

**PREVALENCE OF VIRULENCE AND RESISTANCE GENES IN *Salmonella* Typhi
AMONG INTERNALLY DISPLACED PERSONS IN TWO LOCAL GOVERNMENT
AREAS OF BENUE STATE**

BY

**Ambrose Ashibel ADIE
PG/LSC18102474**

**UNIVERSITY OF BENIN
BENIN CITY**

OCTOBER, 2025

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IN ENVIRONMENTAL AND PUBLIC HEALTH MICROBIOLOGY, UNIVERSITY
OF BENIN, BENIN CITY**

OCTOBER, 2025.

CERTIFICATION

We certify that this work was carried out by **Ambrose Ashibel ADIE** in the Department of Microbiology, Faculty of Life Sciences, University of Benin, Benin City.

Prof. B.A. Omogbai
(Supervisor)

Date

Dr. A.G. Ogofure
(Co-Supervisor)

Date

Prof. E.O. Igbinosa
(Head of Department)

Date

CERTIFICATION OF THESIS

We, the undersigned, attest and declare that the thesis of Ambrose Ashibel ADIE titled: “Prevalence of Virulence and Resistance Genes in *Salmonella* Typhi Among Internally Displaced Persons in two Local Government Areas of Benue State.” has successfully passed the anti-plagiarism test and does not violate any copyright regulation.

Prof. B.A. Omogbai
(Supervisor)

Date

Dr. A.G. Ogofure
(Co-Supervisor)

Date

Prof. E.O. Igbinosa
(Head of Department)

Date

DEDICATION

This research work is dedicated to God Almighty, the most gracious, my lovely wife, Mabel Ambrose, my parents, Sir and Lady Adie, Patrick Betiang, and the entire family.

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I am most grateful to God Almighty for His love and protection during my research work.

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TABLE OF CONTENTS

Page	
Title page	ii
Certification	iii
Certification of Thesis	iv
Dedication	v
Acknowledgement	vi
Table of contents	viii
List of Tables	xiii
List of Figures	xiv
List of Plates	xv

List of Appendices	xvi
Abstract	xvii

CHAPTER ONE

1.0	Introduction	1
1.1	Background of the study	1
1.2	Aim and Objectives	5

CHAPTER TWO

2.0	Literature Review	7
2.1	Internally Displaced Persons	7
2.2	Public Health Concerns Associated with IDPs	11
2.3	Enterobacteriaceae	13
2.3.1	The Genus <i>Salmonella</i>	13
2.3.2	Classification of <i>Salmonella</i>	14
2.4	History of Typhoid Fever	14
2.5.	<i>Salmonella</i> Infections and Pathogenesis	18
2.5.1	<i>Salmonella</i> Infections	18
2.5.2	Transmission of Typhoid Fever	21
2.5.3	Pathogenesis of <i>Salmonella</i>	22
2.5.4	<i>Salmonella</i> in Humans	23
2.5.5	Prevalence of Typhoid Fever	25
2.5.6	Signs and Symptoms	32
2.5.7	Complications Associated with Typhoid Fever	34
2.5.8	Intestinal Complications	35
2.5.9	Intestinal Perforation	36
2.5.10	Gastrointestinal Bleeding	37
2.5.11	Extra-Intestinal Complications	38
2.5.12	Haematological Complications	38
2.5.13	Neurological Complications	38
2.5.14	Diagnosis of Typhoid Fever	38
2.5.14.1	Molecular Survey of <i>Salmonella typhi</i>	40

2.5.14.1.1 PCR (Polymerase Chain Reaction)	40
2.5.15 Prevention and Control	41
2.5.16 Primary Prevention	41
2.5.16.1 Five key steps to safer food	42
2.5.16.2 Vaccination	44
2.5.17 Secondary Prevention	46
2.5.17.1 Treatment	46
2.5.17.1.1 Oral Rehydration Therapy	46
2.5.17.1.2 Surgery	46
2.6 Antibiotic Resistance Profile of <i>Salmonella</i> Species	47
2.7 Spread of Resistance	51
2.7.1 Antimicrobial susceptibility test	55
2.8 Epidemiology of <i>Salmonella typhi</i>	56

CHAPTER THREE

3.0 Materials and Methods	61
3.1 Study areas	61
3.1.1 Guma Local Government of Benue State	61
3.1.2 Logo Local Government of Benue State	62
3.2 Ethical Approval for the study	64
3.3 Sample Size Determination	64
3.4 Questionnaire Design	65
3.5 Sample collection	65
3.6 Sterilisation Methods	65
3.7 Microbiological Analysis	66
3.7.1 Preparation of Media	66
3.7.2 Isolation of <i>Salmonella</i> species	66
3.8 Gram Staining	66
3.9 Biochemical Characterisation of Putative <i>Salmonella</i> Isolates	67
3.10 Preparation of Standard Inocula	72
3.11 Antibiotic used for susceptibility testing	72

3.12	Storage of Pure Isolates for Further Testing	73
3.13	Molecular Analysis	74
3.13.1	Preparation of PCR Reaction Mixture	74
3.13.2.	Protocol for Polymerase Chain Reaction	75
3.13.2.1	Two virulent gene were targeted for PCR	75
3.13.2.2	Two Resistant genes were targeted for PCR	75
3.13.2.3	One <i>S. typhi</i> gene-specific primer was targeted for PCR	75
3.14.1	Electrophoresis for Genomic PCR product	76
3.15	Plasmid Curing of <i>Salmonella typhi</i> isolates	76
3.16	Plasmid Extraction by Alkaline Lysis Method Disruption	77
3.16.1	Agarose gel electrophoresis of plasmid DNA	78
3.17	Multiple antibiotic resistance (MAR) index.	79
3.18	Statistical Analysis	79
CHAPTER FOUR		
4.1	Results	80
4.1.1	Overall Prevalence of <i>Salmonella typhi</i> among Internally Displaced Persons (IDPs)	80
4.1.2	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Camp Area	80
4.1.3	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Gender	80
4.1.4	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Age	84
4.1.5	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Occupation	84
4.1.6	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Personal Hygiene	84
4.1.7	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Risk Factors	
4.1.8	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to History/Knowledge about the disease	90
4.1.9	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Duration in Camp	91
4.1.10	Prevalence of <i>Salmonella typhi</i> among Internally Displaced Persons (IDPs) in Relation to the Toilet System/mode of defecation	91
4.1.11	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Marital Status	95
4.1.12	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Depression from the death of loved ones	96

4.1.13 Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Medication	96
4.1. Detection of the <i>invA</i> virulent gene of <i>Salmonella typhi</i>	102
4.2 Detection of the <i>FliC-d</i> virulent gene of <i>Salmonella typhi</i>	102
4.3 Detection of the <i>STY0307</i> gene Specific to <i>Salmonella typhi</i>	102
4.4 Detection of the <i>BlaTEM</i> resistant gene of <i>Salmonella typhi</i>	103
4.5 Detection of the <i>tetA</i> resistant gene of <i>Salmonella typhi</i>	103
4.6 Agarose gel post-electrophoresis showing plasmid before curing of <i>Salmonella typhi</i> isolates.	109
4.7 Agarose gel post-electrophoresis showing plasmid after curing of <i>Salmonella</i>	109
4.1.14 Antibiotic Sensitivity of <i>Salmonella typhi</i> isolates before curing	112
4.1.15 Antibiotic Sensitivity of <i>Salmonella typhi</i> isolates after curing	112

CHAPTER FIVE

5.1 Discussion	115
5.2 Findings	129
5.3 Contribution to Knowledge	129
5.4 Conclusion	130
5.5 Recommendation	130
References	132
Appendixes	156

LIST OF TABLES

Table	Title	Page
4.1:	An Overall Prevalence of <i>Salmonella typhi</i> among IDPs	81
4.2:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Camp	82
4.3:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Gender	83
4.4:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Age Group	86
4.5:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Occupation	87
4.6:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Personal Hygiene	88
4.7:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Risk Factors	92
4.8:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to History/Knowledge	93
4.9:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Duration in Camp	94
4.10:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to System of the toilet	98
4.11:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Marital Status	99

4.12:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Depression from the deaths of loved ones	100
4.13:	Prevalence of <i>Salmonella typhi</i> among IDPs in Relation to Medication	101

LIST OF FIGURES

Figure	Title	Page
4.1:	Map of Benue state showing the study areas	63
4.2:	Heat map of antibiotic sensitivity of uncured <i>S. typhi</i> Isolates	113
4.3:	Heat map of antibiotic sensitivity of cured <i>S. typhi</i> isolates	114

LIST OF PLATES

Plate	Title	Page
4.1:	Agarose gel picture showing PCR	104
4.2:	Agarose gel post picture showing no PCR	105
4.3:	Agarose gel picture showing PCR	106
4.4:	Agarose gel pictures showing PCR	107
4.5:	Agarose gel picture showing PCR	108
4.6:	Agarose gel post-electrophoresis showing uncured plasmid profile of <i>Salmonella typhi</i> isolates.	110
4.7:	Agarose gel picture showing cured plasmid profile of <i>Salmonella typhi</i> isolates.	111

LIST OF APPENDICES

Appendix I: Statistical Analysis	155
Appendix II: Ethical Clearance	195
Appendix III: Questionnaire	196
Appendix IV: Zone Diameter Interpretive Standards Chart	197
Appendix V: Antibiotic sensitivity before curing <i>S. typhi</i> isolates	198
Appendix VI: Antibiotic sensitivity after curing <i>S. typhi</i> isolates	199
Appendix VII: Biochemical characteristics and Gram staining <i>S. typhi</i> isolates	200
APPENDIX VIII Culture Media	204

ABSTRACT

An internally displaced person (IDP) is someone who is forced to leave his/her home due to a crisis, conflict, or natural disaster to find safety within their country's borders. Internal displacement has significant effects on public health, including the prevalence of typhoid fever. Following decades of several crises in Benue State, there has been an increasing number of internally displaced persons (IDPs). The aim of this study was to assess the prevalence of virulent and resistant genes of *Salmonella typhi* among internally displaced persons in two local government areas of Benue State, Nigeria.

Four hundred (400) stool samples were collected alongside with a well-structured questionnaires, 200 stool samples were collected from each IDP camp (Logo and Guma). The samples were screened for *Salmonella Typhi* following standard bacteriological procedures. *Salmonella* isolates were subjected to antibiotic susceptibility test on Muller-Hinton agar following the Kirby-Bauer disk diffusion technique. Plasmid gel electrophoresis was used to screen the isolates for plasmids. Acridine orange was used for curing experiment. Polymerase chain reaction was used to detect virulent and resistant genes: *inVA*, *FliC-d*, *tetA* and *blaTEM*, respectively. The identification of *Salmonella Typhi* was done by using PCR the *STY0307*-specific gene primers.

The results of this study showed a higher prevalence [50(12.5%)] of *S. typhi* infection in Logo LGA compared to Guma LGA, with 30(7.5%). *Salmonella typhi* infection was highest 5.0% amongst IDPs aged ≤ 10 years in Logo LGA and 3.0% in Guma LGA. Female IDPs had a significantly ($P < 0.05$) higher prevalence rate (8.75%) in Logo LGA than males, with 3.75%. Female IDPs in Guma LGA had a higher infection rate 5.0% in comparison to males with 2.5%. Concerning duration in camps, IDPs who lived longer than 2 years had a higher *Salmonella Typhi* infection rate (4.25% in Guma LGA and 9.5% in Logo LGA). *Salmonella Typhi* isolates exhibited resistance to cephorex (cephalexin), ciprofloxacin (cipro), ampicillin (omnipen), streptomycin (trobicin), gentamycin (gentamicin) and tetracycline (doxycycline). The isolates' multiple antibiotic resistance index (MARI) ranges from 0.4 to 0.7. The study demonstrated a high prevalence of plasmid mediated multidrug resistant potentially virulent strains of

Salmonella Typhi amongst the sample IDP dwellers. The antibiotic resistance was borne on plasmids following the post-curing experimentation. The isolates showed presence of the *blaTEM* resistant gene of 100.00% isolates and *tetA* resistant gene 50.00% isolates. Polymerase chain reaction analysis revealed that 80% of the isolates harboured the *inVA* gene. The *FliC-d* virulent gene was not detected in the isolates. A total of 75.00% of the isolates showed amplification of the *STY0307* gene, for *Salmonella* Typhi. The presence of typhoid fever and high levels of antimicrobial resistance plasmid-mediated in this study implies a significant threat to public health. It is therefore imperative for stakeholders and policymakers to prioritize healthcare infrastructure, routine screening, and education within IDP settings to curb the spread of resistant and virulent *S. typhi* strains.

CHAPTER ONE

INTRODUCTION

1.1 Background of the study

An internally displaced person (IDP) is someone who is forced to leave his/her home due to a crisis, conflict, or natural disaster to find safety within their country's borders. Internal displacement significantly affects public health and the well-being of the affected populations (Olwedo *et al.*, 2008; Adamu and Ben, 2017). Furthermore, few medical facilities are available to diagnose and treat individuals living in displacement camps (IDMC, 2016). However, following decades of communal crisis, Tiv/Jukum crisis, Fulani/Idoma crisis and Fulani/Tiv crisis, Benue state has more IDPs (Adamu and Ben, 2017). The incidence of typhoid fever in Benue State is estimated to be over seven thousand annually, which is among the leading causes of childhood mortality in the country (Umeh and Agbulu, 2009). This study explored some risk factors associated with Salmonella infection among IDPs with a review to curtailing the transmission of this highly infectious disease.

Globally, there are approximately 48 million internally displaced persons (IDPs) who have fled conflict and violence (UNHCR, 2021). IDPs are people who have been forced to leave their place of habitual residence but, unlike refugees, they have not crossed an internationally recognized State border (UNCHR, 1998). Such internal displacement occurs across various contexts - including conflicts, environmental disasters and the negative impacts of climate change - and often results from, and leads to, multiple human rights violations. Nevertheless, compared with the health of other conflict-affected, disadvantaged or mobile populations, including refugees and migrants, IDP health is relatively poorly understood. Given the scale of internal displacement due to conflict or violence and the fact that IDPs are among the most disadvantaged people in affected countries, this is anomalous.

According to UNHCR (2023) the security situation in Benue State remained volatile with persistent attacks by armed herders that claimed over 30 lives, including Internally Displaced

Persons (IDPs) and left scores injured in Guma, Logo and Gwer-West Local Government Areas (LGAs). The insistent threat continues to pose a significant challenge to the safety and security of the local population, particularly women and children. Hosted in overcrowded IDP camps and communities in six LGAs, the IDPs face increased protection risks such as Gender-Based Violence (GBV), trafficking, and exploitation due to poor WASH facilities, food, healthcare, and shelter. UNHCR and its partners are facing a significant challenge in expanding assistance to IDPs due to funding shortfalls and the limited presence of humanitarian agencies.

Public health concerns for Internally Displaced Persons (IDPs) in Benue State include widespread infectious diseases due to overcrowding and poor sanitation, high rates of malnutrition and food insecurity, inadequate maternal and child healthcare leading to increased infant mortality, and disruptions to routine immunization programs. These issues are driven by a lack of proper shelter, clean water, waste management, and limited access to health services, necessitating urgent interventions in Water, Sanitation, and Hygiene (WASH), food security, and healthcare delivery. According to Akpenpuun (2025) the total number of internally displaced persons (IDPs) in sub-Saharan Africa stands at 34.8 million, representing 46% of the global total of 68.3 million IDPs. This worrisome trend underscores the urgent need for concerted regional and international action. In addition to facing forced displacement, most internally displaced persons (IDPs) encountered challenges such as residing in camps unrecognized by national authorities, limited access to essential resources, and the consequences of inadequate support. The primary health issues reported included headaches, eye infections, diarrhoea, fever, typhoid, and malaria. IDPs attributed some of these health problems to the large number of rodents and disease-carrying vectors on the camp premises, including mosquitoes, snakes, and scorpions. The bites from these vectors were linked to increased disease rates and deaths. Long-term well-being issues included trauma, stress, and loss of income. Supplies for the IDPs were insufficient, with food scarcity affecting their health

and leading to speculated deaths. Consequently, it was not surprising to find that hunger was the most significant challenge across all camps, with one IDP noting that some deaths were due to starvation Albert and Abah (2024).

In terms of primary healthcare provision, some camps like Agatu, Logo, and Naka had established a health support team to manage medical issues for the internally displaced persons (IDPs). Sick individuals were typically taken to see a medical doctor, often at distant facilities, who would then prescribe medications. These health services were available in most locations but often required direct financial payments as there were no insurance or subsidy schemes for the IDPs. In such cases, the IDPs usually supported each other financially. However, when their out-of-pocket expenses exceeded their budgets, they turned to alternative treatments such as traditional remedies like herbs or purchasing medicines from street vendors. The use of herbs and medications from street vendors was sometimes found to be ineffective, leading to inadequate treatment of the conditions experienced by the IDPs. Overall, financial constraints posed a significant challenge as the IDPs could not afford proper medical care, resorting instead to self-medication. They also noted that sometimes, because of the high cost of proper treatment, they go get concoctions from chemist stores with 50 or 100 naira, they just tell the chemist person to mix drugs for them Albert and Abah (2024)

Typhoid fever is a problem in IDP camps because these environments have poor sanitation, limited access to clean water, and inadequate healthcare, creating conditions ideal for the spread of this infectious disease. Studying it is crucial to inform strategies like improving hygiene, providing clean water and sanitation, implementing vaccination programs, and enhancing access to effective treatment to protect this vulnerable population from severe illness and death.

Ekezie (2022) highlighted contributing factors in IDP Camps such as lack of proper sanitation facilities and the presence of high volumes of rodents in camp settings create an environment

where the bacterium *Salmonella Typhi* can thrive and spread; scarcity of safe drinking water is a major challenge, as typhoid is spread through contaminated water sources, making the population susceptible to infection; over crowdedness of IDPs camps and resources such as clean water, food, and healthcare are limited, leading to conditions where diseases can spread rapidly; inadequate access to essential healthcare, including medical personnel, logistics, and effective treatment, is often suboptimal and uncoordinated in IDP camp settings and vulnerability in children, in particular, are severely impacted by disease outbreaks in IDP camps.

Virulence and resistance genes increase typhoid incidence in IDP camps by allowing the bacteria to more easily infect, proliferate within, and survive the host's immune system, while simultaneously resisting antibiotics for treatment. The close quarters and poor sanitation of IDP camps facilitate the rapid spread of these more invasive and drug-resistant strains, leading to more severe outbreaks. Genes like the *invA* gene encode proteins necessary for *Salmonella Typhi* to attach to and invade intestinal cells, a key step in the infection cycle. Other virulence factors and genes, often located on pathogenicity islands (SPIs) or virulence plasmids, help the bacteria survive within host cells and multiply, contributing to the severity of the infection. Some virulence factors, like the Vi polysaccharide capsule, help the bacterium evade the host's immune system, further enhancing its ability to cause disease Olorundare *et al.* (2022).

However, genes conferring resistance to antibiotics are often located on plasmids, which are mobile pieces of DNA. Some resistance genes produce enzymes, such as beta-lactamases (like TEM, SHV, and CTX-M), that break down antibiotics, rendering them ineffective. The transfer of these plasmids allows for the rapid spread of antibiotic resistance among bacteria Olorundare *et al.* (2022).

The Combined Impact in IDP Camps such as overcrowding and poor sanitation in IDP camps provide ideal conditions for the transmission of *S. Typhi*. The presence of virulence genes

means that even with proper treatment, the infection is more likely to cause severe illness Olorundare *et al.* (2022) and Ekezie (2022). The combination of virulence and resistance genes allows for the emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains, which are extremely difficult to treat with existing antibiotics. This can lead to more prolonged and fatal outbreaks in vulnerable populations.

Furthermore, following the dearth of information on the prevalence of multidrug resistant, potentially virulent strains of *Salmonella Typhi* in the literature. Hence the current study was put together to fill this gap.

1.2 Aim and Objectives

The aim of this study was to assess the prevalence of virulence and resistance genes in *Salmonella Typhi* isolates among internally displaced persons (IDPs) in Logo and Guma Local Government Area, Benue State, Nigeria.

The specific objectives were to:

1. isolate, enumerate and identify *Salmonella typhi* among Internally Displaced Persons in Guma and Logo local government areas of Benue State.
2. determine the prevalence of *Salmonella typhi* among internally displaced persons in Guma and Logo local government areas of Benue State.
3. determine the antibiotic sensitivity profile of *Salmonella typhi* isolated within the study areas.
4. determine the presence of plasmid-mediated genes in *Salmonella typhi* isolates within the study area.
5. detect virulence and resistance genes in *Salmonella Typhi* isolates.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Internally Displaced Persons

Conflicts and disasters often cause large-scale displacement of people due to destruction of homes and environment, religious or political persecution or economic necessity (Kett, 2005; Umeh and Agbulu, 2009). According to Kett (2005) these persons or groups of people are forced or obliged to flee or leave their homes or places of habitual residence, in particular as a result of, or to avoid the effects of armed conflicts, situations of generalised violence, violations

of human rights or natural or human-made disasters, and who have not crossed an internationally recognized state border (Kett, 2005). They added that IDPs are distinct from refugees displaced outside their national borders. Furthermore, IDPs are often more disadvantaged than refugees because they do not benefit from assistance provided by international agencies unless the national government requests such assistance (Mooney, 2005).

Global estimates indicate that the number of people displaced annually by conflict and violence has increased since 2003 (NRC, IDMC, 2016). Also, on average, 5.2 million have been displaced annually in the past 13 years due to insurgency, political instability and terrorist activities of groups such as the Islamic State of Iraq and Syria (ISIS), Boko Haram and herders/farmers' crisis, particularly in the Middle East and Sub-Saharan Africa (Ferris, 2012). As of December 2015, the global estimate of IDPs due to conflict was 40.8 million (NRC, IDMC, 2016). Three-quarters of these IDPs reside in ten countries of the world, and five of these are located in Sub-Saharan Africa. The total number of people displaced by conflict in the region is almost 12 million (NRC, IDMC, 2015).

IDPs in Africa experience a myriad of health problems. The main health problems identified include physical health and mental health problems, including depression (Olwedo *et al.*, 2008; Guerrier *et al.*, 2009; Asad *et al.*, 2013; Singh *et al.*, 2016). Health problems reported by the studies mainly were communicable and non-communicable diseases, as well as other health-related problems such as sexual abuse and substance use (Kim *et al.*, 2007).

In Nigeria, the insurgent activities of Boko Haram in years back have forced over a million people to flee their homes. This has resulted in an unprecedented humanitarian crisis in the North-eastern part of the country and the Lake Chad region (NRC, IDMC, 2015). Furthermore, inter-communal clashes resulting from ethno-religious disputes, tensions between Fulani herders and farmers have resulted in over 700,000 people being displaced from the Middle Belt

region of Nigeria (NRC, IDMC, 2016). In Central Africa, conflict and violence have resulted in over a million displacements of people in the Democratic Republic of Congo (NRC, IDMC, 2016). Other African countries which have had large numbers of IDPs in the past decade are Somalia, Uganda, Kenya and Sudan (Ferris, 2012).

Furthermore, apart from conflicts and violence, natural disasters resulting from floods, storms, wildfires, earthquakes and droughts have caused the displacement of 203.4 million people globally in the past (Lam *et al.*, 2015). In 2015, 19.2 million people in 113 countries were displaced by natural disasters. Most of these displacements occurred in South and Eastern Asian countries, while slightly over a million occurred in Sub-Saharan Africa (NRC, IDMC, 2016).

Internal displacement significantly affects public health and the well-being of the affected populations. These impacts may be categorised as direct due to violence and injury or indirect, such as increased rates of infectious diseases and malnutrition (Olwedo *et al.*, 2008; Guerrier *et al.*, 2009; Lam *et al.*, 2015). Several risk factors that promote communicable diseases work in synergy during displacement. These factors include movement of mass populations and resettlement in temporary locations, overcrowding, economic and environmental degradation, poverty, inadequate safe water, poor sanitation and waste management. These conditions are further compounded by the absence of shelter, food shortages and inadequate access to healthcare (Connolly *et al.*, 2004;Lam *et al.*, 2015). Depending on the location in Sub-Saharan Africa, the combined effects of these factors among IDPs result in increased risk of diseases such as acute respiratory infections (ARI) (4%) and diarrhoeal diseases (18%-22%) recorded in Nyala Province, South Darfur, Sudan (Kim *et al.*, 2007). Getanda *et al.* (2015) recorded 18% -22% of diarrhoeal diseases among IDPs living in Nakuru County, Kenya and scabies (77%-86%) among IDPs. Furthermore, malnutrition has been reported among children under five in Indonesia (Owoaje *et al.*, 2016). In the region, the spectrum includes stunting (38.6%),

underweight (28.4%) and wasting (7.2%) (Owoaje *et al.*, 2016). According to Owoaje *et al.*(2016), diarrhoeal diseases are significant causes of morbidity and mortality among IDPs and mainly result from substandard or inadequate sanitation facilities, poor hygiene and scarcity of soap.

The disruption in public health services also hinders prevention and control programmes, resulting in the rise of vector-borne diseases such as malaria and yellow fever (Owoaje *et al.*, 2016). Similarly, routine immunisation services are disrupted, thus increasing the number of individuals susceptible to diseases and the risk of vaccine-preventable disease (VPDs) epidemics (Shultz *et al.*, 2009). Depending on the geographical location, outbreaks of VPDs which have been reported among IDPs include measles (20%-30%) and meningococcal meningitis (0.3%) in Northern Uganda (Santaniello-Newton and Hunter, 2000). Similarly, epidemics of cholera in Kenyan refugee camps (WHO, 2008; Shultz *et al.*, 2009), yellow fever in Liberia (Huhn *et al.*, 2006) hepatitis E have been reported in IDP and Refugee camps across Africa (Nicole, 2015). Furthermore, global polio eradication activities have been hampered in three conflict-torn countries, which have large numbers of refugees and IDPs in Afghanistan, Pakistan and Nigeria (NRC/ IDMC, 2016). According to Siriwardhana and Wickramage (2014) and Oluwaremilekun and Mojirayo (2020), epidemics of infectious diseases are quite common in IDP camp settings due to inadequate water and sanitation facilities combined with overcrowding.

More so, women and children constitute over 70% of internally displaced populations, and they experience a wide range of health risks (NRC/ IDMC, 2015; Getanda *et al.*, 2015 and NRC/ IDMC, 2016). They added that IDPs are highly vulnerable to physical and mental health problems. Communicable diseases have been reported among children and adults. The rate of typhoid reported among children was 84.8%, while among adults, it was 48%. Cough/respiratory problems were reported among children at 81.7% and 45% among adults.

Diarrhoea was reported among children at 61.9% and 18.5% among adults. (Olwedo *et al.*, 2008; Bozzoli and Brück, 2010). The high prevalence rates of the communicable diseases reported were attributed to environmental factors such as poor waste disposal, ecological sanitation, overcrowding, inadequate water supply and healthcare services (Bozzoli and Brück, 2010). The prevalence of infectious diseases was higher among children, indicating that children are most vulnerable in IDP camps. Studies conducted among children between 3 months and <10 years showed that acute malnutrition (wasting) ranged between 6% and 21% in the Chad Republic, while chronic malnutrition (stunting) ranged from 2.2% in Sierra Leone (Gbakima *et al.*, 2012) to 52.4% in Uganda (Guerrier *et al.*, 2009).

The study by Singh *et al.* (2016) on the nutritional status of men aged 18 years and above in Kenya reported that 23% of men were underweight. However, these authorities noted that the prevalence was similar to the national malnutrition estimates. This suggests that the findings of their study may have been related to the prevailing socio-economic and environmental conditions rather than the displacement. In addition, the use of Body Mass Index (BMI) and mid-upper arm circumference to assess malnutrition may have also contributed to the high prevalence (Singh *et al.*, 2016).

Furthermore, several studies have reported that women and girls were victims of physical and sexual violence in IDP camps (Amowitz *et al.*, 2002; Kerimova *et al.*, 2003; Ellsberg *et al.*, 2008; Vu *et al.*, 2014; Owoaje *et al.*, 2016). Women are at higher risk of unwanted pregnancies, unsafe abortions, maternal morbidity and mortality (Austin *et al.*, 2008). Thus, the negative impacts of sexual violence are significant and long-term. These may include physical injuries, sexually transmitted infections including HIV, unwanted pregnancies and mental health effects (Campbell, 2002; Austin *et al.*, 2008; McLean *et al.*, 2011; Draughon, 2012).

Moreover, IDPs, particularly those affected by conflict, are at a high risk of mental health problems, including depression, primarily as a result of the death of loved ones. Also reported

are psychological reactions (violence and depression), which cause post-traumatic stress disorders (PTSDs). (Getanda *et al.*, 2015; Mujeeb, 2015; Ugbe *et al.*, 2022) . Other types of mental health problems which have been reported are panic attacks and anxiety disorders (Saxon *et al.*, 2016).

2.2 Public Health Concerns Associated with IDPs

Public health for refugees, internally displaced persons and other conflict-affected populations has evolved as a specialised field with its policies, procedures, manuals, indicators and reference materials (Craig, 2010; Judy and Kelly, 2012). Displacement of a population always affects health status and health care. In the epidemiological triad of host, agent and environment interaction, displacement exposes IDPs to new hazard dynamics: Infectious agents and vectors might be present in the new environment, to which IDPs may lack immunity and or coping skills; in general, poor quality of water and sanitation and overcrowding, as in temporary settlements, modify interaction with existing infectious agents; absolute and relative food shortages occur due to disruptions in the production and supply systems; psychosocial balance is disrupted by being uprooted, insecurity, lacking meaningful employment and death of loved ones, etc; displacement can also lead to an increase in hazardous behaviours (such as promiscuity and sexual and/or intra-household violence); weather vagaries and other natural hazards may be present in the new environment (Leus *et al.*, 2001; Mooney, 2005).

These new hazards are compounded by accrued vulnerability due to loss of assets and entitlements, loss of social networks and caring capacities, and often disruption of households. This has a particularly profound impact on women, children and the elderly (Leus *et al.*, 2001). Lack of knowledge and information on the new environment, decreased food security and dependence on external aid, often inadequate shelter, sanitation and access to safe water, reduced access to health care facilities and health care services: IDPs lose access to the health

services they knew and are at a disadvantage, in cultural, financial, and functional terms in accessing health services in areas of relocation (Judy and Kelly, 2012; Akinwusi *et al.*, 2013). Exposure to new hazards and greater vulnerability result in a greater risk of illness and death for these populations. Even in a best-case scenario, functional access is difficult, and the host population shares the sufferings of the internally displaced (Akinwusi *et al.*, 2013). The arrival of many people can strain local health systems that are not sufficiently resilient. If the new arrivals are unexpected, or if information is uncertain and slow, personnel, supplies and facilities rapidly become inadequate. Furthermore, this translates into reduced access to health care and poor health outcomes for all. Internally displaced persons and host communities may also compete for access to food, infrastructure and environmental resources (Shultz *et al.*, 2009). In addition, IDPs may introduce diseases not typically seen in the host population, thus the hosts could perceive the IDPs as public health threats (Wisner *et al.*, 2003; Ben *et al.*, 2003; Mooney, 2005; Shultz *et al.*, 2009).

2.3 Enterobacteriaceae

Members of the family Enterobacteriaceae are Gram-negative, non-sporing straight rods. Some genera are motile using peritrichous flagella, except *Tatumella*, *Shigella* and *Klebsiella* species, which are non-motile humans (Hafez and Jodas, 2000). They are facultative anaerobes and most species grow well at 37°C, although some grow better at 25-30°C (Hong *et al.*, 2007). They grow well on peptone and meat extract media. Some strains grow on D-glucose as the sole carbon and energy source, but others require vitamins and/or amino acids (Hong *et al.*, 2007). They are oxidase negative, and catalase reactions vary among Enterobacteriaceae. They are distributed worldwide and may be found in soil, water, plants, humans and animals. Enterobacteriaceae contain many harmless symbionts and many more familiar pathogens, such as *Salmonella*, *Escherichia coli*, *Yersinia pestis*, *Klebsiella* and *Shigella*. Other disease-causing

bacteria in this family include *Proteus*, *Enterobacter*, *Serratia*, and *Citrobacter* (Hong *et al.*, 2007).

2.3.1 The Genus *Salmonella*

The genus *Salmonella* incorporates Gram-negative, facultative anaerobic, rod-shaped bacilli members of Enterobacteriaceae. This genus, which is estimated to have diverged from *Escherichia coli* (*E. coli*) approximately 100 to 150 million years ago (Hong *et al.*, 2007), has adapted to colonise many different niches. *Salmonella* can roughly be classified into three groups. The first group includes highly host-adapted and invasive serovars such as *S. gallinarum*, *S. pullorum* in poultry, and *S. typhi* in humans. The second group comprises non-host adapted and invasive serovars such as *S. typhimurium*, *S. arizonae* and *S. enteritidis*. The third group contains non-host-adapted and non-invasive serovars. Most of these serovars are harmless to animals and humans (Hafez and Jodas, 2000).

2.3.2 Classification of *Salmonella*

Salmonella taxonomy divide the genus into two species: *Salmonella bongori* and *Salmonella enterica*. *Salmonella bongori* contains fewer than 10 serovars, while *S. enterica* contains more than 2500 serovars and is divided into six subspecies, namely *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae* and *indica* (Tindall *et al.*, 2005)

Salmonella belongs to the Domain: Bacteria, Kingdom: Monera, Phylum: Proteobacteria, Order: Enterobacteriales, Family: Enterobacteriaceae and Genus: *Salmonella* (Adeolu *et al.*, 2016). The order ‘*Enterobacteriales*’ is a large and diverse group of Gram-negative, facultatively anaerobic, non-spore-forming, rod-shaped bacteria within the class *Gamma proteobacteria*. Members of this group inhabit several different ecological niches and have been found in soil and water and in association with living organisms, including plants, insects, animals and humans (Brenner and Farmer, 2005).

2.4 History of Typhoid Fever

Historically, in the pre-antibiotic era, the case fatality rate of typhoid fever was 10–20%. Today, with prompt treatment, it is less than 1% (Heymann, 2008). However, about 3–5% of infected individuals will develop a chronic infection in the gall bladder. Since *S. Typhi* is human-restricted, these chronic carriers become the crucial reservoir, which can persist for decades for further spread of the disease, further complicating the identification and treatment of the disease (Gonzalez *et al.*, 2011). Lately, the study of *S. Typhi* associated with a large outbreak and a carrier at the genome level provides new insights into the pathogenesis of the pathogen (Yap *et al.*, 2016; Bhandari *et al.*, 2024).

In industrialised nations, water, sanitation and food handling improvements have reduced the number of cases (Crump, 2016). Developing countries, such as those in parts of Asia and Africa, have the highest rates of typhoid fever. These areas lack access to clean water, sanitation systems, and health care facilities. For these areas, such access to basic public health needs is not in sight in the near future (Bhandari *et al.*, 2024).

Previously, in 430 BC, a plague, which some believe to have been typhoid fever, killed one-third of the population of Athens, including their leader Pericles (Bhandari *et al.*, 2024). Following this disaster, the balance of power shifted from Athens to Sparta, ending the Golden Age of Pericles that had marked Athenian dominance in the ancient Greek world (Bhandari *et al.*, 2024). The ancient historian Thucydides also contracted the disease, but he survived to write about the plague. His writings were the primary source of this outbreak, and modern academics and medical scientists consider typhoid fever the most likely cause (Bhandari *et al.*, 2024). In 2006, a study detected DNA sequences similar to those of the bacterium responsible for typhoid fever in dental pulp extracted from a burial pit dated to the time of the outbreak of typhoid (Smith, 2023). The cause of the plague has long been disputed, and other scientists have disputed the findings, citing serious methodological flaws in the dental pulp-derived DNA

study. The disease is most commonly transmitted through poor hygiene habits and public sanitation conditions; during the period related to Athens above, the whole population of Attica was besieged within the Long Walls and lived in tents (Smith, 2023).

Furthermore, a pair of epidemics struck the Mexican highlands in 1545 and 1576, causing an estimated 7 to 17 million deaths (Acuna-Soto *et al.*, 2002; Vågene *et al.*, 2018). Some historians believe that the English colony of Jamestown, Virginia, died from typhoid. Typhoid fever killed more than 6000 settlers in the New World between 1607 and 1624 (Smith, 2023).

During the American Civil War, 81,360 Union soldiers died of typhoid or dysentery, far more than died of battle wounds (Walter, 2014). In the late 19th century, the typhoid fever mortality rate in Chicago averaged 65 per 100,000 people a year (Smith, 2023).. The worst year was 1891, when the typhoid death rate was 174 per 100,000 people (Chicago Timeline, 2007).

A long-held belief is that the 9th US President William Henry Harrison died of pneumonia, but recent studies suggest he likely died from typhoid (Smith, 2023). This disease may also have been a contributing factor in the death of the 12th US President Zachary Taylor due to the unsanitary conditions in Washington, D.C., in the mid-19th century (Death in the White House, 2014; The New York Times, 2014)

During the Spanish–American War, American troops were exposed to typhoid fever in stateside training camps and overseas, mainly due to inadequate sanitation systems. The Surgeon General of the Army, George Miller Sternberg, suggested that the War Department create a Typhoid Fever Board (Walter, 2014).

Major Walter Reed, Edward O. Shakespeare, and Victor C. Vaughan were appointed on August 18, 1898, with Reed being designated the President of the Board. The Typhoid Board determined that during the war, more soldiers died from this disease than from yellow fever or from battle wounds (Walter, 2014). The Board promoted sanitary measures, including latrine policy, disinfection, camp relocation, and water sterilisation. Still, the most successful anti-

typhoid method was vaccination, which became compulsory in June 1911 for all federal troops (Walter, 2014).

The most notorious carrier of typhoid fever, but by no means the most destructive, was Mary Mallon, also known as Typhoid Mary. In 1907, she became the first carrier in the United States to be identified and traced. She was a cook in New York who was closely associated with 53 cases and three deaths (Nova, 2010). Public health authorities told Mary to give up working as a cook or have her gall bladder removed, as she had a chronic infection that kept her active as a carrier of the disease (Nova, 2010). Mary quit her job, but returned later under a false name. She was detained and quarantined after another typhoid outbreak (Nova, 2010). She died of pneumonia after 26 years in quarantine (Nova, 2010).

A notable outbreak occurred in the Democratic Republic of Congo (DRC), which is the epicentre of typhoid fever, a survey shows. According to the Severe Typhoid in Africa programme, which offers new typhoid fever burden estimates from six high-burden countries on the continent, DRC, Madagascar, Burkina Faso, Ethiopia, Ghana and Nigeria, the country is exhibiting a high incidence rate with 315 cases per 100,000 individuals (Kairu, 2024). Four countries recorded more than 100 cases for every 100,000 person-years of observation (Kairu, 2024). Which is considered a high burden. In DRC, children between 2 and 14 years of age were shown to be at the highest risk across all 25 study sites (Kairu, 2024).

The number of suspected typhoid intestinal perforations was notably high, particularly in DRC and Ghana, suggesting that a substantial proportion of typhoid infections go undetected and untreated (Kairu, 2024).

Salmonella Typhi is the aetiological agent of typhoid fever, while paratyphoid fever is caused by *S. paratyphi* A, B and C. Since the clinical symptoms of paratyphoid fever are indistinguishable from typhoid fever, the term 'enteric fever' is used for both fevers, and both *S. typhi* and *S. paratyphi* are referred to as typhoid *Salmonella* (Thielman *et al.*, 2004). Humans

are the sole reservoir for the two strains of typhoid *Salmonella* (Patel *et al.*, 2010; Galan, 2016). Enteric fever is characterised by an incubation period of one week or more, with prodromal symptoms such as headache, abdominal pain and diarrhoea (or constipation), followed by the onset of fever. Diarrhoea is more commonly observed in children, whereas patients with immune suppression are more likely to develop constipation (Thielman *et al.*, 2004; Kuvandik *et al.*, 2009).

Enteric fever displays a specific fever pattern with an initial low-grade fever ($>37.5^{\circ}\text{C}$ to 38.2°C) which slowly develops to high-grade fever ($>38.2^{\circ}\text{C}$ to 41.5°C) in the second week (Parry *et al.*, 2002). If the patient is left untreated, fever can persist for a long time (Patel *et al.*, 2010). Besides fever, infected patients may also develop hepatomegaly (enlarged liver), splenomegaly (enlarged spleen), and rose spots on their chest and abdomen (Parry *et al.*, 2002). In endemic regions, approximately 15% of the infected patients develop gastrointestinal complications, which include pancreatitis, hepatitis and cholecystitis. Haemorrhage is one of the most severe gastrointestinal complications that occur as a result of perforation of Peyer's patches and lymphatic nodules located at the terminal ileum, resulting in bloody diarrhoea (Parry *et al.*, 2002).

2.5. *Salmonella* Infections and Pathogenesis

2.5.1 *Salmonella* Infections

Salmonella are well-known pathogens, highly adaptive and potentially pathogenic for humans and/or animals. *Salmonella* can produce serious infections that are often foodborne and present as gastroenteritis. However, a small percentage of these infections may become invasive, resulting in bacteremia and severe extra-intestinal disease (Bibek *et al.*, 2024). The main reservoirs for non-typhoid *Salmonella* are animals such as poultry, livestock, pets and reptiles (Bibek *et al.*, 2024). *Salmonella* Typhi and *Salmonella* paratyphi colonise only humans, so

they can be acquired only from close contact with a person who has typhoid fever, from a chronic carrier, or water or food contaminated by human faeces (Bibek *et al.*, 2024).

