptibility testing was performed to determine the resistance profiles of bacterial isolates recovered from cockroaches. The Kirby-Bauer disk diffusion method was employed using Mueller-Hinton agar plates. Pure bacterial colonies were suspended in sterile saline and adjusted to match the 0.5 McFarland turbidity standard. A sterile swab was used to evenly inoculate the surface of the agar plates, after which commercially prepared antibiotic discs were placed on the inoculated surface. Plates were incubated at 37°C for 18–24 hours. Zones of inhibition around each disc were measured in millimeters using a calibrated ruler as shown in figure 3.9, and the results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) M100 guidelines. Commercial antibiotic discs were utilized, including oxytetracycline (30 µg), gentamicin (10 µg), ciprofloxacin (5 µg), chloramphenicol (10 µg), amoxicillin (25 µg), ampicillin (10 µg), Clindamycin (30 µg), azithromycin (30 µg), and erythromycin (15 µg).

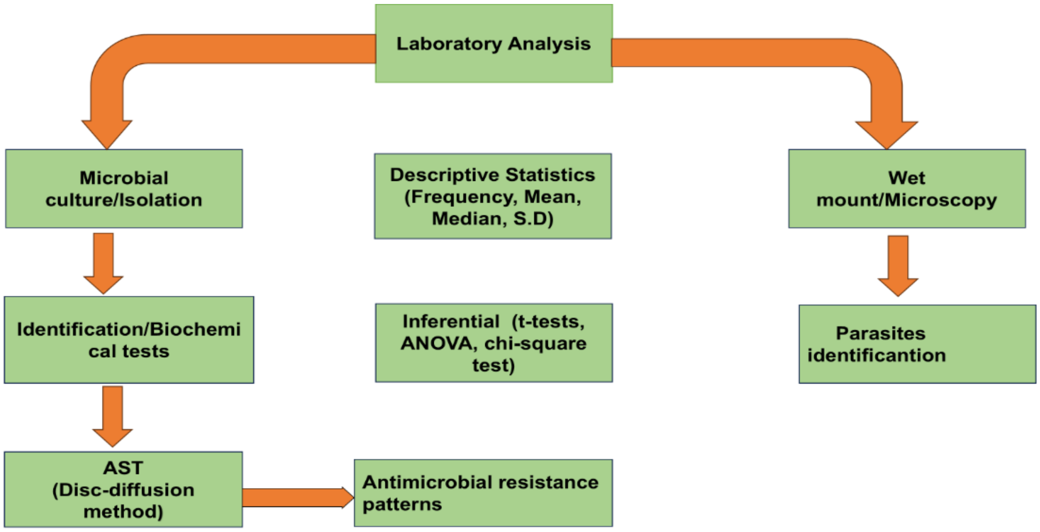


Figure 3. 5: Flow chart of laboratory analysis

3.9 Data Analysis

Data from microbiological and parasitological studies were entered systematically into Microsoft Excel and exported into SPSS version 26.0 (IBM Corp., Armonk, NY, USA) and RStudio for analysis. Descriptive statistics of frequencies, percentages, and means were calculated to describe the prevalence of bacterial species, parasites, and antimicrobial resistance patterns. Chi-square (χ^2) tests were employed to compare the rates of microbial carriage and resistance prevalence across the three study environments (hospitals, households, and catering centers). Statistical significance was placed at $p < 0.05$.

3.10 Quality Control and Assurance

Rigorous quality control measures were followed during specimen collection, laboratory processing, and data analysis to ensure confidence in the reliability and reproducibility of results. During field collection, only intact and live cockroaches were included to avoid contamination from damaged or degraded specimens. In the laboratory, all culture media were batch-tested for sterility using uninoculated controls, and function was confirmed using standard reference organisms.

3.11 Ethical Considerations

Ethical clearance for this study was provided by the Institutional Review Board (IRB) at Kwame Nkrumah University of Science and Technology, with the reference number CHREP/AP/188/61. Cockroaches are considered invertebrates and thus are not specifically covered by animal protection law. Nevertheless, since the study involved contact with the human environment, including hospitals, residential areas, and food service facilities, an ethical review was sought. Approval was gained from hospital managers, household heads, and food sellers prior to sampling.

CHAPTER FOUR

RESULTS

4.1 Demographic Characteristics of Cockroaches Collected

A total of 358 cockroaches were collected from households, eateries, and hospitals in Asante Mampong. The demographic distribution of species, sex, and study locations is presented in Table 4.1.

Table 4. 1: Distribution of Collected Cockroach Samples by Sex, Species and Location

Variable	Frequency	Percentage (%)
Sex		
Female	192	53.6
Male	166	46.4
Species		
Blatta orientalis	2	0.6
Periplaneta americana	239	66.8
Blattella germanica	117	32.7
Location		
Eatery	87	24.3
Hospital	77	21.5
Household	194	54.2

(*Source: Field data, 2025)*

Table 4.1 shows that *Periplaneta americana* was the most dominant species, representing (239;66.8%) of the total cockroaches collected. *Blattella germanica* accounted for (117;32.7%), while *Blatta orientalis* was the least represented at (2;0.6%). In terms of sex distribution, females were slightly higher at (192;53.6%) than males at (166;46.4%). By location, the highest number of cockroaches was collected from Household (194;54.2%) and the lowest was collected from hospitals (77;21.3%). Table 4.2 shows that, across the three—sites, eateries, hospitals and households. *Periplaneta americana* was the dominant species accounting for 50.6%, 85.7% and 66.5% respectively

Table 4. 2: Distribution of cockroach species across the three study sites

	Species		
Study sites	***Periplaneta americana (%)***	***Blatella germanica (%)***	***Blatta orientalis (%)***
Eatery	44 (50.6)	43 (49.4)	0
Hospital	66 (85.7)	9 (11.7)	2 (2.6)
Household	129 (66.5)	65 (33.5)	0

(Source: Field data, 2025)

4.2 Prevalence of Parasite Carriage

Out of the 358 cockroaches examined, 242 (67.6%) were found to be positive for parasites. The prevalence was higher in females (68.7%) than in males (66.3%), but the difference was not statistically significant ($\chi^2 = 0.15$, $p = 0.698$). With respect to species, *Blattella germanica* showed the highest parasite prevalence (74.4%), followed by *Periplaneta americana* (64.4%) and *Blatta orientalis* (50.0%); however, these differences were not significant ($\chi^2 = 3.82$, p =

0.148). Considering location, cockroaches collected from eateries recorded a prevalence of 69.0%

4.3 Parasite Species Prevalence

In figure 4.1, out of the 358 cockroaches examined, *Ascaris* spp. showed the highest prevalence (199;55.6%), followed by *Toxoascaris* spp (172;48.0%). *Oxyurid* was detected in 68 (19.0%) samples, *Strongyloides* in 35 (9.8%), while Hookworm was the least prevalent parasite, detected in 32 (8.9%) samples. These results indicate that cockroaches carried a range of intestinal parasites, with *Ascaris* and *Toxoascaris* being the most dominant.

Table 4. 3: Prevalence of Parasite Carriage in Cockroaches by Demographics

Factors	**Number Examined**	**Positive n (%)**	**χ²**	**p-value**
Overall	358	242 (67.6)	—	—
Sex				
Female	192	132 (68.7)	0.15	0.698
Male	166	110 (66.3)		
Species				
Blatta orientalis	2	1 (50.0)	3.82	0.148
Blattella germanica	117	87 (74.4)		
Periplaneta americana	239	154 (64.4)		
Location				
Eatery	87	60(69.0)	0.14	0.93
Hospital	77	51(66.2)		
Household	194	131(67.5)		

(Source: Field data,2025)

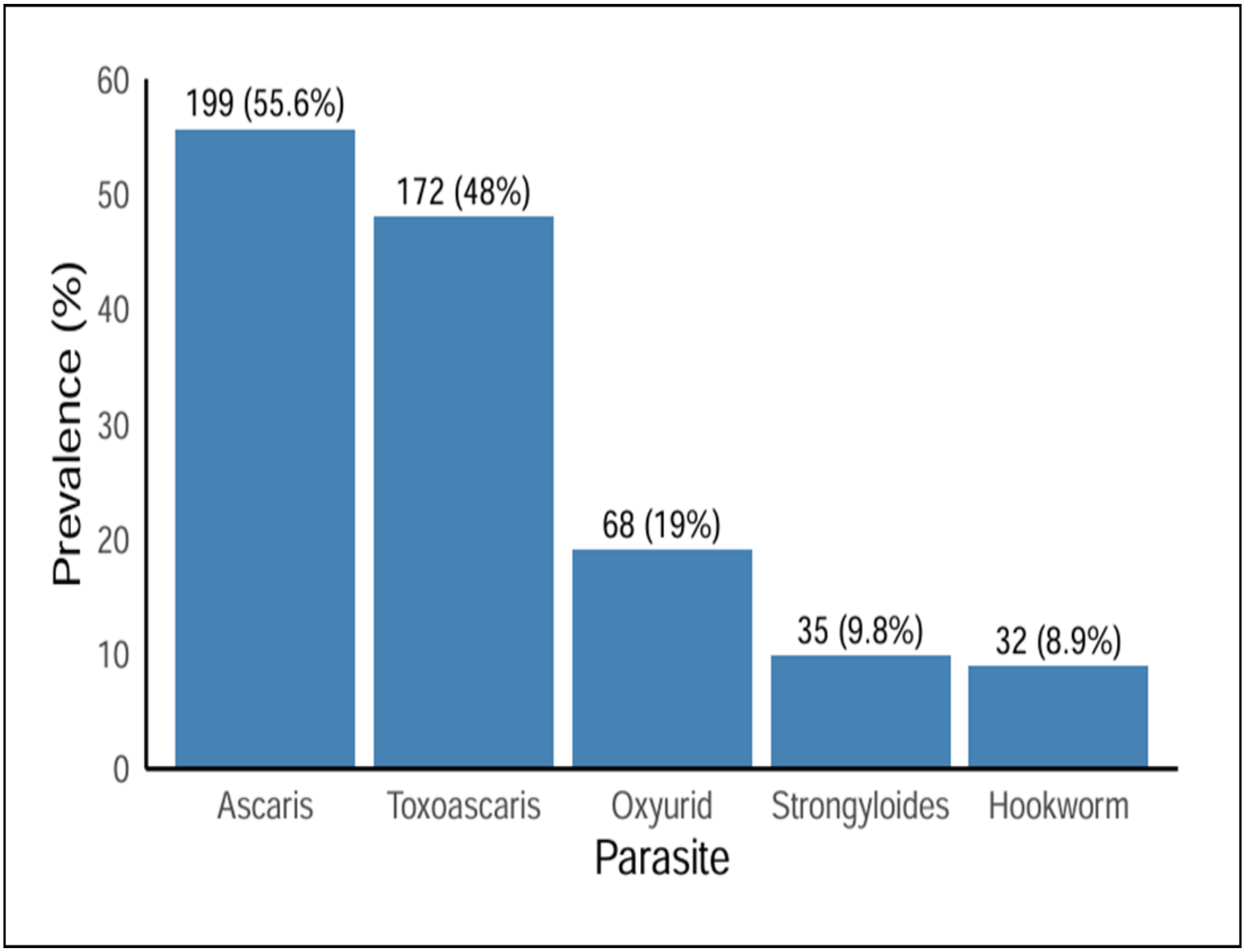


Figure 4. 1: Prevalence of Specific Parasites in Cockroaches

(Source: Field data, 2025)

Among females, 49.0% were infected with *Toxoascaris*, 6.8% with hookworm, 16.1% with *Oxyurid*, 7.8% with *Strongyloides*, and 58.3% with *Ascaris*. In males, the prevalence was 47.0% for *Toxoascaris*, 11.4% for hookworm, 22.3% for *Oxyurid*, 12.0% for *Strongyloides*, and 52.4% for *Ascaris*. There was no significant difference in infection prevalence between males and females ($p > 0.05$). By species, *Blattella germanica* carried 46.2% *Toxoascaris*, 11.1% hookworm, 23.1% *Oxyurid*, 11.1% *Strongyloides*, and 52.1% *Ascaris*. *Periplaneta americana* carried 49.0% *Toxoascaris*, 7.5% hookworm, 17.2% *Oxyurid*, 9.2% *Strongyloides*, and 57.3% *Ascaris*. *Blatta orientalis* showed only a few infections, as just two specimens were examined.

