FEDERAL UNIVERSITY OF TECHNOLOGY MINNA

THE HUMAN-PATHOGEN PUSH ME AND I PUSH YOU CONUNDRUM: WHEN WILL THIS MUTUALLY ANTAGONISTIC STRUGGLE END?

BY:

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INAUGURAL LECTURE SERIES 126

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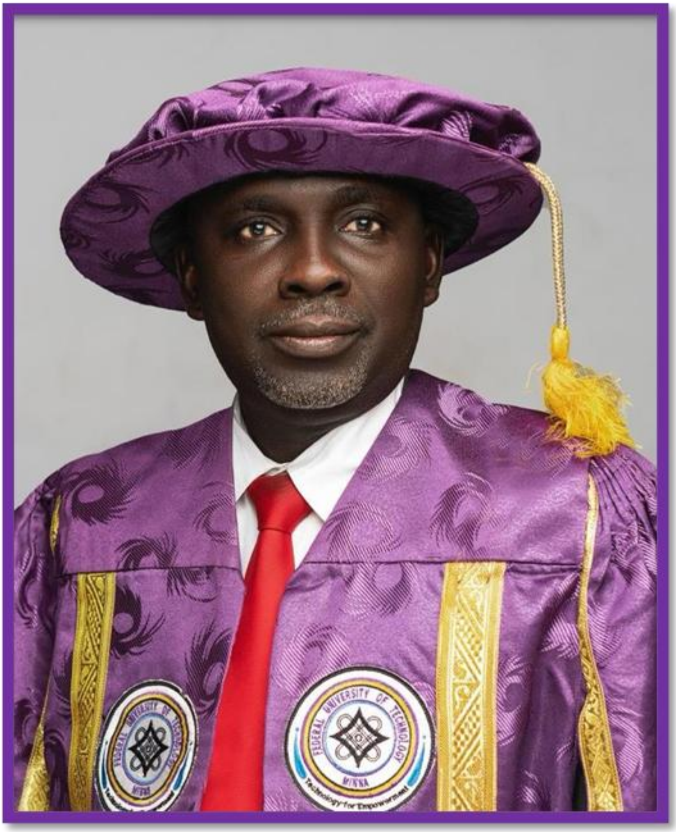

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Preamble

Mr. Vice Chancellor, other Principal Officers of the University, the Deans, Directors and Professors, the Chairman and members of the Colloquium Committee, every member of the University Community and all the distinguished guest here present, let me begin with praises to the Almighty Allah for blessing and giving life to this day. If my father were alive, I would have told him just like Prophet Yusuf/Joseph in the Quran/Bible that Papa, this is the dream I nursed but couldn't explain clearly many years ago.

Mr. Chairman Sir, standing here on this stage today with your permission is all at once unique, historic and symbolic. It is not like any other lecture by a professor because it symbolizes a formal inauguration into the professorial fold with the town and the gown as witness. In a way, it can be likened to the professorial staff of office. The significance of this day is therefore huge and massive for me and in some ways, spiritual. Having to present this lecture under your chairmanship is to me, the Almighty Allah's way of saying that you should perfect what you started. Your role in my rise through the academic ladder, ever since you adopted me as a younger brother, is a story for another day. May the Almighty Allah expand your blessing and may the blessings of your children dwarf your own, Aameen.