More so, specific serovars of *Salmonella enterica* cause disease in humans and various animals; other serovars are highly restricted to a specific host. *Salmonella* infections range from gastrointestinal infections accompanied by inflammation of intestinal epithelia, diarrhoea and vomiting, to typhoid fever, a life-threatening disease (Hensel, 2004). The host and the status of the bacterium determine the outcome of *Salmonella* infections. Whereas age, genetic and environmental factors mainly determine the status of the host, the status of the bacterium is determined by its virulence factors (Hensel, 2004).

Serotypes adapted to man, such as *Salmonella typhi* and *Salmonella paratyphi*, usually cause severe diseases in humans as a septicemic typhoid syndrome; these serotypes are not typically pathogenic to animals (Ying *et al.*, 2020). Serotypes highly adapted to animal hosts, such as *Salmonella gallinarum* (poultry) or *Salmonella abortus-ovis* (sheep), typically produce very mild symptoms in humans (Ying *et al.*, 2020). However, *Salmonella choleraesuis*, which has the pig as a primary host, also causes severe systemic illness (Ying *et al.*, 2020). In the same way, *Salmonella dublin*, which prefers bovines, is primarily responsible for the systemic form of Salmonellosis. In young calves, this disease causes high mortality, and in adult cattle, it results in fever, reduced milk yield, diarrhoea, abortion, and occasionally death. Ubiquitous serotypes, such as *Salmonella Enteritidis* or *Salmonella Typhimurium*, which affect both man and animals, generally cause gastrointestinal infections less severe than enteric fever (Ying *et al.*, 2020).. However, they can also produce typhoid-like infections in mice and humans, or asymptomatic intestinal colonisation in chickens (Ying *et al.*, 2020).

The term for infections caused by *Salmonella* is salmonellosis, which is generally divided into two main types: typhoidal and non-typhoidal. Typhoidal salmonellosis or typhoid fever is caused mainly by *Salmonella typhi*, characterized by symptoms such as fever, weakness,

abdominal pain, and loss of appetite (Matheson *et al.*, 2010; Eng *et al.*, 2015; Barnett, 2016; Sohail *et al.*, 2023) and typically acquired through the consumption of contaminated food or water and more common in developing countries (Eng *et al.*, 2015). Salmonellosis includes several syndromes (gastroenteritis, enteric fevers, septicemia, focal infections, and an asymptomatic carrier state) Particular serovars show a strong propensity to produce a particular syndrome (*S. typhi*, *S. paratyphi-A*, and *S. schottmuelleri* produce enteric fever; *S. choleraesuis* produces septicemia or blood infections; *S. typhimurium* and *S. enteritidis* produce gastroenteritis); however, on occasion, any serotype can produce any of the syndromes (Giannella, 1996). In general, more serious infections occur in infants, adults over 50, and subjects with debilitating illnesses (Giannella, 1996).

However, non-typhoidal salmonellosis is caused by a variety of *Salmonella* serotypes and mainly causes food poisoning symptoms, such as diarrhoea, abdominal cramps, and fever and is more common in developed countries (Bhutta, 2006; Majowicz *et al.*, 2010; Matheson *et al.*, 2010; Feasey *et al.*, 2012). Most people infected with *Salmonella* will develop diarrhoea, abdominal cramps, fever, and vomiting, which can last up to a week (Eng *et al.*, 2015; Barnett, 2016; Jajere *et al.*, 2019; White *et al.*, 2019). Other symptoms caused by *Salmonella* infection include the enlargement of the spleen and lymph nodes, accumulation of fluid and blood in organs such as the lungs, and damage to the liver (Matheson *et al.*, 2010; Barnett, 2016; Jajere *et al.*, 2019). In chronic cases, arthritis, known as Reiter's Syndrome, may even occur and can last for months or even years (Dworkin *et al.*, 2001; Canović *et al.*, 2004 and Abdullahi *et al.*, 2014). Different symptoms will occur in various mammals and birds.

2.5.2 Transmission of Typhoid Fever

Following contact with an infected carrier and ingestion of fecally contaminated food or water, the pathogenesis of both typhoid and *Salmonella* enteritis begins with the intestinal phase. In

contrast, only typhoid, caused by *Salmonella typhi* and *paratyphi*, progresses to systemic infection. The transmission of this disease within the human population is generally a result of poor sanitation, which results from faecal contamination of water and food supplies in developing nations.

The broad host-range *Salmonella* serovars are prevalent within warm-blooded animal populations that make up the human food supply, and bacterial transmission generally results from consumption of raw or undercooked food products. The vast majority of *Salmonella* infections are transmitted from animals to humans through food and occasionally from person to person through the faecal-oral route. *Salmonella* generally causes one or more of four broad clinical syndromes, such as gastroenteritis, enteric fever, septicemia with associated focal lesions, and asymptomatic long-term carriage (Jones, 2005).

Furthermore, *Salmonella typhi* is spread through the faecal-oral route by individuals currently infected and by asymptomatic carriers of the bacteria. Unlike other strains of *Salmonella*, there are no animal carriers of *S. typhi*. Humans are the only known carriers of the bacteria. An asymptomatic human carrier is an individual who is still excreting *S. typhi* in their stool a year after the acute stage of the infection. Human carriers are responsible for transmitting the bacteria in endemic regions of the world (Eng *et al.*, 2015).

2.5.3 Pathogenesis of *Salmonella*

S. typhi enters the human host through contaminated food and water sources and tends to pass through the stomach into the epithelial cells of the gut. The first challenge of *Salmonella* colonisation is stomach acidity, and specific situations in which it is either reduced (by the usage of antacids, proton pump inhibitors) or the intestinal integrity is compromised (surgery, antibiotic use, inflammatory bowel disease) elevate the chances of *Salmonella* infection in the host (Lorkowski *et al.*, 2014). According to Giannella (1996) and Gut *et al.* (2018), the invasion of epithelial cells stimulates the release of proinflammatory

cytokines, which induce an inflammatory reaction. The acute inflammatory response causes diarrhoea and may lead to ulceration and destruction of the mucosa. The bacteria can disseminate from the intestine to cause systemic disease (Lorkowski *et al.*, 2014). The bacteria interact with the non-phagocytic cells, such as the epithelial cells of the intestinal mucosa, which adhere to the intestinal epithelial cells by adhesive structures (fimbriae) that promote binding and invade cells to provoke gastroenteritis (Lorkowski *et al.*, 2014). Most *S. Typhi* have virulence factors such as virulence plasmids, toxins, fimbriae and flagella that help establish an infection.

However, epithelial cell cytokine secretion occurs in *Salmonella enteritidis* tissue culture models (Lorkowski *et al.*, 2014). Translocation of *Salmonella* pathogenicity island (SPI-1) proteins into intestinal epithelial cells leads to the synthesis and polarised secretion of inflammatory mediators and neutrophil chemoattractants. Several translocated *Salmonella* pathogenicity island (SPI-1) proteins contribute to intestinal inflammation and fluid secretion (Lorkowski *et al.*, 2014). Intestinal inflammation probably contributes to fluid secretion and diarrhoea by disrupting the epithelial barrier and increasing water flux by an exudative mechanism. Innate immune system activation also contributes to intestinal inflammation (Lorkowski *et al.*, 2014). Finally, *Salmonella typhi* invades macrophages and the migration of infected macrophages to reticuloendothelial organs via the lymphatic system and blood produces systemic illness with fewer diarrhoeas (Lorkowski *et al.*, 2014).

2.5.4 *Salmonella* in Humans

Typhoidal *Salmonella* serovars, such as *S. Typhi* or *S. paratyphi*, are the causative agents of enteric fever, also known as typhoid or paratyphoid fevers, respectively (Reddy *et al.*, 2010). According to Kanungo *et al.* (2008) and Wain *et al.* (2015), typhoid fever is a major human bacterial infection caused by *Salmonella typhi*. Parry *et al.* (2002) opined that *Salmonella typhi* and *Salmonella paratyphi* are pathogenic exclusively for humans, causing systemic infections

and typhoid fever, whereas *Salmonella enterica* serovar Typhimurium causes gastroenteritis. Furthermore, *Salmonella* serotypes can be divided into three groups that cause distinctive clinical syndromes: typhoid fever, bacteremia and enteritis (Chiu *et al.*, 2002). The non-typhoid *Salmonella* serotypes can cause human protean manifestations, including acute gastroenteritis, bacteremia, and extra-intestinal localised infections involving many organs (Chiu *et al.*, 2002). *Salmonella enterica* subspecies *enterica* causes approximately 99% of *Salmonella* infections in humans and warm-blooded animals (Gut *et al.*, 2018). Serotypes in other subspecies are usually isolated from cold-blooded animals and the environment, but rarely from humans (Gut *et al.*, 2018).

Globally, there are 11–21 million instances of typhoid fever and 5 million cases of paratyphoid fever each year, resulting in approximately 135,000–230,000 deaths annually (CDC, 2023).. In the US, around 400 cases of typhoid fever and 5–100 cases of paratyphoid fever were confirmed in cultures between 2016 and 2018. Notably, more than 85% of these cases occurred in individuals who had travelled internationally (CDC, 2023). The incubation period of enteric fever is marked by one week or longer, during which individuals experience symptoms such as high fever, diarrhoea, vomiting, and headache (Bosilevac *et al.*, 2009). Throughout enteric fever, a notable fever pattern emerges. It begins with a low-grade fever (>37.5 °C to 38.2 °C) and gradually progresses to a high-grade fever (>38.2 °C to 41.5 °C) in the second week. The fever can persist without appropriate treatment for a month or even longer (Patel *et al.*, 2010). In addition to fever, infected individuals may experience myalgia, bradycardia, hepatomegaly (enlarged liver), splenomegaly (enlarged spleen), and rose blotches on their chest and abdomen (Kuvandik *et al.*, 2009).

On the contrary, non-typhoidal *Salmonella* affects approximately 93.8 million people and causes 160,000 fatalities globally each year (Balasubramanian *et al.*, 2019; Allen *et al.*, 2023). According to the current surveillance report in the US on Non-typhoidal Salmonella (NTS)

infections in humans, most of the isolated serovars are *S. Enteritidis*, *S. Typhimurium*, and *S. Newport*(CDC, 2023), while *S. enteritidis* are the most common serotype recovered from clinical samples in Asia, Europe, and Latin America (Bakhshandeh *et al.*, 2022). The infection is typically self-limiting, and the symptoms usually last about a week (Turgeon *et al.*, 2018). The incubation period ranges from 6 h to 6 days after initial inoculation, and the infection typically lasts for 4 to 7 days (Acheson *et al.*, 2001). Shedding of the bacteria via faeces may last for a month or longer (Pulford *et al.*, 2021). The most common human symptoms include gastroenteritis, accompanied by clinical signs including nausea, vomiting, headache, abdominal pain, non-bloody diarrhoea, and muscle pain (Acheson *et al.*, 2001). The severity of the infections increases in susceptible individuals such as babies and children under the age of five years, immunocompromised patients, and immunocompromised elderly people (Callan *et al.*, 2011). Conditions like cholecystitis, pancreatitis, and appendicitis may manifest and can escalate to severe levels, leading to life-threatening situations like meningitis and sepsis (Ajene *et al.*, 2013). Inadequate fluid balance due to prolonged loss of bodily fluids can lead to dehydration, which may be fatal in newborns and older adults (Ehuwa *et al.*, 2021). Reactive arthritis, a persistent autoimmune joint inflammation, may supervene even after weeks or months of urogenital or digestive tract infections and occurs in around 20% of clinical cases reported in Europe and the US following *Salmonella* infections (Chempp *et al.*, 2019). Furthermore, *Salmonella* infections are implicated in the development of colonic cancer in patients suffering from chronic inflammatory bowel disease (IBD) (Tsuchiya *et al.*, 2018) and are a risk factor for colorectal and gallbladder cancer (Zha *et al.*, 2019).

2.5.5 Prevalence of Typhoid Fever

The global estimate of typhoid fever caused by *Salmonella enterica* serovar typhi (*S. typhi*) was 26.9 million cases, with 217,000 deaths recorded (Buckle *et al.*, 2012). This is especially

worse in the developing nations of the world, where it is a significant contributor to morbidity and mortality (Buckle *et al.*, 2012). This estimate was adjusted for blood culture sensitivity based on a conservative assumption of 50% (Buckle *et al.*, 2012; Breiman *et al.*, 2012). However, only Egypt and South Africa contributed to this estimate for the African continent. A previous global estimate of the burden of typhoid fever indicated that south-central and east-central Asia had the highest incidences of typhoid fever, with more than 100 cases per 100,000 people annually (Marks *et al.*, 2017); Africa was estimated to have a medium incidence (10–100 cases per 100,000) (Marks *et al.*, 2017). The estimated number of typhoid fever cases in low- and middle-income countries in 2010 was 11.9 million (95% confidence interval: 9.9–14.7) cases with 129,000 (75,000–208,000) deaths (Mogasale *et al.*, 2014). The incidence of typhoid fever in Africa is still poorly understood (Antillón *et al.*, 2017). Out-of-sample validation of the model against data from nine Typhoid Fever Surveillance in Africa Program sites showed that the model has mixed success in predicting incidence for locations outside the estimation sample (Antillón *et al.*, 2017).

The paucity of epidemiological data regarding invasive *Salmonella* disease in sub-Saharan Africa led the World Health Organisation (WHO) to call for a continent-wide approach in generating more accurate disease incidence and antimicrobial susceptibility data in 2008 (Baker *et al.*, 2016).

In Nigeria, typhoid fever remains a significant disease because of factors such as increased urbanisation, inadequate supplies of potable water, regional movement of large numbers of immigrant workers, insufficient facilities for processing human waste, overburdened health-care delivery systems, and overuse of antibiotics that contribute to the development and spread of antibiotic-resistant *S. typhi* (Akinyemi *et al.*, 2005; Odion *et al.*, 2022). However, the true incidence of typhoid fever is difficult to evaluate in Nigeria because of the lack of a proper coordinated epidemiological surveillance system. Nevertheless, information on typhoid fever

prevalence has been documented by several researchers in some states in Nigeria, ranging from 0.071% in Oyo to 47.1% in Osun (Akinyemi *et al.*, 2000; Ameh and Opara, 2004; Akinyemi *et al.*, 2005; Fashae *et al.*, 2010; Uyigüe and Osadolor, 2012; Kingsley *et al.*, 2013; Akinwusi *et al.*, 2013; Obaro *et al.*, 2015).

Blood/stool culture-positive typhoidal *Salmonella* remains the pivotal determinant in estimating the actual burden (Akinyemi *et al.*, 2018). Unfortunately, only a few hospitals, specifically referral hospitals, perform blood/stool cultures to diagnose typhoid cases (Akinyemi *et al.*, 2018). The rate of hospitalisation and prolonged illness of patients with typhoid fever in high-burden regions due to treatment failure with empirical therapy is a continuing public health concern (Akinyemi *et al.*, 2018).

The number of cultures performed and data availability across Lagos, Kano, and Abuja varied. In Lagos, *S. typhi* percent positivity ranged between 7% and 18.6% over 23 years (Akinyemi *et al.*, 2018). There was no clear trend in *S. typhi* isolation over time, and rates have remained less than 10% since 2010 (Akinyemi *et al.*, 2018). The highest positivity rates were recorded in 1997 and 2006 at 17.1% and 18.6%, respectively. Serotyping of isolates was not performed in Lagos, and the culture positivity rates included both *S. typhi* and *S. paratyphi* isolates (Akinyemi *et al.*, 2018). The Kano and Abuja sites measured the trend as the number of *S. Typhi*-positive cultures out of the total number of blood cultures performed to yield a percent positivity trend (Akinyemi *et al.*, 2018). From 2013 to 2017, the blood culture confirmed typhoid incidence in Kano ranged from 3.9% to 10.4%. Moreso, in Abuja, the percent positivity of *S. Typhi* ranged from 0.8% to 2.4% across 2008–2017 (Akinyemi *et al.*, 2018). Abuja showed a generally decreasing trend with a slight increase between 2015 and 2017, whereas no clear trend was evident in Kano. *S. Paratyphi* culture positivity remained consistently low in Kano and Abuja at less than 1% throughout the study period (Akinyemi *et al.*, 2018).

Some studies reported a higher prevalence in females than males, with 71.43% in females and 53.97% in males of Karu LGA of Nasarawa State, Nigeria (Abioye *et al.*, 2017). In Ondo State, Nigeria, prevalence was recorded among the age group 41-60 years with 30.58%, sex related males and females with 41.67% and 58.33% and farmers with 12.00% all for *Salmonella typhi* (Ajayi *et al.*, 2015).

Some studies found that enteric fevers are more prevalent in males than females (Okome-Nkoumou *et al.*, 2000; Akinyemi *et al.*, 2005; Reuben *et al.*, 2013; Njoya *et al.*, 2021). But Zailani *et al.* (2004) found no influence of age, sex and social class on the distribution pattern of *S. typhi/paratyphi* in Ile-Ife, south western Nigeria. Nevertheless, a higher prevalence of *Salmonella* infections and carrier rates was observed in individuals aged 18-45years with 19.27%, 46 – 75years with 7.05% and > 75years with 3.27% respectively, for *Salmonella Typhi* infection as recorded by Sadia *et al.* (2020). Also, the authors recorded a higher rate with males (31.65%) than females (27.35%) for typhoid. Typhoid or paratyphoid fevers are usually associated with unstable living conditions and lack of cleanliness among other factors (Okome-Nkoumou *et al.*, 2000). In some parts of the world, infections appear to be associated with seasonal changes (Fares, 2013), although in others, it seems not to be so (Fares, 2013) .

In Nigeria, enteric fevers caused by *S. typhi* and *S. paratyphi* are not only endemic (Tanyigna *et al.*, 1999; Akinyemi *et al.*, 2018) but also constitute a significant socio-medical problem (Zailani *et al.*, 2004), being responsible for many cases of pyrexia of unknown origin (Akinyemi *et al.*, 2005), high morbidity and mortality (Ekenze *et al.*, 2008; Nasir *et al.*, 2008; and Effa and Bukirwa, 2008). Umeh and Agbulu (2009) and Okome-Nkoumou *et al.* (2000) affirmed that typhoid fevers are associated with poor environmental and living conditions, especially in economically poor countries. Communities in financially poor countries lack treated pipe-borne water, toilet facilities, and effective waste disposal systems, and they obtain their drinking water from streams, wells, and rivers Umeh and Agbulu (2009). Unfortunately,

they defecate in nearby bushes and indiscriminately dispose of domestic waste in the environment, at sites which, in some cases, are very close to the same streams and rivers that provide water for the communities Umeh and Agbulu (2009). Some of these communities' inhabitants bathe in the same body of water used for domestic purposes. Contamination of food materials or drinking water could likely be as a result of washed-off faecal matter from the environment, debris and littered garbage during the early rainy season, which runs into streams and wells used as domestic sources of water (Okome-Nkoumou *et al.*, 2000; Umeh and Agbulu, 2009).

In the central area of Benue State, Nigeria, inadequate water supplies are a serious socio-economic problem that has caused the inhabitants to resort to untreated water and polluted streams for domestic water supplies Umeh and Agbulu (2009). Polluted and untreated water supplies are responsible for waterborne infections such as enteric fevers (Umeh and Agbulu, 2009; Adikwu *et al.*, 2018). The authors noted that the epidemiological data on the distribution of typhoid fever in the area seems lacking. More so, their study recorded the overall prevalence of 57.9% for *Salmonella* Typhi infection in the central part of Benue State (Umeh and Agbulu, 2009). Furthermore, some studies showed the distribution pattern of the infections with geographical variation. In Southern Benue State, Nigeria, Adikwu *et al.* (2018) reported an isolation rate of *S. typhi* in the geographical zones as (64.2%) in Oju LGA, followed by Okpokwu LGA (55.5%), and Ado LGA had the least rate of isolation, (29.8%) for *Salmonella* Typhi. There was a significant difference in the isolation rate of *S. typhi* in various study sites within Benue State (Adikwu *et al.*, 2018). They also reported the prevalence rate of *S. typhi* with respect to the age range of ≤ 10 years, with the highest rate of occurrence, 52.7%, followed by the age range 51-60 years with an occurrence rate of 51.4%. The age group >60 years has the lowest rate of occurrence, 36.4%. There was a significant difference in the prevalence rate

of *S. typhi* among various age groups. Males had a higher isolation frequency, 46.8%, than females, 39.6% (Adikwu *et al.*, 2018).

Another study conducted in Abeokuta, South-Western Nigeria, reported a distribution of *Salmonella typhi* with 54.8% positivity in females and 45.2% in males (Okonko *et al.*, 2010). Similarly, a study in Zaria, Northern Nigeria, found that 45.2% of females and 54.8% of males tested positive for *Salmonella typhi*, contributing to an overall prevalence of 69.0% (Gbonjubola *et al.*, 2009). However, a study conducted in Unwana community, Afikpo North, Ebonyi State, southeastern Nigeria, showed 49.4% were positive for *Salmonella enterica* serovar Typhi. The prevalence was statistically significant in relation to sex ($p < 0.05$); while males had a 57% prevalence for *Salmonella enterica serovar typhi*, females had 42%. In the case of treatment, buying medicine from pharmacy shops was common 48%. This was followed by the use of herbal remedies 31%, while an appreciable number adopted 18% the self-treatment method (Odikamnoru *et al.*, 2017).

In Akure, Ondo State at the State Specialist's Hospital an occurrence of 8.23% *Salmonella typhi* was observed in males of age group 10-25 while the least occurrence 3.00% was observed in females of 61 to 80 years of age (Ajayi *et al.*, 2015). At the Federal Medical Centre, Owo, least (17.06%) was observed in males of age group 41-60 while the highest occurrence of *Salmonella typhi* was (41.67%) observed in females of age group 10-25 (Ajayi *et al.*, 2015). Also, the influence of water source on typhoid fever prevalence in Akure State Specialist Hospital, revealed that patients who sourced their water from wells had the highest frequency (76%) while the least frequency, (3%) was observed in undisclosed water source(s) of *Salmonella typhi*. Additionally, at the Federal Medical Centre in Owo, patients who obtained their water from wells exhibited the highest frequency of *Salmonella typhi* infection at 57.64%. In contrast, those with undisclosed water sources had the lowest frequency at 2.35% (Ajayi *et al.*, 2015). Furthermore, among different occupational groups at Don Bosco Clinic in Akure,

civil servants represented the highest infection rate at 41.20%, while artisans and business workers showed the lowest rate at 7.20% (Ajayi *et al.*, 2015). At the State Specialist Hospital in Akure, civil servants again had the highest frequency of *Salmonella typhi* infections at 38%, whereas farmers experienced a lower occurrence rate of 12% (Ajayi *et al.*, 2015). Similarly, within Federal Medical Centre Owo, civil servants showed a high frequency of 43.53%, while artisans and business individuals exhibited a minimal occurrence rate of 10.59% (Ajayi *et al.*, 2015).

A recent study in Nigeria by Akinyemi *et al.* (2018) based on blood culture, the prevalence rate between 1993 and 2017, revealed positivity rates of 7% to 18.6% in Lagos, 3.9% to 10.4% in Kano and 0.8% to 2.4% in Abuja. A slight increase in incidence was observed between 2015 and 2017 in Abuja (Akinyemi *et al.*, 2018). The incidence of typhoid fever in many parts of Nigeria is unknown. This has been made difficult by the absence of efficient epidemiological surveillance, coupled with poor or non-existent databases of infectious diseases (Akinyemi *et al.*, 2018; Grema *et al.*, 2018). Other contributory factors attributed to the spread of typhoid fever in Nigeria include the absence of adequate human waste processing facilities, abuse of antibiotics, lack of portable drinking water, an increase in movement of people and inefficient healthcare delivery systems (Akinyemi *et al.*, 2018). Moreover, it is common to find patients presenting themselves only after patronising unapproved treatment outlets (Akinyemi *et al.*, 2018; Grema *et al.*, 2018). Grema *et al.* (2018) reported that north eastern Nigeria recorded the occurrence of *Salmonella typhi* among age groups 0-9years with 24.3%, 10-19years with 43.2% and a lower rate greater than 40years with 2.7% respectively for typhoid.

A study in Mahama refugee camp, Rwanda, opined that people who had spent more than 6 months in the camp had the risk of contracting typhoid fever nearly three times individuals who had spent less than 6 months in the camp (Nyamusore *et al.*, 2018). On a similar note, Joshua *et al.* (2017) reported in Stefano's IDP camp, Jos, Nigeria, that the longer the stay in

the camp, the more the chances of being exposed to the risk factors for infection. They added that most respondents (78%) said they fell sick at least once, and about 19.1% of respondents said they were down with an illness at least 5 times within the short time they had stayed in the camp. Many interviewed people said they were sick even at that moment even though there was no confirmation as to whether they were sick of typhoid fever. If so many people could be sick within just about 4 months of setting up the camp, it implies that the risk factors are very high and could get even worse.

According to Nyamusore *et al.* (2018), those who completed pre-school education were twice as likely to be infected. They added that poor awareness about typhoid fever was significantly associated with the illness. At the same time, subjects who reported only sometimes washing their hands after using the latrine were twice as likely to develop typhoid fever compared with those who did it regularly. However, the risk of infection with *S. typhi* was also higher in respondents who reported eating food prepared at home (4.06%) and those who used the community market as a source of food daily (23.88%), compared with a community kitchen (Nyamusore *et al.*, 2018). Low awareness about typhoid fever (1.63%) and inconsistent hand washing after use of the latrine (1.78%) were risk factors significantly associated with typhoid fever (Nyamusore *et al.*, 2018). Households near and far from the latrines were surveyed to identify the risk of living near a latrine. The proportion of cases in households near and far from the latrines was 16.8% and 3%, respectively; people living near the toilets were 7.7% more likely to be affected than those living further away (Nyamusore *et al.*, 2018).

2.5.6 Signs and Symptoms

Untreated typhoid fever is classified into four distinct stages, each lasting about a week. The patient becomes exhausted and emaciated (CDC, 2015). However, in the first week, the body temperature rises slowly, and fever fluctuations are seen with relative bradycardia (Faget sign),

malaise, headache, and cough (Kumar and Kumar, 2017). A bloody nose (epistaxis) is seen in a quarter of cases, and abdominal pain is also possible. A decrease in circulating white blood cells (leukopenia) occurs with eosinopenia and relative lymphocytosis; blood cultures are positive for *Salmonella typhi* or *S. paratyphi* (Kumar and Kumar, 2017).. The Widal test is usually negative in the first week (Kumar and Kumar, 2017).

In the second week, the person is often too tired to get up, with high fever in a plateau around 40 °C (104 °F) and bradycardia (sphygmothermic dissociation or Faget sign), classically with a dicrotic pulse wave (Kumar and Kumar, 2017).. Delirium is frequent, often calm, but sometimes agitated. This delirium gives typhoid the nickname of "nervous fever"(Kumar and Kumar, 2017). Rose spots appear on the lower chest and abdomen in around a third of patients. Rhonchi are heard in the lung bases (Kumar and Kumar, 2017).

The abdomen is distended and painful in the right lower quadrant, where borborygmi can be heard (Chang *et al.*, 1999). Diarrhoea can occur in this stage: six to eight stools per day, green, and comparable to pea soup, with a characteristic smell (Buzğan *et al.*, 2007). However, constipation is also frequent. The spleen and liver are enlarged (hepatosplenomegaly) and tender; liver transaminases are elevated. The Widal test is strongly positive, with anti-O and anti-H antibodies (Buzğan *et al.*, 2007). Blood cultures are sometimes positive at this stage. The primary symptom of this fever is that it usually rises in the afternoon up to the first and second week (Chang *et al.*, 1999; Buzğan *et al.*, 2007; Zhang *et al.*, 2022).

In the third week of typhoid fever, several complications can occur: intestinal haemorrhage due to bleeding in congested Peyer's patches; this can be very serious, but is usually not fatal. Intestinal perforation in the distal ileum: This is a severe complication and is frequently fatal (Sharma *et al.*, 2013) . It may occur without alarming symptoms until septicaemia or diffuse peritonitis sets in. Encephalitis, respiratory diseases such as pneumonia and acute bronchitis, and neuropsychiatric symptoms (described as "muttering delirium" or "coma vigil"), with

picking at bedclothes or imaginary objects (Sharma *et al.*, 2013), can all present significant challenges in clinical management, highlighting the need for comprehensive assessment and multi-disciplinary approaches to treatment (Buzğan *et al.*, 2007).

Metastatic abscesses, cholecystitis, endocarditis, and osteitis are severe medical conditions that require prompt diagnosis and intervention. These conditions can result from underlying infections or systemic diseases, leading to significant morbidity if not addressed promptly (Buzğan *et al.*, 2007). The fever is still very high and oscillates very little over 24 hours. Dehydration ensues, and the patient is delirious (typhoid state). One-third of affected individuals develop a macular rash on the trunk. Platelet count goes down slowly, and the risk of bleeding rises. By the end of the third week, the fever starts subsiding (Buzğan *et al.*, 2007).

2.5.7 Complications Associated with Typhoid Fever

When patients of enteric fever are left untreated, their complications mostly tend to occur in the third and fourth weeks of infection, the complication rate being as high as 15% (Buzğan *et al.*, 2007). The most critical complications encountered in clinical practice include gastrointestinal bleeding, intestinal perforation, bronchitis, encephalopathy with confusion as a result of toxæmia, and toxic myocarditis (Buzğan *et al.*, 2007). The authors noted that it is essential for the treating physician to recognize the various complications of enteric fever early and plan their line of management accordingly because several complications need to be managed in a tertiary medical care centre and hence call for timely referral followed by the medical management with appropriate antibiotics along with any surgical interventions if found to be necessary (Buzğan *et al.*, 2007). It was noted that complications from enteric fever are rarely encountered in primary care settings, with some physicians reporting only one or two complicated cases annually. Children and elderly patients are at a higher risk of developing these complications than other age groups (Shrivastava *et al.*, 2014). The authors noted the importance of early recognition of red flag symptoms such as dehydration, toxæmia, altered

mental status, and abdominal rigidity to prevent severe complications and reduce mortality rates (Marchello *et al.*, 2020). Additionally, physicians should be aware of age and gender-specific complications; for instance, bronchitis is more prevalent in children, while intestinal perforations are more common in males (Marchello *et al.*, 2020).

2.5.8 Intestinal Complications

The gastrointestinal complications of enteric fever can range from something as benign as glossitis or an oesophageal ulcer to a problem that can prove fatal, such as intestinal perforation or bleeding. Gastrointestinal bleeding, seen in 10% of patients, is the most typical complication, and in 2% of these cases, there may be a need for blood transfusion (Buzğan *et al.*, 2007). Severe, untreated cases of enteric fever are associated with the development of intestinal as well as extra-intestinal complications. Surgical interventions may be required to manage certain complications involving the small gut, acalculous cholecystitis, perforation of the gall bladder, or gangrene (Pandove *et al.*, 2014). *Salmonella* cholecystitis, a rare complication of *Salmonella typhi* infection, presents with high-grade fever, jaundice and right-sided abdominal pain (Charcot's triad). Tender hepatomegaly and a distended gallbladder are the usual examination findings (Ali *et al.*, 2013).

2.5.9 Intestinal Perforation

The most serious complication of enteric fever is intestinal perforation, as the morbidity and mortality rates associated with it are high (Shrivastava *et al.*, 2014). An indicator of the endemicity of enteric fever is the incidence of intestinal perforation, which varies geographically. The perforation rate ranges between 0.6% and 4.9% worldwide (Shrivastava *et al.*, 2014). The rate of enteric perforation in India is higher, owing to factors such as drought, illiteracy, poverty, and proliferation of bacterial strains that are multidrug resistant (Shrivastava *et al.*, 2014). Youngsters in their second or third decade are more likely to develop this

complication, as they often eat street food, practice poor hand hygiene, and neglect their health (Shrivastava *et al.*, 2014). Ileal perforation is witnessed more frequently in remote areas due to a lack of good medical facilities (Shrivastava *et al.*, 2014). Factors associated with an increased risk of perforation include male gender, leukopenia, short disease duration, presence of bacterial strains that are multidrug resistant, and incomplete antibiotic therapy (Shrivastava *et al.*, 2014). The surgeon usually finds it difficult to manage such cases, as the patients present themselves or are diagnosed late after being initially treated by quacks (Shrivastava *et al.*, 2014). The indiscriminate use of glucocorticoids, lack of awareness, poverty, and poor medical and transportation facilities complicate matters further (Shrivastava *et al.*, 2014). While the mortality associated with enteric fever related perforation ranges from 0 to 2% in the developed nations, it is much higher (9 to 22%) in the developing countries, due to reasons such as the want of intensive care, poor resuscitation facilities, antibiotic resistance, regional taboos, delay in surgery, more perforations, faecal peritonitis, and increased disease duration (Shrivastava *et al.*, 2014). It is advisable to manage such cases with timely and appropriate surgical interventions, safe anaesthesia, proper operative care, and wide-spectrum antibiotics with low resistance (Shrivastava *et al.*, 2014).

2.5.10 Gastrointestinal Bleeding

Gastrointestinal bleeding generally occurs in the third week as a result of ulceration, due to necrosis in the small bowel. About 20% of the patients with enteric fever test positive for the presence of occult blood in their stool (Buzgan *et al.*, 2007). Massive bleeding is very rarely seen, although gross bleeding may be observed in 10% of the patients (Buzgan *et al.*, 2007). The first signs of bleeding are a sudden decrease in blood pressure and body temperature, the former dropping to 80-90 mmHg or even lower, and the patient going into a state of shock. Before chloramphenicol was discovered and used to treat enteric fever, the incidence rate of

perforations was higher (Buzgan *et al.*, 2007). While perforations usually occur in the third week of infection, with the distal part of the ileum being involved most of the time, they can occur even in the first 2 weeks in fulminant cases (Buzgan *et al.*, 2007). Bleeding in the gastrointestinal tract can occur in the form of either occult blood in stool or melena (Kumar and Kumar, 2017; Reddy *et al.*, 2010). Enteric fever happens due to erosion of Peyer's patches into an intestinal vessel. On colonoscopy, it is seen that the terminal ileum is the most commonly involved site, followed by the ileocecal valve, the ascending colon, and the transverse colon. The ulcers in such cases are usually multiple and punched out in appearance, and their margins are slightly elevated (Reddy *et al.*, 2010; Kumar and Kumar, 2017).

2.5.11 Extra-Intestinal Complications

S. typhi infection may sometimes manifest with extra-intestinal infectious complications, which can involve various systems and organs of the body. It is essential to recognise these complications, specifically in patients who have just been to an endemic region and are returning home. This can help to prevent a delay in the diagnosis of enteric fever (Feasey *et al.*, 2012; Bhandari *et al.*, 2024).

2.5.12 Haematological Complications

Various haematological complications have been witnessed in patients suffering from enteric fever, such as haemolytic anaemia, haemolytic uraemic syndrome (a condition that affects the kidney and blood clotting), and disseminated intravascular coagulation (DIC) (Buzgan *et al.*, 2007). The haemoglobin level and platelet count may be normal or low in these patients, but their leukocyte count can be low, normal, or high. Generally, there is evidence of eosinopenia, and prolongation of the prothrombin time is also detected (Buzgan *et al.*, 2007).

2.5.13 Neurological Complications

The neurological complication rates in enteric fever vary (5-35%) following the extent of drug resistance. Meningismus and acute confusion are the most frequent manifestations. Confusion may have an intermittent character and appear as apathy in many patients (Buzğan *et al.*, 2007). An Indian study found that 27.1% of the patients suffering from enteric fever had neurological manifestations, and the mortality rate was 6.35% (Buzğan *et al.*, 2007). This only shows how vital the early detection of enteric fever (Buzğan *et al.*, 2007).

2.5.14 Diagnosis of Typhoid Fever

Diagnosis is made by any blood, bone marrow or stool cultures along with the Widal test (demonstration of antibodies against *Salmonella* antigens O-somatic and H-flagellar). In epidemics and less wealthy countries, after excluding malaria, dysentery, or pneumonia, a therapeutic trial time with chloramphenicol is generally undertaken while awaiting the results of the Widal test and cultures of the blood and stool (Maidabara *et al.*, 2021).

The Widal test is time-consuming and prone to significant false-positive results (Mehmood *et al.*, 2015). The test may also be falsely negative in the early course of illness. However, unlike the Typhidot test, the Widal test quantifies the specimen with titres. Typhidot is a medical test consisting of a dot ELISA kit that detects IgM and IgG antibodies against the outer membrane protein (OMP) of the *Salmonella typhi*. The typhidot test becomes positive within 2–3 days of infection and separately identifies IgM and IgG antibodies. The test is based on specific IgM and IgG antibodies to a particular 50 Kd OMP antigen, which is impregnated on nitrocellulose strips (Mehmood *et al.*, 2015). IgM shows recent infection, whereas IgG signifies remote infection. The most important limitation of this test is that it is not quantitative, and the result is only positive or negative (Mehmood *et al.*, 2015).

Polymerase chain reaction (PCR) is a promising test that is as sensitive as blood/stool culture but less specific (Bhutta *et al.*, 2006). It has been found to be >90% sensitive and relatively

simple to perform. Moreover, it can amplify DNA from dead or unculturable bacteria, providing an additional sensitivity benefit (Bhutta *et al.*, 2006). Without any validated PCR test, the in-house systems currently in use are open to differing interpretation and do not meet the rigorous quality control standards for worldwide acceptance. Experts observed that PCR might not satisfy the criteria of a ‘gold standard’ for the diagnosis of enteric fever in terms of sensitivity and specificity, since it does not cover all the antigens of the disease (Kim *et al.*, 2023). Only one PCR test picks up antigens 14, 15, and 18. Moreover, this test is not available in remote and peripheral areas. Some authors, observed that PCR is hardly ever used to diagnose enteric fever (Kim *et al.*, 2023).

A nested polymerase chain reaction is more sensitive than PCR and uses H1-d primers to amplify specific genes of *S. typhi* in patients' blood (Prakash *et al.*, 2005). It involves two rounds of PCR using two primers with different sequences within the H1-d flagellin gene of *S. typhi*, offering the best sensitivity and specificity (Prakash *et al.*, 2005). It is a promising rapid diagnosis test, potentially replacing blood culture as the new gold standard (Bhutta and Dewraj, 2006; Afshari *et al.*, 2012). It is so sensitive that it can detect even one bacterium in a given sample within a few hours (Prakash *et al.*, 2005; Afshari *et al.*, 2012). Due to its high sensitivity and specificity, nested PCR can help diagnose clinically suspected, culture-negative cases of enteric fever (Khan *et al.*, 2012).

2.5.14.2 Molecular Survey of *Salmonella typhi*

2.5.14.1.1 PCR (Polymerase Chain Reaction)

PCR (Polymerase Chain Reaction) is a laboratory technique to amplify specific DNA sequences. According to Valones *et al.* (2009), it is a widely used molecular biology tool for detecting and identifying microorganisms (bacteria, viruses, fungi); analysing genetic material (DNA or RNA); cloning genes; diagnosing genetic disorders and forensic analysis. More so, the PCR process involves: denaturation (heating DNA to separate strands), annealing (adding

primers to the target DNA sequence), extension (synthesising new DNA strands using polymerase enzyme) and repeat (cycles of denaturation, annealing, and extension).

This process amplifies the target DNA sequence, which allows the detection of rare or hard-to-find DNA sequences, analysis of small DNA samples, rapid identification of microorganisms, and study of gene expression and regulation. Souzaa *et al.* (2013) opined that PCR has revolutionised molecular biology, enabling scientists to identify genetic disorders, develop genetic tests, study evolutionary relationships, analyse ancient DNA, and detect and track infectious diseases. They added that PCR can detect and identify the bacteria in food, water, or clinical samples, aiding in rapid diagnosis and public health response.

According to Souzaa *et al.* (2013) procedures for performing PCR on *Salmonella typhi* virulent genes involves isolation of DNA from a *Salmonella typhi* sample; designing primers that target the virulent genes of interest; preparing a reaction mixture containing DNA, primers, dNTPs, and Taq polymerase; performing PCR amplification using a thermal cycler with specific temperature profiles; analyzing the amplified DNA using agarose gel electrophoresis or real-time PCR and interpreting the results based on the presence or absence of the targeted virulent genes. They added that PCR conditions and primer sequences may vary depending on the targeted genes and experimental design

2.5.15 Prevention and Control

Primary and secondary strategies are usually adopted to prevent enteric fever and its complications. While secondary prevention stratagems attempt to reduce the morbidity and mortality associated with the disease, the primary prevention approaches entail measures that help to avoid getting infected or at least prevent overt clinical manifestations of the disease (Levine and Lepage, 2005).

2.5.16 Primary Prevention

Environmental measures to ensure the supply of treated water along with proper sanitation, identification of chronic carriers of enteric fever to break the chain of transmission of the disease, and vaccination of susceptible hosts to make them immune to the organism constitute the three main approaches for primary prevention (Bhandari *et al.*, 2024). Unfortunately, owing to cost implications, many parts of developing countries continue to have poor sanitation facilities and drinking water that is not potable. Chlorination of drinking water at home should be advocated. The treated water should preferably be stored in a narrow-mouthed vessel and drawn out by tilting the container or using a tap to avoid contamination (Bhandari *et al.*, 2024). People should be encouraged to use latrines at home, and waste disposal must be done in closed sewerage systems. Raw fruits and vegetables should be washed thoroughly, and the latter should preferably be cooked before consumption (Bhandari *et al.*, 2024).