The differences in parasite prevalence between species were not statistically significant ($p > 0.05$). By sub-location, cockroaches from kitchens carried 50.0% *Toxoascaris* and 56.1% *Ascaris*. Those from washrooms showed 52.9% *Toxoascaris* and 58.8% *Ascaris*. Cockroaches from living rooms recorded 40.0% *Oxyurid*, while those from toilets carried 14.5% hookworm. In storerooms, both hookworm and *Oxyurid* were detected at 11.8%. Although the differences between sub-locations were not significant, the prevalence of *Oxyurid* approached significance ($p = 0.06$).

Table 4. 4: Distribution of Parasite Infections by Demographic Factors

Parasite	**Sex**			**Species**				**Location**			
	Female	Male	**χ2(P-value)**	*Blatta orientalis*	*Blattella germanica*	*Periplaneta americana*	**χ2(P-value)**	Eatery	Hospital	Household	χ2(P-value)
Toxoascaris	94 (49.0)	78 (47.0)	**0.07(0.79)**	1 (50.0)	54 (46.2)	117 (49.0)	**0.25(0.88)**	27(31)	39(50.65)	106(54.64)	13.67(0.001)
Hookworm	13 (6.8)	19 (11.4)	**1.85(0.17)**	1 (50.0)	13 (11.1)	18 (7.5)	**5.4(0.07)**	9(10.34)	7(9.10)	16(8.25)	0.33(0.85)
Oxyurid	31 (16.1)	37 (22.3)	**1.8(0.17)**	0 (0.0)	27 (23.1)	41 (17.2)	**2.26(0.32)**	9(10)	14(18.1)	45(23.2)	6.49(0.04)
Strongyloides	15 (7.8)	20 (12.0)	**1.36(0.24)**	0 (0.0)	13 (11.1)	22 (9.2)	**0.54(0.76)**	10(11.5)	9(11.9)	16(8.2)	1.12(0.57)
Ascaris	112 (58.3)	87 (52.4)	**1.03(0.31)**	1 (50.0)	61 (52.1)	137 (57.3)	**0.88(0.64)**	16(18.4)	52(67.5)	131 (67.53)	64.4(0.001)

(Source: Field data, 2025)

4.2.1 Parasite Co-carriage in Cockroaches

Out of 358 cockroaches examined, 148 (41.3%) carried only one parasite, while 66 (18.4%) carried two parasites. Triple and quadruple co-carriage were detected in 24 (6.7%) and 4 (1.1%) of the cockroaches respectively. Of the 94 co-carriage cases, the most prevalent were *Toxoascaris* with Hookworm (12.8%), *Ascaris* with *Toxoascaris* (10.6%), and *Toxoascaris* with *Oxyurid* (9.6%) (Table 4.5).

Table 4. 5: Co-carriage of Parasites in Cockroaches

Carriage Type	Number of Cockroaches (n)	Percentage (%)
No carriage	116	32.4
Single carriage	148	41.3
Double carriage	66	18. 4
Triple carriage	24	6.7
Quadruple carriage	4	1.1
Total	358	100%

(Source: Field data 2025)

4.2.2 Common Parasite Co-carriage Patterns

A total of 94 co- carriage cases involving various combinations of intestinal parasites were recorded. The most frequent dual co-carriage was *Toxoascaris* + Hookworm, accounting for 12.77% of all cases. This was followed by *Ascaris* + *Toxoascaris* (10.64%) and *Toxoascaris* + *Oxyurid* (9.57%). Mixed carriage involving three parasites were also observed, with *Ascaris* + *Toxoascaris* + Hookworm being the most common (6.38%). Less frequent combinations included those involving four parasites, each representing 2.13% of cases. (Table 4.6).

Table 4. 6: Common Parasite Co-carriage Patterns

Co-Infection Combination	Frequency	Percentage (%)
Ascaris + *Toxoascaris*	10	10.64
Ascaris + Hookworm	8	8.51
Ascaris + *Oxyurid*	6	6.38
Ascaris + *Strongyloides*	5	5.32
Toxoascaris + Hookworm	12	12.77
Toxoascaris + *Oxyurid*	9	9.57
Toxoascaris + *Strongyloides*	7	7.45
Hookworm + *Oxyurid*	4	4.26
Hookworm + *Strongyloides*	4	4.26
Oxyurid + *Strongyloides*	3	3.19
Ascaris + *Toxoascaris* + Hookworm	6	6.38
Ascaris + *Toxoascaris* + *Oxyurid*	5	5.32
Ascaris + *Toxoascaris* + *Strongyloides*	4	4.26
Toxoascaris + Hookworm + *Oxyurid*	2	2.13
Toxoascaris + *Oxyurid* + *Strongyloides*	3	3.19
Toxoascaris + Hookworm + *Strongyloides*	2	2.13
Ascaris + *Toxoascaris* + Hookworm + *Oxyurid*	2	2.13
Ascaris + *Toxoascaris* + *Strongyloides* +Hookworm	2	2.13
Total	**94**	**100.00**

(Source: Field data, 2025)

4.3 Prevalence and Counts of Bacterial Isolates

Figure 4.2 shows overall bacterial prevalence was high, with 217 out of 291 examined samples testing positive, giving an overall rate of 74.6% ($\chi^2 = 0.02$, $p = 0.89$). Analysis showed no statistically significant difference between infection status and sex (95% CI: 0.64–1.50). Species prevalence ranged between 47.7% and 53.6%, and these differences were not significant ($\chi^2 = 1.21$, $p = 0.55$; 95% CI: 0.25–5.08) as shown in Figure 4.2.

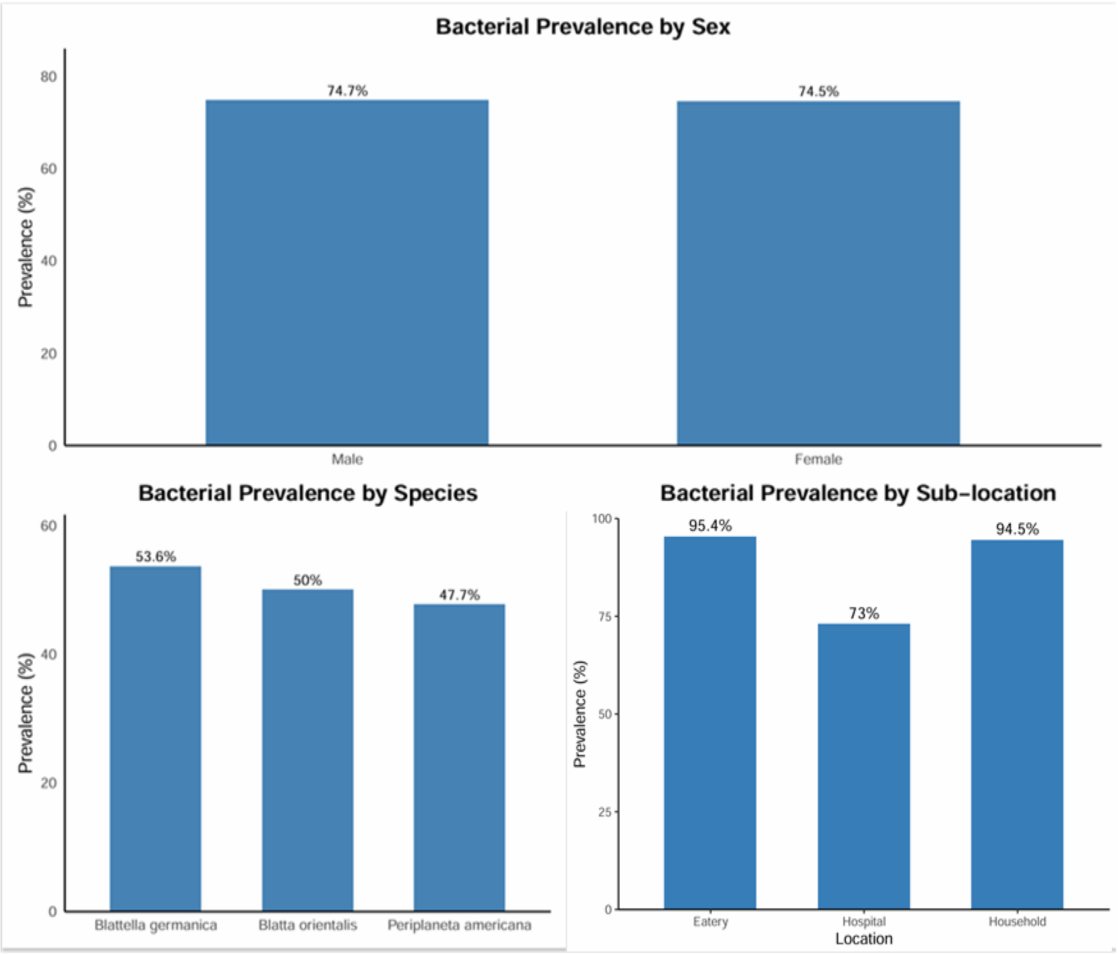


Figure 4. 2: Prevalence of Bacteria by Demographic Characteristics

(Source: Field data, 2025)

The most common bacteria were *Salmonella* (73.5%) and *Enterococcus* spp. (69.1%), followed by *Shigella* spp. (53.3%) and *Klebsiella* (47.8%). E. *coli* (23.4%) and *Proteus* (19.9%) were less frequently identified. Bacterial counts ranged from 8.39 × 10^4 in *Shigella* to 5.52 × 10^5 in *Proteus*. *Salmonella* and *Enterococcus* spp. also showed high bacterial counts as shown in figure 4.3.