Given the aforesaid importance of this day, permit me Mr. Chairman to go down memory lane and provide a little exposition on how this particular journey started. It all began in my primary five sometimes in the 80s, after hearing about a man who was then a Professor of Engineering. Let me quickly confess that I grew up as a bit of a difficult child (not too stubborn though) and Mama faced quite some trouble controlling me anytime dad is not around. In response, my dad came up with a brilliant idea. Each time he is going out, he gives me assignments that will occupy me till he returns back home thereby effectively making me unavailable for troubles and most importantly football. On one such occasion, I had to answer a question on what I wish to be in life. And without hesitation, I answered "Professional", my own version of the word "Professor". To my adulterated childish understanding, anyone who teaches in the university is a professional. My father, who was obviously impressed with my choice of word, being an educationist, took time to explain that a professional is one who dedicatedly practices and is good in a particular occupation. He went further to say that I needed a specific occupation that I can be a professional in. He therefore requested that I choose a particular occupation but each time he asks, I had only one answer which is “Professional” not knowing that the right word is “Professor”. When it became obvious that my little head was impervious to his explanations, he left me out of frustration believing that someday, I will probably understand better and be able to clearly express my career choice. Today, I give praises to the Almighty Lord for making a child’s uncoordinated dream a reality even though Papa is not a witness to this fulfilling occasion. May Allah grant him and all departed faithful eternal rest, Aameen.

1.0 INTRODUCTION

Today I stand before you to discuss a subject matter that historically preceded all of us and which sadly, will certainly outlive all of us: infectious diseases. From prehistoric times, humans and microorganisms have co-existed and co-evolved symbiotically, enjoying a relationship that traverses the entire spectrum between the best and the worst as expediency demands and leaving in its wake a tremendous impact on the world in which they both live or exist.

The struggle between man and pathogenic microbes started blind with man fighting an enemy he does not even know exists. For several centuries, the activities of pathogenic microorganisms made man’s life miserable leaving in its wake miseries and deaths that were attributed to spiritual sources. It can be said without any fear of contradiction that man has never had any enemy as vicious as microorganisms. Ironically, he also will never gain a friend as beneficial as microbes. In wars and other disasters, disease causing microbes usually account for the greater percentages of undesirable health outcomes while in all beneficial natural processes, microbes are almost always the driving force.

It took several centuries before man came to term with his source of misery and ever since then, life has never been the same again marking humanity's eventual transition from vulnerability and superstition to scientific mastery and technological advancement.

1.1 Microorganisms

Microorganisms, simply known as microbes, are no longer described exclusively on the basis of size as was hitherto done because there are organisms which can now be seen without the aid of a microscope. While over 90% of the microbial population are within the micrometres range in size and appear in various shapes cutting across rod, spheres, spirals and several other complex shapes, a few have been discovered that are readily resolvable with the naked eyes. One characteristic that is however common to all of them and which currently defines them is the simplicity of their structure (Kubitschek, 1993).

Microbes are closely associated with human and are found in very large numbers in the gut, skin as well as other anatomical sites in humans as symbionts often playing contradictory roles (Chanda and Joshi, 2022). Although, some microorganisms are capable of causing diseases and are responsible for very serious diseases like tuberculosis, bubonic plague, anthrax, HIV, Ebola, syphilis, cholera, and leprosy among others, the larger majority are harmless and are involved in numberless processes some of which are not just beneficial but essential for human survival (Weiss and Sankaran, 2022).