Practices should be adopted in the storage and preparation of milk. The public health department should do product studies to ascertain the quality of drinking water supplied to the community (Bhandari *et al.*, 2024). Hospital surveillance can help evaluate such interventions' effectiveness (Barac *et al.*, 2018).

2.5.16.1 Five key steps to safer food

Keep clean

Dangerous microorganisms are widely found in soil, water, animals, and people. These are carried on the hands, clothes used for wiping, utensils, and cutting boards, and the slightest contact can transfer them to food and cause foodborne diseases. Hands should be washed before handling food, during food preparation, and after using the toilet. All surfaces and equipment used for food preparation should be washed and sanitised. Kitchen areas and food should be protected from insects, pests, and other animals (WHO, 2006).

Separate raw and cooked Food

Raw food, especially meat, poultry, and seafood, and their juices, can contain pathogenic microorganisms that might be transferred onto other foods during food preparation and storage.

Raw meat, poultry, and seafood should be separated from other foods. Equipment and utensils such as knives and cutting boards should be kept separate for handling raw foods. Food should be stored in containers to avoid contact between raw and prepared foods (WHO, 2006).

Cook thoroughly

Cooking food to a temperature of 70 °C kills almost all pathogenic microorganisms and ensures it is safe for consumption. Foods that require special attention include minced meats, rolled roasts, large joints of meat, and whole poultry (WHO, 2006). Food, especially meat, poultry, eggs, and seafood, should be cooked thoroughly. Soups and stews should be boiled till 70 °C. (WHO, 2006).

Keep at safe Temperatures.

Microorganisms can multiply very quickly if food is stored at room temperature. By keeping the temperature below 5 °C or above 60 °C, the growth of microorganisms is slowed down or stopped (WHO, 2006). Some pathogenic microorganisms still grow below 5°C. Cooked foods should not be kept at room temperature for more than two hours, and should be refrigerated promptly. Cooked and perishable foods should be preserved preferably below 5 °C. Cooked food should be kept piping hot (more than 60 °C) before serving. Food should not be refrigerated too long, and frozen food should not be thawed at room temperature (WHO, 2006).

Safe water and raw Materials

Portable water should be used or treated to make it safe. Fresh and wholesome foods and pasteurised milk should be consumed. Fruits and vegetables should be washed properly, especially if eaten raw. Raw materials, including water and ice, may be contaminated with pathogenic microorganisms and chemicals. Toxic chemicals may be formed in damaged and mouldy foods. Care in selecting raw materials and simple measures such as washing and peeling may reduce the risk. Identifying and treating chronic carriers: Chronic carriers of the pathogen responsible for the development of enteric fever can cause localised or sporadic cases

of the disease, particularly if they handle food consumed by others. Once identified, they should be taken away from the space. Since nearly 90% of chronic carriers demonstrate high titres of serum Vi antibodies (that is, the presence of antibodies in a person's blood serum that specifically target the "Vi antigen," a capsular polysaccharide found on the surface of the bacteria *Salmonella typhi*, the causative agent of typhoid fever, serological tests to detect the same can be helpful in screening (WHO, 2018). Stool cultures can also be done repeatedly after inducing strong purgation. Several weeks of oral ciprofloxacin or norfloxacin therapy have been shown to eradicate the carrier state in up to 90% of the cases, without the need for cholecystectomy, which used to be advocated in the past (WHO, 2018).

2.5.16.2 Vaccination

The use of affordable vaccines seems to be the most lucrative prophylactic intervention. Despite the early attempts to produce resistance against typhoid fever with parenteral vaccination by Pfeiffer and Kolle in 1896, and with oral vaccines by Carroll in 1904, it was not until the 1950s that typhoid vaccine efficacy was prospectively evaluated in both well-controlled field trials and human volunteer studies (Bockemühl, 1983). Among the parenteral whole cell preparations, the acetone-inactivated and heat-phenol-killed vaccines, respectively, demonstrated an efficacy of 60-90% for 3-5 years, and have received most attention (Bockemühl, 1983). Oral killed typhoid vaccines have enjoyed popularity for many years, but their effectiveness has never been proven under statistically and epidemiologically controlled conditions (Khan *et al.*, 2017). Vaccination against typhoid as a routine is not required in countries with high sanitation standards (Khan *et al.*, 2017). However, its administration is recommended for individuals travelling to areas where typhoid is endemic, people in close contact with a chronic typhoid carrier, and laboratory staff handling samples containing *S. typhi* bacteria. The standard old typhoid vaccines included a monovalent vaccine (containing only *S. typhi*), a bivalent vaccine (containing *S. typhi* and *S. paratyphi A*) and the traditional typhoid

paratyphoid A and B (TAB) vaccine (containing *S. typhi*, *S. paratyphi A*, and *S. paratyphi B* (Zein, 2017).

As of now, only two typhoid vaccines are licensed for use for the prevention of typhoid (Milligan *et al.*, 2018): the live, oral Ty21a vaccine (sold as Vivotif by Crucell Switzerland AG) and the injectable typhoid polysaccharide vaccine (sold as Typhim Vi by Sanofi Pasteur and Typherix by Glaxo SmithKline). Both are efficacious and recommended for travellers to areas where typhoid is endemic. Boosters are recommended every five years for the oral vaccine and every two years for the injectable form (Camp and Shorman, 2023). An older, killed-whole-cell vaccine is still used in countries where the newer preparations are unavailable. Still, this vaccine is no longer recommended for use because it has a higher rate of side effects (mainly pain and inflammation at the site of the injection) (Milligan *et al.*, 2018). To help decrease rates of typhoid fever in developing nations, the World Health Organisation (WHO) endorsed the use of a vaccination program starting in 1999 (Bilcke *et al.*, 2019). Vaccinations have proven to be a great way to control outbreaks in high-incident areas; it is also very cost-effective. Vaccination prices are usually low, less than US\$1 per dose. Because the price is low, poverty-stricken communities are more willing to take advantage of the vaccinations. Although vaccine programs for typhoid have proven effective, they alone cannot eliminate typhoid fever. Combining the use of vaccines and increasing public health efforts is the only proven way to control this disease (Bilcke *et al.*, 2019).

Since the 1990s, the World Health Organisation has recommended two typhoid fever vaccines. The ViPS vaccine is given via injection (intramuscular) while the Ty21a is taken through capsules (oral). It is recommended that only people 2 years or older be vaccinated with the ViPS vaccine, and a revaccination after 2–3 years with a 55–72% vaccine efficacy is required. The alternative Ty21a vaccine is recommended for people 5 years or older, and has a 5-7-year

duration with a 51–67% vaccine efficacy. The two different vaccines have been proven to be a safe and effective treatment for epidemic disease control in multiple regions (WHO, 2023).

2.5.17 Secondary Prevention

Secondary prevention aims to decrease the clinical severity of enteric fever and its complications, so that it doesn't prove to be fatal. The most important component of secondary prevention is the judicious use of efficacious antimicrobials early in the disease. When prescribing antibiotics for patients who have acquired the infection from regions where *S. typhi* species are multidrug resistant, it is advisable to select the drug based on the most current reviews (Levine and Lepage, 2005).

2.5.17.1 Treatment

2.5.17.1.1 Oral Rehydration Therapy

The rediscovery of oral rehydration therapy in the 1960s provided a simple way to prevent many deaths from diarrheal diseases in general (Parry and Beeching, 2009).

2.5.17.1.2 Surgery

Surgery is usually indicated in cases of intestinal perforation. Most surgeons prefer simple closure of the perforation with drainage of the peritoneum. Small-bowel resection is indicated for patients with multiple perforations (WHO, 2017). The gallbladder should be resected if antibiotic treatment fails to eradicate the hepatobiliary carriage. Cholecystectomy does not always successfully eliminate the carrier state because of persisting hepatic infection (WHO, 2017).

2.6 Antibiotic Resistance Profile of *Salmonella* Species

This spectrum of activity, which includes the strains that the antibiotic can inhibit, does not vary qualitatively, although the percentages of susceptible bacterial strains in a species may change over time with the development of resistance. The range of bacteria that an antibiotic affects can be divided into narrow and broad spectrum. Narrow-spectrum antibiotics act against

a limited group of Gram-positive or Gram-negative bacteria. For example, sodium fusidate only acts against Staphylococcal species (Muteeb *et al.*, 2023). Broad-spectrum antibiotics act against Gram-positive and Gram-negative bacteria, for example, amoxicillin (Muteeb *et al.*, 2023).

A broad-spectrum antibiotic acts against both Gram-positive and Gram-negative bacteria, in contrast to a narrow-spectrum antibiotic, which is effective against specific families of bacteria. An example of a commonly used broad-spectrum antibiotic is ampicillin. Broad-spectrum antibiotics are appropriately used in the following medical situations: empirically (i.e., based on the practitioner's experience), before the formal identification of the causative bacteria, and when there is a wide range of possible illnesses and a potentially serious illness would result if treatment is delayed (Sohana *et al.*, 2023). This occurs, for example, in meningitis, where the patient can become fatally ill within hours if broad-spectrum antibiotics are not initiated (Muteeb *et al.*, 2023). Broad spectrum antibiotics are also used for drug resistant bacteria that do not respond to other, more narrow spectrum antibiotics and in the case of super infections, where there are multiple types of bacteria causing illness, thus warranting either a broad-spectrum antibiotic or combination antibiotic therapy (Fred *et al.*, 1996; Song *et al.*, 2018; Muteeb *et al.*, 2023) and Sohana *et al.*, 2023).

Gawey and Czaja (2017) listed some examples of broad antibiotics classes which are as follows; class-Penicillins consist of Ampicillin, Amoxicillin, and Augmentin, class-Cephalosporins consist of Ceftriaxone and Cefepime), class-Tetracyclines consist of Doxycycline, Minocycline, and tetracycline); class-Macrolides consist of Azithromycin, Clarithromycin, Chloramphenicol and Erythromycin), class-Fluoroquinolones consist of Ciprofloxacin, and Levofloxacin, and class-Aminoglycosides consist of Gentamicin, Tobramycin, and Streptomycins, class-sulfonamides consist of sulfamethoxazole or Septrin (Gawey and Czaja (2017)).

The emergence of antimicrobial resistance in *Salmonella* strains is a serious health problem worldwide. Years ago, the first incidence of *Salmonella* resistance to a single antibiotic, chloramphenicol, was reported (Montville *et al.*, 2008). Since then, the isolation frequency of *Salmonella* strains with resistance towards one or more antimicrobial agents has increased in many countries, including the USA, UK, Saudi Arabia and Africa. Antimicrobial agents such as ampicillin, chloramphenicol and tetracycline are used as the traditional first-line treatments for *Salmonella* infections. *Salmonella* species resistant towards these agents are referred to as multidrug-resistant strains (MDR) (Montville *et al.*, 2008).

For many years, the phenotypic trait of multidrug-resistant *Salmonella* was widely distributed among *S. Typhi* and, at a lower rate, among *S. paratyphi* (Montville *et al.*, 2008).. Africa and Asia are two continents with a high isolation frequency of *S. Typhi* displaying a multidrug-resistant phenotype (Montville *et al.*, 2008). With the emergence of resistance towards traditional isolates that are resistant to nalidixic acid and ceftriaxone, it has become increasingly essential for healthcare professionals to explore alternative treatment options and develop new strategies for managing infections, as well as to invest in research focused on understanding the mechanisms behind this resistance to mitigate its impact on public health (Crump *et al.*, 2011). This phenomenon has raised concern among public health authorities regarding clinical management and infection prevention (Crump *et al.*, 2011). A surveillance study on 135,000 clinical isolates of Non-typhoidal *Salmonella* (NTS) was conducted in Europe from 2000 to 2004, and the data showed that 15% of the isolates displayed MDR phenotypes and 20% of the isolates were resistant to nalidixic acid (Meakins *et al.*, 2008).

The identification of antimicrobial-resistant *Salmonella* in food has raised concerns about the treatment of foodborne Salmonellosis, especially the development of ceftriaxone and ciprofloxacin-resistant *Salmonella*, as these are important in treating *Salmonella* infections in children and adults (Yoke-Kqueen *et al.*, 2008). The extent of global food trade and the

intercontinental transmission of resistant *Salmonella* via foods underscore the potential impact that local geographical agricultural antimicrobial use may have on consumer health worldwide (Yoke-Kqueen *et al.*, 2008).

Conventional antimicrobial agents, such as ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole, had been the drug of choice in treating Salmonellosis before the 1980s. However, multidrug resistance, with rates of resistance to these antimicrobial agents of more than 50% has been reported in many areas of the world (Chiu *et al.*, 2002). Extended-spectrum cephalosporins and fluoroquinolones have been increasingly reported after 1991 (Chiu *et al.*, 2002). The possible emergence and spread of *Salmonella* strains resistant to antibiotics commonly used as treatment are concerns, because these infections can be invasive and difficult to treat with the drugs of choice for invasive *Salmonella* diseases (Chiu *et al.*, 2002).

A study was undertaken in Bio Merieux, France, to compare the changing trends of the antibiogram of *Salmonella enterica* serovar Typhi and *Salmonella enterica* serovar paratyphi A isolates. A total of 80 isolates of *Salmonella* were obtained from blood cultures during 2001-2004. Sixty isolates were identified as *Salmonella enterica* serovar Typhi, and 20 were identified as *Salmonella enterica* serovar paratyphi A (Lakshmi *et al.*, 2006). Over 67% of *S. typhi* and 80% of *S. paratyphi* A isolates were sensitive to chloramphenicol. Sensitivity of *S. typhi* isolates to cephalosporins was found to have increased from 2001 to 2004, while that of *S. paratyphi* A showed a decline (Lakshmi *et al.*, 2006).

A total of 464 *Salmonella* Typhi were isolated from the blood of patients suspected of having enteric fever in the Calcutta School of Medicine from 1991 to 2003 (Gaind *et al.*, 2006). The 464 isolates were susceptible to Amikacin and Gentamycin. Both antibiotics showed bactericidal activity at concentrations of 2µg/ml after incubation for 6 hrs (Gaind *et al.*, 2006). Previously, there has been molecular characterisation of *Salmonella typhi* with complete resistance to ciprofloxacin (Gaind *et al.*, 2006). According to Gaind *et al.* (2006), the presence

of a plasmid-borne integron in ciprofloxacin-resistant *S. typhi* may lead to a situation of untreatable enteric fever.

In another study, all the *Salmonella typhi* isolates were less sensitive to ciprofloxacin, but no resistance was seen, whereas 76% of the same isolates showed resistance to nalidixic acid (Lakshmi *et al.*, 2006). This work showed that nalidixic acid-resistant isolates had decreased susceptibility to ciprofloxacin (Stevenson *et al.*, 2007). Similar study was carried out by Serpil *et al.* (2006), which revealed the same pattern of results. Changing trends of antibiogram of *S. typhi* and *S. paratyphi A* suggests that 67% of *S. typhi* in a study were sensitive to chloramphenicol, and the sensitivity of *S. typhi* isolates to cephalosporin was found to have increased from 2001 to 2004 in Indian (Lakshmi *et al.*, 2006).

Resistance to amoxicillin, chloramphenicol, ampicillin and co-trimoxazole was significantly high in a study conducted at Kasturba Medical College Asia. Plasmid-mediated multidrug resistance to ampicillin, chloramphenicol and co-trimoxazole has been described in various parts of Asia (Bhutta, 2006).

In Nigeria, Kabiru *et al.* (2018) recorded *S. typhi* isolated from Abuja showed 0% resistance to ceftazidime, ofloxacin, ciprofloxacin, and ceftriaxone, whereas just less than 50% of isolates were resistant to amoxicillin, augmentin, and chloramphenicol. Also, in Kano, antimicrobial resistance results were previously described. The prevalence of resistance to ampicillin, chloramphenicol, and cotrimoxazole was 38.11%, with regional differences in susceptibility to different antibiotics but a high prevalence of resistance to readily available oral antibiotics (Obaro *et al.*, 2015).

2.7 Spread of Resistance

Antimicrobial resistance arises in several ways, including acquiring resistance genes via horizontal gene transfer and selecting resistant variants in the population. In the case of *Salmonella*, the situation is more complicated because the use of antibiotics for therapeutic

or preventive purposes in veterinary medicine and as growth promoters in animal feed may promote the emergence of resistance, thereby presenting a potential risk to public health from zoonotic infections (McEwen, 2002; Song *et al.*, 2018; Sohana *et al.*, 2023). Although the transmission route of antimicrobial-resistant *Salmonellae* is complex, evidence in many epidemiological and laboratory studies suggests that the primary source of antimicrobial-resistant *Salmonella* infection is foods of animal origin. There are several reasons to conclude that antibiotic resistance among human *Salmonella* isolates results from antimicrobial agents in food animal production (Parisi *et al.*, 2020). The trace back from foodborne disease outbreaks has shown food animals as the ultimate source of infection, antimicrobial resistance patterns and genetic fingerprints have shown a strong correlation between animal and human *Salmonella*, and antibiotic resistance in human *Salmonella* isolates have shown more correlation with antibiotic use in animals than with antibiotic use in humans (Aminov, 2010; Parisi *et al.*, 2020).

The prevalence of AMR in *Salmonella* can vary significantly by region, with some areas having higher rates of AMR than others. For example, studies have shown that the prevalence of AMR in *Salmonella* isolates from animals and food in the United States is generally low, with most isolates being susceptible to a range of antimicrobial drugs (WHO, 2018).

Some strains of *Salmonella* have developed resistance to certain antibiotics, making it more difficult to treat infections (Browne *et al.*, 2020; Marchello *et al.*, 2020; Littmann *et al.*, 2020). These are known as antibiotic-resistant *Salmonella* or antimicrobial-resistant (AMR) *Salmonella*. AMR is a growing global health concern because it can make it more difficult to effectively treat bacterial infections, including those caused by *Salmonella* (Marchello *et al.*, 2020; Charani *et al.*, 2022; Rodrigues *et al.*, 2020). The overuse and misuse of antibiotics are major contributing factors to the development of AMR in bacteria (WHO, 2020 and Charani *et al.*, 2022). Antibiotic resistance in *Salmonella* has a long history (Aminov,

2010). *Salmonella* has been known to cause illness for over a century, and antibiotics have been used to treat *Salmonella* infections since the 1940s (Aminov, 2010; Davies and Davies, 2010). However, as with many other bacteria species, *Salmonella* has developed resistance to many antibiotics used for clinical treatment (Prestinaci *et al.*, 2015). More so, one of the first reported cases of antibiotic resistance in *Salmonella* was in the 1950s, when strains of *Salmonella* resistant to streptomycin were identified (Aminov, 2010; Davies and Davies, 2010). Since then, *Salmonella*'s resistance to other antibiotics, such as tetracycline and ampicillin, has also been reported (Jajere, 2019; Ingle *et al.*, 2021), and some strains are now resistant to multiple antimicrobial drugs or antibiotics.

Some common antimicrobial resistance (AMR) genes found in *Salmonella* include the following:

1. ***blaTEM* gene**: encodes for beta-lactamase, an enzyme that hydrolyses beta-lactams such as ampicillin, penicillins, and cephalosporins (Nair *et al.*, 2019).
2. ***sulI* and *sul2* genes**: encode for sulfonamide-resistant dihydropteroate synthases, which, when expressed, can inactivate sulfonamide antibiotics (Wang *et al.*, 2019; Pavelquesi *et al.*, 2021).
3. ***tetA*, *tetC*, and *tetB* genes**: encode for tetracycline efflux pumps, which can pump tetracycline antibiotics out of the bacterial cell, making the bacteria resistant to these drugs (Adesiji *et al.*, 2014; Pavelquesi *et al.*, 2021).
4. ***qnr* gene encodes**: for the quinolone resistance-determining region, which can make *Salmonella* resistant to quinolone antibiotics (Pribul *et al.*, 2016; Song *et al.*, 2018; Marchello *et al.*, 2020).
5. ***mcr* gene encodes**: phosphoethanolamine transferase, which transfers the phosphatidyl-ethanolamine residue to the lipid A of the cell membrane and provides resistance to

colistin, last-resort antibiotics effective against multidrug-resistant *Salmonella* (Monte *et al.*, 2019; Vázquez *et al.*, 2021).

The presence of an AMR gene does not necessarily mean that the bacterium will be resistant to the use of the antimicrobial drug (Levy and Marshall, 2004; Prestinaci *et al.*, 2015). The ability of bacteria to survive antimicrobial treatment depends on many factors, including the specific strain of bacteria, the type and dosage of the drug, and the presence of other AMR genes (WHO, 2020; Prestinaci *et al.*, 2015).

Recently, extensively drug-resistant (XDR) or more commonly known as multiple-drug resistant (MDR) *Salmonella* types, that is, *Salmonella* resistance to a wide range of antimicrobial drugs including many antibiotics that are typically used to treat *Salmonella* infections, have been on the rise, especially in developing countries (WHO, 2020; Wang *et al.*, 2022). XDR *Salmonella* is of particular concern because it can be more challenging to treat and may lead to more severe or even fatal infections (WHO, 2020). XDR *Salmonella* can be transmitted through contaminated food, water, or surfaces and through contact with infected animals or people (Levy *et al.*, 2001). XDR phenotype in *Salmonella* arises through acquiring multiple AMR genes, which enables the bacteria to survive exposure to multiple drugs (Levy *et al.*, 2001; Levy *et al.*, 2004). The specific AMR genes present in XDR *Salmonella* can vary, but they may include genes that confer resistance to antibiotics such as ciprofloxacin, amoxicillin, and ceftriaxone drugs (Levy *et al.*, 2001). China has recently reported the first case of a waterborne outbreak caused by XDR *S. typhi* in Beijing (Wang *et al.*, 2022). Similarly, the World Health Organisation (WHO) recorded about 5274 cases of XDR typhoid fever in Pakistan from November 2016 to December 2018 (WHO, 2018).

However, the prevalence of AMR *Salmonella* isolates from humans in the United States is higher, with some studies reporting resistance rates as high as 30–40% (Charani *et al.*, 2022).

In other parts of the world, the prevalence of AMR *Salmonella* may be higher. For example, studies have shown that the prevalence of AMR *Salmonella* isolates from humans in some European countries is as high as 50–60% (WHO,2022). The distribution of AMR *Salmonella* in developing countries can vary significantly depending on the specific country and region. However, in general, the prevalence of AMR in *Salmonella* in developing countries tends to be higher than in developed countries (WHO, 2020). Several factors may contribute to the higher prevalence of AMR in *Salmonella* in developing countries, including the following (WHO, 2018):

1. Limited access to clean water and sanitation: In some developing countries, access to clean water and adequate sanitation facilities is limited, increasing the risk of bacterial infections, including salmonellosis and the spread of AMR.
2. Poor infection control practices: In certain countries, infection control practices are inadequate, which can increase the risk of *Salmonella* infections and the spread of AMR.
3. High use of antimicrobial drugs in animals: In some developing countries, there is high and uncontrolled use of antimicrobial drugs in animals, contributing to the development and spread of AMR.
4. Limited surveillance and monitoring: In developing countries, there are usually limited surveillance and monitoring systems for the presence of *Salmonella* in food and food-related environments, leading to increased prevalence of infections, including *Salmonella* infections and the spread of AMR *Salmonella*.

2.7.1 Antimicrobial susceptibility test

Antimicrobial susceptibility tests measure the ability of an antimicrobial agent to inhibit bacterial growth *in vitro*. This ability may be estimated by either the dilution or diffusion methods (WHO, 2003). The concept of sensitivity testing has remained remarkably constant

since it was first introduced on a broad scale almost 40 years ago (WHO, 2003). Four sensitivity testing methods are common: agar diffusion, agar incorporation, broth macrodilution and broth microdilution. According to Balouiri *et al.* (2016), agar diffusion is most commonly used in most laboratories as the routine method. The zones of inhibition of growth due to the diffused antimicrobial agents are measured and related to those of known “sensitive” or “resistant” organisms Balouiri *et al.* (2016). The disk diffusion sensitivity test is performed on agar plates. This consists of a small disk of filter paper, pre-impregnated with a defined quantity of antibiotic, which is placed on the surface of an agar plate that has already been inoculated with a suspension of the isolate. The antibiotic diffuses from the disk into the agar, along a concentration gradient, as the plates were incubated for 18–24 hours Balouiri *et al.* (2016). According to CLSI (2020), if the bacterial strain is sensitive to the antibiotic, a zone of inhibition (no growth) occurs around the disk. The diameter of the zone depends on several factors, which among others include: the concentration of antibiotics within the disk, the degree of susceptibility of the bacteria to the antibiotic, the physicochemical properties of the antibiotic, the depth of the agar plate and the concentration of bacteria in the inoculum Balouiri *et al.* (2016).

2.8 Epidemiology of *Salmonella typhi*

In recent years, there have been some changes in the epidemiological patterns of typhoid and related diseases in third-world countries, involving most of the countries in Africa, Asia and Latin America. More than 20 million cases a year occur in the hygienically compromised areas of developing countries, and out of them, Pakistan, India, and Bangladesh together bear the brunt of the attack, accounting for 85% of the cases occurring globally (Paul and Bandyopadhyay, 2017). The highest age-specific rates of typhoid and allied diseases are borne by children and young adults (Paul and Bandyopadhyay, 2017). Studies in Pakistan and Bangladesh show that the mean age of patients affected by typhoid fever is 7 years (Paul and

Bandyopadhyay, 2017). Typhoid is found to be a seasonal disease; in the monsoon itself, there is an occurrence of 45% of the total annual reported cases (Paul and Bandyopadhyay, 2017). In South Asia, the disease occurrence is highest from July to October because of heavy rainfall (Paul and Bandyopadhyay, 2017).

Enteric fever is endemic in many regions of the African and Asian continents, as well as countries such as Europe, South and Central America, and the Middle East. The incidence of enteric fever in the USA and some European countries is low, with the total number of *Salmonella* cases being less than 10 per 100,000 annually (Eng *et al.*, 2015). Most of the cases reported in these countries are related to travel, with the disease being imported by foreigners or travellers returning from Africa, India or Pakistan (Muresu *et al.*, 2020). Israel has a very low incidence of enteric fever, reducing from 0.42 to 0.23 cases per 100,000 (Muresu *et al.*, 2020).

However, the pattern of the causative organism reflects an increasing number of cases of *S. paratyphi*, with this organism being isolated from 57.4% of the patients reported with enteric fever in Israel (Meltzer *et al.*, 2006). This matches the worldwide increase in infection caused by *S. paratyphi*, especially in Asian countries where these strains are responsible for more than 50% of the incidence of enteric fever (Kim *et al.*, 2022).

The increase in *S. paratyphi* infection raises concern over the effectiveness of the typhoid fever vaccines and highlights the need for more extensive epidemiological studies of the pathogen. In many developing countries, especially in sub-Saharan Africa, including Nigeria, the limited diagnostic resources and proper surveillance tools result in poor characterisation of the burden of enteric fever and other *Salmonella* infections (Kim *et al.*, 2022).

WHO (2011) observed that all the standardised studies of typhoid epidemiology data, which were abstracted from 47 countries across the globe, revealed significant variations in the incidence and prevalence of typhoid fever. The findings highlighted that regions with

inadequate sanitation and limited access to clean drinking water experienced higher infection rates. Additionally, the report emphasised that children under five years old were particularly vulnerable to severe outcomes associated with typhoid fever.

The analysis also indicated that urban areas tended to have higher incidences than rural areas due to population density and environmental factors contributing to transmission. Furthermore, WHO (2011) noted that socio-economic status played a crucial role in susceptibility, with lower-income populations facing increased risks due to poor hygiene practices and lack of vaccination coverage. Data were also obtained from population-based and prospective vaccine studies for 13 countries. Typhoid fever surveillance systems collected the remaining incidence data in several developed regions where regular and systematic national-level surveillance was in vogue. Paratyphoid fever incidence data were available for only nine countries, of which the USA did not have even a single case of paratyphoid fever during the entire period (WHO, 2011).

More so, the existing estimate of the global burden of typhoid fever is 16 million illnesses and 600,000 deaths annually (Epstein and Hoffman, 2006). Typhoid fever burdens the 5.5 billion people living in low and middle-income countries (Antillon *et al.*, 2017). In 2000, it was estimated that over 2.6 million episodes of typhoid fever occurred worldwide, resulting in 216,000 deaths and among them, Asians were the major sufferers, with 90% of morbidity and mortality (Acosta *et al.*, 2008; Mweu and English, 2008). Typhoid fever is endemic in the subcontinent, Southeast Asia, the Middle East and South and Central America, with hyperendemicity reported in Pakistan (Hayat *et al.*, 2011).

The distribution pattern of the infections seems uncertain in Nigeria and appears to show geographical variation. Some studies found that enteric fevers are more prevalent in males than females (Kam, 1996; Okome-Nkougou *et al.*, 2000; Okome-Nkougou *et al.*, 2014). But

Zailani *et al.* (2004) found no influence of age, sex and social class on the distribution pattern of *S. typhi/Paratyphi* in Ile-Ife, south western Nigeria.

In 2000, typhoid fever caused 21.7 million illnesses and 217,000 deaths (Crump and Mintz, 2010). These staggering figures underscore this infectious disease's significant public health burden, particularly in low- and middle-income countries where access to clean water and sanitation facilities is often inadequate. It occurs most often in children and young adults between 5 and 19 years old (WHO, 2007). In 2013 it resulted in about 161,000 deaths, down from 181,000 in 1990 (Global Burden of Disease, 2013). Infants, children, and adolescents in South-Central and Southeast Asia experience the most significant burden of illness (Odikamnoru *et al.*, 2018). Outbreaks of typhoid fever are also frequently reported from sub-Saharan Africa and Southeast Asian countries (Kim *et al.*, 2022 and Kim *et al.*, 2024).

Typhoid fever (enteric fever) caused by *Salmonella typhi* is an endemic disease in the tropics and sub-tropics. It has become a significant public health problem in developing countries with an estimated annual incidence of 540 per 100,000. The yearly incidence of typhoid is estimated to be about 17 million cases worldwide (WHO, 2008). It is often encountered in tropical countries, including Nigeria, where they constitute serious sources of morbidities and mortalities (Ibekwe *et al.*, 2008).

Typhoid is spread by eating food or drinking water contaminated with the faeces of an infected person (WHO, 2008). Risk factors include poor sanitation and hygiene (Wain *et al.*, 2015). Those who travel to the developing world are also at risk; only humans can be infected (WHO, 2008). Enteric fever is a condition that is taking its toll even now in India, where its prevalence doesn't seem to be decreasing despite the availability of antibiotics and vaccines in the market. With the emergence of antibiotic-resistant strains of the pathogenic organisms, the management of this disease is becoming more challenging. Further, no standard India-specific guidelines exist to treat this scourge (WHO, 2008).

Outbreaks of typhoid fever are frequently reported from sub-Saharan Africa and Southeast Asian countries (Kim *et al.*, 2022). Other regions of Asia and Africa, Latin America, the Caribbean, and Oceania have a medium incidence of 10 to 100 cases per 100,000 person years (Wain *et al.*, 2015). These estimates, though, are limited by a lack of consistent reporting from all areas of the world and are based on the extrapolation of data across regions and age groups. More recent population-based studies from Latin America, in particular, are lacking, and surveillance suggests that rates have declined substantially over the past 30 years (Marks *et al.*, 2017). Furthermore, subsequent data from Africa have revealed substantial heterogeneity between countries, with some Southern and Northern African countries having very low rates (<5 cases per 100,000 person years) while several countries in Eastern and West Africa have rates >100 per 100,000 (Marks *et al.*, 2017). *Salmonella* has many different serotypes. Some serotypes are only found in one kind of animal or a single place. Others are found in many different animals and all over the world. Some can cause especially severe illnesses when infecting people, while others cause milder ones. Some groups, such as older adults, people with weakened immune systems, and children under five, have a higher risk of *Salmonella* infection (Parra-Flores, 2024). Infections in these groups can be more severe, resulting in long-term health consequences or death. More than 2,500 serotypes have been described for *Salmonella*, but because they are rare, scientists know little about most of them. Less than 100 serotypes account for most human infections (Parra-Flores, 2024).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Study Areas

The study was conducted in two (Guma and Logo) local government areas in Benue State. The area lies within the Guinea savannah region of Central Nigeria (Mid-belt region) and

experiences a tropical climate with moderate rainfall estimated to average 1173 mm. The rainy season is experienced from April to October, while the dry season runs from November to March. It has a population of about 1,307,647.23. Some local government areas in Benue State are Logo, Ado, Agatu, Apa, Buruku, Gboko, Guma, Gwer East, Gwer West, Ukum, Katsina-Ala, and Ushongo (Idoko *et al.*, 2023).

3.1.1 Guma Local Government of Benue State

Guma local government was created from the then Makurdi Local Government of Benue State in May 1989. The local government derives its name from River Guma, which traverses the local government from the Northwest and flows into the Northern bank of River Benue. It is situated in the Northeastern part of Benue State with a landmass of 240,000 sq. km. It shares common boundaries with Tarka and Logo local government areas in the East and Makurdi in the South. In contrast, the Doma local government area of Nasarawa State lies in the West. Gbajimba town, the headquarters of Guma local government area, has a strategic location as it is situated at the confluence of two big rivers of the state. River Benue and Katsina-Ala. Guma Local Government Area has a total land area of 2,882 km², and the Guma River runs through its borders. Guma LGA's average annual temperature is 29 degrees Celsius, and the region receives an average of 1,850 mm of precipitation annually. Guma Local Government Area's humidity level is 61 percent on average. Guma Local Government Area is situated in the northern region of Benue State. Guma LGA is impacted by endemic diseases like urinary schistosomiasis and contaminated water sources, leading to illnesses such as cholera. Mental health issues, particularly Post-Traumatic Stress Disorder (PTSD), are prevalent due to conflict and violence. The area also experiences challenges related to food security caused by violence and a significant population of internally displaced persons (IDPs) facing public health needs. It is located at latitudes 06° 33' and 07° 03' North and longitudes 07° 60' and 08° 12' East (Idoko *et al.*, 2023).

3.1.2 Logo Local Government of Benue State

Logo, LGA, has its headquarters in the town of Ugba. It has an area of 1,408 km² and a population of 169,063 according to the 2006 census. The logo of the local government is located on the map of Benue state, which is around longitude 9°4 east and latitude 7°40 north. Logo LGA, revealed a lack of equipment and essential medicines, leading to poor outcomes for patients. Also, like other areas in Benue State, Logo LGA is affected by water-related diseases, likely exacerbated by poor water supply and the high prevalence of heavy metals in water sources. As part of the Benue Valley, the area is susceptible to recurring floods, which can lead to damaged health infrastructure, increased disease vectors like mosquitoes, and outbreaks of waterborne diseases like malaria, cholera, and typhoid fever. Logo LGA was created in December 1996 out of the Katsina-Ala Local Government Area. The name is derived from the Logo stream, which runs through the local government from the east to the West (Idoko *et al.*, 2023).

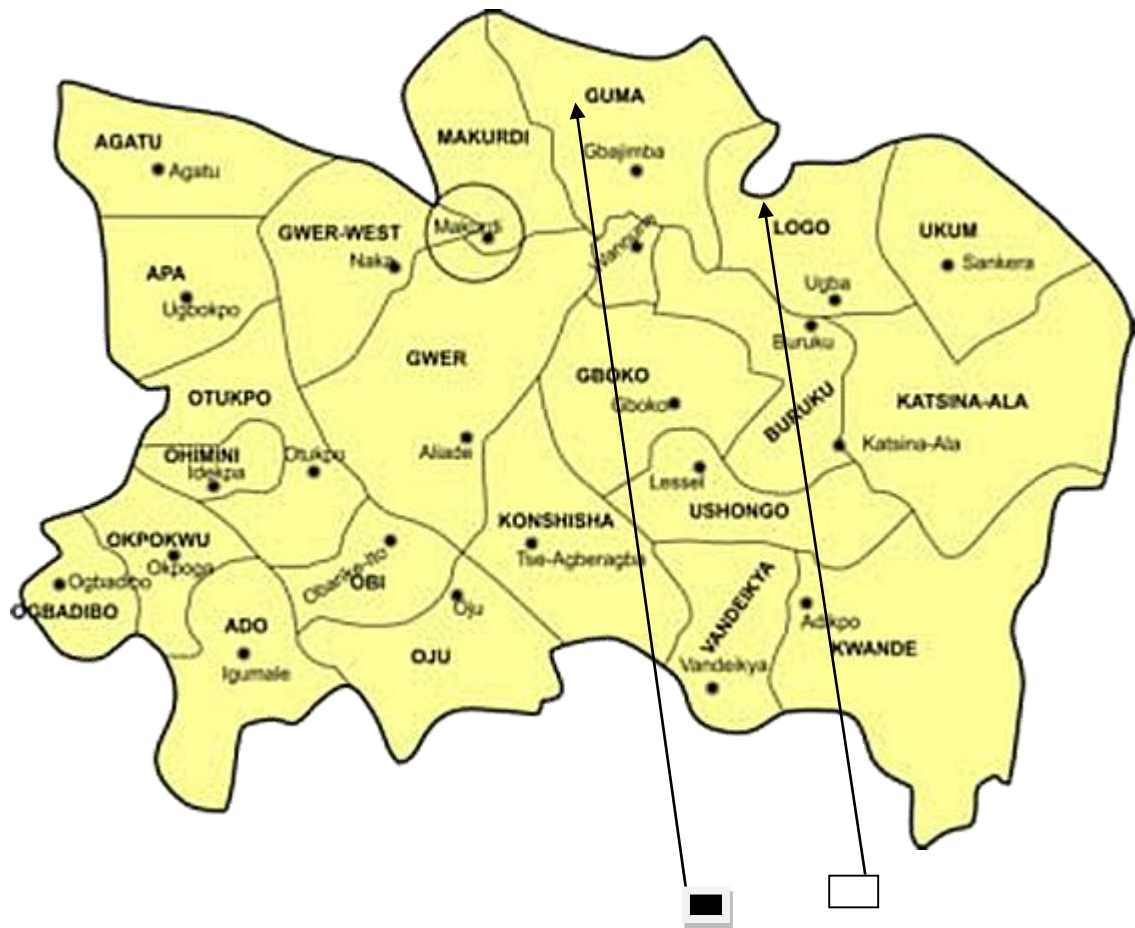


Figure 3.1: Map of Benue State showing the study areas
(Idoko *et al.*, 2023)

Key
 = Guma LGA
 = Logo LGA

3.2 Ethical Approval for the study

This study received ethical approval from the Benue State Emergency Management Agency. Additional permission was obtained from the directors of the Camps that participated in the study. Consent was sought from the IDPs, and they were educated on obtaining stool samples before collection. Confidentiality was maintained following standards of medical practice

3.3 Sample Size Determination

Taro Yamane's sample size determination method was used to determine the sample size for this study. Yamane (1967) suggested the following formula for determining the appropriate sample size for a finite population.

$$n = \frac{N}{1 + N(e)^2}$$

Where:

n = desired sample size

N = the finite size of the survey population

e = the marginal error or confidence interval as determined by the researcher.

1 = statistical or theoretical constant.

Based on the report by the BSEMA (2019) which recorded a total IDP population (N) of 204,193 in Benue state, the sample size was determined. A 5% confidence level was adopted, i.e. 0.05, to reduce the sample size errors.

$$n = \frac{204,193}{1 + 204,193(0.05)^2}$$

n = 399.22

Using the Yamane formula, the sample size determined for the study was 399.9, which was approximated to 400 for the study. The entire sampling process was done in a single step, with each subject selected independently of the other population members. A total of 400 samples,

with 200 samples each, were considered from the camps in Logo and Guma L.G.A.s, respectively. A random sampling technique was employed. In this technique, each member of the population in the camp has an equal chance of being selected as a subject (Groves and Heeringa, 2006).

3.4 Questionnaire Design

In this study, a structured questionnaire was utilized as the primary data collection method. The questionnaire was designed to gather information on socio-demography factors as well as risk-factors relevant to the study. Questions included mix of multiple-choice formats to capture a comprehensive range of responses from participants.

3.5 Sample collection

A total of four hundred (400) stool samples were employed for the study. Early morning stool samples were collected in sterile McCartney containers alongside with a structured questionnaire which were transported to the Microbiology laboratory of the University of Mkar, Gboko, Benue State, Nigeria, for further microbiological analysis (Cheesbrough, 2010). The study was conducted between February, 2020 and January, 2025.

3.6 Sterilisation Methods

All materials used for this study were properly sterilised by observing all the aseptic techniques to prevent contamination (Willey *et al.*, 2008). Glasswares were washed carefully with soap and rinsed in running tap water, and allowed to dry. The glasswares was wrapped in aluminium foil and sterilised in hot air oven at 180⁰C for one hour. Culture media were also sterilised using the autoclave at 121⁰C for 15 min, and those that did not require sterilisation were used according to the manufacturer's specifications. The workbench was disinfected using 70% alcohol. All analyses were carried out close to the naked Bunsen burner flame (Chessbrough, 2010).

3.7 Microbiological Analysis

3.7.1 Preparation of Media

All media: Nutrient agar (NA), Selenite F broth, *Salmonella-Shigella* agar (SSA) and Muller Hinton agar (MHA) used in the research were prepared according to the manufacturer's specifications (Cheesbrough, 2010).