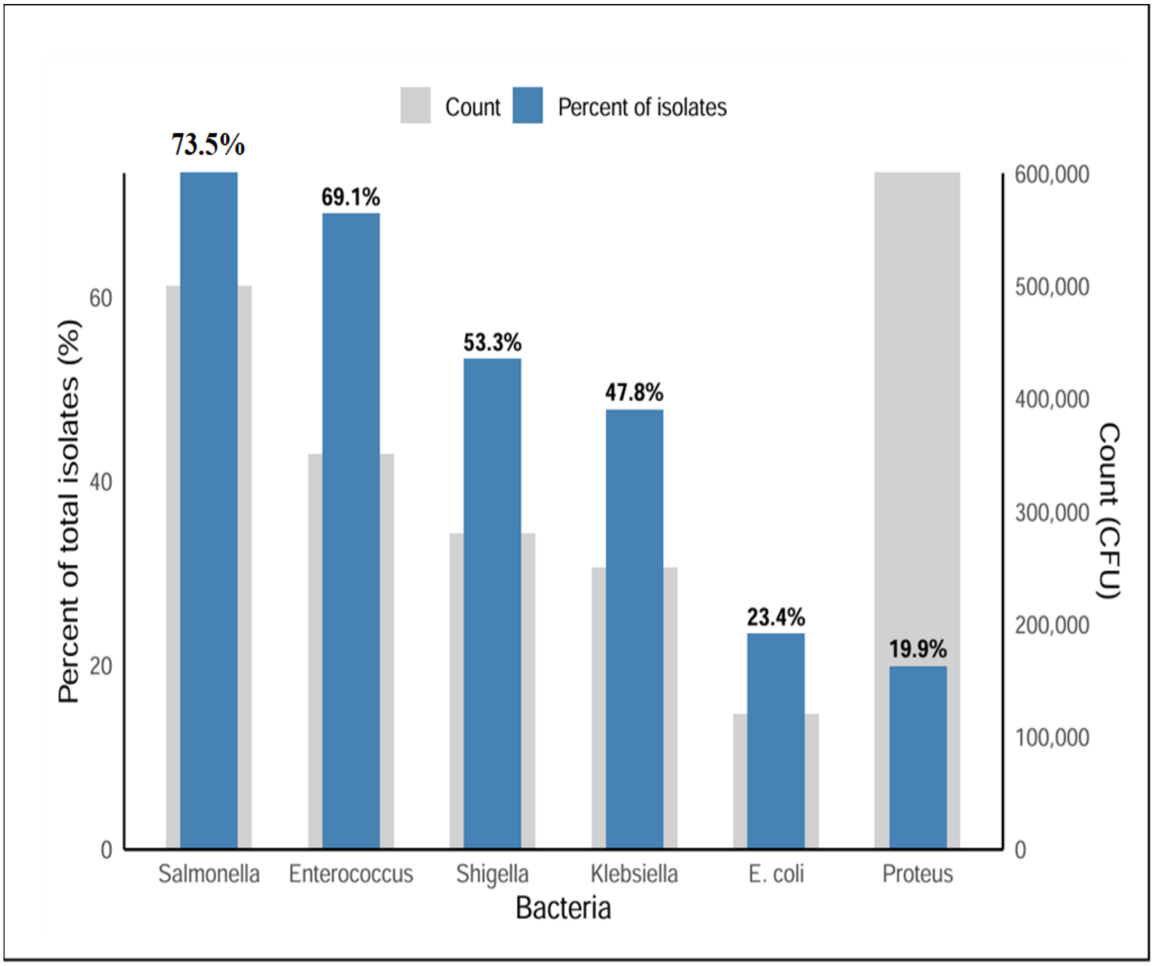


Figure 4. 3: Bacteria Isolate and Count in Cockroaches

(Source: Field Data, 2025)

Table 4. 7: Bacterial Species Distribution among Demographic Factors

Bacteria	Sex			Species			Location			
	Female	Male	χ2(P-value)	*Blattella germanica*	*Periplaneta americana*	χ2(P-value)	Eatery	Hospital	Household	χ2(P-value)
E. coli	34 (23.4)	34 (23.3)	**1.00 (0.99)**	37 (23.1)	31 (23.7)	<0.01 (0.99)	20 (23.0%)	18 (23.4%)	30 (23.6%)	**1.00 (0.99)**
Klebsiella	69 (47.6)	70 (47.9)	**<0.01(0.99)**	77 (48.1)	62 (47.3)	0.001 (0.99)	42 (48.3%)	37 (48.1%)	60 (47.2%)	**<0.01(0.99)**
Proteus	29 (20.0)	29 (19.9)	**<0.01(0.99)**	32 (20.0)	26 (19.8)	<0.01 (0.99)	17 (19.5%)	15 (19.5%)	26 (20.5%)	**<0.01(0.99)**
Enterococcus	99 (68.3)	102 (69.9)	**0.03(0.87)**	110 (68.8)	91 (69.5)	<0.01 (0.91)	60 (69.0%)	53 (68.8%)	88 (69.3%)	**0.03(0.87)**
Salmonella	107 (73.8)	107 (73.3)	**<0.01(0.99)**	118 (73.8)	96 (73.3)	<0.01(0.91)	64 (73.6%)	57 (74.0%)	93 (73.2%)	**<0.01(0.99)**
Shigella	77 (53.1)	78 (53.4)	**<0.01(0.99)**	85 (53.1)	70 (53.4)	<0.01(0.99)	46 (52.9%)	41 (53.2%)	68 (53.5%)	**<0.01(0.99)**

(Source: field data)

4.3.1 Parasite-Bacteria Co-carriage in cockroaches

The analysis of cockroach samples, as shown in figure 4.4 shows that parasites carried different levels of bacterial co-infections. *Ascaris* recorded the highest co-infections, with moderate associations with *Salmonella* (50.3%), *Enterococcus* (47.2%), and *Shigella* (36.4%), followed by *Klebsiella* (32.7%), *E. coli* (16.0%), and *Proteus* (13.6%). *Toxoascaris* also showed high co-infection, with *Salmonella* (43.5%), *Enterococcus* (40.8%), and *Shigella* (31.5%) being the most common, while *Klebsiella* (28.2%), *E. coli* (13.8%), and *Proteus* (11.8%) were less frequent.

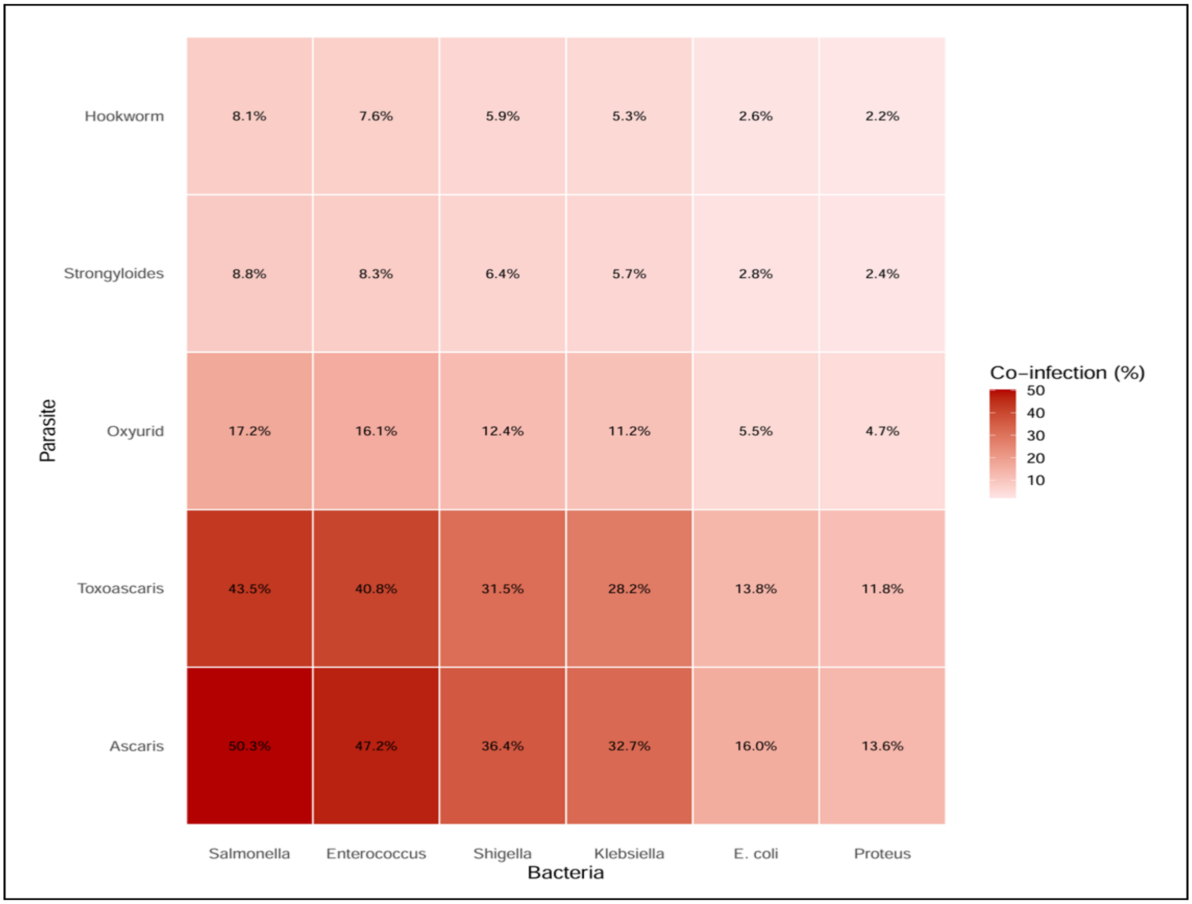


Figure 4. 4: Heatmap of parasitic-bacteria co-infection

(Source: field data, 2025)

4.4 Antimicrobial Resistance

Six bacterial isolates (E. *coli*, *Klebsiella* spp., *Proteus*, *Enterococcus* spp. *Salmonella* spp, and *Shigella* spp.) were tested against nine antibiotics. Resistance levels differed by drug and species. High resistance was found for chloramphenicol, ampicillin, and clindamycin, with most isolates showing values between 55% and 75%. Moderate resistance was recorded for erythromycin and amoxicillin-clavulanate, generally ranging between 45% and 67%. Gentamicin showed lower resistance (about 35% to 47%). Ciprofloxacin and azithromycin had the lowest resistance, mostly below 27% and 11% respectively. The heatmap confirmed these findings.