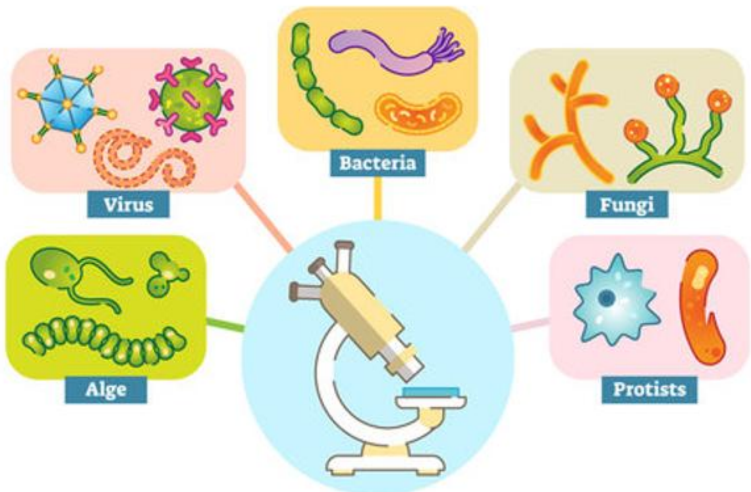

Figure 1: Diagrammatic Representation of Microorganisms (Anonymous, 2026)**.**

1.1.2 The Different Microbial Groups

1.1.2.1. Bacteria

Bacteria which are prokaryotes are the most abundant microorganisms. In size, bacteria range from 0.15 to 700µm (Doetsch & Cook, 2012). While the larger majority are beneficial to humans, a few are pathogenic and have caused notable diseases in plants and animals through the production of toxins, enzymes and/or by activation of inappropriate immune responses (Srivastava *et al*., 2003). Bacteria may be rod shaped (bacillus), spherical (coccus), spiral (Treponema), comma shaped (vibrio), filiform etc. On the basis of cell wall structure, bacterial cell can either be Gram-positive, Gram-negative or wall less. They reproduce asexually by binary fission.

Examples of Bacteria and the Diseases they cause in Humans

Bacteria	Diseases
Clostridium tetani	Tetanus
Salmonella typhi	Typhoid
Mycobacterium tuberculosis	Tuberculosis
Corynebacterium diphtheria	Diphtheria
Streptococcus pneumoniae, Haemophilus influenzae	Pneumonia
Mycobacterium leprae	Leprosy
Treponema pallidum	Syphilis

(Doron & Gorbach, 2008)

1.1.2.2 Viruses

Viruses which are commonly called particles are not strictly living as they can only replicate when they are inside a living host. A virus contains either DNA or RNA enclosed within a protein coat called the capsid and are very small in size (ranging from 20 to 300 nm) (Cliver, 2014; Forni *et al*., 2022). A virus may either be enveloped or non-enveloped.

Examples of Viruses and the Diseases they caused in Humans

Viruses	Diseases
Variola major and *Variola minor*	Smallpox
Rhinoviruses	Common cold
Mumps orthorubulavirus or mumps virus (MuV)	Mumps
Simplexvirus	Herpes
Influenza viruses (A, B, C and D)	Influenza
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)	COVID-19
Human immunodeficiency virus (HIV)	AIDS
Poliovirus (*Enterovirus C*)	Polio

(Forni *et al*., 2022).

1.1.2.3 Protozoans

Protozoans are unicellular eukaryotes that lack the cell wall found in plants and are often referred to as one-celled animals. They are heterotrophic in nature and are either free-living or parasitic, some (parasites) of which are known to cause notable diseases in humans. Protozoans ranges from 1 µm to several mm (Custodio, 2016; Vaisusuk & Saijuntha, 2021). Protozoa possess various locomotion organs which includes flagella, pseudopodia and cilia. Their reproduction is both asexual and sexual.

Examples of Protozoans and the Diseases they caused in Humans

Protozoan	Diseases
Trypanosoma brucei	African sleeping sickness
Plasmodium spp.	Malaria
Leishmania	Leishmaniasis
Entamoeba histolytica	Amoebiasis
Trypanosoma cruzi	Chagas disease
Toxoplasma gondii	Toxoplasmosis

(Scholar, 2007)

1.1.2.4 Fungi

Fungi are eukaryotic heterotrophic organisms whose cell walls are made up of chitin and other polysaccharides. They are mostly saprophytes and absorb organic matter from dead and decaying matter (Blackwell, 2011). Pathogenic fungi derive nutrients from living plants and animals and in the process produce diseases. Fungi can either be multicellular as filamentous fungi (Moulds) or unicellular like bacteria (yeast) and they reproduce generally by vegetative, asexual and sexual means.