3.7.2 Isolation of *Salmonella* species

Four hundred (400) early morning stool samples were collected from the internally displaced persons from the two LGAs. The samples were processed via the broth enrichment method using Selenite F broth, followed by subculturing onto *Salmonella-Shigella* agar and incubating overnight at 37°C. Colonies growing on the agar plates that exhibit morphological and biochemical properties typical of *Salmonella* spp were selected for Gram staining and biochemical tests (Cheesbrough, 2005; Isenberg, 2015; Abioye *et al.*, 2017)

3.8. Gram Staining

Gram staining was carried out according to the method described by Fred *et al* (1996) and Golam *et al.* (2020). A thin smear of 18-24 h culture of each isolate was made on a clean, grease-free glass slide and heat-fixed by passing it gently over a flame. Each smear was stained with crystal violet solution for 1 min and poured off. It was then flooded with Gram's iodine solution and allowed to react for 1 min.

The iodine solution was washed off, and the slide was flooded with acetone for 1 min. Then, the slides were washed off with distilled water. The slides were then stained with safranin for 1 minute and washed with distilled water. Slides were allowed to air-dry and be observed under the microscope using an oil immersion objective lens. Gram-negative cells were pink (red) because they retain the counterstain. In contrast, Gram-positive cells appeared purple (blue) because they have a thick peptidoglycan cell wall, which retains crystal violet stain.

3.9 Biochemical Characterisation of Putative *Salmonella* Isolates

For further identification, Suspected *Salmonella* colonies on *Salmonella-Shigella* agar were subjected to a series of biochemical tests and probable identity was determined as described by (Cheesbrough, 2010)

(i) Catalase test

This test detects the presence of the enzyme catalase, which breaks down hydrogen peroxide into oxygen and water. Catalase test was carried out according to the method described by Golam *et al.* (2020) and Abioye *et al.* (2017). A thick emulsion of each isolate from 18-24 h culture was made on a clean, grease-free glass slide. A drop of 3% hydrogen peroxide was added to each emulsion. A positive result was indicated by the production of gas bubbles while the absence of bubbles indicated a negative result.

(ii) Hydrogen sulphide Test

This test was used to identify bacteria that can reduce sulphur-containing compounds to hydrogen sulphide during metabolism. According to Golam *et al.* (2020) and Cheesbrough (2010), this method is more sensitive in the detection of H₂S than Triple Sugar Iron (TSI) or Kligler's Iron Agar (KIA), because of its semisolid nature, its lack of interfering carbohydrates, and the use of peptonized iron as an indicator. Sulfite Indole Motility (SIM) agar medium was used for this test and prepared according to the manufacturer's specifications. Five (5 ml) each was dispensed into test-tubes of 5cm depth, sterilised by autoclaving at 121 °C for 15 min and allowed to set in semi-solid (paste) form. The fresh culture of each isolate was stab-inoculated into each medium and incubated at 30 °C for 48 h. After the incubation period, each inoculated isolate was checked for hydrogen sulphide gas (H₂S) production. A positive result was indicated by black colouration at the base of the test tube, while the absence of black colouration indicated a negative result.

(iii) Indole test

This test detects the presence of the enzyme tryptophanase, which breaks down tryptophan. Indole test was carried out according to the method described by Cheesbrough (2010) and Golam *et al.* (2020). Sulfite Indole Motility (SIM) agar medium was used for this test and prepared according to the manufacturer's specifications. Five millilitres (5ml) each were dispensed into test tubes and sterilised by autoclaving at 121 °C for 15 min and allowed to set in semi-solid (paste) form. The fresh culture of each isolate was stab-inoculated into each medium and incubated at 30 °C for 48 h. After incubation, 3-4 drops of Kovac's reagent were added to each culture. A pinkish red colour indicated a positive reaction in a ring form on the surface of the medium, while the absence of this indicated negative result.

(iv) Motility test

Sulfite Indole Motility (SIM) agar medium was used for this test and prepared according to the manufacturer's specifications. A motility test was carried out according to the method described by Cheesbrough (2010). Five millilitres (5ml) each was dispensed into test tubes sterilised by autoclaving at 121 °C for 15 min and allowed to set. Each of the tubes was stab-streaked to about half-depth of the medium. The tubes were incubated at 30 °C for 48 h and examined for diffuse or fuzzy growth along the stabbed line, an index for motility (Abioye *et al.*, 2017).

(v) Methyl red test

The methyl red test was done to detect acid production during the fermentation of glucose and the maintenance of acidic conditions. Methyl Red-Voges Proskauer medium (Glucose phosphate broth) was used for this test and prepared according to the manufacturer's specifications. Methyl red test was carried out according to the method described by Cheesbrough (2010). Five millilitres (5ml) each of the medium was dispensed into screw capped tubes and sterilised at 121 °C for 15 min. The glucose phosphate broth was inoculated

and incubated at 30 °C for 24 hours. After the incubation period, 2-3 drops of methyl red reagent were added. Red colouration indicated a positive result (i.e, acid production) while yellow indicated a negative reaction.

(vi) Voges-Proskauer test

This is a test for producing acetyl-methyl-carbinol ($\text{CH}_3\text{-CO-CHOCH}_3$) from glucose. Methyl Red-Voges Proskauer medium (Glucose phosphate broth) was used for this test and prepared according to the manufacturer's specifications. Voges-Proskauer test was carried out according to the method described by Isenberg (2015) and Abioye *et al.* (2017). Five (5 ml) of the medium was dispensed into screw capped tubes and sterilised at 121 °C for 15 min. The glucose phosphate broth was inoculated with a fresh culture of each bacterial isolate and incubated for 72 h at 30 °C. At the end of the incubation period, 0.5 ml of 5% α -naphthol solution and 0.5 ml of 40 % potassium hydroxide (KOH) were added to 1 ml of the culture. The content of each tube was shaken vigorously. A positive reaction was indicated by the development of red colouration within 30 min to 1 h, while non-red colouration indicated a negative result.

(vii) Urease test

The urease test was done to detect urease production, which breaks down urea into ammonia and carbon dioxide. An ureagar base medium was used for this test and prepared according to the manufacturer's specifications. According to the method described by Abioye *et al.* (2017) and Golam *et al.* (2020), urea was typically added to the medium after the initial preparation of the agar medium, which usually contains other nutrients and indicators. Five millilitres (5ml) each was dispensed into McCartney bottles and autoclaved at 121 °C for 15 min and then allowed to set in a slanting position. The isolate was stab-streaked and streaked on the medium

in each bottle and incubated at 30 °C for 24 h. After the period of incubation, the bottles were checked for colour change. A change in the colour of the medium from orange to pink indicated a positive result, while the negative result was a creamy to yellowish colour.

(viii) Citrate utilization

Citrate utilisation test was carried out according to Cheesbrough's (2010) and Golam et al. (2020) method. This is a test for the production of citrase enzyme for citrate utilisation. Simon citrate agar medium was prepared according to the manufacturer's specifications. Five millilitres (5 ml) was dispensed in McCartney bottles. These were sterilised 121 °C for 15 min and allowed to set in a slanting position. Each pure bacterial isolate was stabbed-streaked, streaked on each citrate medium, and incubated at 30 °C for 24-48 h. After the period of incubation, the bottles were checked for colour change. A change in colour of the medium from green to blue indicated a positive result, while a negative result was shown by green colour.

(ix) Triple Sugar Iron Agar (TSIA) Test

The TSIA test was carried out according to the method of Cheesbrough (2010) described. This test is based on the distinct metabolic pattern of the different bacterial genera to metabolise glucose, lactose, sucrose, and sodium thiosulfate (a sulfur compound). Fermentation of these sugars will produce acid, decreasing the pH of the medium and turning it red. Similarly, the metabolism of sodium thiosulfate is indicated by turning the medium black. Triple Sugar Iron agar medium was prepared according to the manufacturer's specifications. Five millilitres (5 ml) was dispensed into a sterile test tube. These were sterilised and allowed to set in a slanting position. Each pure bacterial isolate was stabbed-streaked, streaked on each TSIA medium, and incubated at 35 °C for 24-48 h. After incubation, the test tubes were checked for colour change.

Change in colour of the medium from slant to butt indicated positive while negative result was indicated no reaction from red slant and yellow butt (Red/yellow or Alkaline/Acidic) which means only glucose was fermented indicating the presence of *Salmonella typhi*, yellow slant and yellow butt (yellow/yellow or acid/acid) which means the three sugars i.e glucose, lactose and sucrose were fermented, red slant and red butt (red/red or alkaline/alkaline) which means none of the three sugars were fermented, blackening of the media indicated hydrogen sulfide gas production (H₂S) indicating the presence of *Samonella typhi*. At the same time, *Salmonella paratyphi* A did not produce H₂S, cracking of the media, gas bubbles or forming of a gap in the media indicates gas production, which does not indicate the presence of *Salmonella typhi* but suggests the presence of *Salmonella typhimurium* and *Salmonella paratyphi* A (Isenberg, 2015).

3.10 Preparation of Standard Inocula

The inocula were prepared for ten (10) uncured and cured *Salmonella typhi* isolates by using a sterile inoculating loop to pick each pure isolate and emulsified in each 5 ml sterile phosphate buffer saline (PBS) in a test tube and standardized according to Clinical and Laboratory Standards Institute description (CLSI, 2008) by comparing with 0.5 McFarland Standard solution (consist of .05 mL of 1.175% barium chloride dihydrate (BaCl₂•2H₂O) with 9.95 mL of 1% sulfuric acid (H₂SO₄). Stock inoculum suspensions were prepared by taking five colonies (>1 mm in diameter) from 24h cultures into 5 ml sterile saline. Each suspension was shaken for 15 s and density adjusted visually to 0.5 McFarland turbidity standards. This was done by adding more organisms when the suspension is too light or diluting with sterile distilled water when it is too heavy. The turbidity of each suspension was compared by holding both the

standard and the inoculum tubes side by side in front of a white paper with black lines. Dilutions of these suspensions were also sub-cultured on Muller Hinton agar to determine antibiotic sensitivity (Cheesbrough, 2010; Santos *et al.*, 2011).

3.11 Antibiotic used for susceptibility testing

Salmonella isolates were tested against nine antimicrobial agents using the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar following the description of the Clinical and Laboratory Standards Institute (CLSI, 2008; CLSI, 2020). The antimicrobials were chosen from a wide range of commonly used options of broad spectrums, two from each class of antibiotic, including the Cephalosporins: Cefixime clavulanate (Czm) (10 µg); Ceporex (CEP) (10 µg); was used, Fluoroquinolone: Ornidazole/ofloxacin (spoz) (25 µg), Ciprofloxacin (CIP) (5 µg); Penicillin: Augmentin (AU) (30 µg), Amplicin (PN) (30 µg); Aminoglycosides: Streptomycin (S) (30 µg); Gentamycin (CN) (10 µg); and Tetracycline (TET) 30(µg); of class Tetracycline. The susceptibility of the isolated *Salmonella* to various antibiotics was tested using commercially available antibiotic discs from different manufacturers: Cephalosporins from Mayo Diagnostic Limited (Nigeria), Fluoroquinolone and Penicillin from Tyonex Nigeria Limited, and Tetracycline from Nexon Diagnostic Services.

Twenty four hour (24h) culture of each of the test isolated were used to inoculate sterile Mueller Hinton Media plates using nine commercial antibiotic discs following the guide lines of CLSI (2020). The antimicrobial disks were placed evenly with a minimum gap of 24 mm from the centre on the agar medium using sterile forceps. The plates were then incubated at 37°C for 24 h. Zones of inhibition that appeared as clean circles around the disk were recorded by measuring the circle's diameter in millimetres. A metric ruler was placed across the zone of inhibition, at the widest diameter and measured from one edge of the zone to the other. Sensitivity discs with no zone at all were reported as zero, even though the disc was around 7

mm. Zone diameter was reported in millimetres. It was cross-checked on the chart, and the result was reported as resistant, intermediate or susceptible as described by CLSI (2020). Uninoculated media with an antibiotic disc were used as a reference for the negative control.

3.12 Storage of Pure Isolates for Further Testing

The pure cultures were preserved on nutrient agar slants and stored in a refrigerator. The pure isolates were sub-cultured onto each time before further testing was carried out on them.

3.13 Molecular Analysis

The study was conducted at the Africa Centre of Excellence for Neglected Tropical Diseases and Forensic Biotechnology at the Department of Veterinary Public Health at Ahmadu Bello University, Zaria. Sequencing was done commercially by Inqaba Biotec West Africa, Ibadan Nigeria.

3.13.1 Preparation of PCR Reaction Mixture

Amplification of markers was done with slight modification of the methods of Levy *et al* (2008) and Pui *et al* (2011). Twenty-five (25) μ l volume each was prepared for polymerase chain reaction (PCR) in a PCR tube, containing 12.5 μ l of master mix (New England Biolabs containing a mixture of dNTP(Deoxyribonucleotide triphosphate), Taq polymerase, MgCl₂ and PCR buffer), 2 μ l forward primer, 2 μ l reverse primer, 2 μ l of extracted DNA and 6.5 μ l of nuclease-free water.

3.13.2. Protocol for Polymerase Chain Reaction

The PCR thermal cycling protocol consisted of several key steps. Initially, the reaction began with a denaturation phase at 94 °C for 5 minutes, during which the double-stranded DNA template was heated to separate it into single strands. This was followed by 30 cycles of thermal

cycling. Each cycle started with a denaturation step at 94 °C for 40 seconds, further ensuring the separation of the DNA strands. The temperature was then lowered to 54 °C for 30 seconds to allow annealing, permitting the primers to attach to their complementary target DNA sequences. Following annealing, the temperature was raised to 72 °C for 1 minute to facilitate the elongation phase, during which the Taq DNA polymerase extended the primers to synthesize new DNA strands. Finally, a concluding extension step was performed at 72 °C for 5 minutes to ensure that the DNA polymerase could complete the synthesis of any strands that remained unfinished (Levy *et al.*, 2008; Pui *et al.*, 2011). The primers used for PCR of the expected genes were as follows:

3.13.2.1 Two virulent gene were targeted for PCR with the following primer sequence:

Target gene: *invA* gene with 284 base pairs

F: 5'- GTG AAA TTA TCG CCA CGT TCG GGC AA -3'

R: 5'-TCA TCG CAC CGT CAA AGG AAC C-3'

Chaudhary *et al.* (2015)

Target gene: *fliC-d* virulent gene with 763 base pairs

F: 5'-ACT CAG GCT TCC CGT AAC GC-3'

R: 5'- GGC TAG TAT TGT CCT TAT CG G-3'

Phumkhachorn and Rattanachaikunsopon (2017)

3.13.2.2 Two Resistant genes were targeted for PCR with the following primers sequence:

Target gene: *tetA* with 635 base pairs (bp)

F: 5'- GCTGTAGGCATAGGCTTGGT -3'

R: 5'- GCCGGAAGCGAGAAGAATCA -3' Aslam *et al.* (2012)

Target gene: *BLATem* with 862 base pairs (bp)

F: 5'-ATGAGTATTCAACATTTCCG-3'

R: 5'-GACAGTTACCAATGCTTAATCA-3' Fabre *et al.* (2009)

3.13.2.3 One *S. typhi* gene-specific primer was targeted for PCR with the following sequence:

Target gene: *STY0307* with 495 base pairs

F: 5'- ATGAAACCTTTATTCTCAGTGC -3'

R: 5'- TTAGCGTAATTCCCAGAACC -3' (Goay *et al.*, 2016)

3.14.1 Electrophoresis for Genomic PCR product

To detect the distinctive *invA* and *fliC-d* virulent genes, *tetA* and *BLATEM* resistance genes and the *STY0307* gene specific for *Salmonella typhi* in ten (10) biochemically identified isolates, they were evaluated using a Polymerase Chain Reaction (PCR) technique. Two grams (2.0 g) of agarose powder was dissolved in 100 ml of Tris-Boric EDTA (TBE) buffer, boiled to obtain a clear solution, and allowed to cool before adding 4 µl of ethidium bromide dye used for staining. The agarose solution was poured into a preset tray containing twenty combs and allowed to solidify. The set of combs was carefully removed to create wells, and the agarose gel was placed inside the electrophoresis apparatus tank. The samples were loaded by pipetting 5 µl of each sample into each gel well. The inherent dye in the master mix prevented the floating of the loaded DNA sample and also helped track the movement of DNA samples during electrophoresis. After loading, the power pack was put on, both voltage and time were set (80V and time 60 min) to run the DNA samples, where they were separated in sizes, the smaller DNA fragments were seen to move faster and migrate farther than the larger DNA fragments. On completion of electrophoresis, the result was read in the UV transilluminator at 365nm to visualise the DNA bands. The ethidium bromide solution binds to the DNA double helix and emits a bright orange fluorescence when the UV light is excited, verifying the presence of the target DNA sequence (Olawale *et al.*, 2020).

3.15 Plasmid Curing of *Salmonella typhi* isolates

Plasmid curing of 10 resistant *Salmonella typhi* isolates was carried out according to the method of Olawale *et al.*(2020). The curing was carried out using acridine orange at 0.1mg/ml concentration. Acridine orange solution (0.1% w/v) was prepared by adding 0.1 g of the acridine orange powder into 100 mL of sterile distilled water. This mixture was subsequently filtered through a Millipore filter of 0.45 µm. This solution is equivalent to 1 mg/ml of acridine orange. One millilitre of the acridine orange solution was dispensed aseptically to each bottle containing 9 ml of sterile nutrient broth. The concentration of acridine orange in each 10 ml broth-acridine solution is 0.1 mg/ml and was sterilised at 121 °C for 15 min. A fresh culture of each test bacterial isolate was inoculated into each tube. After inoculation, each tube was vortexed using a shaker for 25min for even distribution of cells and incubated at 30 °C for 72h. After incubation, each cultured isolate was streaked on each sterile solidified nutrient agar plate and incubated at 37 °C for 24h. It was further sub-cultured on *Salmonella* Shigella agar plate and incubated at 37 °C for 24h. After incubation, cured isolates (mutants) were selected from the 10 plates based on colony size and colour. Cured isolates were streaked on fresh sterile nutrient agar and prepared for an antibiotic sensitivity profile. Antibiotic susceptibility test was done again for the bacterial isolates that showed resistance to antibiotics before the curing (those with MAR index ≥ 0.8), and the changes in resistance patterns were noted. The bacteria that displayed clear changes in resistance pattern after curing were regarded as bearing their resistance factor in the plasmid.

3.16 Plasmid Extraction by Alkaline Lysis Method Disruption

Overnight cultures of *Salmonella* isolates in microcentrifuge tubes were centrifuged at 10,000 rpm for 1 min to concentrate the cells into pellets and the supernatants was decanted. The pellets were resuspended by vortexing and washed by adding 100 microlitre (µl) GET buffer or a modification of a TE buffer (50mM millimolar glucose/10 mM EDTA/10 mM TrisCl, pH8.0) through centrifuging at 14000 rpm for 5min and the supernatants decanted. The pellets were

re-suspended again by vortexing, and 200 microlitres (μl) of lysis solution (0.2 M NaOH 1% sodium dodecyl sulfate [SDS]) was added into each tube. Then, the tubes were inverted 3 times to enhance the activity of the lysis buffer and 150 microlitres (μl) of 7.5 M potassium acetate and 150 microlitres (μl) of chloroform were added into each tube to stop the activity of the lysis buffer and incubated for 5min at room temperature (Padilla-Zamudio *et al.*, 2018).

Lysates were centrifuged at 14000 rpm for 5 min, and clear supernatants were pipetted into another clean, labelled microcentrifuge tube. An equal volume of cold absolute ethanol was added to each microcentrifuge tube to precipitate plasmid DNA, and then centrifuged at 14000 rpm for 5 min. After centrifugation, the supernatants were carefully decanted. Each plasmid DNA pellet was washed thrice by adding 1ml of 70% isopropanol and centrifuged at 14000 rpm for 1 min each time. After the plasmid DNA pellets in microcentrifuge tubes were dried for 15min in a DNA concentrator (centrifuge) and eluted by adding 50 microlitres (μl) TE buffer to the pellets and vortexed to re-suspend the purified plasmid DNA, the procedure was adopted from Zhou *et al.* (1997) and Padilla-Zamudio *et al.* (2018).

3.16.1 Agarose gel electrophoresis of plasmid DNA

To ensure that the reversal of antibiotic resistance was due to loss of a plasmid and not due to mutation, agarose gel electrophoresis of the crude DNA extract prepared from the original host and its respective cured derivatives was performed. Loss of plasmid bands in the cured derivative was the physical confirmation of plasmid curing (Patwardhan *et al.*, 2018)

After the crude extraction process, the plasmid band were detected using agarose gel electrophoresis as follows:

1-5 microlitre (μl) of the extract was mixed with 1-2 microlitre (μl) of 6X loading dye (containing bromophenol blue and xylene Cyanol). The mixture was loaded into a well of 0.8% -1.2% agarose gel. The gel electrophoresis was run at 100-120V for 30-40min, until the

bromophenol blue reached the gel's end. The gel was stained with ethidium bromide and visualised under UV light (300-360nm). A distinct band corresponding to the plasmid DNA, typically ranging from 2-10kb in size, was looked for and then photographed as carried out by Sambrook and Russella (2001)

3.17 Multiple antibiotic resistance (MAR) index.

MAR index was calculated for each isolate; it is the ratio of the number of antibiotics to which an organism was resistant to the total number of antibiotics it was exposed to (Osundiya *et al.*, 2013). The formula for calculating the Multiple Antibiotic Resistance (MAR) index is:

$$\text{MAR index} = \frac{\text{(Number of antibiotics the isolate is resistant to)}}{\text{(Total number of antibiotics tested)}}$$

3.18 Statistical Analysis

The data obtained from this study were entered into Microsoft Excel and exported to SPSS version 20.0 for data analysis. Pearson Chi square (χ^2) analysis was employed to determine a significant relationship between infection, age, gender and risk factors. Significance was determined at an alpha level of 0.05.

CHAPTER FOUR

4.1

RESULTS

4.1.1 Overall Prevalence of *Salmonella typhi* among Internally Displaced Persons (IDPs)

Table 4.1 shows the prevalence of *Salmonella typhi* among IDPs in Guma and Logo. From the findings, IDPs in Guma had a prevalence rate of 7.5%, while Logo had a prevalence rate of 12.5% for *Salmonella typhi* infection. The rate of infection was significantly different between Guma and Logo IDPs ($\chi^2= 80.000$, $df=1$, $P<0.05$).

4.1.2 Prevalence of *Salmonella typhi* among IDPs in Relation to Camp Area

Data in Table 4.2 shows the prevalence of *Salmonella typhi* in relation to the accommodation arrangement for IDPs. Results obtained indicated prevalence in Guma IDPs of 3.0% in Block A and 4.5% in Block B for *Salmonella typhi* infection, while Logo IDPs had a higher prevalence of 7.0% in Block A and 5.5% in Block B for *Salmonella typhi* infection, respectively. The degree of infection was not significantly different for both Guma and Logo IDPs in relation to residential area ($\chi^2= 1.920$, $P>0.05$)

4.1.3 Prevalence of *Salmonella typhi* among IDPs in Relation to Gender

The prevalence of *Salmonella typhi* infection with respect to gender, as given in Table 4.3, shows a high prevalence of *Salmonella typhi* infection in females 5.0% in Guma compared to 2.5% in males. At the same time, Logo IDPs had a higher prevalence rate of 8.75% in females compared to 3.75% in males for *Salmonella typhi* infection. The chi-square analysis shows no significant difference in infection between male and female IDPs in Guma and Logo ($\chi^2= 0.035$, $P > 0.05$).

Table 4.1: An Overall Prevalence of *Salmonella typhi* among IDPs

L.G.A.	No. Examined	No. Infected	Percentage (%)	χ^2	P-value
Guma	200	30	(7.5)	80.000	0.000
Logo	200	50	(12.5)		
Total	400	80	(20.0)		

$\chi^2 = 80.000$; $df=1$, $P < 0.05$ for Guma and Logo IDPs

Table 4.2: Prevalence of *Salmonella typhi* among IDPs in Relation to Camp area

Area	No. examined	No. infected	Percentage (%)	χ^2	P-value
Guma					
Block A	100	12	(3.0)	1.920	0.166
Block B	100	18	(4.5)		
Total	200	30	(7.5)		
Logo					
Block A	100	28	(7.0)		
Block B	100	22	(5.5)		
Total	200	50	(12.5)		

$\chi^2 = 1.920$; df= 1, P > 0.05 for Guma and Logo IDPs

Table 4.3: Prevalence of *Salmonella typhi* among IDPs in Relation to Gender

Gender	No. examined	No. infected	Percentage (%)	χ^2	P- value
Guma					
Female	122	20	(5.0)	0.035	0.852
Male	78	10	(2.5)		
Total	200	30	(7.5)		
Logo					
Female	130	35	(8.75)		
Male	70	15	(3.75)		
Total	200	50	(12.5)		

$\chi^2 = 0.035$; df = 1 P > 0.05 for Guma and Logo IDPs

4.1.4 Prevalence of *Salmonella typhi* among IDPs in Relation to Age

In Table 4.4, the data shows the prevalence of *Salmonella typhi* with respect to age group among IDPs. In Guma, IDPs had a higher prevalence rate of 3.0% for the age group 5-10years, 11 – 21years had 1.25%, 22 – 32years had 0.5%, 33 – 43years had 0.5%, and above 43years had 2.25% for *Salmonella typhi* infection, Logo IDPs had a higher prevalence rate of *Salmonella typhi* of 5.0% for the age group 5 – 10years, 11 – 21years had 1.0%, 22 – 32years had 0.5%, 33 – 43years had 2.25%, and above 43years had 3.75% for the infection. There was no significant difference in infection in relation to age groups for IDPs in Guma and Logo ($\chi^2=3.270$, $P>0.05$).

4.1.5 Prevalence of *Salmonella typhi* among IDPs in Relation to Occupation

Table 4.5 shows the distribution of *Salmonella typhi* with regard to the occupation of IDPs. From the table, Guma and Logo IDPs had the same prevalence rate of 0.25% for civil servants and 0.5% for business people, respectively. Also, a prevalence rate of 3.25% for Students and 3.5% for Farmers, respectively, for *Salmonella typhi* infection in Guma, compared to a prevalence rate of 4.75% for Students and 7.0% for Farmers, respectively, for *Salmonella typhi* infection in Logo. The result reveals no significant variation in the isolation rate of *Salmonella typhi* infection ($\chi^2=0.844$, $P> 0.05$) for Guma and Logo IDPs.

4.1.6 Prevalence of *Salmonella typhi* among IDPs in Relation to Personal Hygiene

The data presented in Table 4.6 reveal significant associations between personal hygiene practices and the prevalence of *Salmonella typhi* infections among IDPs residing in Guma and Logo. Hand hygiene after defecation or toilet use appeared to be a critical determinant of infection rates in both locations. In Guma, individuals who consistently washed their hands after defecation or toilet use exhibited a lower infection rate of 0.75% compared to those who washed only sometimes, 4.5% or were unsure about their practices, 2.25%. This trend was statistically significant, as shown by the chi-square (χ^2) value of 10.423 and a corresponding p-

value of 0.005, indicating a strong association between handwashing and reduced *S. typhi* infection risk. A similar pattern was observed in the Logo IDP camp. Among the 200 individuals examined, those who always washed their hands after using the toilet had an infection rate of just 0.5%, compared to 11.25% among those who sometimes washed, and 0.75% among those uncertain of their hygiene routine. Again, the association was statistically significant ($\chi^2 = 10.423$, $p = 0.005$), reinforcing the importance of proper hand hygiene in minimising enteric infections in displaced populations.

Conversely, sanitation practices (e.g., environmental cleanliness and latrine availability) did not show a statistically significant relationship with *S. typhi* prevalence in either Guma or Logo. In Guma, the infection rates were 2.0% for those reporting consistent sanitation, 4.75% for those with intermittent sanitation practices, and 0.75% for those without sanitation efforts. Despite these variations, the χ^2 value of 2.853 and a p-value of 0.240 suggest no meaningful association. Similar trends were observed in Logo, with infection rates of 2.0% (always), 10.0% (sometimes), and 0.5% (none), and the same non-significant χ^2 and p-value. Regarding methods of refuse disposal, the type of disposal system used (waste bin, incineration, or open dumping) did not show a statistically significant association with *S. typhi* prevalence in either site. In Guma, infection rates were 1.0%, 0.25%, and 6.25% for waste bin, incineration, and open dumping, respectively, but the association lacked statistical significance ($\chi^2 = 1.270$, $p = 0.530$). In Logo, a similar distribution was observed with infection rates of 0.75% (waste bin), 0.5% (incineration), and 11.25% (open waste), also not statistically significant ($\chi^2 = 1.270$, $p = 0.530$).

Table 4.4: Prevalence of *Salmonella typhi* among IDPs in Relation to Age Group

Age group	No. Examined	No. Infected	Percentage (%)	χ^2	P-value
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Guma					
5 – 10	94	12	(3.0)	3.270	0.514
11 – 21	38	5	(1.25)		
22 – 32	19	2	(0.5)		
33 – 43	16	2	(0.5)		
>43	33	9	(2.25)		
Total	200	30	(7.5)		
Logo					
5 – 10	53	20	(5.0)		
11 – 21	28	4	(1.0)		
22 – 32	18	2	(0.5)		
33 – 43	28	9	(2.25)		
>43	73	15	(3.75)		
Total	200	50	(12.5)		

$\chi^2 = 3.270$, $df = 4$; $P > 0.05$ for Guma and Logo IDPs

Table 4.5: Prevalence of *Salmonella typhi* among IDPs in Relation to Occupation

Occupation	No examined	No infected	Percentage (%)	χ^2	P-value
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Guma					
Civil servant	6	1	(0.25)	0.844	0.839
Business	8	2	(0.5)		
Farmer	120	14	(3.5)		
Student	66	13	(3.25)		
Total	200	30	(7.5)		
Logo					
Civil servant	5	1	(0.25)		
Business	10	2	(0.5)		
Farmer	115	28	(7.0)		
Student	70	19	(4.75)		
Total	200	50	(12.5)		

$\chi^2 = 0.844$; $df= 3$, $P > 0.05$ for Guma and Logo

Table 4.6: Prevalence of *Salmonella typhi* among IDPs in Relation to Personal Hygiene

Personal Hygiene	No examined	No infected	Percentage χ^2 (%)	P-value
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Guma					
Washing of hands after defecation					
Always	36	3	(0.75)	10.423	0.005
Sometimes	138	18	(4.5)		
Not sure	26	9	(2.25)		
Total	200	30	(7.5)		
Sanitation					
Always	40	8	(2.0)	2.853	0.240
Sometimes	150	19	(4.75)		
None	10	3	(0.75)		
Total	200	30	(7.5)		
Method of refuse disposal					
Waste bin	30	4	(1.0)	1.270	0.530
Incinerate	10	1	(0.25)		
Open waste	160	25	(6.25)		
Total	200	30	(7.5)		
Logo					
Washing of hands after defecation					
Always	25	2	(0.5)	10.423	0.005
Sometimes	162	45	(11.25)		
Not sure	13	3	(0.75)		
Total	200	50	(12.5)		
Sanitation					
Always	35	8	(2.0)	2.853	0.240
Sometimes	160	40	(10.0)		
None	5	2	(0.5)		
Total	200	50	(12.5)		
Method of refuse disposal					
Waste bin	25	3	(0.75)	1.270	0.530
Incinerate	10	2	(0.5)		
Open waste	165	45	(11.25)		
Total	200	50	(12.5)		

4.1.7 Prevalence of *Salmonella typhi* among IDPs in Relation to Risk Factors

The analysis of risk factors associated with the prevalence of *Salmonella typhi* among IDPs in both Guma and Logo reveals significant insights into the environmental and lifestyle

determinants of infection, as shown in Table 4.7. Three major risk factors were assessed: overcrowding, the source of daily meals, and water.

In both camps, overcrowding did not statistically correlate with *S. typhi* prevalence. In Guma, of the 200 IDPs examined, 190 individuals lived in overcrowded conditions, among whom 28 had 7.0% were infected. Conversely, only 2 out of 10 had 0.5% non-overcrowded individuals were infected. Despite this apparent difference, the chi-square (χ^2) value of 0.281 and a p-value of 0.596 indicate no statistically meaningful relationship between overcrowding and infection rate. A similar pattern was observed in Logo, where 48 out of 195 overcrowded individuals were infected 12.0%, compared to 2 out of 5 in the non-overcrowded category 0.5%, with the same χ^2 and p-value values as in Guma, reaffirming the lack of significance.

However, the source of daily meals showed a highly significant association with *S. typhi* prevalence in both locations. In Guma, 20 of the 81 individuals 5.0% who sourced their meals from the camp market were infected, whereas only 10 of the 119 who prepared their meals in personal kitchens 2.5% tested positive. The difference was statistically significant ($\chi^2 = 28.024$, $p = 0.000$), suggesting that food from communal or shared sources may pose a greater infection risk due to potential hygiene lapses during preparation, handling, or storage. This trend was even more pronounced in Logo, where 45 out of 163 IDPs relying on personal kitchens were infected 11.25%, while just 5 out of 37 1.25% camp market consumers tested positive. The same statistical significance was observed ($\chi^2 = 28.024$, $p = 0.000$), though the reverse trend here may point to improved hygiene in centralised meal services or variability in preparation standards across camps.

In contrast, the sources of drinking water, borehole and rainwater, did not significantly influence infection rates. In Guma, borehole users (150 individuals) recorded 21 infections 5.25%, while those using rainwater (50 individuals) had 9 infections 2.25%. In Logo, the

pattern remained consistent with 35 infections among 160 borehole users 8.75% and 15 infections among 40 rainwater users 3.75%. In both locations, statistical analysis yielded a chi-square value of 0.000 and a p-value of 1.000, indicating no significant association between the water source and infection.

4.1.8 Prevalence of *Salmonella typhi* among IDPs in Relation to History/Knowledge about the disease

From table 4.8, a notable prevalence of 6.25% was observed among IDPs in Guma who reported not knowing the disease. In contrast, those who had received treatment 1 – 3 times exhibited a significantly lower prevalence rate of 0.25%. Furthermore, individuals who were aware of their treatment history and had received treatment 4 – 6 times or more than 7 times had a prevalence rate of 0.5% each.

Among Logo IDPs, the highest prevalence rate was 11.0% among those without knowledge of the disease, which is higher than in Guma. Like Guma, Logo IDPs who knew they had been treated 1 – 3 times recorded a low prevalence of 0.25%. Participants who knew they had been treated 4 – 6 times and those treated more than 7 times had prevalence rates of 0.5% and 0.75%, respectively.

The comparison of prevalence rates between Guma and Logo IDPs reveals that those who were unaware of the disease presented higher infection rates in both groups. Specifically, Logo IDPs showed a more pronounced susceptibility to *Salmonella typhi* infection in the same group of non-aware IDPs. However, the statistical analysis indicates that there was no significant difference in the prevalence rates of *Salmonella typhi* infection between the Guma and Logo IDP populations, as indicated by a Chi-square statistic ($\chi^2 = 0.46$) with a p-value greater than 0.05 ($P > 0.05$).

4.1.9 Prevalence of *Salmonella typhi* among IDPs in Relation to Duration in Camp

The analysis in Table 4.9 indicates that among Guma IDPs, those who spent less than 1 year in the camp exhibited a prevalence rate of 0.75% for *Salmonella typhi*. Those who spent 1 – 2 years had a slightly increased prevalence 2.5%. The highest prevalence was observed among individuals who spent more than 2 years, with a rate of 4.25%.

For Logo IDPs, those spending less than 1 year in the camp recorded an even lower prevalence of 0.5%. Like Guma, those who spent 1 – 2 years showed a prevalence rate of 2.5%. However, Logo IDPs who spent more than 2 years in the camp had the highest reported prevalence rate of 9.5% for *Salmonella typhi* infection.

A comparison of the prevalence rates indicates a general trend where the increased duration of stay in the camp correlates with higher rates of *Salmonella typhi* infection for both Guma and Logo IDPs. Specifically, Logo IDPs demonstrate a significantly higher prevalence 9.5% among those who spent more than 2 years compared to Guma IDPs 4.25%. Despite the observed trends, the statistical analysis reveals no significant difference in the infection rates between Guma and Logo IDPs across the duration categories. This is supported by the Chi-square statistic ($\chi^2 = 3.433$), which indicates a p-value greater than 0.05 ($P > 0.05$). Consequently, the data suggest that while there are differences in prevalence rates, these differences are not statistically significant.

Table 4.7: Prevalence of *Salmonella typhi* among IDPs in Relation to Risk factors

Risk factors	No examined	No infected	Percentage (%)	χ^2	P-value
Guma					
Are you overcrowded					
Yes	190	28	(7.0)	0.281	0.596

No	10	2	(0.5)		
Total	200	30	(7.5)		
Daily meals					
Camp market	81	20	(5.0)	28.024	0.000
Personal kitchen	119	10	(2.5)		
Total	200	30	(7.5)		
Sources of water					
Borehole	150	21	(5.25)	0.000	1.000
Rain	50	9	(2.25)		
Total	200	30	(7.5)		
Logo					
Are you overcrowded					
Yes	195	48	(12.0)	0.281	0.596
No	5	2	(0.5)		
Total	200	50	(12.5)		
Daily meals					
Camp market	37	5	(1.25)	28.024	0.000
Personal kitchen	163	45	(11.25)		
Total	200	50	(12.5)		
Sources of water					
Borehole	160	35	(8.75)	0.000	1.000
Rain	40	15	(3.75)		
Total	200	50	(12.5)		

Table 4.8: Prevalence of *Salmonella typhi* among IDPs in Relation to History/Knowledge

History/Knowledge	No. Examined	No. infected	Percentage (%)	χ^2	P-value
Guma					
Number of times treated					

1 – 3 times	2	1	(0.25)	0.461	0.927
4 – 6 times	5	2	(0.5)		
Above 7 times	7	2	(0.5)		
No knowledge	186	25	(6.25)		
Total	200	30	(7.5)		

Logo

Number of times

treated

1 – 3 times	3	1	(0.25)		
4 – 6 times	5	2	(0.5)		
Above 7 times	8	3	(0.75)		
No knowledge	184	44	(11.0)		
Total	200	50	(12.5)		

$\chi^2 = 0.461$; df= 3, P > 0.05 for Guma and Logo

Table 4.9: Prevalence of *Salmonella typhi* among IDPs in Relation to Duration in Camp

Duration	No examined	No. Infected	Percentage (%)	χ^2	P-value
Guma					
<1yr	17	3	(0.75)	3.433	0.180

1 – 2yrs	47	10	(2.5)
>2yrs	136	17	(4.25)
Total	200	30	(7.5)
Logo			
<1yr	5	2	(0.5)
1 – 2yrs	15	10	(2.5)
>2yrs	180	38	(9.5)
Total	200	50	(12.5)

$\chi^2 = 3.433$; df= 2, P > 0.05 for Guma and Logo

4.1.10 Prevalence of *Salmonella typhi* among Internally Displaced Persons (IDPs) in Relation to the Toilet System/mode of defecation

Table 4.10 shows the variation in isolation with respect to the toilet system. Among Guma IDPs, those practising open defecation exhibited a higher prevalence rate of 4.25% for *Salmonella typhi* infection. In comparison, those using pit latrines had a lower prevalence rate of 3.25%. For Logo IDPs, the trend is similar, with those using open defecation presenting the highest prevalence rate of 7.0%. Conversely, the prevalence among those utilising pit latrines was 5.5%.

The data shows that individuals using open defecation had higher *Salmonella typhi* infection rates for both Guma and Logo IDPs than those using pit latrines. Specifically, Guma IDPs' open defecation rate of 4.25% is lower than Logo IDPs' 7.0%, indicating a significant disparity.

However, the statistical analysis reveals that the percentage occurrence rates concerning the toilet system in both camps did not differ significantly, as indicated by the Chi-square statistic ($\chi^2 = 0.274$) with a p-value greater than 0.05 ($P > 0.05$).

4.1.11 Prevalence of *Salmonella typhi* among IDPs in Relation to Marital Status

Table 4.11 shows the variation in isolation with respect to marital status. Among Guma IDPs, married individuals had a *Salmonella typhi* infection rate of 2.5%. In contrast, the unmarried individuals exhibited a higher infection rate of 5.0%. For Logo IDPs, the infection rates reflected a similar pattern, with married individuals having an infection rate of 3.25%. Conversely, unmarried individuals showed a notably higher infection rate, 9.25%.

In both camps (Guma and Logo), unmarried individuals experienced higher rates of *Salmonella typhi* infection than their married counterparts. Specifically, the infection rates increased from 2.5% (married) to 5.0% (unmarried) in Guma, and from 3.25% (married) to 9.25% (unmarried) in Logo.

Despite these observed differences, the statistical analysis indicates no significant difference in the infection rates based on marital status between the two groups, as evidenced by the Chi-square statistic ($\chi^2 = 0.492$) with a p-value greater than 0.05 ($P > 0.05$).