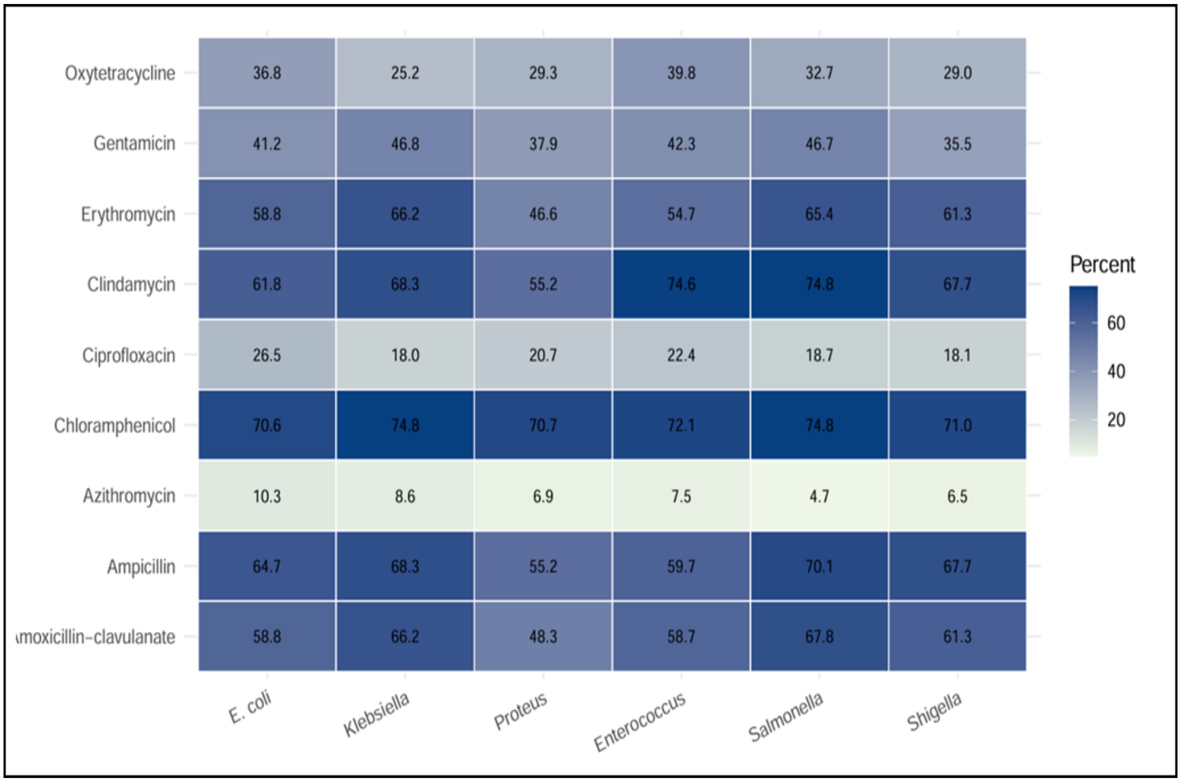


Figure 4. 5: Heatmap of antibiotic resistance test

(Source: Field data, 2025)

Table 4. 8: Antibiotic Resistance Profile of Bacterial Isolates

Antibiotic	*E. coli* (n=68)	*Klebsiella* (n=139)	*Proteus* (n=58)	*Enterococcus* (n=201)	*Salmonella* (n=214)	*Shigella* (n=155)
Chloramphenicol	48 (70.6%)	104 (74.8%)	41 (70.7%)	145 (72.1%)	160 (74.8%)	110 (71.0%)
Ampicillin	44 (64.7%)	95 (68.3%)	32 (55.2%)	120 (59.7%)	150 (70.1%)	105 (67.7%)
Erythromycin	40 (58.8%)	92 (66.2%)	27 (46.6%)	110 (54.7%)	140 (65.4%)	95 (61.3%)
Oxytetracycline	25 (36.8%)	35 (25.2%)	17 (29.3%)	80 (39.8%)	70 (32.7%)	45 (29.0%)
Ciprofloxacin	18 (26.5%)	25 (18.0%)	12 (20.7%)	45 (22.4%)	40 (18.7%)	28 (18.1%)
Clindamycin	42 (61.8%)	95 (68.3%)	32 (55.2%)	150 (74.6%)	160 (74.8%)	105 (67.7%)
Amoxicillin-clavulanate	40 (58.8%)	92 (66.2%)	28 (48.3%)	118 (58.7%)	145 (67.8%)	95 (61.3%)
Gentamicin	28 (41.2%)	65 (46.8%)	22 (37.9%)	85 (42.3%)	100 (46.7%)	55 (35.5%)
Azithromycin	7 (10.3%)	12 (8.6%)	4 (6.9%)	15 (7.5%)	10 (4.7%)	10 (6.5%)

(Source: Field data, 2025)

CHAPTER FIVE

DISCUSSION

5.1 Introduction

This study investigated the prevalence of intestinal parasites, bacterial carriage, and antimicrobial resistance in cockroaches collected from hospitals, households, and restaurants. The results show that cockroaches carry various parasites and bacteria with significant public health relevance. *Ascaris* and *Toxoascaris* were the predominant parasites and *Salmonella* and *Enterococcus* were the leading bacteria. In addition, bacterial isolates exhibited high resistance tendencies towards older antibiotics, such as chloramphenicol and ampicillin; however, ciprofloxacin and azithromycin still demonstrated high efficacy. These results suggest the potential mechanical vector activity of cockroaches in transporting multidrug-resistant pathogens in domestic and clinical settings.

5.2 Cockroach Species Abundances at Different Sites

Periplaneta americana was the most frequently encountered species in hospitals and households in West Africa, attributing this to its adaptability to warm climates and abundant breeding sites (Bisetegn et al., 2024; Turki Jalil et al., 2023; Bahrami et al., 2021;Donkor, 2020;Obeng-Nkrumah et al., 2019). Similar observations have been made in Nigeria, where Dokmaikaw & Suntaravitun (2019) found *P. americana* to dominate in healthcare facilities and residential areas, highlighting its public health importance in African contexts. The present study aligns with these findings, showing that P. americana was the most abundant species across all sites, with its highest prevalence in hospitals (85.7%), followed by households (66.5%) and eateries (50.6%). This dominance of

P.americana consistent with reports from other African and global studies that describe *P. americana* as highly adaptable, thriving in humid environments and exploiting structural niches such as drainage systems and waste areas (Nasirian & Salehzadeh, 2019; Gebreyohans et al., 2024). *Blattella germanica* was the second most common species, showing nearly equal proportions with *P. americana* in eateries (49.4%), but much lower levels in hospitals (11.7%) and households (33.5%). This aligns with the findings of Kassiri et al., (2020), Bahrami et al., (2021) and Memona et al., (2017) who emphasized that *B. germanica* is associated with kitchens, restaurants, and food-handling areas where food residues provide favorable breeding conditions. In contrast, *Blatta orientalis* was rarely detected in this study, occurring only in hospitals at 2.6%. This low occurrence is consistent with global reports that *B. orientalis* is less competitive in tropical and indoor environments, often being displaced by the more adaptable *P. americana* and *B. germanica* (Luckyjane et al., 2023; Memona et al., 2017).

Abundant cockroach populations increase the likelihood of mechanically transmitting pathogenic microorganisms, such as bacteria, fungi, parasites, and viruses. Owing to their ability to frequently move between contaminated areas such as drains, waste sites, and food preparation surfaces, they can easily transfer these pathogens onto food, utensils, and other surfaces humans come into contact with.

5.3 Presence of Parasite Carriage in Cockroaches

The current study revealed that 67.6% of cockroaches carried at least one intestinal parasite, with *Ascaris* spp (55.6%) and *Toxoascaris* spp. (48.0%) as the most dominant species. Studies in Nigeria by Adenusi et al., (2018) reported high levels of *Ascaris* in cockroaches, suggesting the potential role of cockroaches in transmitting Ascaris and other intestinal parasites.

The findings in this study are relatively similar to those of 96.4% of *Ascaris lumbricoides* reported in a study in Nigeria (Adenusi et al., 2018) and Ethiopia (Debash et al., 2022). The consistent predominance of *Ascaris* across these studies may be attributed to the remarkable resilience of its eggs, which can survive for prolonged periods in moist, contaminated environments, making them well-suited for mechanical transfer by cockroaches. These finding highlights the role of cockroaches as carriers of intestinal parasites and the public health risk they pose in both household and public places. In contrast, a study from Thailand reported lower prevalence rates, ranging from 35% to 45% (Dokmaikaw & Suntaravitun, 2019). These differences may reflect variations in environmental sanitation, waste disposal practices, and climate. The elevated prevalence observed in the current study may likely reflect poor sanitation infrastructure. It may also be influenced by the availability of breeding sites, particularly in urban areas with high levels of waste accumulation. We report for the first time in Ghana, the presence of *Toxoascaris* and *Oxyurid* species (pinworm) in cockroaches. Both single-species crrige and mixed carriage were common, with 41.3% of the cockroaches carrying a single parasite and 18.4% carrying more than one. The co-carriage most commonly encountered were those involving *Ascaris* and *Toxoascaris*, as well as *Toxoascaris* and hookworm. Similar multi-carriage profiles were reported in Nigeria and Ethiopia (Victor et al., 2024; Debash et al., 2022). The lack of marked differences in cockroach species and site suggests general contamination and a universal risk of parasitic transmission.

5.3.1 Parasite Carriage in Cockroaches in the Different Locations

The present study demonstrated notable differences in parasitic carriage across environments. *Toxoascaris* and *Ascaris* were most frequently detected in household cockroaches, with *Ascaris* recording the highest prevalence (67.5%). Similarly, *Oxyurid* carriage was significantly higher in households and hospitals compared to eateries, suggesting that domestic environments may provide favorable conditions for the persistence and transmission of these parasites. In contrast, Hookworm and *Strongyloides* occurred at relatively low and uniform rates across all three environments, indicating a more consistent distribution that is less dependent on specific settings (Dokmaikaw & Suntaravitun, 2019). Collectively, these results highlight that although cockroaches universally harbor intestinal parasites, households present a higher risk for Ascaris, *Toxoascaris*, and *Oxyurid*. This underpins the urgent need for improved sanitation and pest management interventions at the household level to minimize the risk of parasite transmission.

5.5 Presence of bacteria carriage in cockroaches

The overall study indicated that 74.6% of cockroaches carried at least one species of bacteria, the predominant ones being *Salmonella* spp. (73.5%) and *Enterococcus* spp. (69.1%). For each bacterium, the prevalence across the three settings remains nearly the same, with *E. coli* around 23%, *Klebsiella* spp. around 47–48%, *Proteus* at about 20%, *Enterococcus* spp. at 69%, *Salmonella* spp. at 73–74%, and *Shigella* spp. at roughly 53%. This consistency shows that cockroaches act as carriers of these bacteria regardless of the location in which they are found.

Recent studies in Ghana linked cockroaches to carriers of pathogenic bacteria such as *Salmonella*, *E. coli*, *Klebsiella*, and *Enterococcus*, particularly in food-handling environments and hospitals (Donkor et al., 2024; Donkor, 2019). The present study supports these findings, with 74.6% of cockroaches carrying at least one bacterium, and *Salmonella* (73.5%) and *Enterococcus* (69.1%) being the most dominant. The similarity in prevalence across households, eateries, and hospitals suggests that cockroaches act as mechanical vectors irrespective of the setting, raising concerns for both community and healthcare-associated infections. These results are comparable to those reported in Iraq and Ethiopia, in which high rates of *Salmonella*, *Klebsiella,* and *Enterococcus* were isolated and identified among cockroaches collected from hospitals and households (Bisetegn et al., 2024; Turki Jalil et al., 2023) In the current study, the prevalence of *Escherichia coli* (23.4%) was lower than that reported in similar studies in Uganda, which found 48.3% *E. coli* in the cockroach gut homogenates and 58.3% in the cuticle washes collected from the communities (Kakooza et al., 2025). Likewise, in Iran, *E. coli* was the predominant bacterial isolate in cockroaches in urban communities and exhibited high-frequency resistance to antimicrobial agents in numerous instances (Crespo et al., 2025). The prevalence differences reported in this study and in previous studies may indicate disparities in environmental sanitation and hygiene, as well as the nature of household facilities and the surveying methodologies employed in the areas. Carriage by bacteria was highly heterogeneous at the location level, with the highest prevalence observed in households and eateries. This trend reflects outcomes from studies in Nigeria and Thailand, in which households and food handling areas were identified as high-risk areas for bacterial carriage by cockroaches (Victor et al., 2024; Adenusi et al., 2018; Dokmaikaw &

Suntaravitun, 2019). These areas have high moisture, warmth, and rich food supplies, which promote cockroach activity and survival by providing a habitat for bacteria.

5.6 Specific Microbial Species Transmitted by Cockroaches

The identification of a high variety of bacteria, like *Shigella* (53.3%), *Klebsiella* (47.8%), and *Proteus* (19.9%), supports the fact that cockroaches act as reservoirs for various clinically important pathogens. Recent studies have also presented similar results, with *Enterobacteriaceae*, such as *Salmonella, Klebsiella,* and *Shigella*, consistently representing the dominant cockroach-associated organisms at all times (Bisetegn et al., 2024; Crespo et al., 2025). The lower prevalence of *Proteus* in this study compared to other areas may indicate variations in regional hygiene levels and the degree of environmental contamination. High loads of *Enterococcus* and *Salmonella* are of concern, as these bacteria are leading causes of nosocomial illness and the chief worldwide causes of food-related gastroenteritis, respectively (Navarra et al., 2025; Sarkodie-Addo et al., 2025). The fact that these bacteria are found in cockroaches collected from households and hospitals reflects the potential for these bacteria to interconnect healthcare and community reservoirs.

3.6.1 Public health importance of bacterial isolates from cockroaches

Escherichia coli represents a significant public health concern, as pathogenic strains are capable of causing diarrheal diseases, urinary tract infections, and in severe cases, life-threatening conditions such as hemolytic uremic syndrome (Khalil et al, 2018; Xu et al., 2022) Likewise, *Klebsiella* spp. are associated with respiratory infections, septicemia, and urinary tract infections, and their capacity to develop antimicrobial resistance, particularly through the production of extended-spectrum beta-lactamases (ESBLs), heightens their clinical importance (Temkin et al., 2018). *Proteus* spp. function as opportunistic pathogens, frequently implicated in urinary tract and wound infections (Chakkour et al., 2024; Slate et al., 2023). *Enterococcus* spp. also poses a considerable challenge in healthcare settings, where they are implicated in hospital-acquired infections such as bloodstream infections and endocarditis; the emergence of vancomycin-resistant enterococci (VRE) further exacerbates their impact (Hammerum et al., 2024).

Additionally, *Salmonella* remains a globally recognized pathogen responsible for foodborne illnesses and gastroenteritis, often associated with large outbreaks (Turner et al., 2024; Donkor, 2020)(Popa & Papa, 2021). *Shigella*, another critical pathogen, is the causative agent of bacillary dysentery, a severe diarrheal disease characterized by its exceptionally low infectious dose, enabling transmission even at minimal exposure (Donkor, 2020; Moges et al., 2016; Donkor et al., 2024; Adejumo B-F et al., 2016). Collectively, these bacterial isolates highlight the capacity of cockroaches to serve as reservoirs and mechanical vectors for clinically important pathogens, thereby underscoring their role in the persistence and dissemination of infectious diseases within domestic, food service, and healthcare environments.

5.7 Antibiotic Resistance Patterns of Bacteria

Antibiotic susceptibility testing revealed extensive resistance to older antibiotics, including chloramphenicol, ampicillin, and clindamycin, with resistance rates ranging from 55% to 75% in these cases. These results align with current global reports indicating that older-generation antibiotics are becoming less effective due to years of improper use in human health and animal husbandry (Bisetegn et al., 2024; Turki Jalil et al., 2023). In comparison, ciprofloxacin and azithromycin exhibited the lowest resistance (<27% and <11%, respectively), suggesting that these agents retain significant effectiveness. This trend is similar to a systematic review by Crespo et al., (2025) which indicates that a recent report by this research group suggests that fluoroquinolones and macrolides continue to have relatively lower resistance rates in environmental isolates compared to beta-lactam antibiotics and tetracyclines. Nevertheless, the fact that resistance was detected in the case of some of these newer agents underscores the need for continued surveillance and stewardship. In the isolated bacteria, maximum resistance was exhibited by *Klebsiella* and *Salmonella*, in complete agreement with recent studies that have shown the emergence of multidrug-resistant forms of these bacteria in hospitals and communities worldwide (Kakooza et al., 2025; Bisetegn et al., 2024; Murray et al., 2022). The fact that cockroaches carry such resistant organisms shows the startling potential for mechanical transfer of resistance genes.

CHAPTER SIX

SUMMARY, CONCLUSION, AND RECOMMENDATIONS

6.1 Summary of Key Findings

The results showed that 242 (67.6%) of the cockroaches carried at least one parasite, with *Ascaris* being the most prevalent, found in 199 (55.6%) of the cockroaches, and *Toxoascaris* in 172 (48.0%) of the cockroaches. *Toxoascaris* and *Oxyurid* species (pinworm) were reported for the first time in Ghana. Multiple infections were common, with 66 (18.4%) carrying two parasites and 28 (7.8%) carrying three or more. Bacterial prevalence was also high, with 217 (74.6%) of samples testing positive. *Salmonella* 214 (73.5%) and *Enterococcus* 201 (69.1%) were the most frequently isolated, while *E. coli* 68 (23.4%) and *Proteus* 58 (19.9%) were less common. Antibiotic susceptibility testing revealed high resistance to chloramphenicol, ampicillin, and clindamycin, ranging between 55% and 75%. Moderate resistance was observed for erythromycin and amoxicillin-clavulanate (45–67%), while ciprofloxacin and azithromycin showed the lowest resistance levels (below 27% and 11%, respectively). *Klebsiella* and *Salmonella* were the most resistant bacteria, while *Proteus* and *Shigella* exhibited moderate resistance.

6.2 Conclusions

The study revealed that cockroaches from hospitals, households, and eateries commonly carry intestinal parasites. Species such as *Ascaris, Toxoascaris,* and *Oxyurid* were more prevalent in household cockroaches, suggesting that domestic environments may provide favorable conditions for parasite carriage. This highlights the potential health risk posed by cockroaches across all settings, with households being particularly vulnerable.

Bacterial carriage was also widespread in cockroaches from all three environments. Organisms such as *Salmonella, Enterococcus, Klebsiella, E. coli,* and *Shigella* were found at high prevalence, with little variation between hospitals, households, and eateries. This demonstrates that cockroaches consistently act as reservoirs of bacteria regardless of their habitat.

The study further confirmed that cockroaches can harbor and transmit a wide range of microbial species. Both parasites and bacteria of significant public health concern were successfully isolated and identified, reinforcing the role of cockroaches as mechanical vectors capable of spreading multiple pathogens in different environments.

Finally, the investigation into antibiotic resistance profiles showed that some bacterial isolates carried by cockroaches exhibited resistance to commonly used antibiotics. This raises concern about their role in the spread of antimicrobial-resistant organisms and emphasizes the need for integrated pest management strategies and continuous antimicrobial resistance surveillance.

6.3 Recommendations

6.3.1 Hospital

1. Strengthening pest control measures and implement regular monitoring programs to reduce cockroach populations within their facilities.
2. Infection control units should include cockroach management as part of their hospital-acquired infection prevention strategies.

6.3.2 Households

1. Improve sanitation practices through proper food storage and waste disposal.
2. Seal entry points and ensure routine cleaning of kitchens and toilets.
3. Promote public health education on the risks posed by cockroaches

6.3.3 Eateries

1. Enforce strict hygiene and pest control measures, including regular fumigation.
2. Maintain clean food preparation areas and ensure proper waste management.
3. Subject eateries to regular inspections by food safety authorities to ensure compliance

6.3.4 Individual

1. Practice good personal hygiene, such as frequent handwashing before meals and after toilet use.
2. Store food in sealed containers and cook thoroughly to prevent infection.
3. Limit exposure to cockroach-contaminated environments.

6.3.5 Future Studies

1. Conduct research on microbial load, genetic diversity, and antimicrobial resistance in cockroach-associated pathogens.
2. Undertake longitudinal studies across ecological zones to assess seasonal variations and environmental influences.

REFERENCES

Abbasi, E. (2025). Pr pr oo f. *IJID One Health*, 100086. https://doi.org/10.1016/j.ijidoh.2025.100086

Adegnika, A. A., Vries, S. G. De, Zinsou, F. J., Honkepehedji, Y. J., Agobé, J. D., Vodonou, K. G., Bikangui, R., Yazdanbakhsh, M., Hotez, P. J., Bottazzi, M. E., Li, G., Bethony, J. M., Diemert, D. J., & Grobusch, M. P. (2021). *Safety and immunogenicity of co-administered hookworm vaccine candidates Na -GST-1 and Na -APR-1 in Gabonese adults : a randomised , controlled , double-blind , phase 1*. *21*(February), 275–285. https://doi.org/10.1016/S1473-3099(20)30288-7

Adejumo B-F, A. E., Alabi ACD-F, O. S., & Adeleke C-F, O. E. (2016). Antibiotic Resistance Profile and Phenotypic Detection of Beta-Lactamase-producers among Gram-negative Bacteria Isolated from the Gut of Household Cockroaches in and around University of Ibadan. *J. Pharm. Res*, *12*(2), 117–126. http://www.nigjpharmres.com

Adenusi, A. A., Akinyemi, M. I., & Akinsanya, D. (2018). *Domiciliary Cockroaches as Carriers of Human Intestinal Parasites in Lagos Metropolis , Southwest Nigeria : Implications for Public Health*. *12*(June), 141–151.