4.1.12 Prevalence of *Salmonella typhi* among IDPs in Relation to Depression from the death of loved ones

Table 4.12 shows the variation in isolation with respect to Depression from the death of loved ones. Among Guma IDPs, those who reported being depressed due to the death of a loved one had a *Salmonella typhi* infection rate of 4.5%. In contrast, those who were not depressed

exhibited a lower infection rate of 3.0%. For Logo IDPs, the situation was similar: individuals who were depressed from the loss of a loved one showed an infection rate of 6.75%. Conversely, non-depressed individuals displayed an infection rate of 5.75%.

The data indicate that both in Guma and Logo IDPs, individuals experiencing depression due to the death of a loved one had higher rates of *Salmonella typhi* infection compared to those who were not depressed. In Guma, the infection rates increased from 3.0% (not depressed) to 4.5% (depressed), and in Logo, from 5.75% (not depressed) to 6.75% (depressed).

However, the statistical analysis resulted in a Chi-square statistic ($\chi^2 = 0.274$) with a p-value greater than 0.05 ($P > 0.05$).

4.1.13 Prevalence of *Salmonella typhi* among IDPs in Relation to Medication

Table 4.13 shows the variation in isolation with respect to Medication. From the table, among Guma IDPs, those who engaged in self-medication exhibited a *Salmonella typhi* infection rate of 4.5%. In contrast, those who utilised the Camp clinic had a lower infection rate of 3.0%. For Logo IDPs, the infection rates were higher. Those who practised self-medication had an infection rate of 8.0%. Conversely, individuals who accessed the Camp clinic had a lower rate of 4.5%. In Guma, self-medication had an infection rate of 4.5%, while the Camp clinic users had a rate of 3.0%. Logo rates were 8.0% (self-medication) versus 4.5% (Camp clinic).

However, the statistical analysis yielded a Chi-square statistic ($\chi^2 = 0.128$) with a p-value greater than 0.05 ($P > 0.05$).

Table 4.10: Prevalence of *Salmonella typhi* among IDPs in Relation to toilet system

Toilet system	No. Examined	No. Infected	Percentage (%)	χ^2	P-value
Guma					
Open defecation	150	17	(4.25)	0.274	0.600
Pit latrine	50	13	(3.25)		
Total	200	30	(7.5)		
Logo					
Open defecation	170	28	(7.0)		
Pit latrine	30	22	(5.5)		
Total	200	50	(12.5)		

$\chi^2 = 0.274$; df= 1, P > 0.05 for Guma and Logo

Table 4.11: Prevalence of *Salmonella typhi* among IDPs in Relation to Marital Status

Marital status	No. examined	No. infected	Percentage (%)	χ^2	P-value
Guma					
Married	70	10	(2.5)	0.492	0.483
Single	130	20	(5.0)		
Total	200	30	(7.5)		
Logo					
Married	120	13	(3.25)		
Single	80	37	(9.25)		
Total	200	50	(12.5)		

$\chi^2 = 0.492$; df= 1, P > 0.05 for Guma and Logo

Table 4.12: Prevalence of *Salmonella typhi* among IDPs in Relation to Depression from deaths of loved ones

Depression	No. Examined	No. Infected	Percentage (%)	χ^2	P-value
Guma					
Depressed					
Yes	40	18	(4.5)	0.274	0.600
No	160	12	(3.0)		
Total	200	30	(7.5)		
Logo					
Depressed					
Yes	60	27	(6.75)		
No	140	23	(5.75)		
Total	200	50	(12.5)		

$\chi^2 = 0.274$; df= 1, P > 0.05 for Guma and Logo

Table 4.13: Prevalence of *Salmonella typhi* among IDPs in Relation to Medication

Medication	No. Examined	No. Infected	Percentage (%)	χ^2	P-value
Guma					
Self-medication	135	18	(4.5)	0.128	0.721
Camp clinic	65	12	(3.0)		
Total	200	30	(7.5)		
Logo					
Self-medication	150	32	(8.0)		
Camp clinic	50	18	(4.5)		
Total	200	50	(12.5)		

$\chi^2 = 0.128$; df= 1, P > 0.05 for Guma and Logo

4.1. Detection of the *invA* virulent gene of *Salmonella typhi*

Plate 4.1 showed the PCR amplification product for *Salmonella typhi*'s *invA* virulent gene on an agarose gel. Successful amplification of the *invA* gene indicates its presence in the selected isolates, suggesting that these isolates possess the genetic material linked to the virulence of *Salmonella typhi*. A molecular ladder (or DNA ladder) was used for size comparison, with bands corresponding to known DNA fragment sizes ranging from 100 base pairs (bp) upwards. Isolation wells numbered 1 through 10 showed PCR product. The discernible bands in wells indicate that the *invA* gene was present within these samples. The PCR results revealed that wells (1, 2, 3, 6, 7, 8, 9, and 10) exhibited bands at around 284 bp. This is consistent with the expected size of the *invA* gene fragment, which is characteristic of *Salmonella typhi*. Clear bands at this specific size confirm the successful amplification of the *invA* gene across isolates tested.

4.3 Detection of the *STY0307* gene Specific to *Salmonella typhi*

Plate 4.2 shows the PCR amplification product for *Salmonella typhi*'s *FliC-d* virulent gene on an Agarose gel. A molecular ladder was utilised for size comparison, with bands corresponding to a

known DNA size marker starting from 100 base pairs (bp). Wells numbered 1 through 12 contain samples subjected to PCR for the *FliC-d* gene. The results indicated that none of the wells (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12) exhibited bands corresponding to the *FliC-d* gene. The lack of visible bands in these wells implies no amplification of the *FliC-d* gene fragment in any of the selected isolates.

The absence of amplification of the *FliC-d* virulent gene in the examined isolates signifies that these specific *Salmonella typhi* strains do not possess this particular virulence factor.

4.3 Detection of the *STY0307* gene Specific to *Salmonella typhi*

Plate 4.3 below shows the PCR amplification product for *Salmonella typhi*'s *STY0307* gene, Specific to an Agarose gel. The molecular ladder was 100bp, and 1,2,3,4,5,6,7,8,9,10,11 and 12 were the wells containing samples. The presence of the bands at 1,2,3,4,5,6,7,8,9, and 12 at 495 bp in the PCR products confirms that the gene *STY0307* was present in the tested *Salmonella typhi* isolates.

4.2 Detection of the *FliC-d* virulent gene of *Salmonella typhi*

4.4 Detection of the *BlaTEM* resistant gene of *Salmonella typhi*

Plate 4.4 shows the successful amplification of the *BlaTEM*-resistant gene among the 10 *Salmonella typhi* isolates, which indicates that this specific resistance gene was present in the tested strains of *Salmonella typhi*.

4.5 Detection of the *tetA* resistant gene of *Salmonella typhi*

Plate 4.5 shows the successful amplification of the *tetA*-resistant gene among the 10 *Salmonella typhi* isolates 5 isolates indicated that this specific resistance gene was present in the tested strains of *Salmonella typhi*.

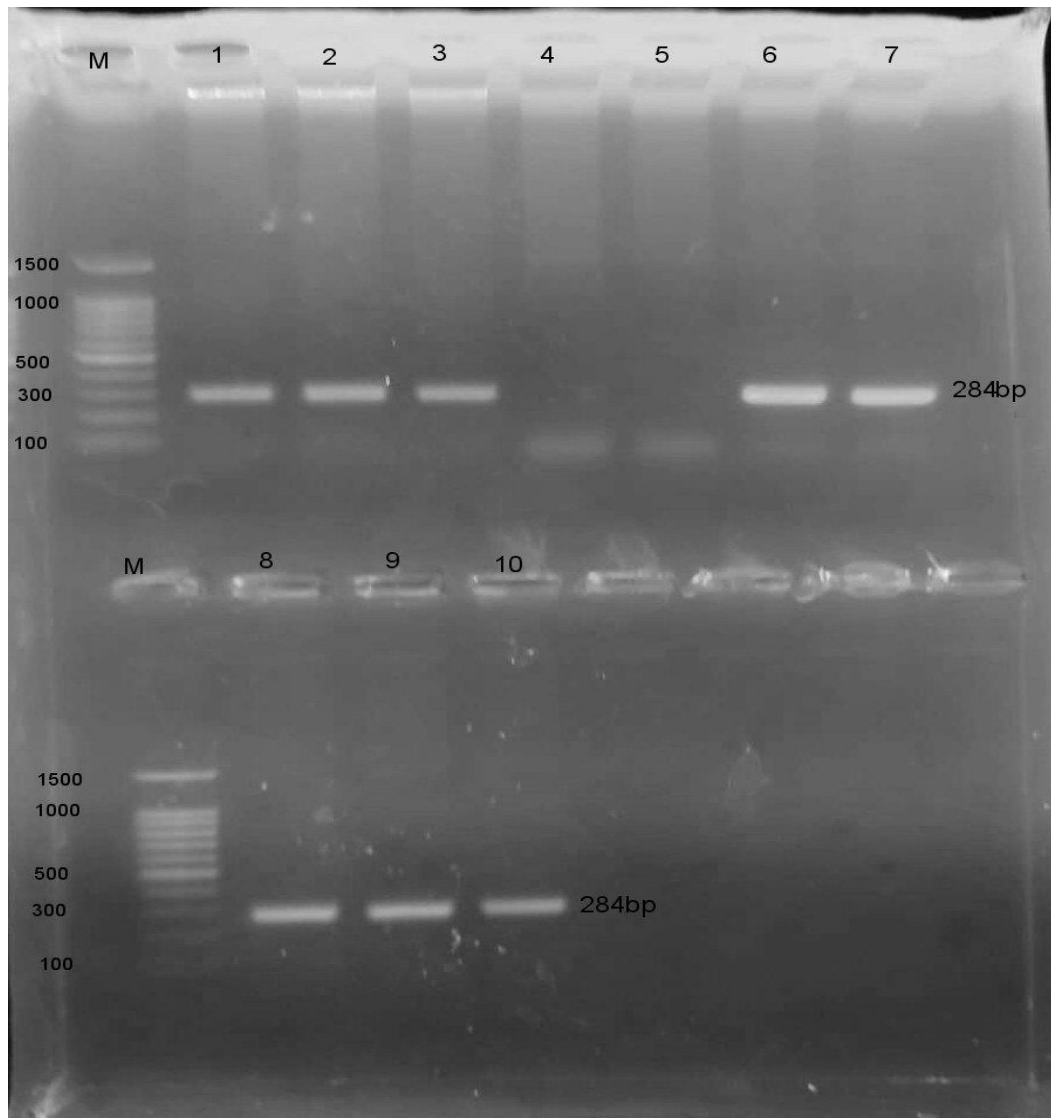


Plate 4.1: Agarose gel picture showing PCR amplification product of the *invA* virulent gene for *Salmonella typhi* at 284 bp.

Key: M = Molecular Ladder, (1, 2,3,4,5,6,7,8,9,10,) – Wells containing samples

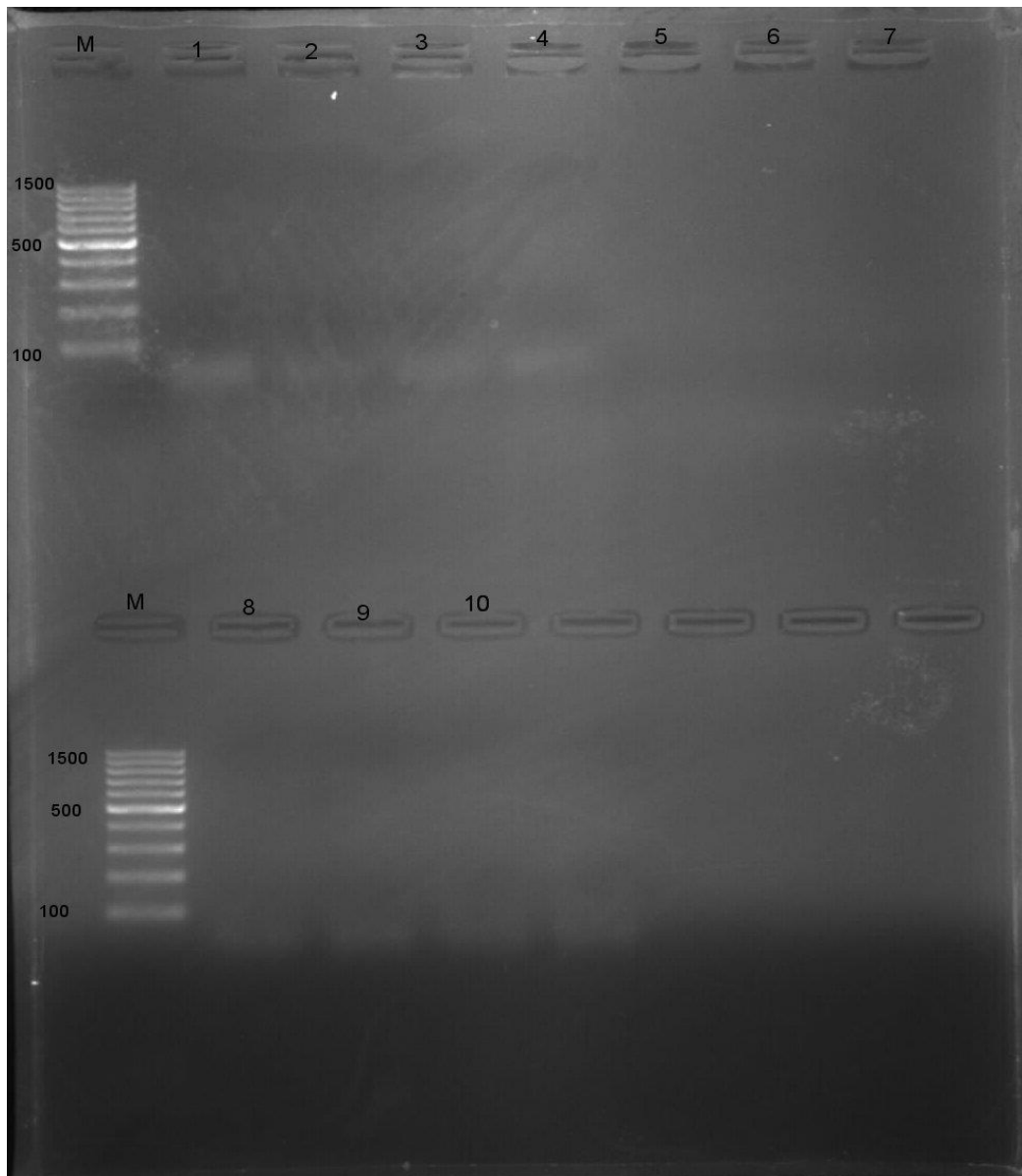


Plate 4.2: Agarose gel post picture showing no PCR amplification product of the *FliC-d* virulent gene for *Salmonella typhi*

Key: M = Molecular Ladder, (1,2,3,4,5,6,7,8,9,10) – Wells containing samples

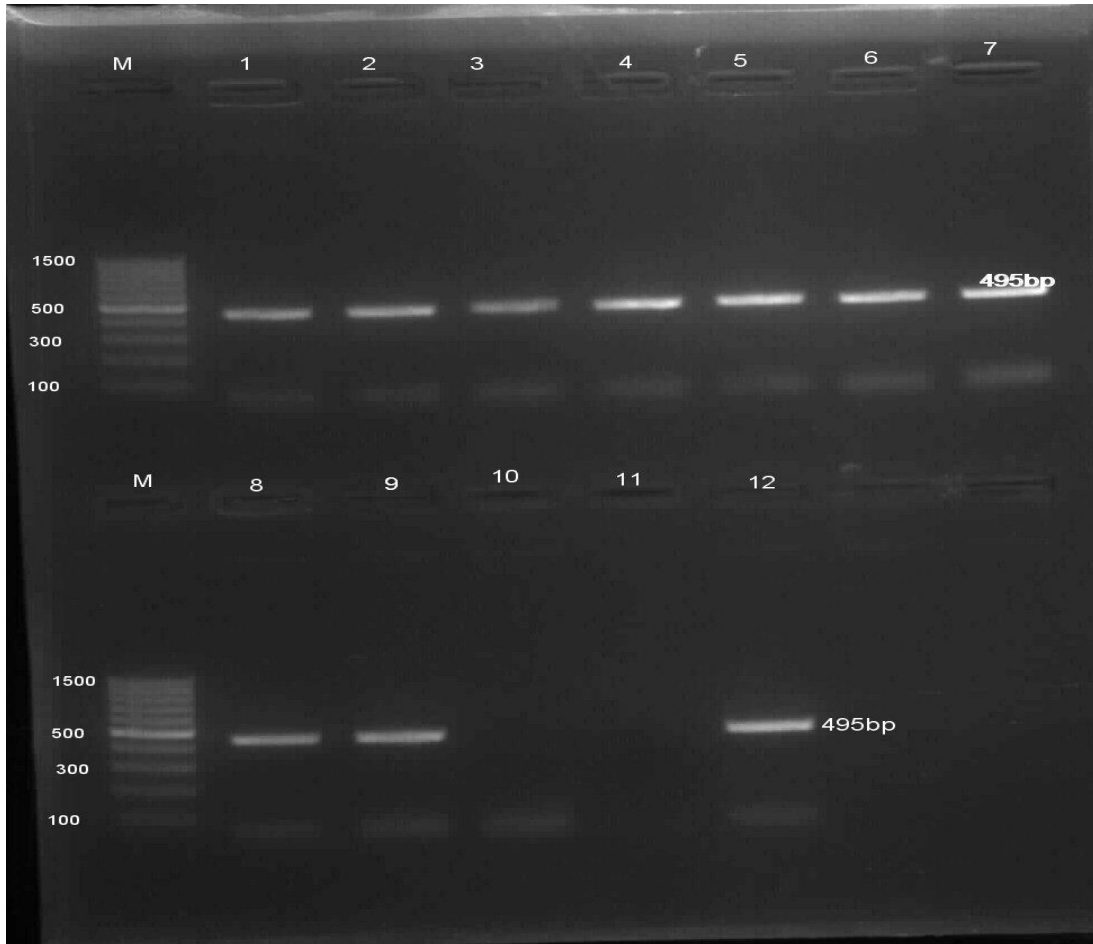


Plate 4.3: Agarose gel picture showing PCR amplification product of the *STY0307* gene, Specific for *Salmonella typhi* at 495 bp.

Key: M = Molecular Ladder, (1, 2,3,4,5,6,7,8,9,10,11,12) – Wells containing samples

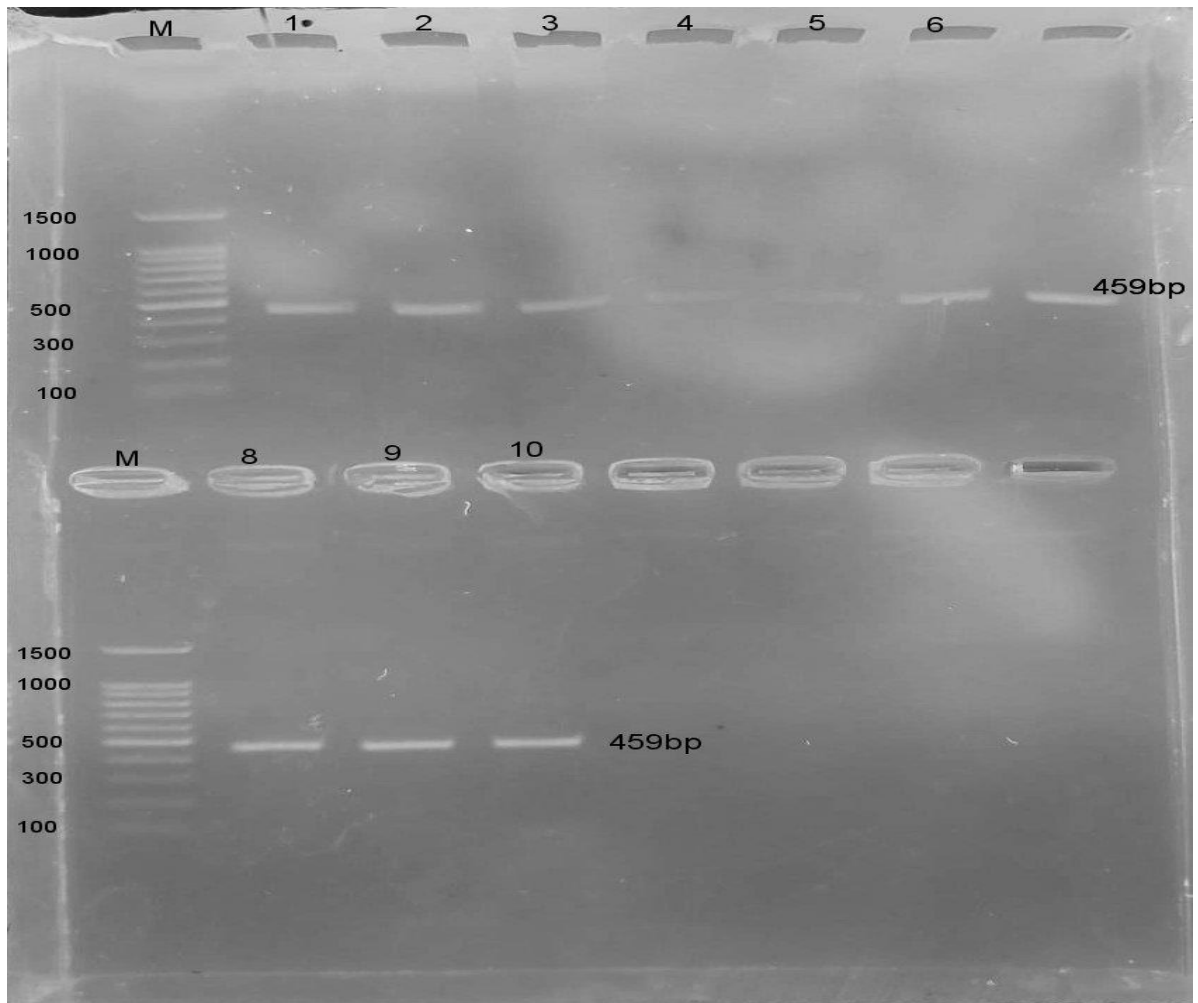


Plate 4.4: Agarose gel pictures showing PCR amplification product of *Blatem* resistant gene for *Salmonella typhi* at 459 bp.

Key: M = Molecular Ladder, (1, 2, 3, 4, 5, 6, 7, 8, 9, 10) – Wells containing samples

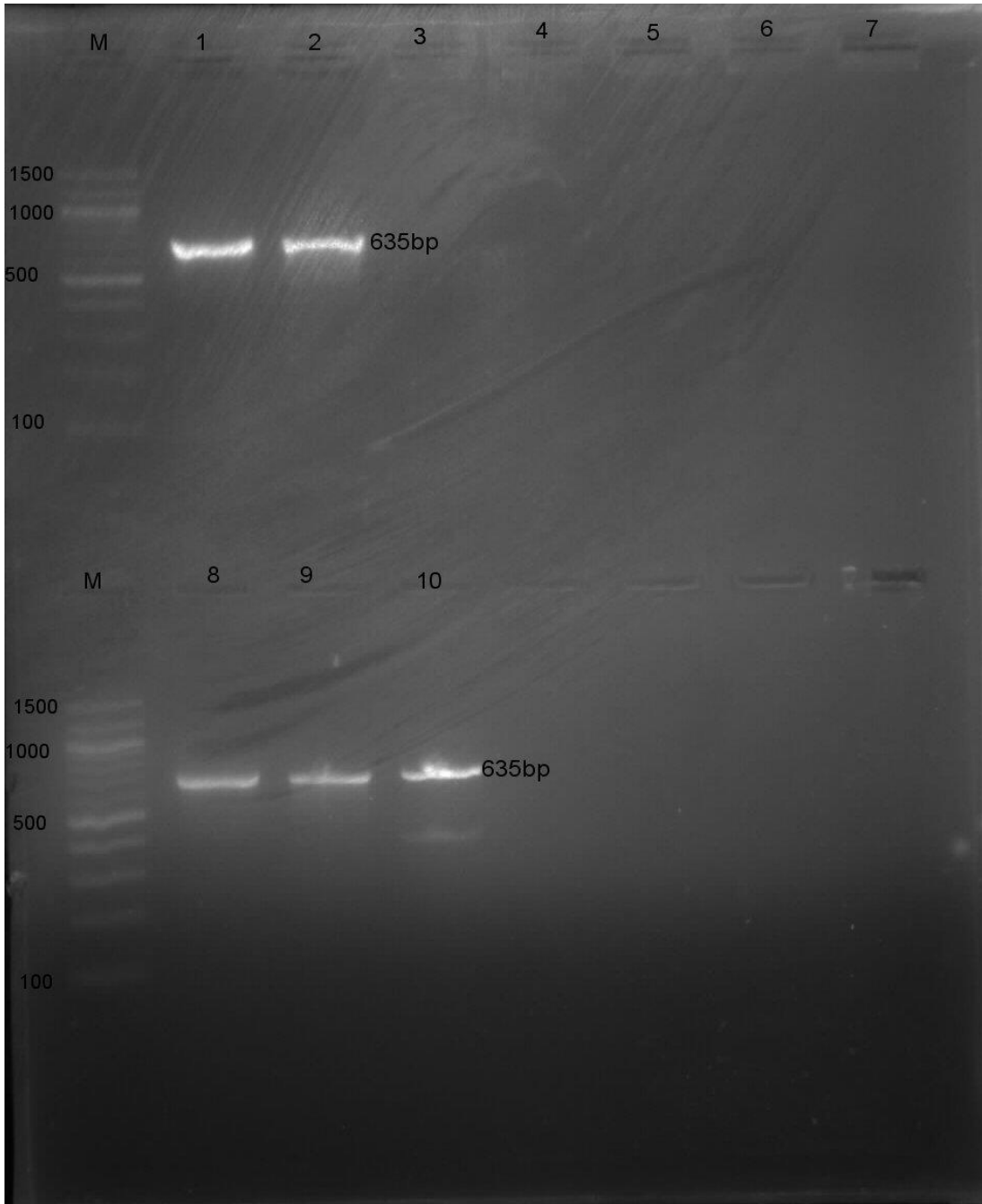


Plate 4.5: Agarose gel picture showing PCR amplification product of the *tetA* resistant gene for *Salmonella typhi* at 635 bp.

Key: M = Molecular Ladder, (1, 2,3,4,5,6,7,8,9,10) – Wells containing samples

4.6 Agarose gel post-electrophoresis showing plasmid before curing of *Salmonella typhi* isolates.

Plate 4.6 shows the plasmid electrophoresis profile of ten uncured *Salmonella typhi* isolates. The plasmid profiling for the ten *Salmonella typhi* isolates initially revealed the presence of DNA. The DNA ladder in the wells showed standard bands. The molecular weights of the DNA ladder used are: 10, 3, 1 and 0.5 kilobase pairs (kbp). Most of the bands (representing plasmids) found in resistant *Salmonella typhi* isolates were in the region of high molecular weight plasmids (10kbp). Also, isolates exhibited plasmids of high molecular weight ranging from 3kbp to 10kbp (Plate 6)

4.7 Agarose gel post-electrophoresis showing plasmid after curing of *Salmonella typhi* isolates.

Plate 4.7 shows the plasmid electrophoresis profile of ten cured *Salmonella typhi* isolates. The plasmid electrophoresis profile of the resistant *Salmonella typhi* isolates after curing showed no plasmid bands detected in most of the wells (representing plasmids), an indication that they were cured plasmids or that the DNA the plasmid-mediated *Salmonella typhi* isolates, except the DNA isolate from well 4.

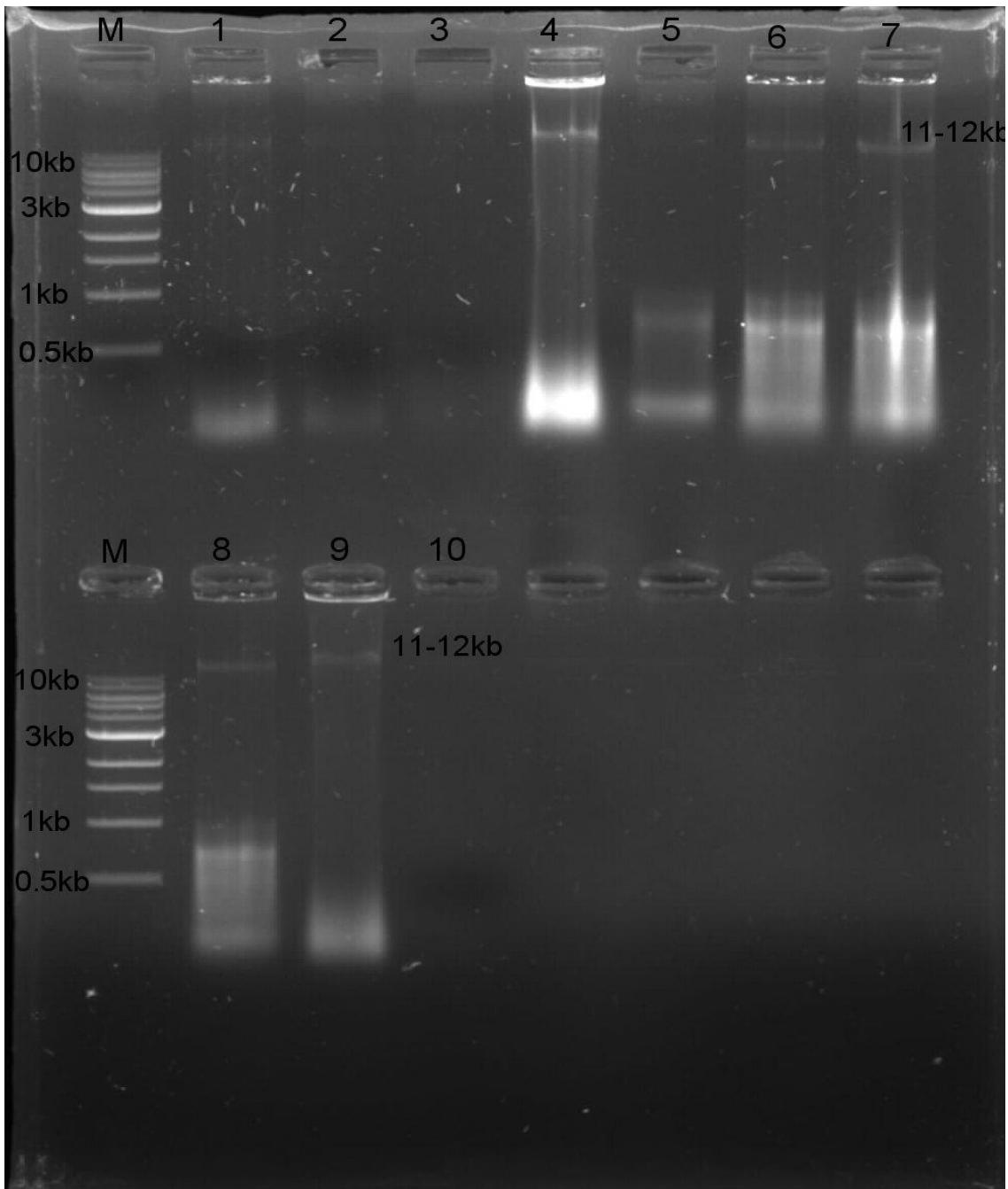


Plate 4.6: Agarose gel post-electrophoresis showing uncured plasmid profile of *Salmonella typhi* isolates.

Key: M = Molecular Ladder, (1, 2,3,4,5,6,7,8,9,10) – Wells containing samples

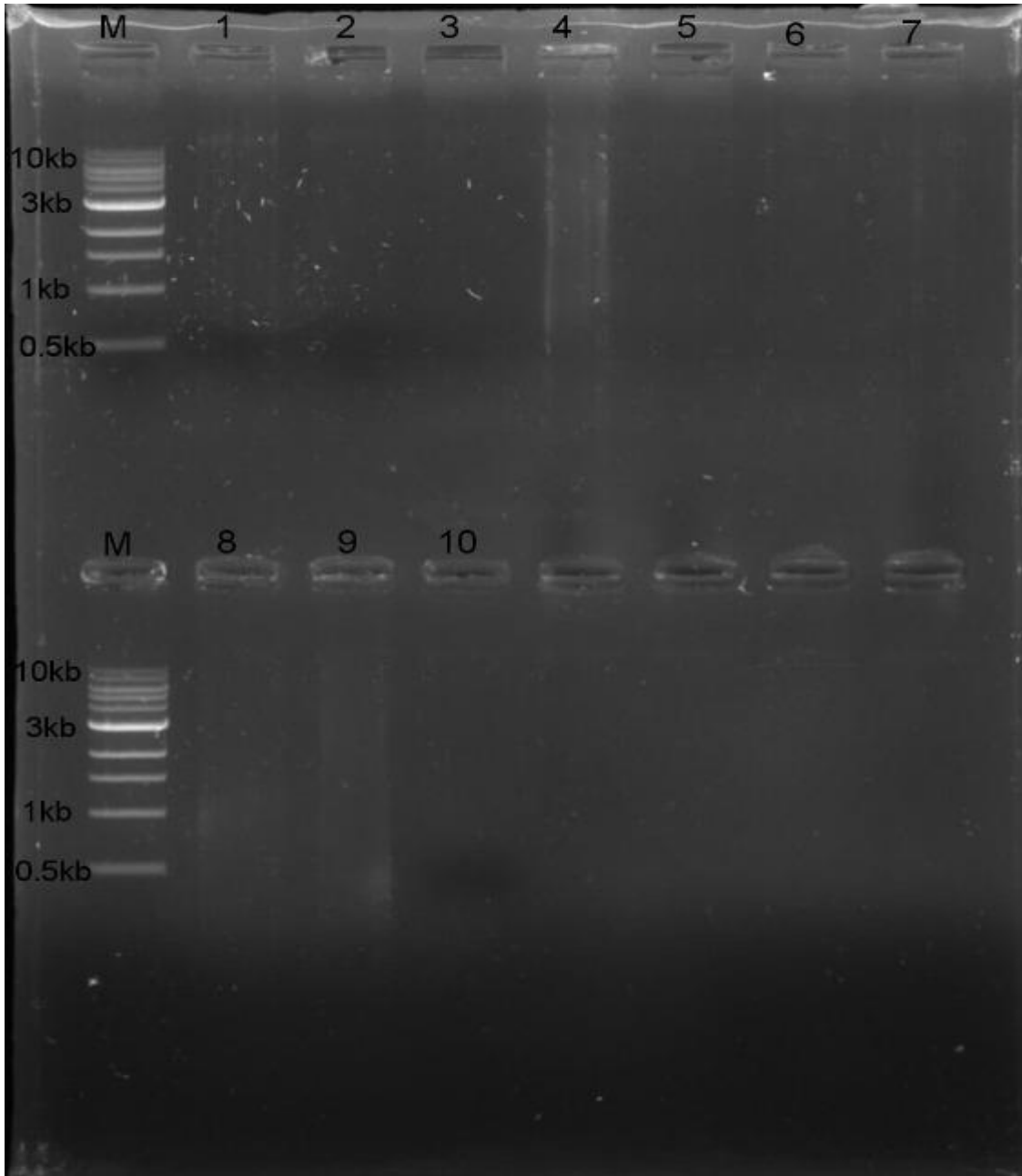


Plate 4.7: Agarose gel picture showing cured plasmid profile of *Salmonella typhi* isolates.

Key: M = Molecular Ladder, (1, 2,3,4,5,6,7,8,9,10) – Wells containing samples

4.1.14 Antibiotic Sensitivity of *Salmonella typhi* isolates before curing

Table 4.14 shows the antibiotic sensitivity of *Salmonella typhi* isolates before curing. From the table, the antibiotic sensitivity of uncured *Salmonella typhi* isolates showed the zones of inhibition measured in millimetres and compared to the Clinical Laboratory Standards Institute (Sarker *et al.*, 2014; CLSI, 2020) Chart. *Salmonella typhi* exhibited high resistance to Ceporex(CEP), Ciprofloxacin(CIP), Ampicillin (PN), Streptomycin(S), Gentamycin(CN) and Tetracycline(TET). The Multiple Antibiotic Resistance Index (MARI) was calculated, with isolate Samples 02, 10, 30, 25, 80 and 88 having the highest index (0.7), followed by Samples 70 and 65 with 0.6 each. Isolates Sample 40 and 100 had the lowest MARI (0.4) each.

4.1.15 Antibiotic Sensitivity of *Salmonella typhi* isolates after curing

Table 4.15 shows the antibiotic sensitivity of *Salmonella typhi* isolates after curing. From the table, isolates with more than four resistances to certain antibiotics underwent plasmid curing and subsequent antibiotic sensitivity testing to confirm the removal of plasmids causing resistance. After curing, the isolates exhibited low resistance to Ceporex (CEP), followed by Ciprofloxacin(CIP), Tetracycline(TET), while the lowest resistance was observed against Gentamycin(CN). The Multiple Antibiotic Resistance (MAR) index was calculated, with isolate Samples 30 and 25 having a lower index (0.2), followed by Samples 10,02,80 and 88 with (0.1), and the zero indices observed in isolates Sample 40, 100, 65 and 70 (0.0) each.

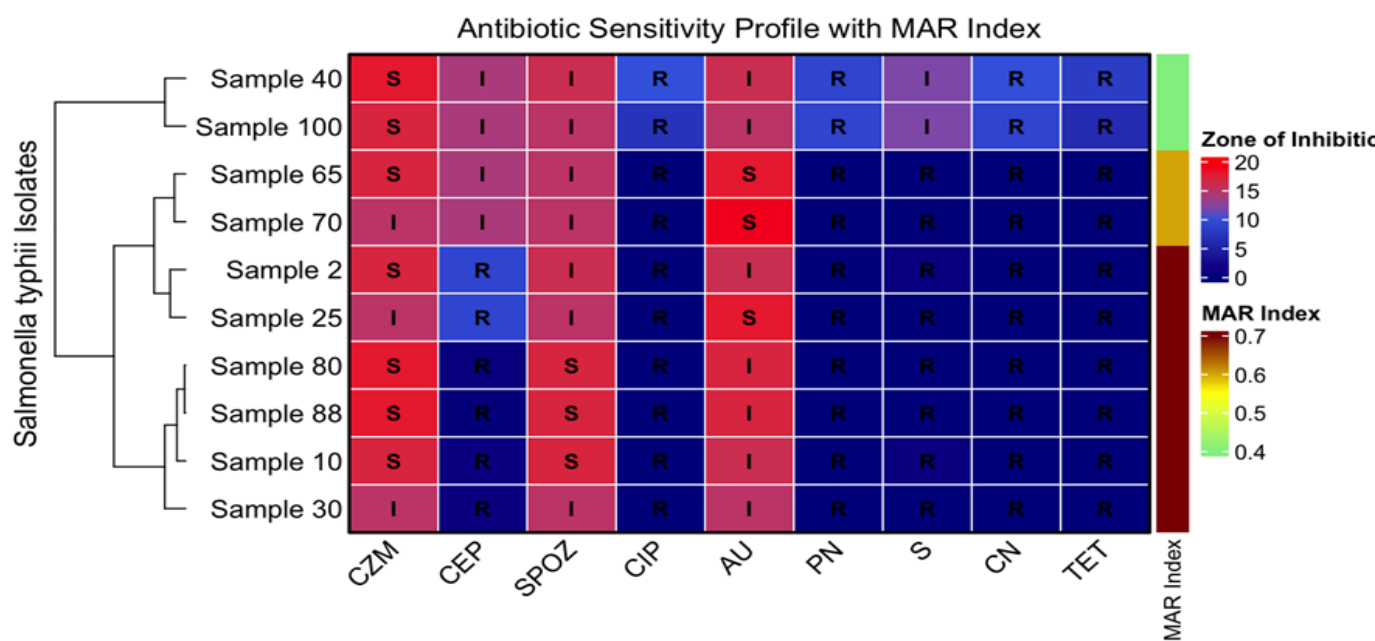


Figure 2: Antibiotic Sensitivity of uncured *Salmonella typhi* isolates

Key : R – Resistant, S – Susceptible, I - Intermediate, CZM – Cefixime clavulanate 10(μg) of class Cephalosporins , CEP – Ceporex 10(μg) of class Cephalosporins , SPOZ – Ornidazole/ofloxacin 25(μg) of class Fluoroquinolone , CIP – Ciprofloxacin 5(μg) of class Fluoroquinolone , AU – Augmentin 30(μg) of class Penicillin, PN - Amplicin 30(μg) of class Penicillin, S – Streptomycin 30(μg) of class Aminoglycoside, CN – Gentamycin 10(μg) of class Aminoglycoside, TET - Tetracycline 30 (μg) of class Tetracycline and MAR- Multiple antibiotic resistance.