Appel, A. G., Dingha, B. N., Eva, M. J., & Jackai, L. E. N. (2022). Toxicity, Repellency, and Laboratory Performance of Consumer Bait Products for German Cockroach (Blattodea: Ectobiidae) Management. *Florida Entomologist*, *105*(2), 115–125. https://doi.org/10.1653/024.105.0203

Awere-Duodu, A., & Donkor, E. S. (2024a). Rotavirus in Water Environments: A Systematic Review and Meta-Analysis. *Environmental Health Insights*, *18*. https://doi.org/10.1177/11786302241276667/SUPPL_FILE/SJ-DOCX-1-EHI-10.1177_11786302241276667.DOCX

Awere-Duodu, A., & Donkor, E. S. (2024b). Rotavirus in Water Environments: A Systematic Review and Meta-Analysis. *Environmental Health Insights*, *18*(December). https://doi.org/10.1177/11786302241276667

Bahrami, A., Kouhestani, F., Firoozfar, F., Yusuf, M. A., Taherpour, M., & Saghafipour, A. (2021). Bacterial and parasitic contamination of cockroaches in hospital and non-hospital places in Alborz province, Northern Iran. *Journal of Entomological Research*, *45*(3), 572-576.

Bengtsson-Palme, J., Kristiansson, E., & Larsson, D. G. J. (2018). Environmental factors influencing the development and spread of antibiotic resistance. *FEMS Microbiology Reviews*, *42*(1), 68–80. https://doi.org/10.1093/femsre/fux053

Bisetegn, F. S., Azene, H., Ahmed, K. S., Wadilo, F., & Tufa, E. G. (2024). Extended spectrum and metalo beta lactamase producing gram negative bacterial pathogens from cockroaches collected at hospital, Southern Ethiopia. *Antimicrobial Resistance and Infection Control*, *13*(1), 1–8. https://doi.org/10.1186/s13756-024-01442-0

Bogri, A., Jensen, E. E. B., Borchert, A. V., Brinch, C., Otani, S., & Aarestrup, F. M. (2024). Transmission of antimicrobial resistance in the gut microbiome of gregarious cockroaches: the importance of interaction between antibiotic exposed and non-exposed populations. *MSystems*, *9*(1). https://doi.org/10.1128/msystems.01018-23

Brenner, R. J., & Kramer, R. D. (2018). Cockroaches (blattaria). *Medical and Veterinary Entomology*, 61–77. https://doi.org/10.1016/B978-0-12-814043-7.00006-6

Brenner, R. J., & Kramer, R. D. (2019). Cockroaches (Blattaria). *Medical and Veterinary*

Entomology, 61–77. https://doi.org/10.1016/B978-0-12-814043-7.00006-6

Brown, C., & Alhassan, A. (2015). Multiple-antibiotic-resistant bacteria from cockroaches trapped from a public hospital and a nearby students' hostel in Accra, Ghana. *International Journal of Biological and Chemical Sciences*, *8*(4), 1859. https://doi.org/10.4314/ijbcs.v8i4.44

Centers for Disease Control and Prevention. (2019). Centers for Disease Control and Prevention. (2019). Antibiotic resistance threats in the United States, 2019. US Department of Health and Human Services, Centres for Disease Control and Prevention. *Centers for Disease Control and Prevention.*

Chakkour, M., Hammoud, Z., Farhat, S., El Roz, A., Ezzeddine, Z., & Ghssein, G. (2024). Overview of Proteus mirabilis pathogenicity and virulence. Insights into the role of metals. *Frontiers in Microbiology*, *15*(April), 1–17. https://doi.org/10.3389/fmicb.2024.1383618

Chala, B., & Hamde, F. (2021). *Emerging and Re-emerging Vector-Borne Infectious Diseases and the Challenges for Control : A Review*. *9*(October), 1–10. https://doi.org/10.3389/fpubh.2021.715759

Chen, J., Gong, Y., Chen, Q., Li, S., & Zhou, Y. (2024). *Global burden of soil-transmitted helminth*. 68–77.

Chilanga, F., Kasozi, K. I., Mazeri, S., Paterson, G. K., & Muwonge, A. (2025). A systematic review of antimicrobial resistance transmission inferences at the human-livestock interface in Africa. *Npj Antimicrobials and Resistance*, *3*(1), 1–11. https://doi.org/10.1038/s44259-025-00126-y

Colella, V., Khieu, V., Worsley, A., Senevirathna, D., Muth, S., Huy, R., Odermatt, P., & Traub, R. J. (2021). The Lancet Regional Health - Western Pacific Risk profiling and efficacy of albendazole against the hookworms Necator americanus and Ancylostoma ceylanicum in Cambodia to support control programs in Southeast Asia and the Western Pacific ☆. *The Lancet Regional Health - Western Pacific*, *16*, 100258. https://doi.org/10.1016/j.lanwpc.2021.100258

Crespo, A., de Armas, Y., Capó, V., Iglesias, E., Palomares-Marín, J., Fonte, L., Plascencia-Hernández, A., Cueto-Aragón, C. L., Calderón, E. J., & Pérez-Gómez, H. R. (2025). Pathogens of Medical Importance Identified in Hospital-Collected Cockroaches: A Systematic Review. *Microorganisms*, *13*(2), 1–14. https://doi.org/10.3390/microorganisms13020337

Davin-Regli, A., Lavigne, J. P., & Pagès, J. M. (2019). Enterobacter spp.: update on taxonomy, clinical aspects, and emerging antimicrobial resistance. *Clinical Microbiology Reviews*, *32*(4). https://doi.org/10.1128/CMR.00002-19

de Luna, M., Estrada-Álvarez, J. C., Rodríguez-Rojas, J. J., Solís-Rojas, C., & García-Barrios, R. (2025). Introduced and Medically Important Cockroaches (Blattodea) for Nuevo Leon, With New Records for Other States in Mexico. *The Southwestern Naturalist*, *69*(3). https://doi.org/10.1894/0038-4909-69.3.3

Debash, H., Alemu, M., & Ayehu, A. (2022). Species composition and parasite carriage rate of cockroaches among households of Sekota town , Northeast Ethiopia. *International Journal of Tropical Insect Science*, *October*. https://doi.org/10.1007/s42690-022-00906-3

Dokmaikaw, A., & Suntaravitun, P. (2019). Prevalence of parasitic contamination of cockroaches collected from fresh markets in Chachoengsao province, Thailand. *Kobe Journal of Medical Sciences*, *65*(4), E118–E123.

Donkor, E. S. (2019). Nosocomial pathogens: an in-depth analysis of the vectorial potential of cockroaches. *Tropical Medicine and Infectious Disease*. https://www.mdpi.com/2414-

6366/4/1/14

Donkor, E. S. (2020). Cockroaches and Food-borne Pathogens. *Environmental Health Insights*, *14*. https://doi.org/10.1177/1178630220913365

Donkor, E. S., Odoom, A., Osman, A. H., Darkwah, S., & Kotey, F. C. N. (2024). A Systematic Review on Antimicrobial Resistance in Ghana from a One Health Perspective. *Antibiotics*, *13*(7). https://doi.org/10.3390/antibiotics13070662

Du, E., Wang, Q., Wang, C., Wu, W., Chen, H., Fang, D., & Xing, H. (2022). *Convergent adaptation of ootheca formation as a protective strategy for cockroach eggs*.

Du, E., Wang, S., Luan, Y. X., Zhou, C., Li, Z., Li, N., Zhou, S., Zhang, T., Ma, W., Cui, Y., Yuan, D., Ren, C., Zhang, J., Roth, S., & Li, S. (2022). Convergent Adaptation of Ootheca Formation as a Reproductive Strategy in Polyneoptera. *Molecular Biology and Evolution*, *39*(3), 1–15. https://doi.org/10.1093/molbev/msac042

Eslahi, A. V., Badri, M., Khorshidi, A., Majidiani, H., Hooshmand, E., Hosseini, H., Taghipour, A., Foroutan, M., Pestehchian, N., Firoozeh, F., Riahi, S. M., & Zibaei, M. (2020). Prevalence of Toxocara and Toxascaris infection among human and animals in Iran with meta-analysis approach. *BMC Infectious Diseases*, *20*(1), 1–17. https://doi.org/10.1186/s12879-020-4759-8

Fenollar, F., & Mediannikov, O. (2018). Emerging infectious diseases in Africa in the 21st century. *New Microbes and New Infections*, *26*, S10–S18. https://doi.org/10.1016/J.NMNI.2018.09.004

Fuller, W. L., Hamzat, O. T., Aboderin, A. O., Gahimbare, L., Kapona, O., Yahaya, A. A., Kasambara, W., Nikiema, J. B., Ilboudo, D. W., & Mpundu, M. M. (2022). National action plan on antimicrobial resistance: An evaluation of implementation in the World Health Organization Africa region. *Journal of Public Health in Africa*, *13*(2). https://doi.org/10.4081/jphia.2022.2000

Gebreyohans, G., Ibrahim, N., Muche, T., Kalayou, N., Bacha, K., Gershe, S., & Ango, Z. (2024). Isolation and identification of major cockroaches associated pathogenic bacteria in Bonga town , Ethiopia. *The Microbe*, *5*(April), 100158. https://doi.org/10.1016/j.microb.2024.100158

Geng, D., Yu, H., Zhao, T., & Li, C. (2025). *The Medical Importance of Cockroaches as Vectors of Pathogens : Implications for Public Health*. https://doi.org/10.15212/ZOONOSES-2024-0045

Getahun, H. (2023). Antimicrobial Resistance. In *Global Health Essentials* (pp. 143-147). Cham: Springer International Publishing.

Gondhalekar, A. D., Appel, A. G., Thomas, G. M., & Romero, A. (2021). A review of alternative management tactics employed for the control of various cockroach species (Order: Blattodea) in the USA. *Insects*, *12*(6), 1–20. https://doi.org/10.3390/insects12060550

Guyader, A., Rivault, C., Chaperon, J., Boparai, J. K., Sharma, P. K., Brown, C., Alhassan, A., Lucero-Prisno, D. E. I. I. I., Kouwenhoven, M. B. N., Adebisi, Y. A., Miranda, A. V., Gyeltshen, D., Suleman, M. H., Chiumia, I. K., Lowe, M., Dorji, T., Huang, J., Gacutno-Evardone, A. J., Lin, X., … Ruan, S. (2019). Resistance Status of Bacteria from a Health Facility in Ghana: A Retrospective Study. *Epidemiology and Infection*, *2021*(3), 485–492. https://doi.org/10.4314/ijbcs.v8i4.44

Gwenzi, W., Chaukura, N., Muisa-zikali, N., Teta, C., Musvuugwa, T., Rzymski, P., Luther, A., & Abia, K. (2021). *of Antimicrobial Resistance*. 1–42.

Endale, H., Mathewos, M., & Abdeta, D. (2023). Potential causes of spread of antimicrobial resistance and preventive measures in one health perspective-a review. *Infection and drug resistance*, 7515-7545.

Hammerum, A. M., Karstensen, K. T., Roer, L., Kaya, H., Lindegaard, M., Porsbo, L. J., Kjerulf, A., Pinholt, M., Holzknecht, B. J., Worning, P., Nielsen, K. L., Hansen, S. G. K., Clausen, M., Søndergaard, T. S., Dzajic, E., Østergaard, C., Wang, M., Koch, K., & Hasman, H. (2024). Surveillance of vancomycin-resistant enterococci reveals shift in dominating clusters from vanA to vanB Enterococcus faecium clusters, Denmark, 2015 to 2022. *Eurosurveillance*, *9*(23). https://doi.org/10.2807/1560-7917.ES.2024.29.23.2300633

Hashemi-Aghdam, S. S., & Oshaghi, M. A. (2015). A checklist of Iranian Cockroaches (Blattodea) with description of Polyphaga sp as a new species in Iran. *Journal of Arthropod-Borne Diseases*, *9*(2), 161–175.

Hassan, B., Ijaz, M., Khan, A., Sands, K., Serfas, G. I., Clayfield, L., El-Bouseary, M. M., Lai, G., Portal, E., Khan, A., Watkins, W. J., Parkhill, J., & Walsh, T. R. (2021). A role for arthropods as vectors of multidrug-resistant Enterobacterales in surgical site infections from South Asia. *Nature Microbiology 2021 6:10*, *6*(10), 1259–1270. https://doi.org/10.1038/s41564-021-00965-1

Ifeanyi, O. T. (2015). *Microbiology of Cockroaches – A Public Health Concern Science Microbiology of Cockroaches - A Public Health Concern*. *January*.

Irfan, M., Almotiri, A., & AlZeyadi, Z. A. (2022). Antimicrobial Resistance and Its Drivers—A Review. *Antibiotics*, *11*(10). https://doi.org/10.3390/antibiotics11101362

Kakooza, S., Ssajjakambwe, P., Nalubega, R., Namazi, B., Nantume, A., Ssentamu, G., Nabatta, E., Nalumenya, D., Wanyana, M., Munyiirwa, D. F. N., Namuyinda, D., Tsuchida, S., Ushida, K., & Kaneene, J. B. (2025). *Cockroaches as Reservoirs , Vectors , and Potential Sentinels of Multidrug-Resistant Bacteria in Ugandan Communities : A Retrospective Analysis*. *2025*(1). https://doi.org/10.1155/ghe3/5940509

Kassiri, H., Dehghani, R., Doostifar, K., Rabbani, D., Limoee, M., & Chaharbaghi, N. (2020). *Insecticide Resistance in Urban Pests with Emphasis on Urban Pests Resistance in Iran : A Review*. *7*(3), 32–54.

Khalil, I. A., Troeger, C., Blacker, B. F., Rao, P. C., Brown, A., Atherly, D. E., Brewer, T. G., Engmann, C. M., Houpt, E. R., & Kang, G. (2018). Morbidity and mortality due to shigella and enterotoxigenic Escherichia coli diarrhoea: the Global Burden of Disease Study 1990–2016. *The Lancet Infectious Diseases*.

Lim, C., Takahashi, E., Hongsuwan, M., Wuthiekanun, V., Thamlikitkul, V., Hinjoy, S., Day, N. P. J., Peacock, S. J., & Limmathurotsakul, D. (2016). Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. *ELife*, *5*(September), 1–18. https://doi.org/10.7554/eLife.18082

Lin, L., Wen, J., Li, S., & Liu, F. (2022). Life-History Traits from Embryonic Development to Reproduction in the American Cockroach. *Insects*, *13*(6). https://doi.org/10.3390/insects13060551

Liu, J., Yuan, Y., Feng, L., Lin, C., Ye, C., Liu, J., & Li, H. (2024). Intestinal pathogens detected in cockroach species within different food - related environment in Pudong , China. *Scientific Reports*, 1–10. https://doi.org/10.1038/s41598-024-52306-x

Lu, T., Das, S., Howlader, D. R., Picking, W. D., & Picking, W. L. (2024). Shigella Vaccines: The Continuing Unmet Challenge. *International Journal of Molecular Sciences*, *25*(8), 1–25. https://doi.org/10.3390/ijms25084329

Luckyjane, M. M., Tobias, B., & Nisha, N. (2023). *Control strategies for domestic cockroach (B*

. germanica , B . orientalis and P . americana) pests : A scoping review. *10*, 20–40. https://doi.org/10.22192/ijamr

Ma, J., Wang, M., Sun, Y., Zheng, Y., Lai, S., Zhang, Y., Wu, Y., Jiang, C., & Shen, F. (2024). Cockroach Microbiome Disrupts Indoor Environmental Microbial Ecology with Potential Public Health Implications. *Environment and Health*. https://doi.org/10.1021/ENVHEALTH.4C00216/SUPPL_FILE/EH4C00216_SI_001.PDF

Ma, J., Wang, M., Sun, Y., Zheng, Y., Lai, S., Zhang, Y., Wu, Y., Jiang, C., & Shen, F. (2025). Cockroach Microbiome Disrupts Indoor Environmental Microbial Ecology with Potential Public Health Implications. *Environment and Health*, *3*(4), 380–391. https://doi.org/10.1021/envhealth.4c00216

Maillard, J., Bloom, S. F., Courvalin, P., Essack, S. Y., Gandra, S., Gerba, C. P., Ba, J. R. R., & Scott, E. A. (2020). *American Journal of Infection Control Reducing antibiotic prescribing and addressing the global problem of antibiotic resistance by targeted hygiene in the home and everyday life settings : A position paper*. *48*, 1090–1099. https://doi.org/10.1016/j.ajic.2020.04.011

Marín-Miret, J., Pérez-Cobas, A. E., Domínguez-Santos, R., Pérez-Rocher, B., Latorre, A., & Moya, A. (2024). Adaptability of the gut microbiota of the German cockroach Blattella germanica to a periodic antibiotic treatment. *Microbiological Research*, *287*. https://doi.org/10.1016/j.micres.2024.127863

Memona, H., Manzoor, F., & Riaz, S. (2017). *Original Article Species Diversity and Distributional Pattern of Cockroaches in Lahore ,*. *11*(June), 249–259.

Merad, Y., Belkacemi, M., Merad, Z., Bassaid, A., & ... (2023). Fungal carriage of hospital trapped cockroaches: A prospective study. *New Microbes and New ...*. https://www.sciencedirect.com/science/article/pii/S2052297523000057

Mloka, D. A., Bwire, G. M., & Mwambete, K. (2020). *Isolation frequency of medically important fungi and fluconazole resistant of Candida sp from hospital cockroaches.* researchsquare.com. https://www.researchsquare.com/article/rs-14898/latest

Moges, F., Eshetie, S., Endris, M., Huruy, K., Muluye, D., Feleke, T., Silassie, F. G., Ayalew, G., & Nagappan, R. (2016). Cockroaches as a Source of High Bacterial Pathogens with Multidrug Resistant Strains in Gondar Town, Ethiopia. *BioMed Research International*, *2016*. https://doi.org/10.1155/2016/2825056

Molewa, M. L., Barnard, T., & Naicker, N. (2022). A potential role of cockroaches in the transmission of pathogenic bacteria with antibiotic resistance: A scoping review. *Journal of Infection in Developing Countries*, *16*(11), 1671–1678. https://doi.org/10.3855/jidc.16893

Mouwenda, Y. D., Ongwe, M. E. B., Sonnet, F., Stam, K. A., Labuda, L. A., De Vries, S., Grobusch, M. P., Zinsou, F. J., Honkpehedji, Y. J., Agobe, J. C. D., Diemert, D. J., van Leeuwen, R., Bottazzi, M. E., Hotez, P. J., Kremsner, P. G., Bethony, J. M., Jochems, S. P., Adegnika, A. A., Loembe, M. M., & Yazdanbakhsh, M. (2021). Characterization of t cell responses to co-administered hookworm vaccine candidates na-gst-1 and na-apr-1 in healthy adults in gabon. *PLoS Neglected Tropical Diseases*, *15*(10), 1–16. https://doi.org/10.1371/journal.pntd.0009732

Mullally, C. A., Fahriani, M., Mowlaboccus, S., Coombs, G. W., Mullally, C. A., Fahriani, M., Mowlaboccus, S., & Coombs, G. W. (2024). *Manifestations , Virulence Factors , and Antimicrobial Resistance*.

Murray, C. J., Ikuta, K. S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A., Han, C., Bisignano, C., Rao, P., Wool, E., Johnson, S. C., Browne, A. J., Chipeta, M. G., Fell, F., Hackett, S., Haines-Woodhouse, G., Kashef Hamadani, B. H., Kumaran, E. A. P., McManigal, B., … Naghavi, M. (2022). Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *The Lancet*, *399*(10325), 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Muzny, C. A., & Sobel, J. D. (2022). *The Role of Antimicrobial Resistance in Refractory and Recurrent Bacterial Vaginosis and Current Recommendations for Treatment*.

Naghavi, M., Vollset, S. E., Ikuta, K. S., Swetschinski, L. R., Gray, A. P., Wool, E. E., ... & Dekker, D. M. (2021). *Global burden of bacterial antimicrobial resistance 1990 – 2021 : a systematic analysis with forecasts to 2050*. https://doi.org/10.1016/S0140-6736(24)01867-1

Nasirian, Hassan, and A. S. (2019). Control of cockroaches (Blattaria) in sewers: a practical approach systematic review. *Journal of Medical Entomology*.

Nasirian, H. (2019). Contamination of cockroaches (Insecta: Blattaria) by medically important bacteriae: a systematic review and meta-analysis. *Journal of Medical Entomology*. https://academic.oup.com/jme/article-abstract/56/6/1534/5521082

Navarra, A., Cicalini, S., D'Arezzo, S., Pica, F., Selleri, M., Nisii, C., Venditti, C., Cannas, A., Mazzarelli, A., Vulcano, A., Carrara, S., Vincenti, D., Bartolini, B., Giacomini, P., Bocci, M. G., & Fontana, C. (2025). Vancomycin-Resistant Enterococci: Screening Efficacy and the Risk of Bloodstream Infections in a Specialized Healthcare Setting. *Antibiotics*, *14*(3), 1–12. https://doi.org/10.3390/antibiotics14030304

Nery, S. V., Traub, R. J., McCarthy, J. S., Clarke, N. E., Amaral, S., Llewellyn, S., Weking, E., Richardson, A., Campbell, S. J., Gray, D. J., Vallely, A. J., Williams, G. M., Andrews, R. M., & Clements, A. C. A. (2019). Wash for worms: A cluster-randomized controlled trial of the impact of a community integrated water, sanitation, and hygiene and deworming intervention on soil-transmitted helminth infections. *American Journal of Tropical Medicine and Hygiene*, *100*(3), 750–761. https://doi.org/10.4269/ajtmh.18-0705

Nielsen, M. (2022). Anthelmintic resistance in equine nematodes: current status and emerging trends. *International Journal for Parasitology: Drugs and Drug Resistance*.