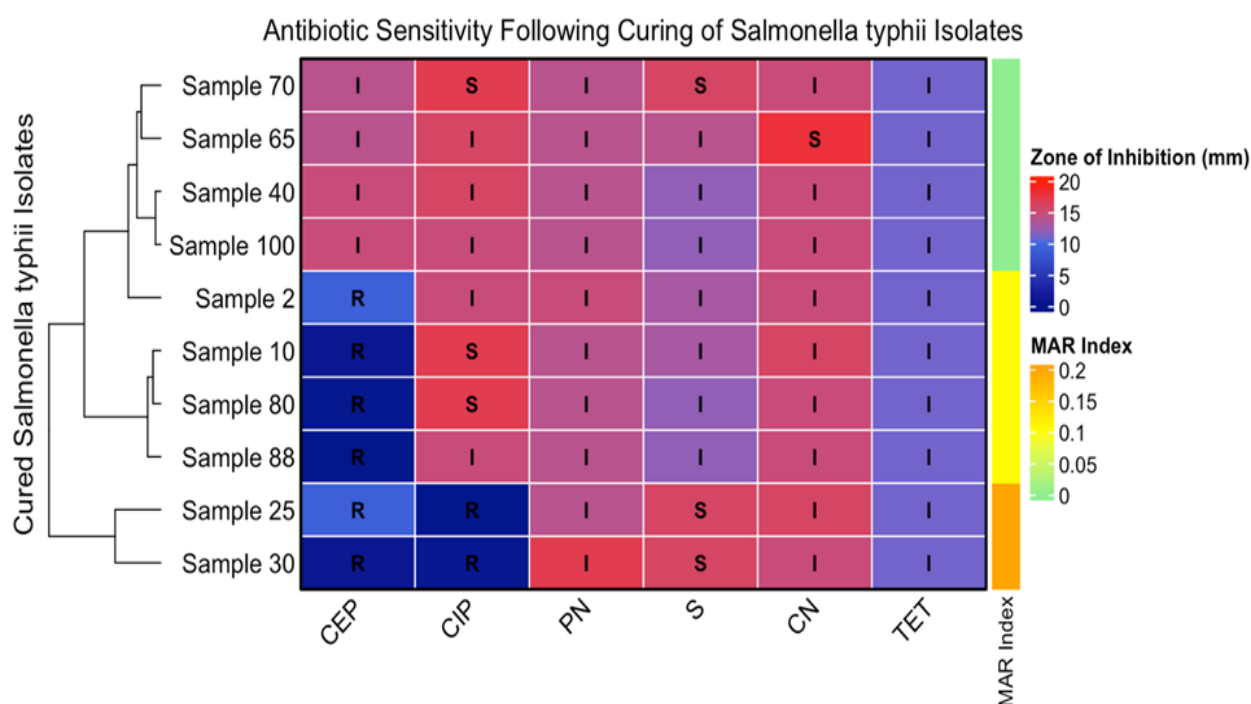


Figure 3 Heat map of the **Antibiotic Sensitivity of cured *Salmonella typhi* isolates**

Key : R – Resistant, S – Susceptible, I - Intermediate, CZM – Cefixime clavulanate 10(µg) of class Cephalosporins , CEP – Ceporex 10(µg) of class Cephalosporins , SPOZ – Ornidazole/ofloxacin 25(µg) of class Fluoroquinolone , CIP – Ciprofloxacin 5(µg) of class Fluoroquinolone , AU – Augmentin 30(µg) of class Penicillin, PN - Amplicin 30(µg) of class Penicillin, S – Streptomycin 30(µg) of class Aminoglycoside, CN – Gentamycin 10(µg) of class Aminoglycoside, TET - Tetracycline 30(µg) of class Tetracycline and MAR- Multiple antibiotic resistance.

CHAPTER FIVE

5.1

DISCUSSION

Salmonella infections are endemic in developing countries of Africa, including Nigeria. The findings of this study revealed the presence of *Salmonella* among IDPs in Guma, with a prevalence rate of 7.5%. In comparison, Logo had a prevalence rate of 12.5% for *S. typhi* infection, respectively. The difference in the isolation rates recorded between the two IDPs was significant, with $P = 0.000$. The variation in the isolation of the infection could be attributed to the location of the IDP camps. The Logo IDP camp was close to the central market. Some camp

areas were used as market extension, characterised by an unhygienic littered environment and poor living conditions. However, the prevalence rate of *Salmonella typhi* is inconsistent with that of Umeh and Agbulu(2009), who recorded an overall prevalence of 57.9% for *Salmonella typhi* infection in the central part of Benue State. Adikwu *et al.* (2018) in Southern Benue State, Nigeria reported a much higher prevalence isolation rate of *S. typhi* in the geographical zones of 64.2% in Oju LGA, followed by Okpokwu LGA, 55.5% and Ado LGA, with an isolation rate of 29.8% for *Salmonella typhi*, respectively. Uttah *et al.* (2013) reported 63.8% prevalence in Akwa Ibom State of Nigeria, Abioye *et al.* (2017) reported 62.70% prevalence in Karu LGA of Nasarawa State, Nigeria, Gbonjubola *et al.* (2009) recorded a prevalence rate of 69.0% in Zaria, Nigeria, and Odikamnoru *et al.* (2018) reported a prevalence rate of 49.4% in Afikpo North LGA, Ebonyi State, Nigeria. However, the findings of this study are higher than those of Akinyemi *et al.* (2018), who recorded a prevalence rate of 0.8% to 2.4% for *Salmonella typhi* in Abuja, Nigeria.

However, Tesfahun *et al.* (2016) reported a 10.8% occurrence of *Salmonella* spp. from diarrheic stools in a study conducted in Ethiopia, while Kabir *et al.* (2007) reported a 17% occurrence of *Salmonella* spp. from stool specimens of patients with gastroenteritis in a study conducted in Lagos, Nigeria. Several studies have reported the burden of typhoid fever in Africa. Knowledge of the burden of disease is essential in understanding the effects and trends of the disease on human health. In Egypt, Smith *et al.* (2016) reported an estimated incidence of typhoid fever of 59/100,000 persons/year. A study conducted in Ghana reported that typhoid fever was among the leading causes of outpatient illness, accounting for 0.92 % of hospital admissions.

Although the IDPs (Internally Displaced Persons) in Guma and Logo camps had access to boreholes for water supply, which may have contributed to the relatively low isolation rate of *Salmonella typhi* in these specific camps, the overall presence of *S. typhi* including in the

present study still indicates the persistence of unhygienic and poor living conditions typical of many IDP settings. This underscores a significant public health hazard in developing countries like Nigeria, where infrastructure and sanitation in IDP camps often remain inadequate. These findings align with WHO (2010), which highlights that waterborne diseases such as typhoid fever are closely linked to poor sanitation and hygiene, especially in vulnerable populations. , which opined that the vast majority of typhoid fever cases occur in Asia, Africa and Latin America, where water-borne diseases are highly prevalent, as well as unstable living conditions. Also, according to Okome-Nkoumou *et al.* (2000), typhoid or paratyphoid fevers are usually associated with unstable living conditions and lack of cleanliness. Antillon *et al.* (2017) stated that typhoid fever burdens the 5.5 billion people living in low and middle-income countries. Thus, the overall prevalence obtained from the study suggests concern for control measures of the infection in the affected IDP camps.

Regarding age, the difference in the prevalence rate of *S. typhi* within the age groups among IDPs in Guma and Logo was not significant. Age groups of 5 – 10years in Guma and Logo had the highest prevalence rate of 3.0% and 5.0% for *Salmonella typhi* infection, respectively. It could be inferred that children form the most vulnerable group in areas of poor environmental hygiene. Furthermore, their level of knowledge, which accounts for the quest or desire to satisfy their thirst irrespective of the water source, especially if the water appears to be clean and without colour adds to this challenge. Also, the higher prevalence in young children could be characterized by their underdeveloped immune systems and limited understanding of disease transmission, which heightens risk of infection. This corroborates previous reports by Adikwu *et al.* (2018), who reported a prevalence rate of *S. typhi* concerning the age range of ≤ 10 years, though with a much higher prevalence occurrence of 52.7%. Also, an age group with a slightly higher range of 1 – 15years differ with the highest prevalence rate of 80.95% reported by

Abioye *et al.* (2017). According to WHO (2018), Crump and Mintz (2010), the burden of typhoid fever is highest in infants, children and young adults.

A high isolation rate was recorded among the older group of >43 years with 2.25% in Guma and 3.75% in Logo. The infection rate could be due to occupational hazards ranging from farming related water contact activities as many IDPs were out to do jobs so as to feign for their families. Also, this could be attributable to suppressed immune system associated with older adults and consumption of poorly prepared or unhygienic food. This is consistent with the findings of Adikwu *et al.* (2018), who recorded an age range of >43 years with an occurrence rate of 51.4% for *Salmonella typhi* infection.

With regards to gender, the *Salmonella typhi* isolation rate showed a female preponderance over males. In Guma, IDPs had 5.0% for females and 2.5% for males, while Logo had 8.75% for females and 3.75% for males, respectively. This could be attributed to the higher population of females available for exercise than males. According to a report by one of the IDPs, attention from concerned authorities towards the IDPs' upkeep was poor and not enough to cater for their family needs. Thus, most men were out to do casual jobs to provide for their families. Additionally, male folks in the study areas engaged in farming activities away from their camps, while some men returned to defend their farms, believing that giving up their ancestral inheritance to the Fulani was taboo. However, the higher exposure of females to *S. typhi* could be due to their physiological status (pregnancy, malnutrition and postpartum period such as low immunity due to blood loss), hormonal imbalance and gender specific activities (food preparations may exposed them to contaminated raw foods, caregivers to children which may exposed them to fecal contaminants as wells transmission from the sick loved ones). This is in consistent with earlier findings in different Nigerian cities, including Abeokuta, South-Western Nigeria, where the distribution of *Salmonella typhi* was 54.8% in females and 45.2% in males (Okonko *et al.*, 2010), and Abioye *et al.* (2017) reported an infection rate of 71.43%

in females and 53.97% in males of Karu LGA of Nasarawa State, Nigeria. The findings of the present study were not consistent with reports by Adikwu *et al.* (2018), who recorded males with an isolation rate of 46.8% compared to females of 39.6% and Gbonjubola *et al.* (2009), who recorded 45.2% female and 54.8% male positivity for *Salmonella typhi*. Regarding accommodation in Camps, Guma, IDPs in Block B had a higher prevalence rate of 4.5% while in Logo, Block A had a higher prevalence rate of 7.0%. The prevalence rate of *Salmonella typhi* could be attributed to their locations close to nearby bushes where they defecate and indiscriminately dispose of domestic waste. This is consistent with the reports of Umeh and Agbulu (2009) and Okome-Nkoumou (2000), who opined that most communities with limited toilet facilities and effective waste disposal systems were observed defecating in nearby bushes and indiscriminately disposing of domestic wastes. It also corroborates with Ajayi *et al.* (2015) who stated that people with limited good toilet facilities resort to nearby bushes for defecation. Pertaining to Occupation, Guma IDPs had a least rate of 0.25% for Civil servant, 0.5% for Business men, high rate of 3.25% for Students and higher occurrence rates among Farmers with 3.5% while in Logo, Civil servant had least rate of 0.25%, Business men had 0.5%, Students had high rate of 4.75% and Farmers had higher rate of 7.0% for *Salmonella typhi* infection respectively. The higher prevalence among students could be inferred from the fact that the population of this status consists of children and young adults whose intellectual and mental capability is not developed enough to maintain required hygiene. This is consistent with the previous reports by WHO (2010) and Crump and Mintz (2010), who reported burden of typhoid fever higher in infants, children, and young adults. Also, their level of ignorance accounts for quest or desire to satisfy their thirst irrespective of the water source, especially if the water appears clean and without colour. Furthermore, the prevalence rate of 7.0% was recorded among farmers in the study. This could be attributed to the fact that farming leads to disease transmission through direct and indirect contact of contaminated soil, water,

equipment, and contaminated animal or plant products while farming. Many farmers in the study areas engaged in farming activities away from their camps, exposing themselves to ingesting other water sources and foods. This is not consistent with the findings of Ajayi *et al.* (2015), who recorded a prevalence rate of 38% in civil servants and farmers, showing at least an occurrence rate of 12%. More so, low educational status is associated with ignorance, poverty and poor personal hygiene as supported by a report conducted by Ajayi *et al.*, (2015). On personal hygiene, IDPs in Guma who were inconsistent with washing their hands after using the toilet had a higher prevalence rate of 4.5% while Logo IDPs had the highest prevalence rate of 11.25%. This infection could be attributed to contact with faecal contamination, which increases the risk of transmission of *Salmonella typhi* infection. This finding is supported by a study conducted by Nyamusore *et al.* (2018), who opined that inconsistent washing of hands after using the latrine/toilet was a risk factor in disease transmission. They added that having close contact with cases and poor hand washing practices with no soap were risk factors that increased person-to-person transmission of *Salmonella typhi*. IDPs who were inconsistent in carrying out sanitation in Guma had a higher prevalence rate of 4.75% while Logo IDPs had the highest prevalence rate of 10.0%. The littered environment with debris and garbage may have contaminated food materials or drinking water, which could increase the risk of *Salmonella typhi* transmission. Also, with the level of ignorance of children, they can pick up contaminated materials into their mouths as well as use unwashed, contaminated hands for eating. Another factor with regard to personal hygiene was their methods of refuse disposal. In Guma, IDPs who disposed of refuse indiscriminately (open waste) had a higher rate of 6.25% while Logo IDPs had the highest occurrence rate of 11.25% for *Salmonella typhi* infection. It is possible that the littered environment with garbage could have contaminated food materials or drinking water, which could increase the risk of disease transmission. House flies and other insects could increase the chances of having the disease.

This is in line with Nyamusore *et al.* (2018), who opined that young children who were infected with *Salmonella typhi* were playing in and around littered environments and open waste water trenches that were likely contaminated in Mahama refugee camp, Rwanda.

Regarding risk factors, IDPs who agreed they were overcrowded in Guma had a high rate of 7.0%, while those who disagreed had a low occurrence rate of 0.5%. In contrast, IDPs who agreed they were overcrowded in Logo had the highest rate of 12.0% compared to those who disagreed, with a low % occurrence rate of 0.5%. There was a lack of adequate space in the camps; therefore, many families were observed to be preparing and consuming their food next to open waste water trenches, which could predispose IDPs and increase the risk of food contamination. This is corroborated by previous studies in Zimbabwe by Muti *et al.* (2011) and in Indonesia, Vollaard *et al.* (2004). In Rwanda, Nyamusore *et al.* (2018) opined that crowded living conditions and poor sanitation were associated with outbreaks of typhoid fever. Moreover, IDPs whose meals were from camp markets in Guma had a high rate of 5.0% while those from personal kitchens had 2.5%. While in Logo, those whose meals were from the camp market had an occurrence rate of 1.25% while those whose meals were from a personal kitchen had the highest prevalence rate of 11.25%. The high prevalence of IDPs whose meals were from the camp market indicated that foods sold in the market may have been infected by *Salmonella typhi*, and poor enforcement of food safety and hygiene in the camp markets was lacking, although, it was not the case in both camps. This is in line with Nyamusore *et al.* (2018), who stated that foods prepared in the camp markets possess a higher risk of disease transmission as they were poorly prepared or unhygienic for consumption. They added that Utensils such as cups were not properly cleaned and were being shared between multiple clients of the alcoholic beverage sellers in the market. However, the prevalence rate with regard to IDPs who prepared personal meals could suggest the presence of a higher rate of person-to-person transmission, poor living conditions, poorly prepared food, as well as poor personal

hygiene practices among IDPs. Another factor concerning risk factors was the sources of water. IDPs using a borehole as a water source in Guma had 5.25% while those using rain had 2.25% for *Salmonella typhi* infection. IDPs in Logo who used a borehole as water source had a higher prevalence rate of 8.75% while those who used rain had a prevalence rate of 3.75% for *Salmonella typhi* infection. The prevalence rate of IDPs that use borehole water could be attributed to contamination of water, which may result from unhygienic practices and poor awareness of the safety measures of water usage among IDPs. In addition, rainwater without disinfection increases the risk of transmission of *Salmonella typhi* infection. This finding is lower than the report by Ajayi *et al.* (2015), who recorded a prevalence rate of 35.60% for persons who sourced their water from the borehole.

As for awareness of the Disease, Guma IDPs who did not know about the disease as well as previous treatment had higher prevalence rate of 6.25% compare to those who were treated 1 – 3 times, had low occurrence rate 0.25%, those who were treated 4 – 6 times had 0.5% and those who were treated above 7 times had 0.5% while Logo IDPs with no knowledge of the disease as well as previous treatment had the highest prevalence rate of 11.0% than those who were treated 1 – 3 times had low occurrence rate 0.25%, those who were treated 4 – 6 times had 0.5% and those who were treated above 7 times had 0.75% all for *Salmonella typhi* infection respectively. The higher prevalence rate concerning IDPs who had no awareness of the disease could be due to a lack of understanding, which is known to be associated with poor compliance with typhoid prevention and control practices. This is supported by findings conducted by Issa *et al.*(2015) and Nyamusore *et al.*(2018), who opined that a lack of awareness is associated with poor compliance with typhoid prevention and control practices.

On the subject of duration in camps, Guma IDPs who spent <1year (less than a year) had less occurrence rate of 0.75%, those who spent 1 – 2years had prevalence rate of 2.5% and those who spent more than 2years had a higher prevalence rate of 4.25% while Logo IDPs who spent

<1year (less than a year) had less occurrence rate of 0.5%, those who spent 1 – 2years had prevalence rate of 2.5%. Those who spent more than 2years had highest prevalence rate of 9.5% all for *Salmonella typhi* infection respectively. The prevalence rate associated with IDPs who had spent more years in camp could be due to the unhygienic and poor living conditions. This is consistent with a report by Nyamusore *et al.*(2018) who opined that Refugees in Mahama camp who spent more than six months had a higher prevalence rate of 76.9%. Also, according to a report by one of the IDPs, who said that longer stay in the camp was enough risk to kill anyone, as they were not receiving adequate attention from concerned authorities.

About toilet systems, Guma IDPs who indulged in open defecation or nearby bush had higher infected rate of 4.5% than those who used latrine had occurrence rate of 3.25% while Logo IDPs who indulged in open defecation or nearby bush had highest infected rate of 7.0% than those who made used latrine with occurrence rate of 5.5% for *Salmonella typhi* infection. The prevalence rate with respect to IDPs who used nearby bushes could be as a result of the infection being transmitted through house flies, inconsistent washing of hands, and other factors such as rain and wind Nyamusore *et al.* (2018). More so, according to one of the IDPs, going to nearby bushes was easier, as was accessing leaves used as toilet paper for cleaning, which indeed is unhygienic and ineffective. House flies and inconsistent hand washing could cause the transmission of infection. This is consistent with the findings of Nyamusore *et al.* (2018) and Akullian *et al.* (2015), who stated that infection via house flies from human waste to food may also be possible in the environment. They added that typhoid fever cases were clustered around latrines, where houseflies were usually prevalent. According to Ajayi *et al.* (2015), nearby bushes are traditionally considered for defecation wherever good toilet facilities are lacking.

Concerning marital status, IDPs who were married in Guma had an occurrence rate of 2.5%. In comparison, those who were single (unmarried) had a higher occurrence rate of 5.0% for

Salmonella typhi infection. More so, Logo IDPs who were married had an infection rate of 3.25% and those who were single had the highest occurrence rate of 9.25% for *Salmonella typhi* infection. The prevalence rate associated with the unmarried could be attributed to the living habits of this group, as a greater proportion of the population were children with poor knowledge of the prevention and control of the disease. Also, it could be that unmarried persons had unrestricted liberty to eat outdoor foods, which increases the risk of *Salmonella typhi* transmission. This is in agreement with Ajayi *et al.*, (2015) who opined that the unmarried have unrestricted liberty to eat hawked food, patronize restaurants and eateries, most of which encourage chain transmission of typhoid fever infection. In contrast, the married group as marriage demands makes it mandatory for a sizeable number of them to cook in their homes paying close attention to basic hygienic practices.

Concerning emotional needs, the results presented highlight significant concerns regarding the emotional and psychological well-being of internally displaced persons (IDPs) and their vulnerability to *Salmonella typhi* infections. In Guma IDPs, those who experienced depression due to loss, physical trauma (like fractures and amputations) had a *Salmonella typhi* infection rate of 4.5%, compared to 3.0% among those who were not depressed. In Logo IDPs, the rates were higher, with depressed individuals showing a 6.75% infection rate vs. 5.75% for non-depressed individuals. The study suggests a correlation between emotional distress and increased susceptibility to infections. Psychological stress resulting from substantial life changes, such as losing loved ones and coping with disabilities, can weaken the immune system, making individuals more prone to infections such as *Salmonella typhi* Mooney (2005). Depression itself can lead to changes in behaviour, hygiene practices, and healthcare-seeking behaviours, which may further increase susceptibility to infection Mooney (2005).

The findings align with WHO/EHA (2000) and Mooney (2005), who opined that displacement can negatively affect health status and IDPs often face a loss of social support, instability, and

limited access to healthcare services, all of which can exacerbate both mental and physical health issues. Also, studies have been conducted about health problems, including depression among IDPs in Darfur (Hamid *et al.*, 2010), in Northern Uganda (Roberts *et al.*, 2008) and malnutrition among IDPs in Northern Uganda, in Eastern Chad and Sierra Leone (Olwedo *et al.*, 2008; Guerrier *et al.*, 2009; Gbakima *et al.*, 2012) and infectious diseases, including typhoid (Guerrier *et al.*, 2009; Kim *et al.*, 2007).

Concerning medication, Guma IDPs who carried out self-medication had an occurrence rate of 4.5% while those who made use of the Camp clinic had an occurrence rate of 3.0%. In Logo, IDPs who carried out self-medication had the highest occurrence infection rate of 8.0%, compared to those who made use of the Camp clinic, who had an occurrence rate of 4.5% for *Salmonella typhi* infection. The higher frequency of self-medication and prevalence rate could be because healthcare facilities were lacking. According to one of the IDPs, only one community healthcare worker was assigned, and there were inadequate healthcare facilities available in the camp. This is in line with a report by Nyamusore *et al.* (2018), who opined that lack of good healthcare services was the primary motivator for self-medication in refugees in Rwanda, which further supports this finding.

Antibiotic-resistant *Salmonellae* are a significant public health concern, especially in Africa and Nigeria. Findings from previous studies indicate an increase in the emergence of antibiotic-resistant strains. The spread of antimicrobial resistance has become a global public health problem, resulting in treatment failure, causing economic and health retardation. It is generally acknowledged that the misuse of antimicrobial agents brings about the emergence and proliferation of antimicrobial-resistant microorganisms and the subsequent dissemination of drug-resistant bacteria and resistant genes. In this study, *Salmonella typhi* isolates were most resistant to Ciprofloxacin (CIP), Ampicillin (PN), Gentamycin (CN) and Tetracycline (TET). This is consistent with the findings of Abdullahi *et al.* (2014), who reported high resistance to

Ampicillin (94.2 %), Chloramphenicol (72.8 %) and lower resistance (31.8 %) to Cotrimoxazole among *Salmonella* serotypes in Katsina State, Nigeria.

Gaind *et al.*, (2006) and Smith *et al.* (2016) added that multidrug resistance to the traditional first-line antimicrobial agents, namely Ampicillin, Chloramphenicol and Tetracycline, is common among *S. typhi*. This implies a significant challenge for healthcare systems because effective treatment options for the disease are reduced, hence leading to complications and death. Also, the Multiple Antibiotic Resistance Index (MARI) of the uncured *Salmonella typhi* isolates was calculated. Samples 02, 10, 30, 25, 80 and 88 had the highest index (0.7), followed by Samples 70 and 65 (0.6 each). Isolates Sample 40 and 100 had the lowest MARI (0.4 each). This is in line with the findings of Ekwem *et al.*(2024), who recorded higher results of the Multiple Antibiotic Resistance Index (MARI) of *Salmonella typhi* isolates S11 having the highest index (1.0), followed by S6 and S12 (0.7 each). Isolates S15, N2, N3, and N10 had the lowest MARI (0.2 each) in Enugu state.

Furthermore, the Multiple Antibiotic Resistance (MAR) index of *Salmonella typhi* isolates before and after plasmid curing was measured, with higher values indicating greater antibiotic resistance. The MAR index of bacterial isolates before plasmid curing represents their resistance profile with plasmids present. This aligns with Mirza *et al.* (2000), Holt *et al.* (2011) and Ekwem *et al.*(2024), who stated that plasmids often carry antibiotic resistance genes, contributing to higher MAR indices.

However, after plasmid curing, which involves the removal or deactivation of plasmids, a significant decrease in the MAR index was observed in most isolates. This indicates that the plasmids were responsible for the antibiotic resistance in these isolates. The Multiple Antibiotic Resistance (MAR) index of Samples 30 and 25 was lower (0.2), followed by Samples 10,02,80 and 88 with (0.1), and the zero indices observed in isolates Sample 40, 100, 65 and 70 (0.0)

each. This aligns with the findings of Ekwem *et al.*(2024), who recorded a lower Multiple Antibiotic Resistance (MAR) index of *Salmonella typhi* isolates after plasmid curing.

The plasmid profiling for the ten *Salmonella typhi* isolates initially revealed the presence of plasmids within the high molecular weight range of 11kbp to 12kbp. This suggests diverse plasmid sizes among the isolates, reflecting the strains within *Salmonella typhi* isolates. This was in line with Ekundayo (2021), who reported different plasmid weights of *Salmonella typhi* isolates.

In this study, specific alterations in the plasmid profiles were observed following the plasmid curing process. Isolates in wells 01, 02, 03, 05, 06, 07, 08, 09 and 10 notably changed by losing their bands. This outcome indicates a targeted impact of plasmid curing, potentially associated with antibiotic resistance. This concurs with the findings of Ekwem *et al.*(2024), who recorded alterations in the plasmid profiles, which exhibited a notable change by losing their bands.

Conversely, this present study did not retain many plasmids (resistance genes) after curing, unlike the findings of Perez-Perez *et al.*(2002), Ekundayo (2021), and Okoye *et al.* (2022), who recorded some bacterial isolates that retained plasmid resistance, totally or partially, to the same drugs after curing. This suggests that plasmid elimination did not significantly impact the plasmid content in these isolates within the observed molecular weight range, stating that the antibiotic resistance from those isolates could be due to the resistance genes that were chromosomally mediated.

The identification of *Salmonella typhi* by molecular methods indicated the presence of the *STY0307* gene, a specific genetic marker for *Salmonella typhi* from the isolates. This aligns with the study of Goay *et al.* (2016), who recorded similar genes. They added that the *STY0307* genes in *Salmonella typhi* demonstrated 100% sensitivity (39/39). PCR assays using *STY0307*

were developed and found to be highly specific at single-gene target resolution to diagnose typhoid fever (Goay *et al.*, 2016).

The detection of *bla-TEM* resistance genes among the *Salmonella typhi* isolates in the study implies that these genes were most likely responsible for the phenotypic resistance observed, hence conferring resistance to the *beta-lactam* antibiotics, including resistance to Ampicillin. This concurs with Nuanmuang *et al.*(2024), who reported a high level of ampicillin resistance among *Salmonella typhi* isolates. He added that ampicillin-resistant *Salmonella typhi* isolates carried the *blaTEM* gene, making it the most prevalent beta-lactamase resistance gene. Nair *et al.* (2018) reported that the *blaTEM* gene encodes for beta-lactamase, an enzyme that hydrolyses beta-lactams, e.g., ampicillin, penicillins, cephalosporins, etc. According to Mohammedkheir *et al.* (2024), Gram-negative bacilli, including *Salmonella typhi* isolates, were resistant to amikacin, cefotaxime, ceftazidime, ceftriaxone, cefixime, ciprofloxacin, gentamycin, imipenem, meropenem, norfloxacin, and trimethoprim. It was attributed to the encode of betalases which hydrolyses betalactam in some antibiotic causing treatment failure.

The *tetA* gene, which confers resistance to most antibiotics such as tetracycline, was detected in the study. This is in harmony with the study of Aslam *et al.* (2012), who reported that the *tetA* gene in *Salmonella typhi* encodes an efflux pump that can expel tetracycline from the bacterial cell, rendering the antibiotic ineffective. They added that the *tetA* genes in *Salmonella typhi* consist of strong tetracycline resistance genes. This work reveals the presence of the *invA* gene among *Salmonella* isolates. This is in harmony with the studies of Marcus *et al.* (2000), who recorded that the gene is located in *Salmonella* Pathogenicity Island (SPI); the DNA region is related to the pathogenicity of *Salmonella enterica* and is owned by all serotypes. They added that the SPI1 is a 40 kb island that encodes for the type III secretion system (T3SS) that contributes to the pathogenesis of *Salmonella* by transporting effector protein complexes into

host cells. More so, Darwin and Miller (1999) and Akinyemi *et al.* (2021) reported that the first step in the intracellular pathogenicity cycle of *Salmonella* is the invasion of intestinal epithelial cells, and the *invA* gene controls this step. They added that the *invA* gene encodes proteins in bacterial cell membranes that are needed for invasion into host epithelial cells. Akinyemi *et al.* (2021) detected the *invA* gene among 75% of the isolated *Salmonella* spp. in Lagos. Almas *et al.* (2021) reported that 70% of isolated *Salmonella* spp. in Lahore had confirmed the presence of *invA* genes. Kanteh *et al.* (2021) reported that invasive *Salmonella* spp constituted about 10% of the total *Salmonella* spp in the Gambia. Isolates had *invA* genes.

This study recorded no amplification of virulent gene *fliC-d* among the chosen isolates, indicating that the selected virulence gene does not exist, but does not rule out the presence of other virulence genes. This work differs from the findings of Yulian *et al.* (2020), who recorded the virulent gene *fliC-d* located in the *Salmonella* virulence plasmid. They added that the plasmid contains genes that contribute to the virulence of *Salmonella*, including the *fliC-d* gene, which encodes for the flagellin protein. The flagellin protein is a key component of the flagellum, which is a whip-like structure that allows *Salmonella* to move and colonise its host. *fliC-d* encodes the synthesis of Vi (capsule), O (LPS), and antigen H (flagellar). Each antigen becomes the basis of detection and classification for *Salmonella* by the Kauffmann-White scheme, which is a classification system that permits serological varieties of the genus *Salmonella* to be differentiated from each other (Kumar *et al.*, 2006; Figueira and David, 2012; Mthembu, 2019).

5.2 Findings

The findings from the study are as follows:

1. The prevalence rate of *Salmonella typhi* infection was higher in Logo IDP camp 50(12.5%) than in Guma IDP camp 30(7.5%), and of the 400 samples, 80(20.0%) were positive for *Salmonella typhi*
2. *Salmonella typhi* isolates from Logo and Guma were generally resistant to Ceporex, Ciprofloxacin, Ampicillin, Streptomycin, Gentamycin and Tetracycline
3. *Salmonella typhi* isolates had *invA* virulent gene with 80% , *tetA* resistance gene 50%, and *blaTEM* resistance gene with 100%.
4. Most resistant genes in *Salmonella typhi* isolates in the study areas were plasmid-mediated
5. *Salmonella typhi* isolates in the study areas showed specificity for the gene *STY0307* with 75%.

5.3 Contribution to Knowledge

The contributions of this study are as follows:

1. The prevalence rate of *Salmonella typhi* among IDPs in Guma and Logo is now documented.
2. Virulent and antibiotic-resistant genes were detected in *Salmonella typhi* isolates from Logo and Guma IDPs in Benue state.
3. This research contributes to the growing body of knowledge on the epidemiology of *S. typhi* in displaced populations and underscores the necessity for integrated public health interventions.
4. Antibiotic-resistant *Salmonella typhi* isolates in the study were plasmid-mediated.

5.4 Conclusion

This study provides critical insights into the prevalence of potentially virulent and multidrug resistant *Salmonella typhi* among internally displaced persons (IDPs) in Logo and Guma local government areas of Benue State, Nigeria. The findings underscore a significant public health concern, with a notable burden of *S. typhi* infections detected among the IDP populations. Molecular analyses revealed the presence of key virulence-associated genes and antimicrobial resistance determinants, highlighting the adaptive potential of *S. typhi* strains circulating in these communities. Detecting multidrug-resistant (MDR) profiles and virulent gene markers raises alarms regarding the treatment potentials and disease management among vulnerable populations. These outcomes not only emphasise the urgent need for strengthened surveillance and targeted antimicrobial stewardship programs but also call attention to the broader socio-environmental determinants contributing to disease transmission, including poor sanitation, overcrowding, and limited access to healthcare within IDP camps. Stakeholders and policymakers must prioritise health infrastructure, routine screening, and education within IDP settings to curb the spread of resistant and virulent *S. typhi* strains.

5.5 Recommendations

A number of specific strategies are hereby recommended for effectively controlling and managing *Salmonella typhi* infection in the study areas.

- (i) The Government should institute a clinic with good healthcare facilities and basic life utilities, such as a sound toilet system in IDP camps.
- (ii) Government provision of free routine screening, adequate treatment, and a management plan for those who test positive.
- (iii) Enlightenment programs on basic rules of personal hygiene and disinfection of drinking water, either by boiling, chlorination or addition of sodium aluminate (alum), should be encouraged.

- (iv) There should be provision of counsellors (experts) who would give help to the psychological and emotional needs of depressed IDPs.
- (v) The government should provide suitable accommodation in good sites and decongest the population spike among IDPs.
- (vi) Organising health education classes for the IDPs about the various risk factors of *Salmonella typhi* infection and designing an effective preventive program through routine assemblies.
- (vii) Diagnosis of *Salmonella typhi* by molecular methods.

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APPENDIX I
Statistical Analysis

Age-related values
Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Age group * Number infected	80	100.0%	0	0.0%	80	100.0%

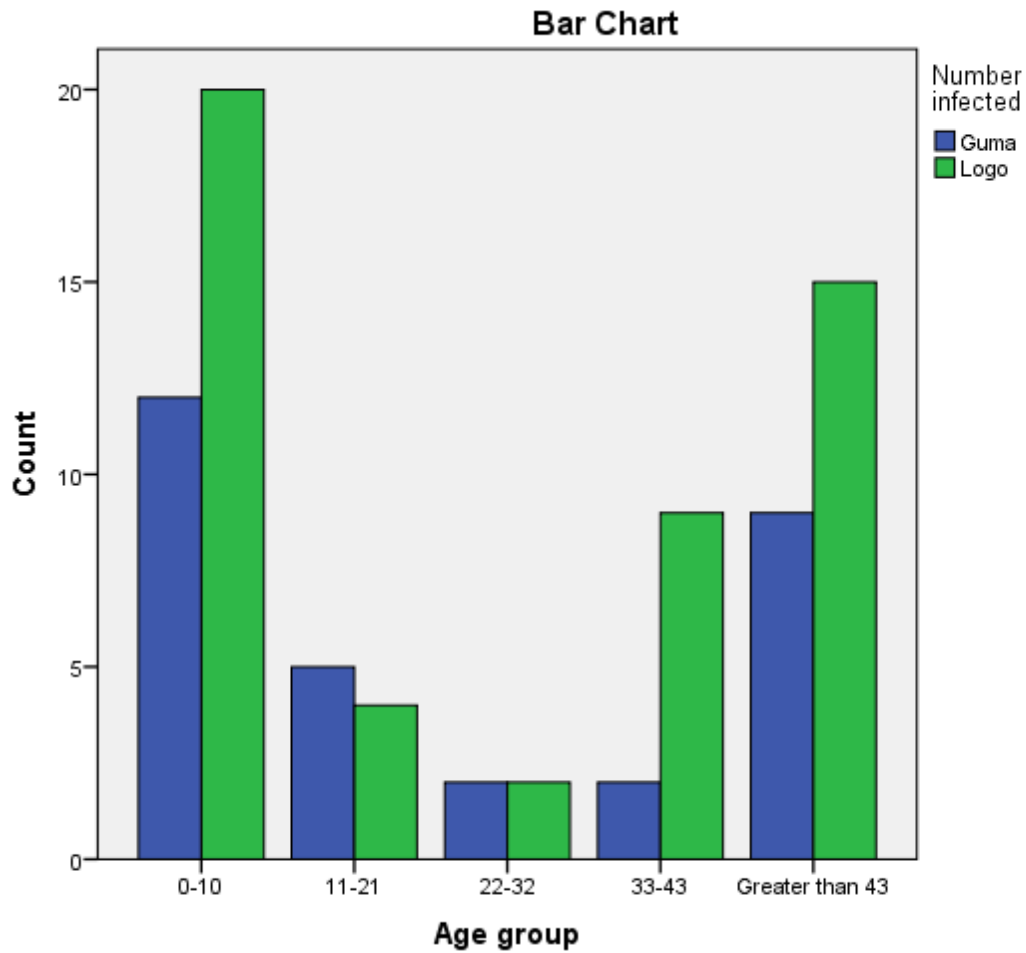
Age group * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
0-10	Count		12	20	32
	Expected Count		12.0	20.0	32.0
11-21	Count		5	4	9
	Expected Count		3.4	5.6	9.0
22-32	Count		2	2	4
	Expected Count		1.5	2.5	4.0
33-43	Count		2	9	11
	Expected Count		4.1	6.9	11.0
Greater than 43	Count		9	15	24
	Expected Count		9.0	15.0	24.0
Total	Count		30	50	80
	Expected Count		30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.270 ^a	4	.514
Likelihood Ratio	3.413	4	.491
Linear-by-Linear Association	.245	1	.620
N of Valid Cases	80		

a. 4 cells (40.0%) have expected count less than 5. The minimum expected count is 1.50.