O'Neill, J. (2016). O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. London: Review on Antimicrobial Resistance. *Cabidigitallibrary.Org*.

Obeng-Nkrumah, N., Labi, A. K., Blankson, H., Awuah-Mensah, G., Oduro-Mensah, D., Anum, J., Teye, J., Kwashie, S. D., Bako, E., Ayeh-Kumi, P. F., & Asmah, R. (2019). Household cockroaches carry CTX-M-15-, OXA-48- And NDM-1-producing enterobacteria, and share beta-lactam resistance determinants with humans. *BMC Microbiology*, *19*(1), 1–11. https://doi.org/10.1186/s12866-019-1629-x

Onohuean, H., Olot, H., Onohuean, F. E., Bukke, S. P. N., Akinsuyi, O. S., & Kade, A. (2025). A scoping review of the prevalence of antimicrobial-resistant pathogens and signatures in ready-to-eat street foods in Africa: implications for public health. *Frontiers in Microbiology*, *16*(April). https://doi.org/10.3389/fmicb.2025.1525564

Organization, W. H. (2023). *Antimicrobial resistance*.

Patel, C., Coulibaly, J. T., Hofmann, D., N'Gbesso, Y., Hattendorf, J., & Keiser, J. (2021). Efficacy and safety of albendazole in hookworm-infected preschool-aged children, school-aged children, and adults in Côte d'Ivoire: a phase 2 randomized, controlled dose-finding trial. *Clinical Infectious Diseases*.

Patel, A., Jenkins, M., Rhoden, K., & Barnes, A. N. (2022). A Systematic Review of Zoonotic Enteric Parasites Carried by Flies, Cockroaches, and Dung Beetles. *Pathogens*, *11*(1), 1–23. https://doi.org/10.3390/pathogens11010090

Pattnaik, M., Pattnaik, S., Pradhan, J., & Bhattacharya, D. (2023). Antimicrobial resistance and its possible implications in the future: a mini review. *International Journal Of Community Medicine And Public Health*, *10*(11), 4485–4491. https://doi.org/10.18203/2394-6040.ijcmph20233499

Perlin, D. S., Rautemaa-Richardson, R., & Alastruey-Izquierdo, A. (2017). The global problem of antifungal resistance: prevalence, mechanisms, and management. *The Lancet Infectious Diseases*, *17*(12), e383–e392. https://doi.org/10.1016/S1473-3099(17)30316-X

Pikkemaat, M. G., Yassin, H., van der Fels-Klerx, H. J., & Berendsen, B. J. A. (2016). Antibiotic Residues and Resistance in the Environment. *RIKILT Report 2016.009.*, 32. http://dx.doi.org/10.18174/388253%0Awww.wageningenUR.nl/en/rikilt

Prinzi, A. M., & Moore, N. M. (n.d.). Change of Plans : Overview of Bacterial Taxonomy , Recent Changes of Medical Importance , and Potential Areas of Impact. *Open Forum Infectious Diseases*, *10*(7), 1–9. https://doi.org/10.1093/ofid/ofad269

Ramalho-Ortigao, M., & Gubler, D. J. (2020). Human Diseases Associated With Vectors (Arthropods in Disease Transmission). *Hunter's Tropical Medicine and Emerging Infectious Diseases*, 1063–1069. https://doi.org/10.1016/B978-0-323-55512-8.00147-2

Rose Jepkosgei Kimosop1, Chrispinus Siteti Mulambalah1, M. M. N. (2018). *Prevalence of Enteric Parasitic Diseases among Patients Referred at a Teaching Hospital in Kenya*. 78–85. https://doi.org/10.4103/jhrr.jhrr

Rust, M. K., Lee, C. Y., Bennett, G. W., & Robinson, W. H. (2024). The Emergence and Sustainability of Urban Entomology. *Annual Review of Entomology*, *69*, 59–79. https://doi.org/10.1146/annurev-ento-012423-110612

Sarkodie-Addo, P., Aglomasa, B. C., & Donkor, E. S. (2025). Prevalence and antimicrobial resistance patterns of nontyphoidal Salmonella in Ghana: a systematic review and meta-analysis. *Tropical Medicine and Health*, *53*(1). https://doi.org/10.1186/s41182-025-00731-7

Slate, A. J., Jones, B. V, Clarke, O. E., Kerio, M., Nzakizwanayo, J., & Patel, B. A. (2023). *Infection responsive coatings to reduce biofilm formation and encrustation of urinary catheters*. *June*, 1–9.

Solomon, F., Kibru, G., & Ali, S. (2018). Multidrug-resistant pattern of food borne illness associated bacteria isolated from cockroaches in meal serving facilities, Jimma, Ethiopia. *African Health Sciences*, *18*(1), 32–40. https://doi.org/10.4314/AHS.V18I1.6

Tamma, P. D., Heil, E. L., Justo, J. A., Mathers, A. J., Satlin, M. J., & Bonomo, R. A. (2024). Infectious Diseases Society of America 2024 Guidance on the Treatment of Antimicrobial-Resistant Gram-Negative Infections. *Clinical Infectious Diseases*, *00*(0), 1–56. https://doi.org/10.1093/cid/ciae403

Temkin, E., Fallach, N., Almagor, J., Gladstone, B. P., Tacconelli, E., & Carmeli, Y. (2018). Estimating the number of infections caused by antibiotic-resistant Escherichia coli and Klebsiella pneumoniae in 2014: a modelling study. *The Lancet Global Health*, *6*(9), e969–e979. https://doi.org/10.1016/S2214-109X(18)30278-X

Turki Jalil, A., Abdulhadi, M. A., Al-Ameer, L. R., Jaafar Naser, S., Merza, M. S., Alsandook, T., al-hili, A., & Zabibah, R. S. (2023). Bacterial contamination of cockroaches in different wards of hospital, restaurant and home. *Heliyon*, *9*(11), e22103. https://doi.org/10.1016/j.heliyon.2023.e22103

Turner, M., Van Hulzen, L., Guse, K., Agany, D., & Pietri, J. E. (2024). The gut microbiota confers resistance against Salmonella Typhimurium in cockroaches by modulating innate immunity. *IScience*, *27*(12), 111293. https://doi.org/10.1016/j.isci.2024.111293

Victor, A., Titus, A., Olusi, A., Tyra, R., & Obi, E. (2024). Intestinal Parasites Associated with American Cockroach (Periplaneta americana) in Akure , Ondo State , Nigeria. *Journal of Parasitic Diseases*, *0123456789*. https://doi.org/10.1007/s12639-024-01645-7

Wada-katsumata, A., & Schal, C. (2024). Glucose aversion : a behavioral resistance mechanism in the German cockroach. *Current Opinion in Insect Science*, *63*, 101182. https://doi.org/10.1016/j.cois.2024.101182

Waindok, P., Raulf, M.-K., Springer, A., & Strube, C. (2020). The zoonotic dog roundworm Toxocara canis, a worldwide burden of public health. In Dog parasites endangering human health. *Springer International Publishing*.

Wang, C., & Cooper, R. (2025). Advances in monitoring of indoor pests. *Current Opinion in Insect Science*, *69*, 101366. https://doi.org/10.1016/j.cois.2025.101366

Werneburg, G. T., & Werneburg, G. T. (2022). *Catheter-Associated Urinary Tract Infections : Current Challenges and Future Prospects Catheter-Associated Urinary Tract Infections : Current Challenges and Future Prospects*. *2447*. https://doi.org/10.2147/RRU.S273663

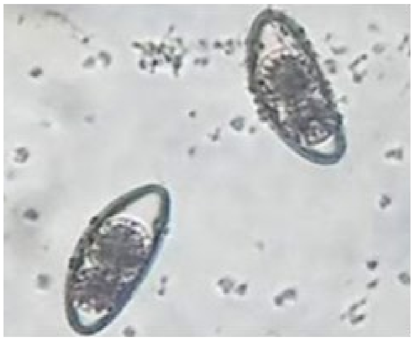
Wesevich, A., Sutton, G., Ruffin, F., Park, L. P., Thaden, J. T., Fouts, D. E., Fowler, V. G., De, F., Vg, F., & Jt, T. (2020). *crossm aerogenes) Is Associated with Poor Clinical Outcomes Relative to Other Enterobacter Species in Patients with Bloodstream Infection*.

Xu, C., Kong, L., Liao, Y., Tian, Y., Wu, Q., Liu, H., & Wang, X. (2022). Mini-Review: Antibiotic-Resistant Escherichia coli from Farm Animal-Associated Sources. *Antibiotics*, *11*(11), 1–17. https://doi.org/10.3390/antibiotics11111535

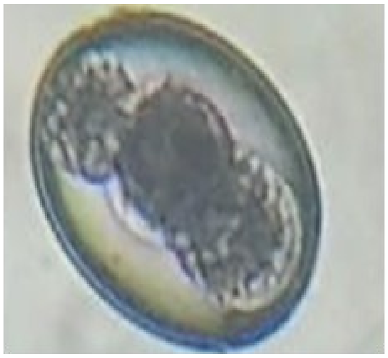
Yang, A., Tian, Y., & Li, X. (2024). *Unveiling the hidden arsenal : new insights into Proteus mirabilis virulence in UTIs*. *November*, 1–12. https://doi.org/10.3389/fcimb.2024.1465460

Zajac, A. M., Conboy, G. A., Little, S. E., & Reichard, M. V. (2021). Veterinary clinical parasitology. *John Wiley & Sons*.

APPENDIX



A



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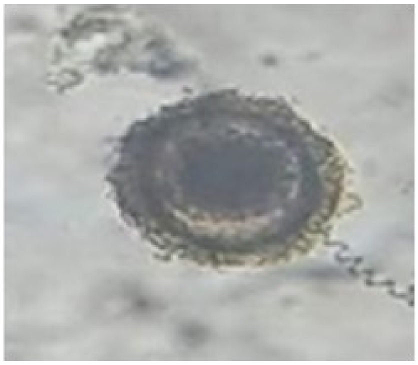

C

D

E

A= *Oxydurid* spp

B= *Toxoascaris*

C= *Ascaris* spp

D= Hookworm

E= *Strongyloides* spp