Age prevalence of *Salmonella typhi* infection

**Depression from death of love ones
Case Processing Summary**

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Depression from death of love ones * Number infected	80	100.0%	0	0.0%	80	100.0%

Depression from death of love ones * Number infected Crosstabulation

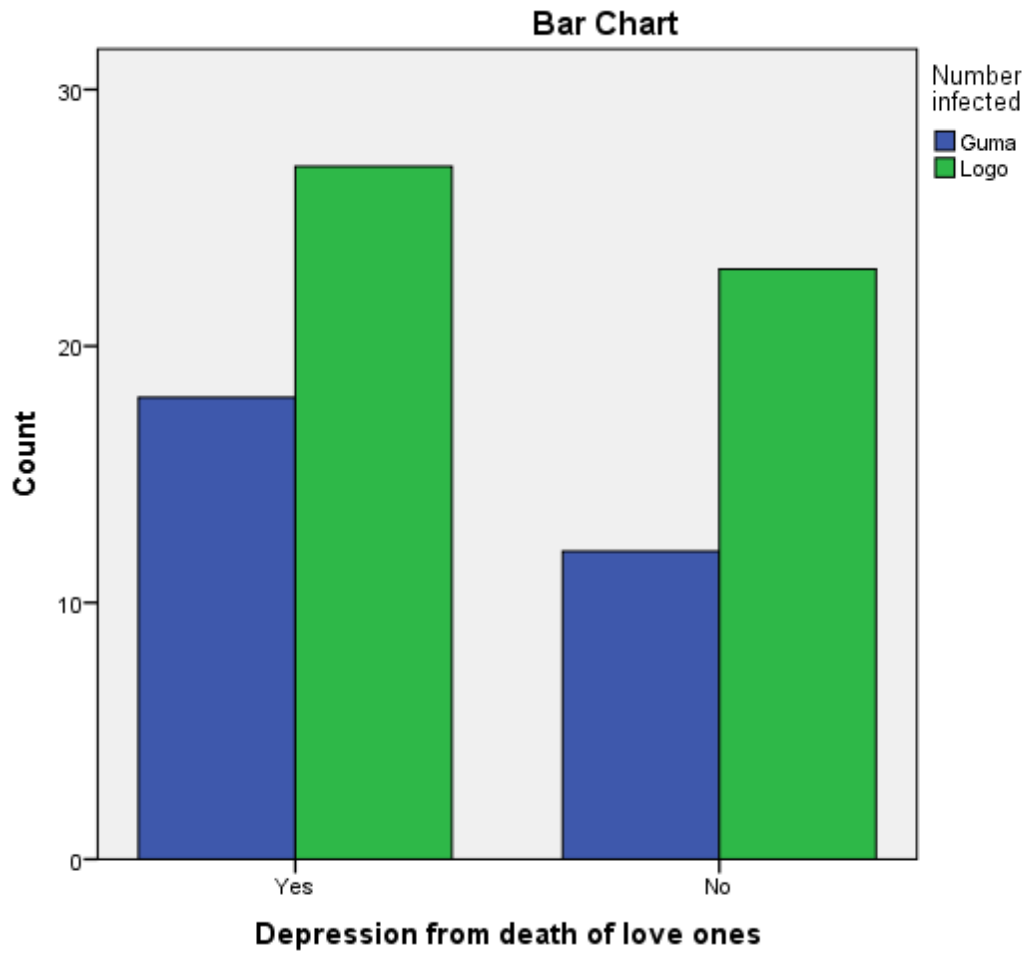
			Number infected		Total
			Guma	Logo	
Depression from death of love ones	Yes	Count	18	27	45
		Expected Count	16.9	28.1	45.0
	No	Count	12	23	35
		Expected Count	13.1	21.9	35.0
Total	Count	30	50	80	
	Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.274 ^a	1	.600		
Continuity Correction ^b	.085	1	.771		
Likelihood Ratio	.275	1	.600		
Fisher's Exact Test				.647	.387
Linear-by-Linear Association	.271	1	.603		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 13.13.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to Depressed IDPs

**Camp area-related
Case Processing Summary**

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Camp Area * Number infected	80	100.0%	0	0.0%	80	100.0%

Camp Area * Number infected Crosstabulation

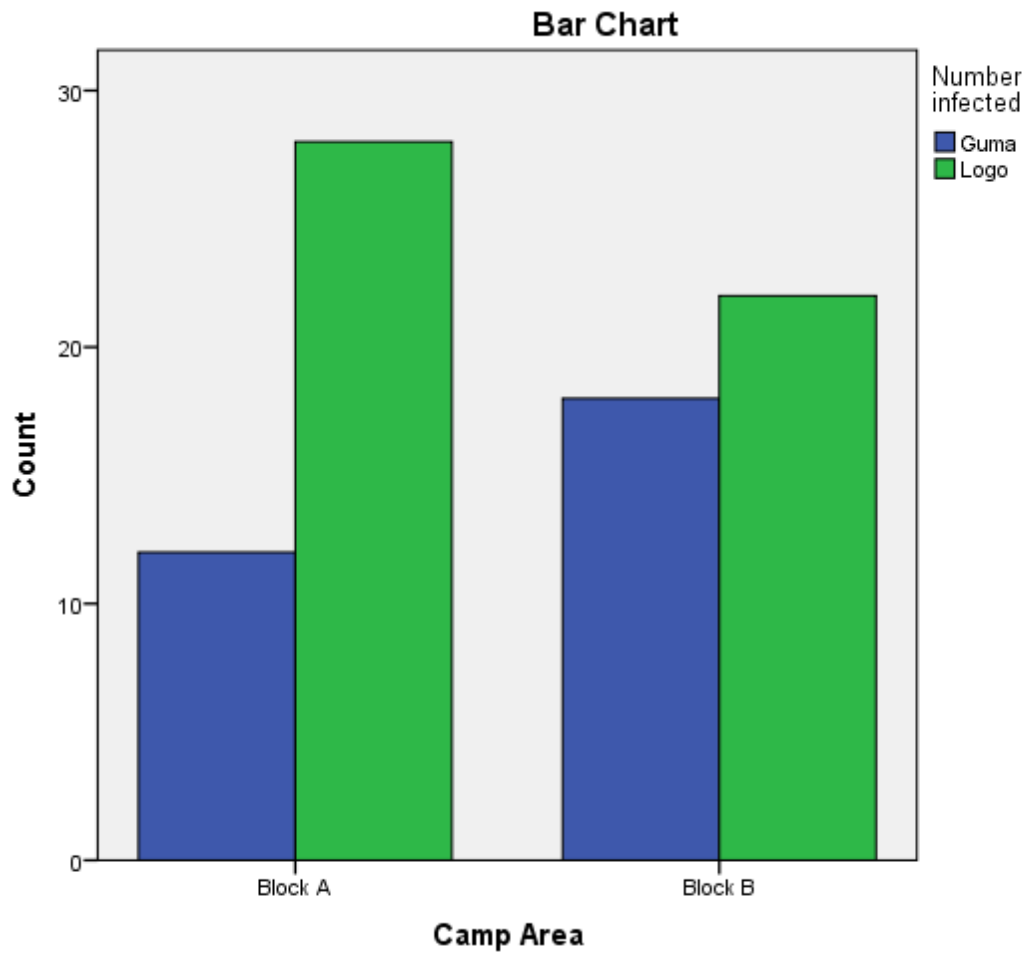
		Number infected		Total	
		Guma	Logo		
Camp Area	Block A	Count	12	28	40
		Expected	15.0	25.0	40.0
	Block B	Count	18	22	40
		Expected	15.0	25.0	40.0
Total		Count	30	50	80
		Expected	30.0	50.0	80.0

Chi-Square Tests

	Value	Df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	1.920 ^a	1	.166		
Continuity Correction ^b	1.333	1	.248		
Likelihood Ratio	1.930	1	.165		
Fisher's Exact Test				.248	.124
Linear-by-Linear Association	1.896	1	.169		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 15.00.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* in relation to accomodation

Camp duration-related

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Camp duration * Number infected	80	100.0%	0	0.0%	80	100.0%

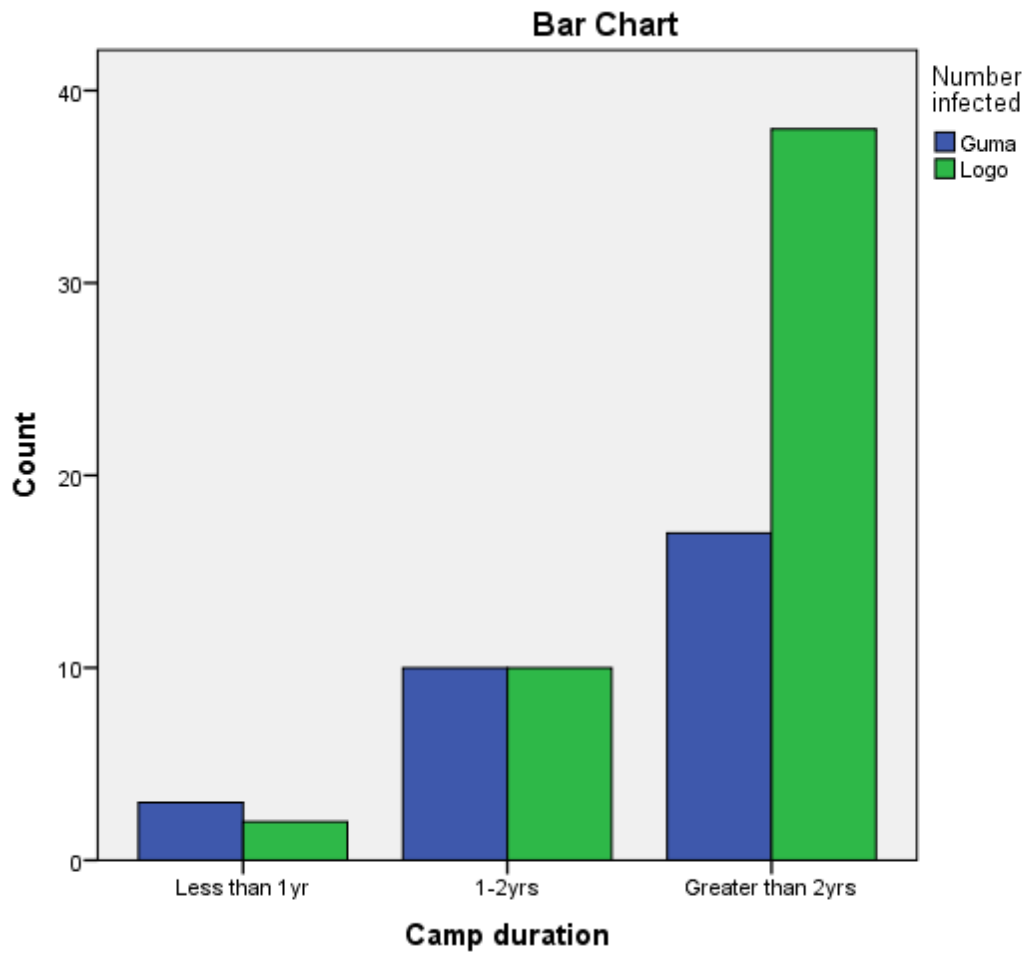
Camp duration * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Camp duration	Less than 1yr	Count	3	2	5
		Expected Count	1.9	3.1	5.0
	1-2yrs	Count	10	10	20
		Expected Count	7.5	12.5	20.0
	Greater than 2yrs	Count	17	38	55
		Expected Count	20.6	34.4	55.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.433 ^a	2	.180
Likelihood Ratio	3.373	2	.185
Linear-by-Linear Association	3.307	1	.069
N of Valid Cases	80		

a. 2 cells (33.3%) have expected count less than 5. The minimum expected count is 1.88.



Prevalence of *Salmonella typhi* infection in relation to duration in camp

**Daily Meals
Case Processing Summary**

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Daily meals * Number infected	80	100.0%	0	0.0%	80	100.0%

Daily meals * Number infected Crosstabulation

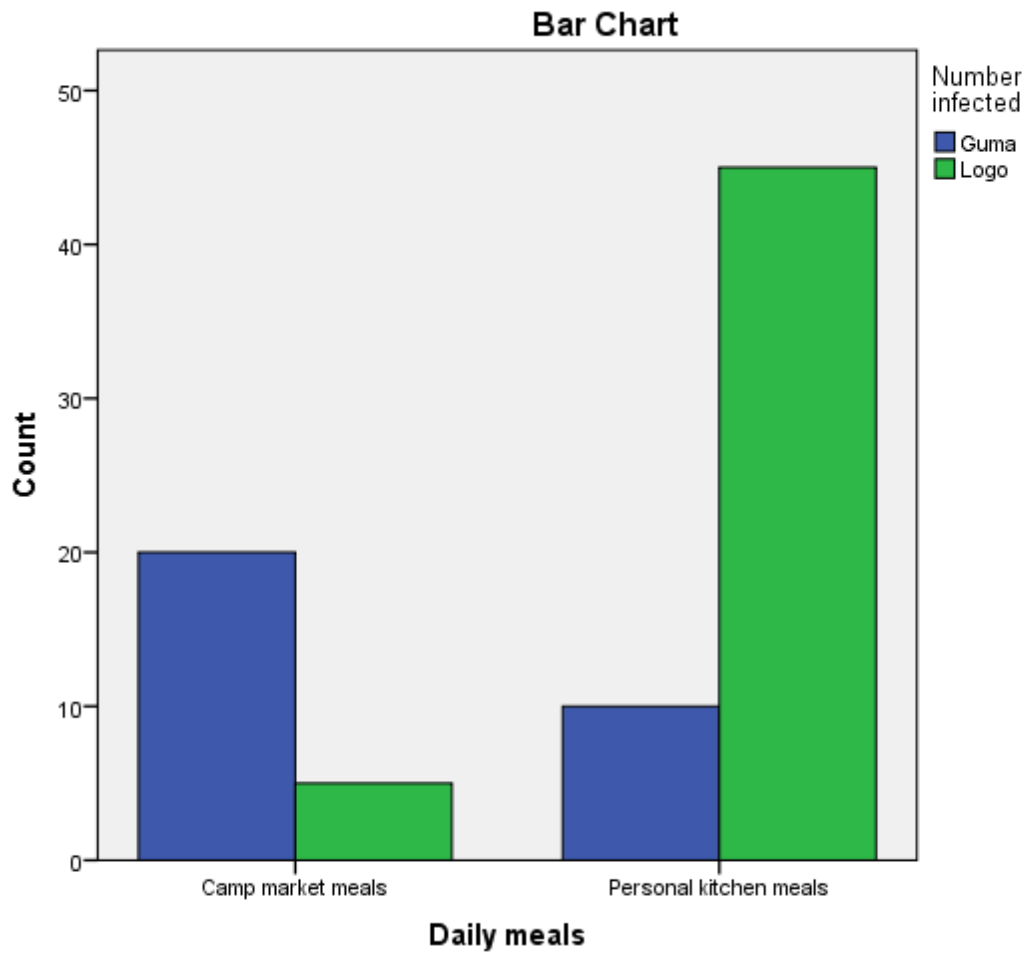
			Number infected		Total
			Guma	Logo	
Daily meals	Camp market meals	Count	20	5	25
		Expected Count	9.4	15.6	25.0
	Personal kitchen meals	Count	10	45	55
		Expected Count	20.6	34.4	55.0
Total	Count	30	50	80	
	Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	28.024 ^a	1	.000	.000	.000
Continuity Correction ^b	25.449	1	.000		
Likelihood Ratio	28.675	1	.000		
Fisher's Exact Test					
Linear-by-Linear Association	27.674	1	.000		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 9.38.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to daily meals

**Gender-related
Case Processing Summary**

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Gender * Number infected	80	100.0%	0	0.0%	80	100.0%

Gender * Number infected Crosstabulation

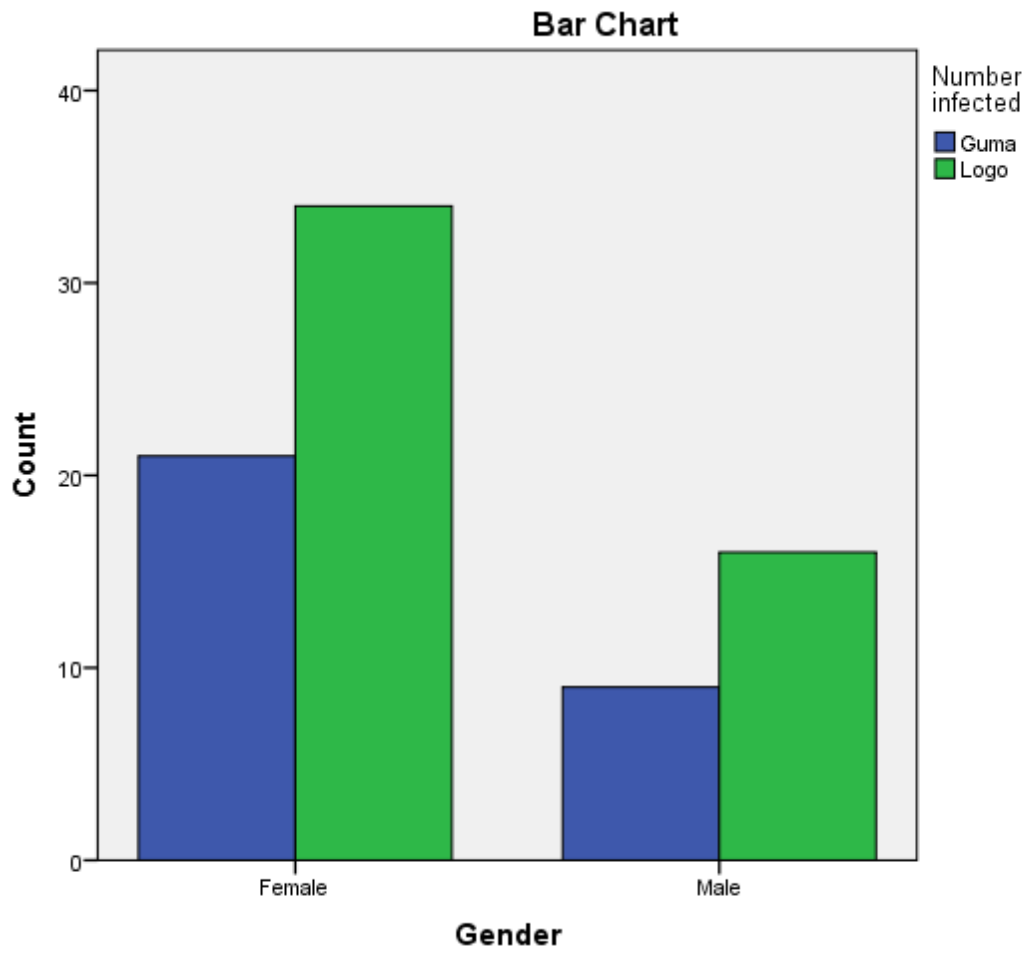
		Number infected		Total	
		Guma	Logo		
Gender	Female	Count	21	34	55
		Expected	20.6	34.4	55.0
		Count	9	16	25
	Male	Expected	9.4	15.6	25.0
		Count	30	50	80
	Total	Expected	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.035 ^a	1	.852	1.000	.528
Continuity Correction ^b	.000	1	1.000		
Likelihood Ratio	.035	1	.852		
Fisher's Exact Test					
Linear-by-Linear Association	.034	1	.853		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 9.38.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to Gender

Daily Meals

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Daily meals * Number infected	80	100.0%	0	0.0%	80	100.0%

Daily meals * Number infected Crosstabulation

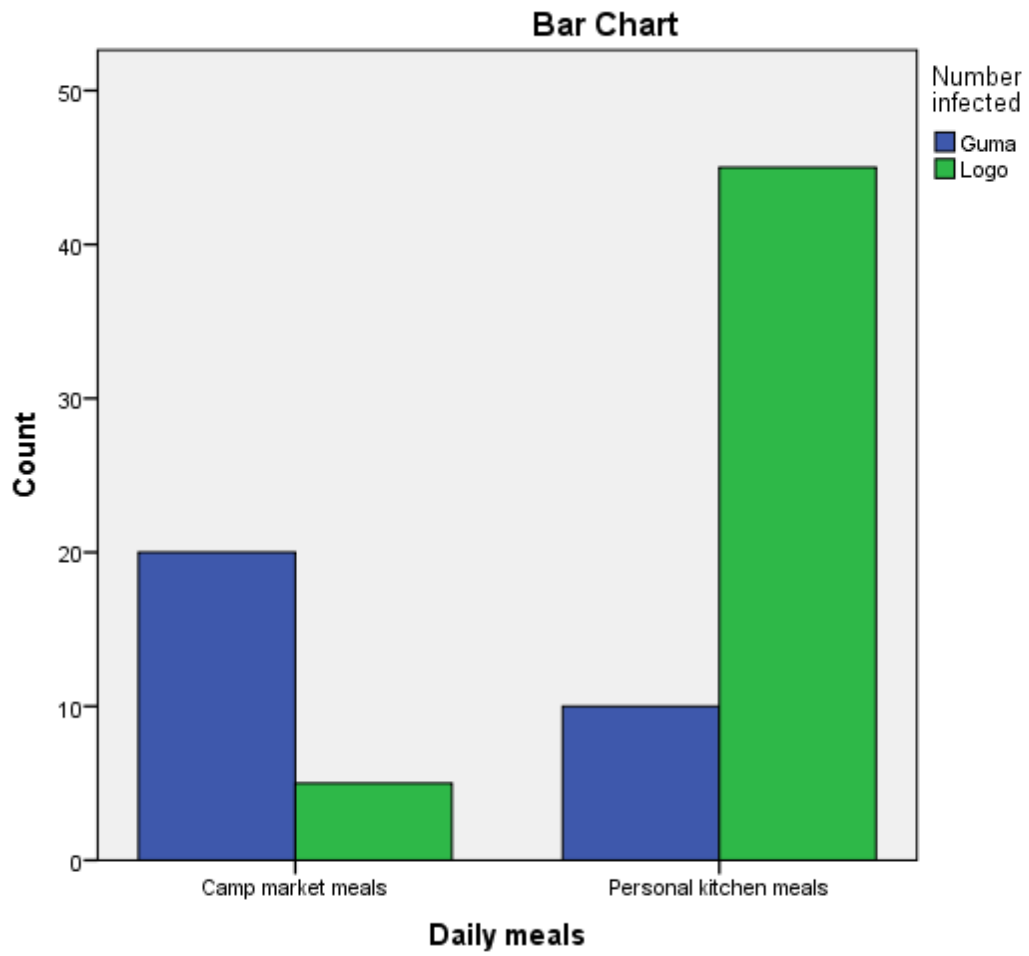
				Number infected		Total
				Guma	Logo	
Daily meals	Camp market meals	Count	20	5	25	
		Expected Count	9.4	15.6	25.0	
	Personal kitchen meals	Count	10	45	55	
		Expected Count	20.6	34.4	55.0	
Total		Count	30	50	80	
		Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	28.024 ^a	1	.000	.000	.000
Continuity Correction ^b	25.449	1	.000		
Likelihood Ratio	28.675	1	.000	.000	.000
Fisher's Exact Test					
Linear-by-Linear Association	27.674	1	.000	.000	.000
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 9.38.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to daily meals

Knowledge

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Knowledge of dis. * Number infected	80	100.0%	0	0.0%	80	100.0%

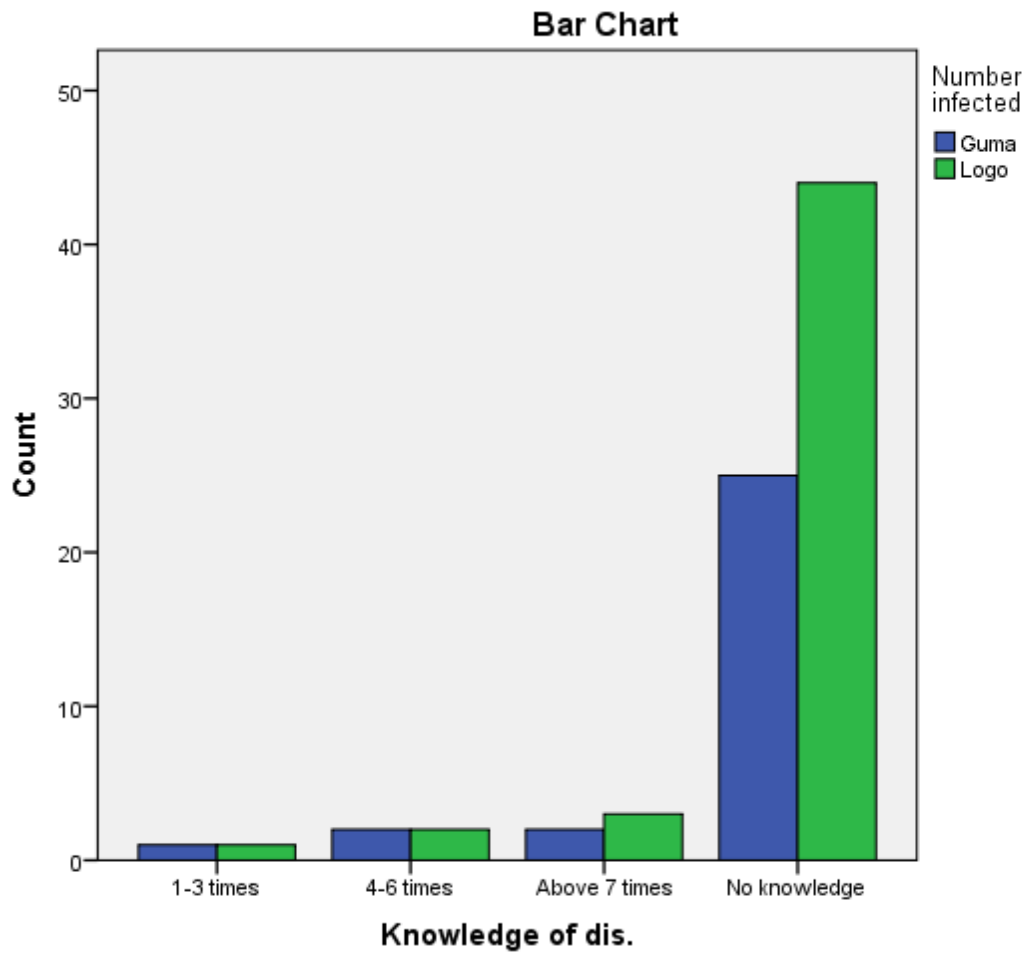
Knowledge of dis. * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Knowledge of dis.	1-3 times	Count	1	1	2
		Expected Count	.8	1.3	2.0
	4-6 times	Count	2	2	4
		Expected Count	1.5	2.5	4.0
	Above 7 times	Count	2	3	5
		Expected Count	1.9	3.1	5.0
	No knowledge	Count	25	44	69
		Expected Count	25.9	43.1	69.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.461 ^a	3	.927
Likelihood Ratio	.448	3	.930
Linear-by-Linear Association	.430	1	.512
N of Valid Cases	80		

a. 6 cells (75.0%) have expected count less than 5. The minimum expected count is .75.



Prevalence of *Salmonella typhi* infection in relation to Knowledge

Marital status-related

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Marital Status * Number infected	80	98.8%	1	1.2%	81	100.0%

Marital Status * Number infected Crosstabulation

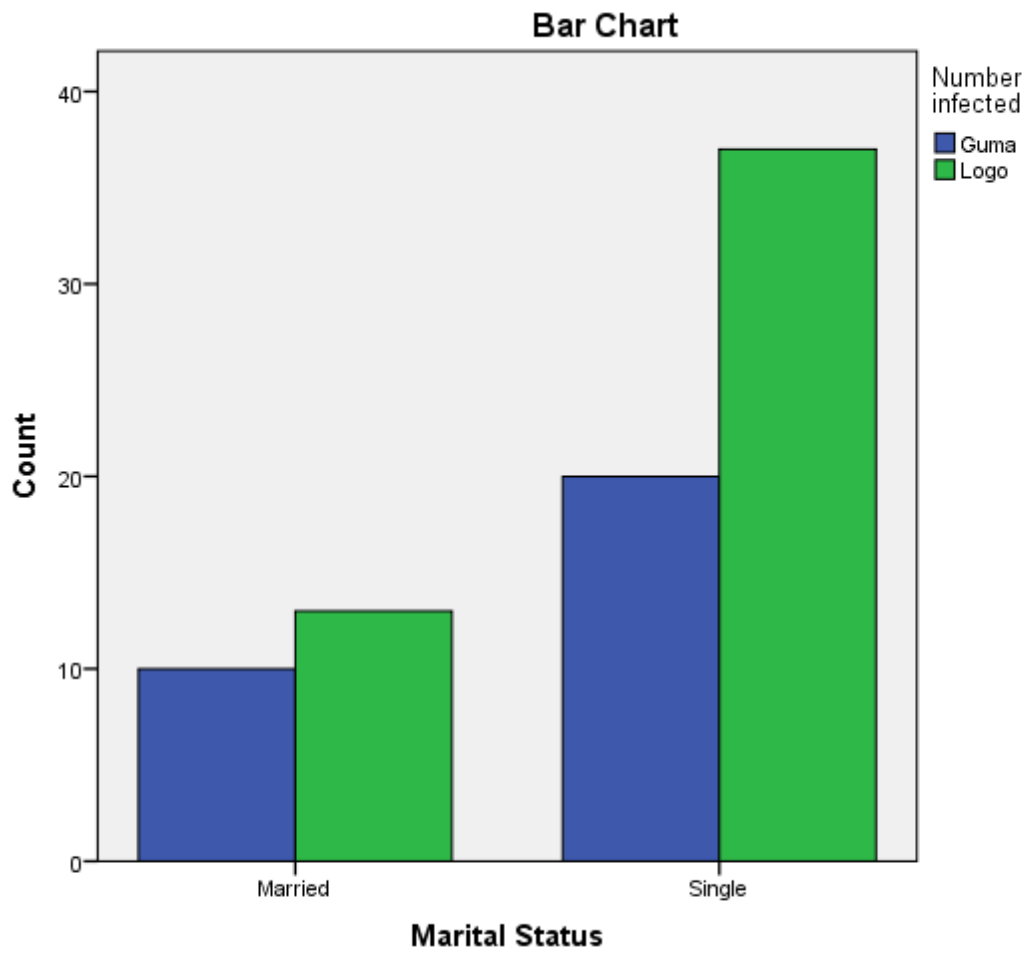
		Number infected		Total	
		Guma	Logo		
Marital Status	Married	Count	10	13	23
		Expected	8.6	14.4	23.0
	Single	Count	20	37	57
		Expected	21.4	35.6	57.0
		Count	30	50	80
	Total	Expected	30.0	50.0	80.0
	Count				

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.492 ^a	1	.483		
Continuity Correction ^b	.199	1	.655		
Likelihood Ratio	.487	1	.485		
Fisher's Exact Test				.611	.325
Linear-by-Linear Association	.486	1	.486		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 8.63.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to marital status

Type of Medication

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Medication type * Number infected	80	98.8%	1	1.2%	81	100.0%

Medication type * Number infected Crosstabulation

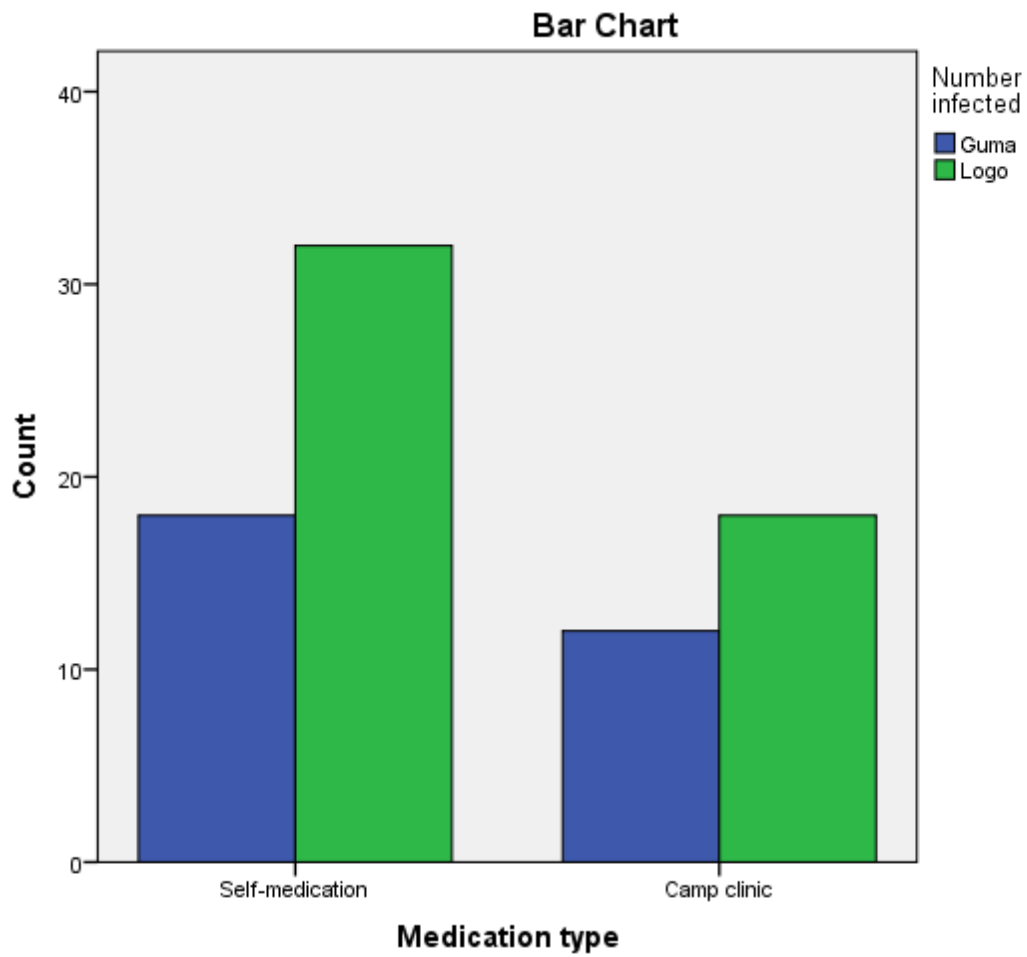
			Number infected		Total
			Guma	Logo	
Medication type	Self-medication	Count	18	32	50
		Expected Count	18.8	31.3	50.0
	Camp clinic	Count	12	18	30
		Expected Count	11.3	18.8	30.0
Total	Count	30	50	80	
	Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.128 ^a	1	.721		
Continuity Correction ^b	.014	1	.905		
Likelihood Ratio	.128	1	.721		
Fisher's Exact Test				.813	.451
Linear-by-Linear Association	.126	1	.722		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 11.25.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to medication

Method of refuse Disposal

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Method of refuse disposal * Number infected	80	100.0%	0	0.0%	80	100.0%

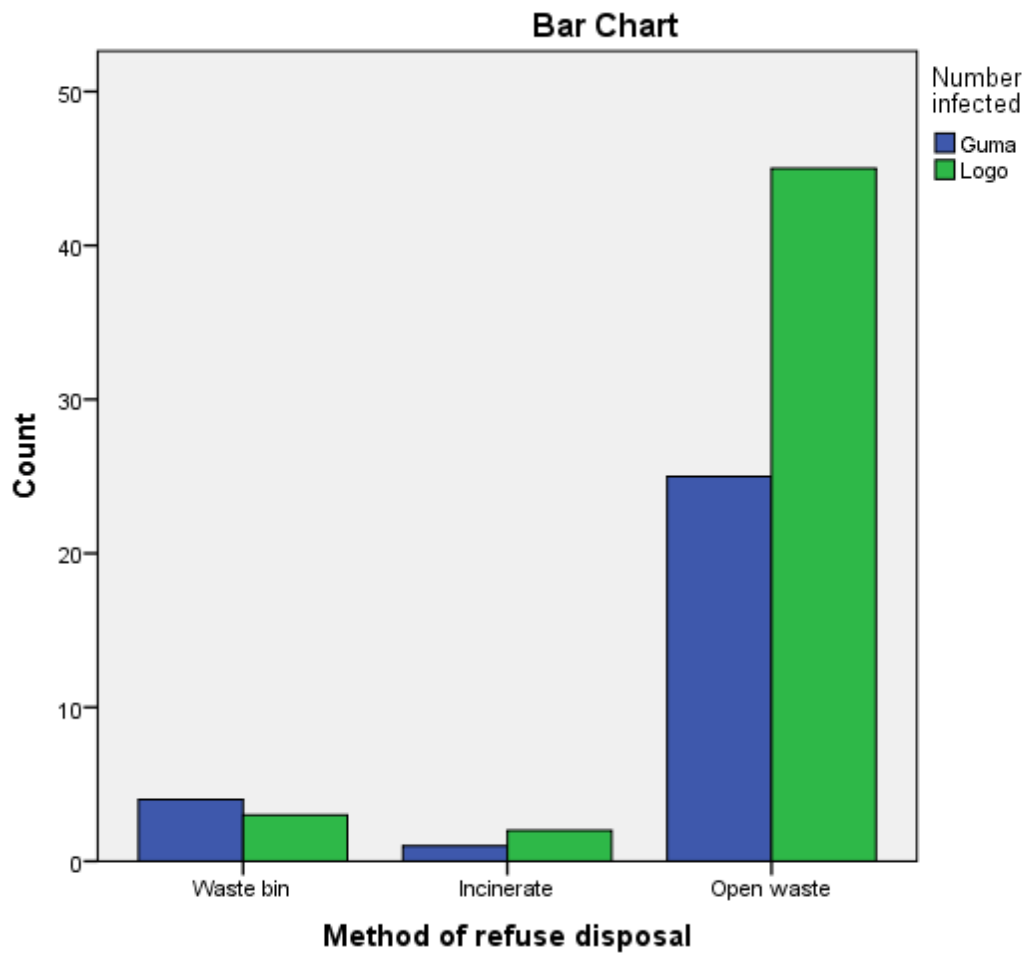
Method of refuse disposal * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Method of refuse disposal	Waste bin	Count	4	3	7
		Expected Count	2.6	4.4	7.0
	Incinerate	Count	1	2	3
		Expected Count	1.1	1.9	3.0
	Open waste	Count	25	45	70
		Expected Count	26.3	43.8	70.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.270 ^a	2	.530
Likelihood Ratio	1.224	2	.542
Linear-by-Linear Association	1.060	1	.303
N of Valid Cases	80		

a. 4 cells (66.7%) have expected count less than 5. The minimum expected count is 1.13.



Prevalence of *Salmonella typhi* in relation to method of refuse disposal

Nature of Toilet

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Nature of toilet * Number infected	80	100.0%	0	0.0%	80	100.0%

Nature of toilet * Number infected Crosstabulation

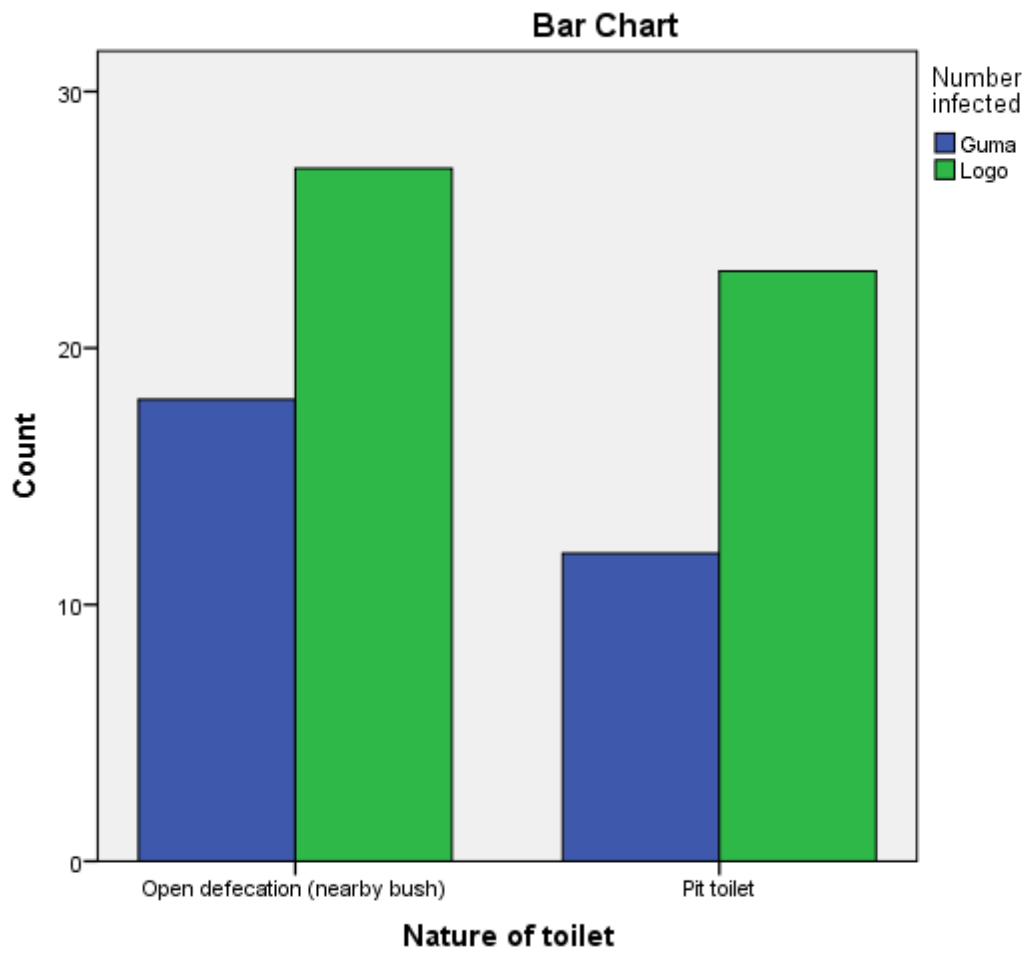
				Number infected		Total
				Guma	Logo	
Nature of toilet	Open defecation (nearby bush)	Count	18	27	45	
		Expected Count	16.9	28.1	45.0	
	Pit toilet	Count	12	23	35	
		Expected Count	13.1	21.9	35.0	
Total		Count	30	50	80	
		Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.274 ^a	1	.600		
Continuity Correction ^b	.085	1	.771		
Likelihood Ratio	.275	1	.600		
Fisher's Exact Test				.647	.387
Linear-by-Linear Association	.271	1	.603		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 13.13.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to nature of toilet

Camp Duration

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Camp duration * Number infected	80	98.8%	1	1.2%	81	100.0%

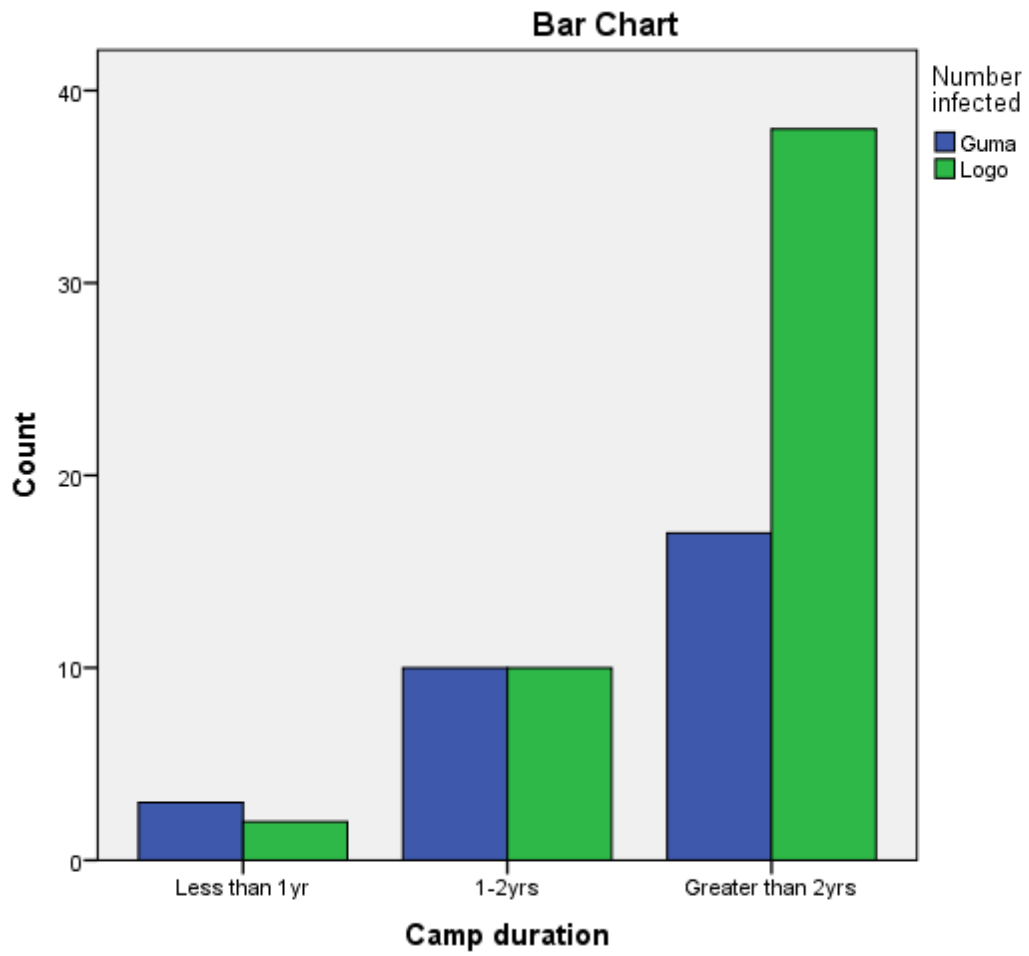
Camp duration * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Camp duration	Less than 1yr	Count	3	2	5
		Expected Count	1.9	3.1	5.0
	1-2yrs	Count	10	10	20
		Expected Count	7.5	12.5	20.0
	Greater than 2yrs	Count	17	38	55
		Expected Count	20.6	34.4	55.0
Total	Count	30	50	80	
	Expected Count	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	3.433 ^a	2	.180
Likelihood Ratio	3.373	2	.185
Linear-by-Linear Association	3.307	1	.069
N of Valid Cases	80		

a. 2 cells (33.3%) have expected count less than 5. The minimum expected count is 1.88.



Prevalence of *Salmonella typhi* infection in relation to period in camp

Psychology in-balance

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Psycho. In-balance * Number infected	80	98.8%	1	1.2%	81	100.0%

Psycho. In-balance * Number infected Crosstabulation

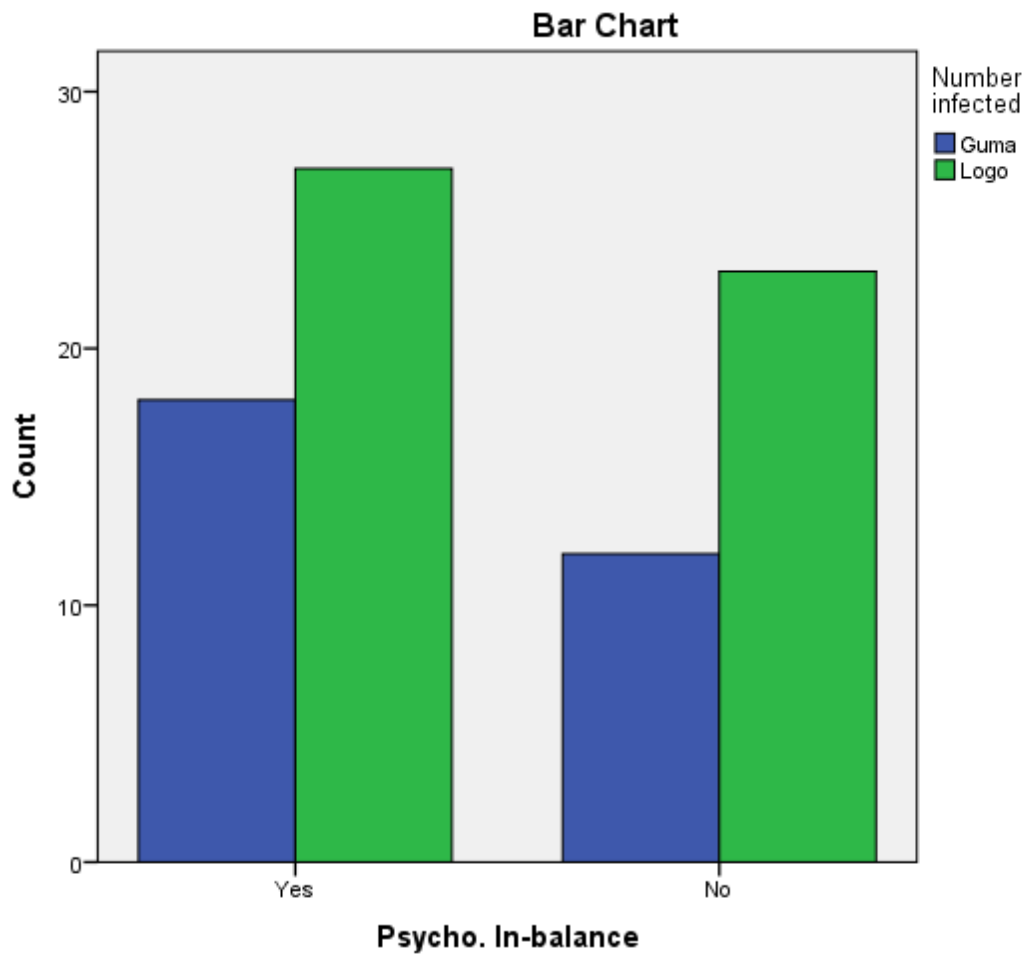
			Number infected		Total
			Guma	Logo	
Psycho. In- balance	Yes	Count	18	27	45
		Expected Count	16.9	28.1	45.0
	No	Count	12	23	35
		Expected Count	13.1	21.9	35.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2- sided)	Exact Sig. (1- sided)
Pearson Chi-Square	.274 ^a	1	.600	.647	.387
Continuity Correction ^b	.085	1	.771		
Likelihood Ratio	.275	1	.600		
Fisher's Exact Test					
Linear-by-Linear Association	.271	1	.603		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 13.13.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to Psycho-in-balance

**Occupation
Case Processing Summary**

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Occupation * Number infected	80	100.0%	0	0.0%	80	100.0%

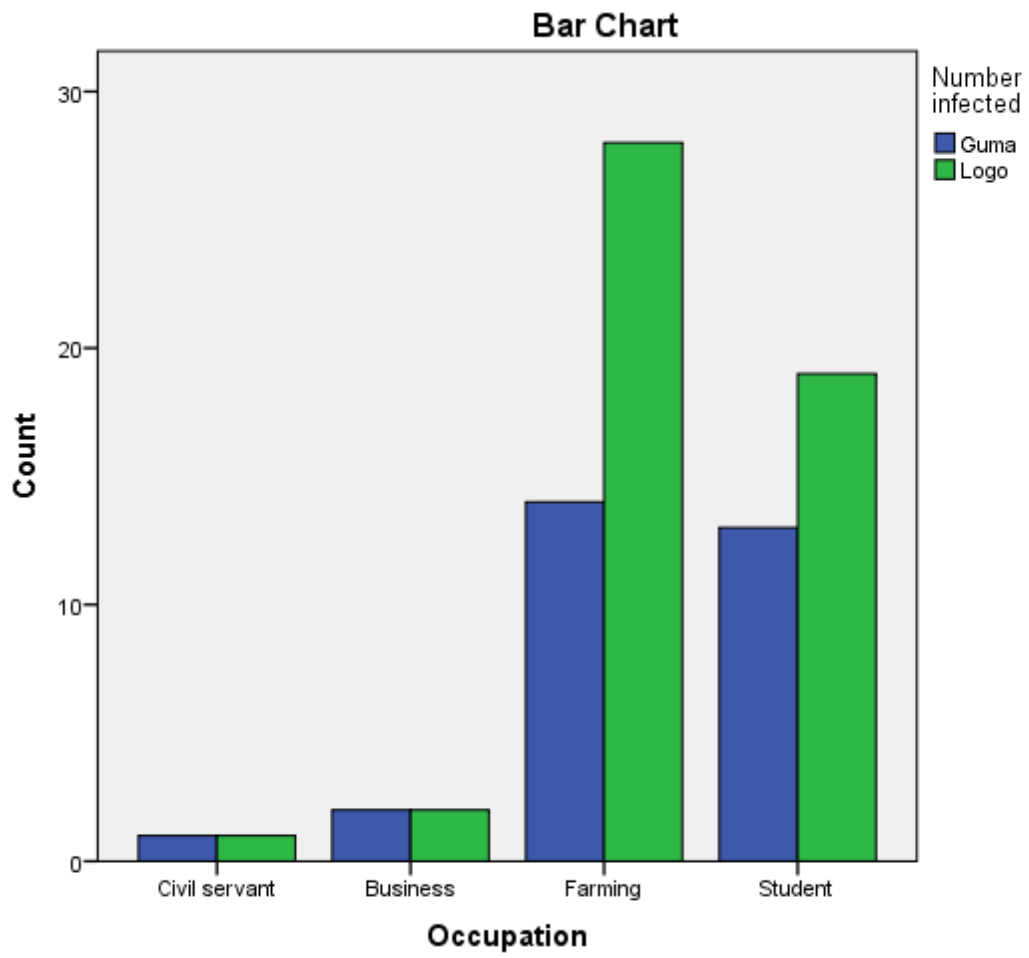
Occupation * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Occupation	Civil servant	Count	1	1	2
		Expected Count	.8	1.3	2.0
	Business	Count	2	2	4
		Expected Count	1.5	2.5	4.0
	Farming	Count	14	28	42
		Expected Count	15.8	26.3	42.0
	Student	Count	13	19	32
		Expected Count	12.0	20.0	32.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.844 ^a	3	.839
Likelihood Ratio	.835	3	.841
Linear-by-Linear Association	.000	1	1.000
N of Valid Cases	80		

a. 4 cells (50.0%) have expected count less than 5. The minimum expected count is .75.



Prevalence of *Salmonella typhi* infection in relation to occupation

Overall Prevalence

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Overall Prevalence * Number infected	80	98.8%	1	1.2%	81	100.0%

Overall Prevalence * Number infected Crosstabulation

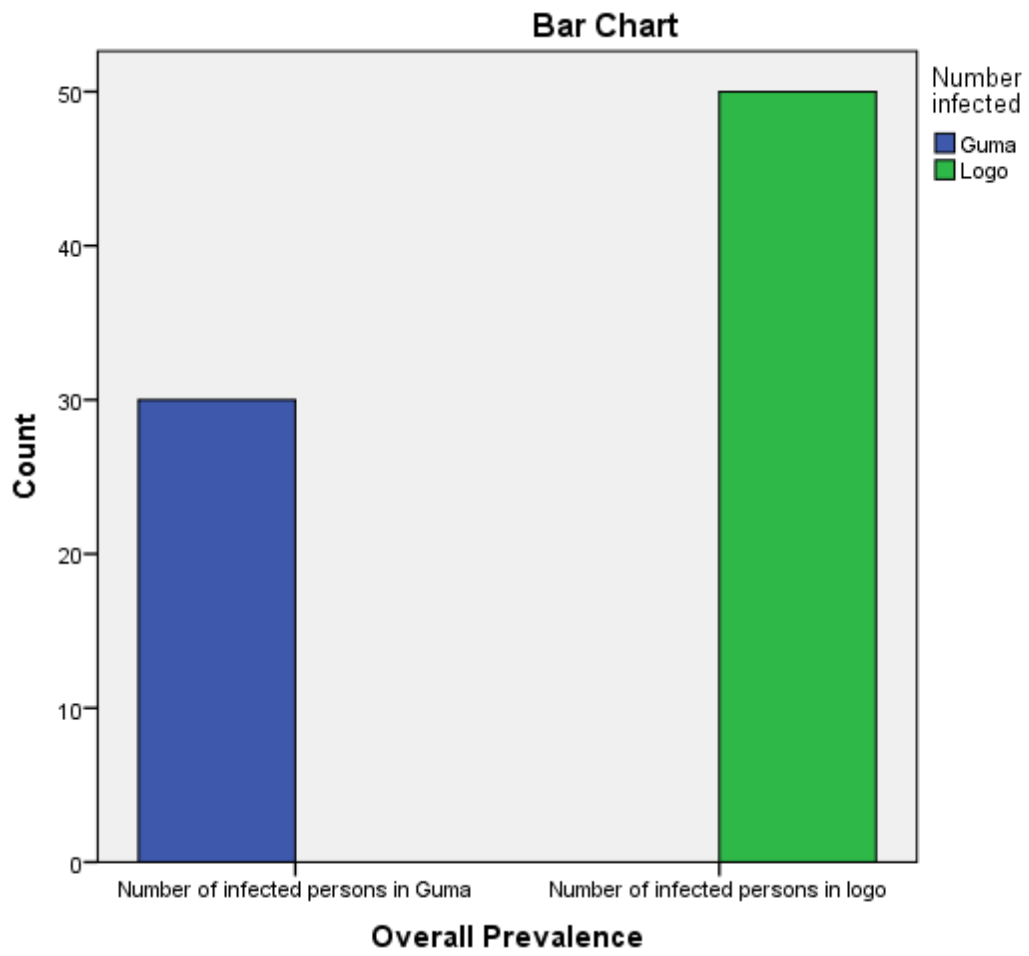
			Number infected		Total
			Guma	Logo	
Overall Prevalence	Number of infected persons in Guma	Count	30	0	30
		Expected Count	11.3	18.8	30.0
	Number of infected persons in logo	Count	0	50	50
		Expected Count	18.8	31.3	50.0
Total		Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2- sided)	Exact Sig. (1- sided)
Pearson Chi-Square	80.000 ^a	1	.000		
Continuity Correction ^b	75.790	1	.000		
Likelihood Ratio	105.850	1	.000		
Fisher's Exact Test				.000	.000
Linear-by-Linear Association	79.000	1	.000		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 11.25.

b. Computed only for a 2x2 table



Salmonella typhi infection in relation to overall Prevalence

Sanitation

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Sanitation as P. hygiene * Number infected	80	100.0%	0	0.0%	80	100.0%

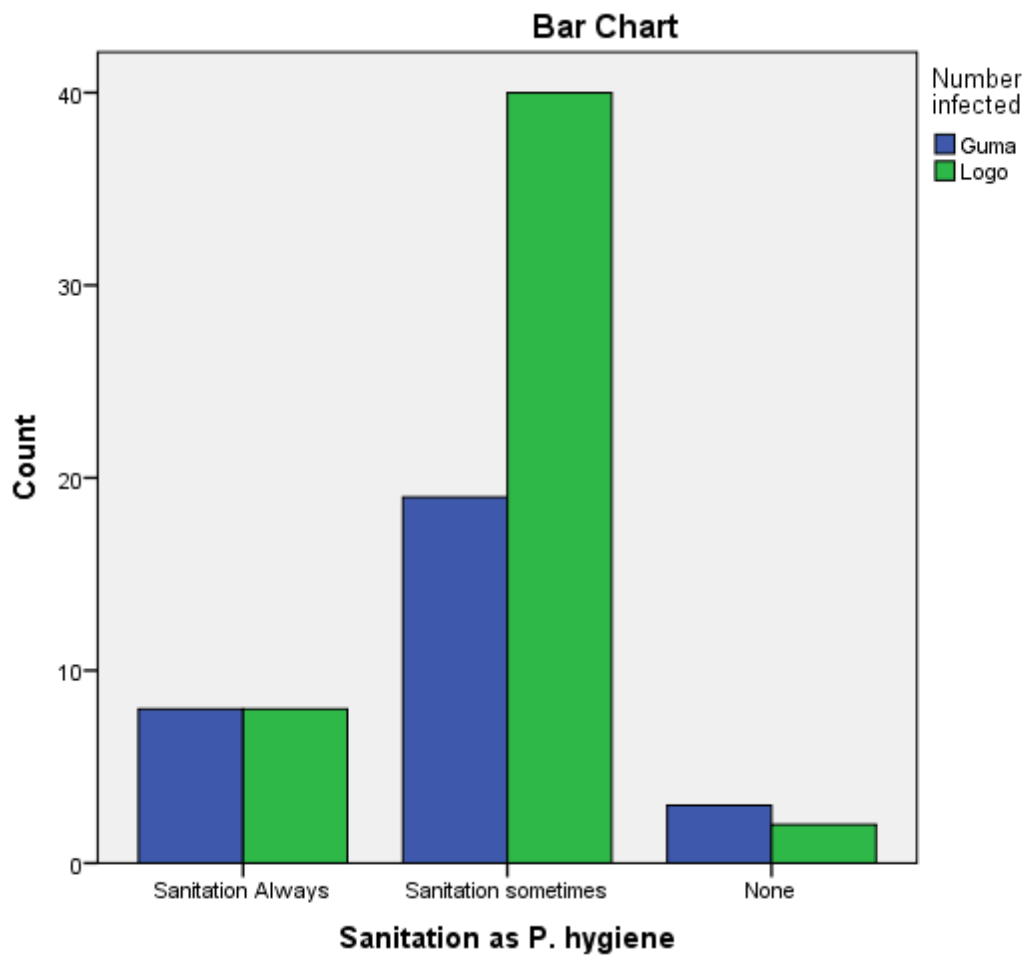
Sanitation as P. hygiene * Number infected Crosstabulation

			Number infected		Total	
			Guma	Logo		
Sanitation as P. hygiene	Sanitation Always	Count	8	8	16	
		Expected Count	6.0	10.0	16.0	
	Sanitation sometimes	Count	19	40	59	
		Expected Count	22.1	36.9	59.0	
	None	Count	3	2	5	
		Expected Count	1.9	3.1	5.0	
	Total		Count	30	50	80
			Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.853 ^a	2	.240
Likelihood Ratio	2.789	2	.248
Linear-by-Linear Association	.166	1	.684
N of Valid Cases	80		

a. 2 cells (33.3%) have expected count less than 5. The minimum expected count is 1.88.



Prevalence of *Salmonella typhi* infection in relation to sanitation

Sources of water

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Sources of water * Number infected	80	100.0%	0	0.0%	80	100.0%

Sources of water * Number infected Crosstabulation

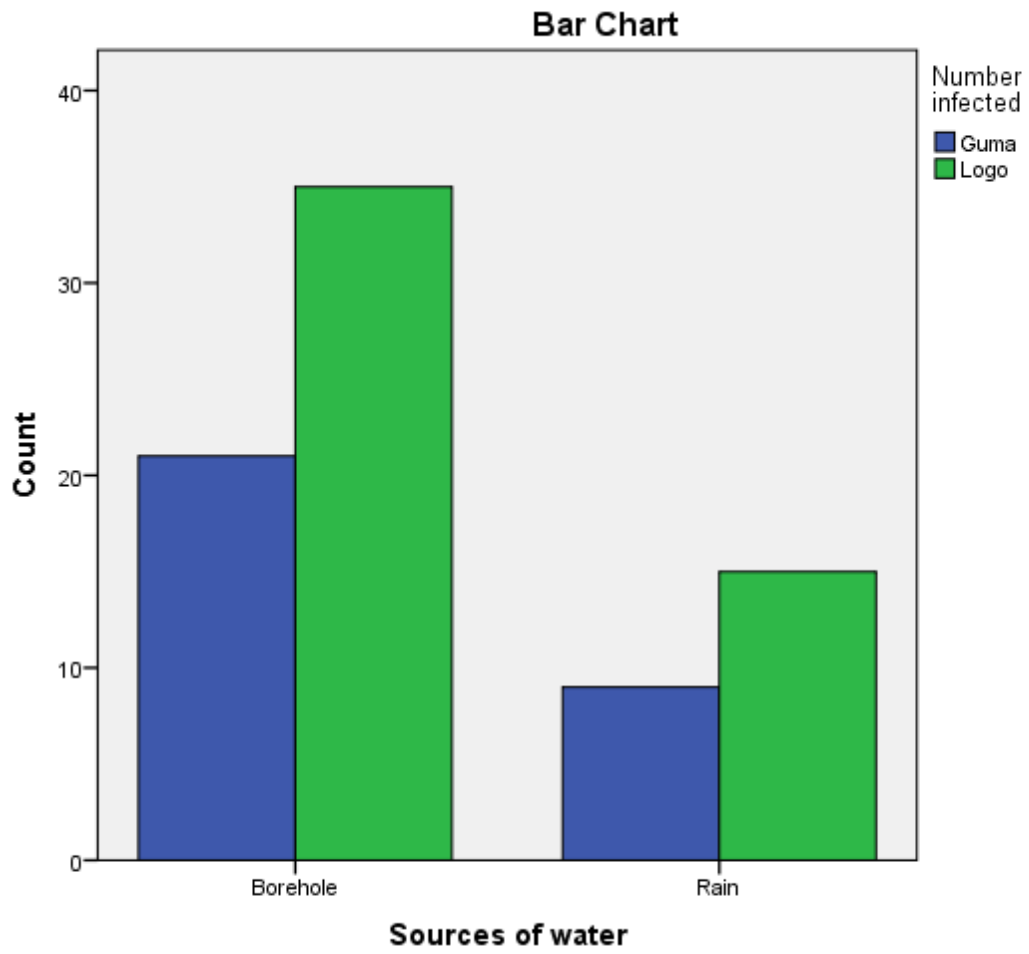
		Number infected		Total	
		Guma	Logo		
Sources of water	Borehole	Count	21	35	56
		Expected	21.0	35.0	56.0
		Count	9	15	24
	Rain	Expected	9.0	15.0	24.0
		Count	30	50	80
	Total	Expected	30.0	50.0	80.0
		Count			

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.000 ^a	1	1.000		
Continuity Correction ^b	.000	1	1.000		
Likelihood Ratio	.000	1	1.000		
Fisher's Exact Test				1.000	.596
Linear-by-Linear Association	.000	1	1.000		
N of Valid Cases	80				

a. 0 cells (.0%) have expected count less than 5. The minimum expected count is 9.00.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to sources of water

Washing of hands

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Personal Hygiene * Number infected	80	100.0%	0	0.0%	80	100.0%

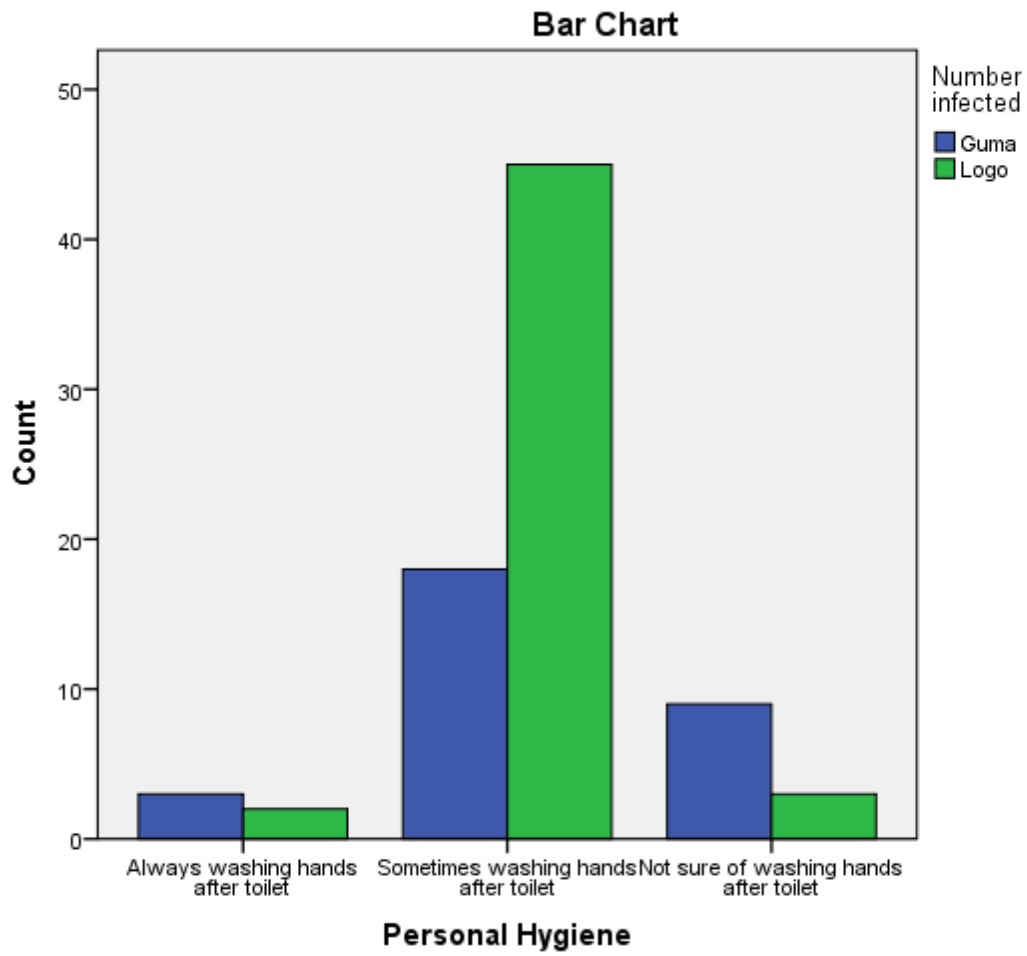
Personal Hygiene * Number infected Crosstabulation

			Number infected		Total
			Guma	Logo	
Personal Hygiene	Always washing hands after toilet	Count	3	2	5
		Expected	1.9	3.1	5.0
	Sometimes washing hands after toilet	Count	18	45	63
		Expected	23.6	39.4	63.0
	Not sure of washing hands after toilet	Count	9	3	12
		Expected	4.5	7.5	12.0
Total	Count	30	50	80	
	Expected	30.0	50.0	80.0	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	10.423 ^a	2	.005
Likelihood Ratio	10.242	2	.006
Linear-by-Linear Association	2.929	1	.087
N of Valid Cases	80		

a. 3 cells (50.0%) have expected count less than 5. The minimum expected count is 1.88.



Prevalence of *Salmonella typhi* infection in relation to hygiene

Risk factors

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
Risk factors * Number infected	80	100.0%	0	0.0%	80	100.0%

Risk factors * Number infected Crosstabulation

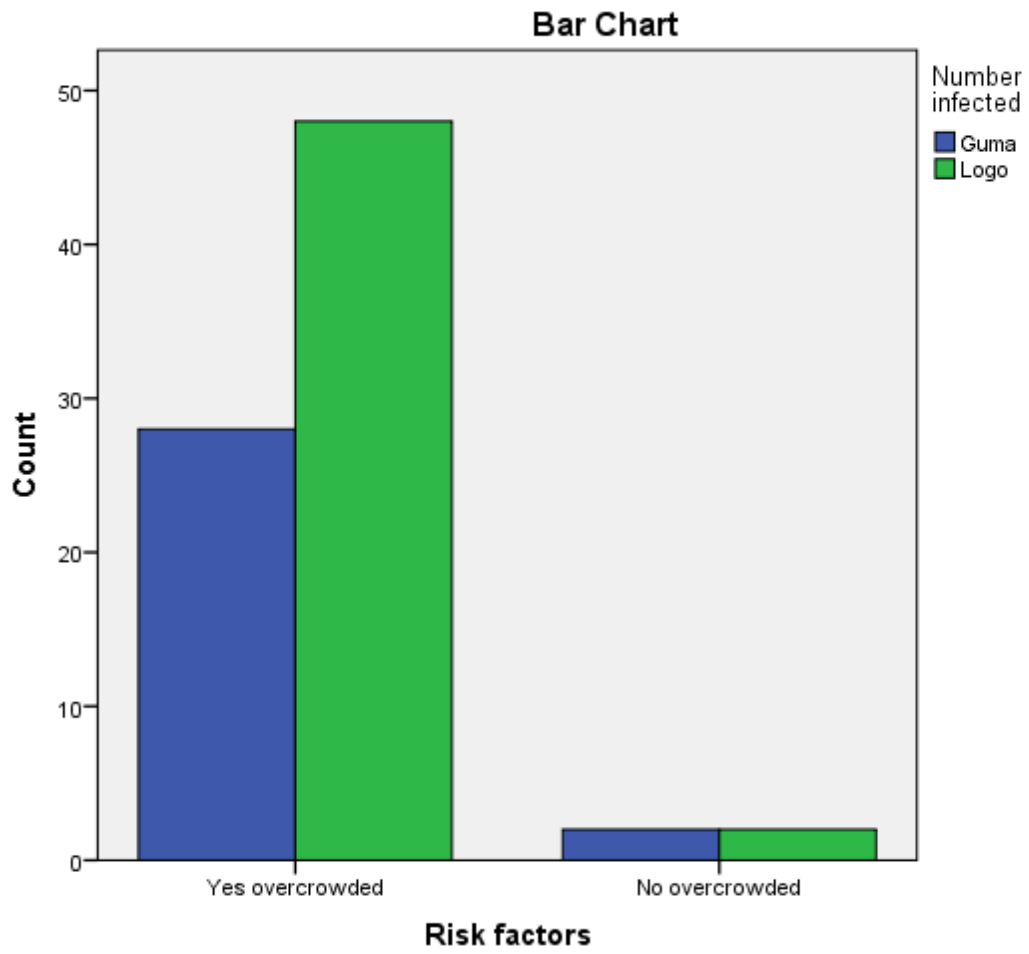
			Number infected		Total
			Guma	Logo	
Risk factors	Yes overcrowded	Count	28	48	76
		Expected Count	28.5	47.5	76.0
	No overcrowded	Count	2	2	4
		Expected Count	1.5	2.5	4.0
	Total	Count	30	50	80
		Expected Count	30.0	50.0	80.0

Chi-Square Tests

	Value	Df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.281 ^a	1	.596		
Continuity Correction ^b	.000	1	1.000		
Likelihood Ratio	.272	1	.602		
Fisher's Exact Test				.628	.483
Linear-by-Linear Association	.277	1	.599		
N of Valid Cases	80				

a. 2 cells (50.0%) have expected count less than 5. The minimum expected count is 1.50.

b. Computed only for a 2x2 table



Prevalence of *Salmonella typhi* infection in relation to risk-factors

APPENDIX II
Ethical Clearance

GOVERNMENT OF BENUE STATE OF NIGERIA
STATE EMERGENCY MANAGEMENT AGENCY

Governor's Office
No. 7 Kashim Ibrahim Road,
P.M.B. 102065
Makurdi, Benue State



All Communications should be addressed to
the Executive Secretary of the Agency

BSEMA/OFF/GEN/87/VI/138

6th February, 2020

Our Ref: _____ Your Ref: _____ Date: _____

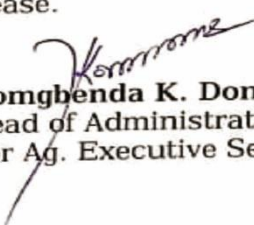
Adie Ambrose Ashibel
Department of Microbiology
University of Benin

**RE: APPLICATION FOR ETHICAL CLEARANCE/PERMISSION TO
CONDUCT A Ph.D RESEARCH AMONG IDPs IN TWO CAMPS IN
THE STATE.**

Your letter dated 27th January, 2020 on the above subject refers

2. I am directed by the Ag. Executive Secretary to convey his approval
to allow you carry out research in the IDPs Camp.

3. Accept the assurance of the Ag. Executive Secretary warm regards
please.


Komghenda K. Donald,
Head of Administration,
For Ag. Executive Secretary.



APPENDIX III
Questionnaire

QUESTIONNAIRE

Thesis: Prevalence and Molecular Characterization of *Salmonella typhi* Infection among Internally Displaced Persons in Two LGAs (Guma and Logo) of Benue State

A) SOCIO-DEMOGRAPHIC INFORMATION OF IDPs

1. Sex: Male Female
2. Age: 5 -10 11-21 22-32 33-43 >44
3. Marital status: Single Married
4. Educational Level:
(a) No formal education (b) Nursery (c) Primary
(d) Tertiary institution
5. Occupational status:
Farming Civil service Trading/Business Artisan ()
Others
5. Religion: Christian Muslim

B) RISK FACTORS OF *Salmonella typhi* INFECTION

7. Time spent in camp
Less than 1yr 1-2yrs >2yrs
8. Sources of waters
Stream/River Borehole Well Rain fall
9. Are you overcrowded
Yes No
10. How often do you wash your hands after toilet
Always Sometimes None
11. Where do you get your meals
Camp kitchen Personal kitchen Community market
12. Method of refuse disposal
Waste bin Incinerate Open waste
13. Sanitation of environment
Every day Once a week Once a month None
14. Have you been tested positive for typhoid before
Yes No
15. When
Less than a month above two months Three months and beyond
16. Where do you defecate.....
Pit toilet Open defecation
17. Are you depressed as from death of love ones.....
Yes No
18. Choice of medication when you have fever
Camp Clinic Self

C) Laboratory findings of *Salmonella typhi* Positive Negative

APPENDIX IV

Zone diameter interpretive standards chart

Table14: Zone diameter interpretive standards chart for the determination of antibiotic sensitivity and resistance status by the Disk Diffusion method (Sarker *et al.*, 2014; CLSI, 2020; CLSI, 2024)

Antibiotic	Resistant (mm)	Intermediate (mm)	Susceptible (mm)
Cefixime clavulanate(Czm)	≤14	15 – 16	≥17
Ceporex (CEP)	≤13	14 -16	≥17
Ornidazole or ofloxacin (spoz)	≤14	15 – 16	≥17
Ciprofloxacin (CIP)	≤14	15 -17	≥17
Augmentin (AU)	≤13	14–17	≥18
Amplicin (PN)	≤13	14–17	≥18
Streptomycin (S)	≤11	12 – 14	≥15
Gentamycin (CN)	≤14	15 – 17	≥18
Septtrin (SXT)	≤10	11 – 15	≥17
Trimethoprim Sulfamethoxazole (TMP)	≤10	11 – 15	≥16
Tetracycline (TET)	≤11	12 - 14	≥15

APPENDIX V

Table 4.14: Antibiotic Sensitivity of plasmid before curing *Salmonella typhi* isolates

Salmonella isolates	Diameter of zone of inhibition (mm)									MAR Index
	CZM	CEP	SPOZ	CIP	AU	PN	S	CN	TET	
Sample 40	S(18)	I(14)	I(16)	R(10)	I(16)	R(9)	I(12)	R(10)	R(8)	0.4
Sample 100	S(17)	I(14)	I(15)	R(7)	I(15)	R(9)	I(12)	R(9)	R(6)	0.4
Sample 02	S(17)	R(9)	I(16)	R(0)	I(16)	R(0)	R(0.7)	R(0)	R(0)	0.7
Sample 10	S(17)	R(0.9)	S(17)	R(0)	I(16)	R(0)	R(0.8)	R(0)	R(0)	0.7
Sample 30	I(15)	R(0.8)	I(15)	R(0)	I(15)	R(0)	R(0)	R(0)	R(0)	0.7
Sample 25	I(15)	R(9)	I(15)	R(0)	S(18)	R(0)	R(0)	R(0)	R(0)	0.7
Sample 70	I(15)	I(14)	I(15)	R(0)	S(19)	R(0)	R(0)	R(0)	R(0)	0.6
Sample 65	S(17)	I(14)	I(15)	R(0)	S(18)	R(0)	R(0)	R(0)	R(0)	0.6
Sample 80	S(18)	R(0.5)	S(17)	R(0)	I(17)	R(0)	R(0)	R(0)	R(0)	0.7
Sample 88	S(18)	R(0.3)	S(17)	R(0)	I(17)	R(0)	R(0)	R(0)	R(0)	0.7

Key: R – Resistant, S – Susceptible, I - Intermediate, CZM – Cefixime clavulanate 10(µg) of class Cephalosporins, CEP – Ceporex 10(µg) of class Cephalosporins, SPOZ – Ornidazole/ofloxacin 25(µg) of class Fluoroquinolone, CIP – Ciprofloxacin 5(µg) of class Fluoroquinolone, AU – Augmentin 30(µg) of class Penicillin, PN - Amplicin 30(µg) of class Penicillin, S – Streptomycin 30(µg) of class Aminoglycoside, CN – Gentamycin 10(µg) of class Aminoglycoside, CTZ – Ceftazidime 30(µg) of class Cephalosporins, TET - Tetracycline 30(µg) of class Tetracycline and MAR- Multiple antibiotic resistance.

APPENDIX VI

Table 4.15 Antibiotic Sensitivity of *Salmonella typhi* isolates after curing

Salmonella isolates	Diameter of zone of inhibition (mm)						MAR Index
	CEP	CIP	PN	S	CN	TET	
Sample 40	I(15)	I(16)	I(14)	I(12)	I(15)	I(12)	0.0
Sample 100	I(15)	I(15)	I(14)	I(12)	I(15)	I(12)	0.0
Sample 02	R(9)	I(15)	I(15)	I(13)	I(15)	I(12)	0.1

Sample 10	R(0.9)	S(17)	I(14)	I(13)	I(16)	I(12)	0.1
Sample 30	R(0.8)	R(0.6)	I(17)	S(16)	I(15)	I(12)	0.2
Sample 25	R(9)	R(0.3)	I(14)	S(16)	I(16)	I(12)	0.2
Sample 70	I(14)	S(17)	I(14)	S(16)	I(15)	I(12)	0.0
Sample 65	I(14)	I(16)	I(14)	I(14)	S(18)	I(12)	0.0
Sample 80	R(0.5)	S(17)	I(14)	I(12)	I(15)	I(12)	0.1
Sample 88	R(0.3)	I(15)	I(14)	I(12)	I(15)	I(12)	0.1

Key: R – Resistant, S – Susceptible, I - Intermediate, CZM – Cefixime clavulanate 10(µg) of class Cephalosporins, CEP – Ceporex 10(µg) of class Cephalosporins, SPOZ – Ornidazole/ofloxacin 25(µg) of class Fluoroquinolone, CIP – Ciprofloxacin 5(µg) of class Fluoroquinolone, AU – Augmentin 30(µg) of class Penicillin, PN - Amplicin 30(µg) of class Penicillin, S – Streptomycin 30(µg) of class Aminoglycoside, CN – Gentamycin 10(µg) of class Aminoglycoside, TET - Tetracycline 30(µg) of class Tetracycline and MAR- Multiple antibiotic resistance.

APPENDIX VII

Table 4.16: Biochemical Characteristics and Gram Staining of *Salmonella typhi*

Bacteria sample	Shape	Gram staining	SIM TEST		MR-VP TEST			Citrate	Catalase	Urease	TSI Agar			
			Sulfite test	Indole test	Motility test	Methylene red test	Voges-proskaur test				Slant	Butt	Glucose	
40	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
100	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
2	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
10	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
30	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
25	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
80	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-
88	Rods	N	+	-	+	+	-	-	+	-	R	Y	+	-

Key: - = Negative, + = Positive, N = Gram-negative rod bacilli

APPENDIX VIII Culturwe Media

Selenite F broth

A Selenite F broth medium was used to selectively enrich *Salmonella* spp. Each sample was first inoculated into Selenite broth base and incubated for 18-24 h at 37 °C for pre-enrichment. However, according to the method described by Chang *et al.* (1999), Aryal (2022) 19 g of selenite F powder was suspended in 100ml of distilled or deionised water. The media solution was heated gently using a water bath at 100 °C for 10 min and equilibrated at 25-45 °C. However, this was further dispensed into sterile test tubes of at least 5cm in depth. Each sample was first inoculated into Selenite broth base using a sterile loop and incubated for 18-24 h at 37 °C for selective pre-enrichment. Broths were not autoclaved to avoid excessive heating, which would have been detrimental to selectivity in the medium. Also, broths were not incubated longer than 24 h as the inhibitory effects of selenite decrease after 6-12 h of incubation. A positive result was indicated by colourless, good growth, suggesting the presence of *Salmonella* spp. In contrast, a negative result was shown in pink with bile precipitate, with

no growth, which suggested *Escherichia coli* or *Enterococcus faecalis*. An uninoculated medium was used as a negative control, and the result had no growth or change in the medium.

Sub-Culturing onto *Salmonella-Shigella* Agar Plate

The pre-enriched samples were sub-cultured onto *Salmonella-Shigella* Agar media using the streaking method and incubated at optimum conditions to obtain pure cultures. *Salmonella* appeared as colourless colonies with a black centre.

***Salmonella-Shigella* agar (SSA)**

Salmonella-Shigella (SS) agar is a moderately selective and differential medium for the isolation, cultivation and differentiation of *Salmonella* spp. and some strains of *Shigella* spp.

Salmonella-Shigella (SS) agar is a modification of the Deoxycholate Citrate Agar. Including Bile Salts, Sodium Citrate, and Brilliant Green, partially or inhibit gram-positive, coliform organisms and inhibit swarming *Proteus* spp. While allowing *Salmonella* spp. to grow (Cheesbrough, 2005; Isenberg, 2015; Abioye *et al.*, 2017). They added that they may overcome the inhibitory effects after prolonged incubation. Also, they said that *Proteus* was a smaller colony than *Salmonella typhi*.

However, according to the method described by Golam *et al.* (2020), 60 grams of *Salmonella-Shigella* Agar was suspended in 1000mL of distilled water and brought to a boil in a water bath at 100 °C, stirring frequently to dissolve the medium completely. The solution medium was not autoclaved or overheated to avoid destruction of selectivity in the medium. It was allowed to equilibrate at a room temperature of 25-45 °C, where the media solution was poured or dispensed into sterile petri plates covered with the lid and allowed to solidify. The plates were placed in inverted position to avoid contamination from condensation on the lid. A loop-full of fresh culture from selenite F broth after 24 h was inoculated (sub-cultured) onto the solidified media of SS agar and was incubated at 37 °C for 18-24 h. Colourless colonies with a black centre indicated a positive result due to hydrogen sulfide (H₂S) gas production, which

suggested *Salmonella typhi*. However, *Proteus* spp had a similar appearance to *Salmonella* colonies, and were smaller in size. On the other hand, a negative result was indicated by a colourless or pink colour. An un-inoculated medium was used as a negative control, and the result had no growth.

Muller Hinton agar (MHA)

Mueller Hinton Media contains beef extract, acid hydrolysate of casein, starch and agar. Beef extract and acid hydrolysate of casein provide nitrogen, vitamins, carbon, amino acids, sulphur and other essential nutrients. Starch is added to absorb any toxic metabolites produced. Starch hydrolysis yields dextrose, which serves as a source of energy. Agar is the solidifying agent.

However, according to the method described by Åhman *et al.* (2020), 38grams of the medium was suspended in 1000 mL of distilled water and heated with frequent agitation and boiled for 1 min to completely dissolve the medium, after which it was autoclaved at 121°C for 15 min. The medium was allowed to equilibrate at a room temperature of 25-45 °C, where the media solution was poured or dispensed into sterile petri plates covered with the lid and allowed to solidify. After solidification of the medium, a fresh culture of each isolate was created, and then antibiotic discs were placed onto the lawn within 15 minutes and incubated at 37 °C for 18- 24 hours. Antibiotic discs were placed onto plates of MHA no closer than 24mm from the centre to centre of the discs. An un-inoculated medium was used as a negative control, and the result had no growth or no change in the medium (Cheesbrough, 2010)