Examples of Fungi and the Diseases they caused in Humans

Fungi	Diseases
Candida albicans	Candidiasis
Cryptococcus neoformans	Cryptococcal meningitis
Microsporum, Trichophyton and Epidermophyton	Ringworms
Histoplasma capsulatum	Histoplasmosis
Mucormycetes	Mucormycosis
Aspergillus	Aspergillosis

(Centre for Diseases Control and Prevention, 2021)

1.1.2.5 Chlamydia

Chlamydia are small Gram-negative coccoid or rod shaped, aerobic, non-motile bacteria that are obligate intracellular parasites of man. They have a very high predilection for sites such as the squamous epithelial cells and macrophages of the respiratory and gastrointestinal tract of human and other animals.

Examples of Chlamydia and the Diseases they caused in Humans

Chlamydia serotypes	**Diseases**
C. trachomatis serotype A, B, Ba, C	Ocular infections
C. trachomatis serotype D to K	inclusion conjunctivitis
C. trachomatis serotype L1, L2, L3)	non-gonococcal urethritis and lymphogranuloma venereum
C. pneumoniae	pneumonia.
C. psittaci	Psittacosis

Source: (Arif, 2023)

1.1.2.6 Rickettsia

Rickettsia are small, pleomorphic, non-motile and non-capsulated Gram-negative bacilli that multiply by binary fission. They are fastidious in nature and are characterized by obligate intracellular parasitism. They normally require a blood sucking arthropod vector as part of their natural life cycle who also serve as the source of transmission to man. They possess both DNA and RNA. Their cell wall is made of peptidoglycan. They are susceptible to antibacterial agents (Osip *et al*., 2024). However, they are not resolvable by light microscopy. The genus was named after Howard Taylor Rickett who died of typhus fever contracted while carrying out his pioneering work on this special group of organisms.

Examples of Rickettsia and the Diseases they caused in Humans

Rickettsia serotypes	**Diseases**
C. trachomatis serotype A, B, Ba, C	Ocular infections
C. trachomatis serotype D to K	inclusion conjunctivitis
C. trachomatis serotype L1, L2, L3)	non- gonococcal urethritis and lymphogranuloma venereum
C. pneumoniae	pneumonia.
C. psittaci	Psittacosis

(Biggs *et al*., 2016)

1.1.2.7 Miscellaneous Infectious Agent

Prions are misfolded protein that are infectious in nature and have been discovered to cause fatal, rare and incurable neurodegenerative diseases.

1.1.3 Pathogenic Microorganisms

Pathogenic microbes or pathogens are actually microbes that are capable of infecting and causing diseases, either frankly or opportunistically, in their hosts which may be human, animals or plants (Shanson, 2014). A pathogen can be bacteria, fungi, helminths, protozoa, viruses, rickettsia, chlamydia etc (Maraz and Khan, 2021). They are called **frank** pathogens when they are characteristically pathogenic or **opportunistic** pathogens when they are situationally pathogenic usually as a result of changes in the microbe-host dynamics.

The ability of a microorganism to cause disease in a host is described as pathogenicity. This ability, which is not entirely qualitative varies not just between two different species of microorganisms but also between different hosts for a specific microorganism. This variation in pathogenicity between microbes is known as virulence and is defined as the degree of pathogenicity of any given pathogen. Variation in pathogenicity of specific microbes in different hosts may be due to the infectious dose of the pathogen or the competence level of the host immune system. Virulence is characterized by the ability of pathogens to invade covertly, replicate, and damage host tissues often through the production of toxins or related molecules (Leitao, 2020; Soni *et al*., 2024).

The body is naturally full of microbes, many of which only cause problems if the immune system is weak or if they manage to enter a strange or a normally sterile site within the body. All that a pathogen needs to thrive and survive is a suitable host. Once the pathogen sets itself up within a host's body, it struggles to avoid the body's protective responses and uses the body's resources to grow and multiply before exiting and spreading to a new host (Basu *et al*., 2025). Transmission can be through skin contact, body fluids, airborne particles, contact with faeces or contaminated surfaces etc.

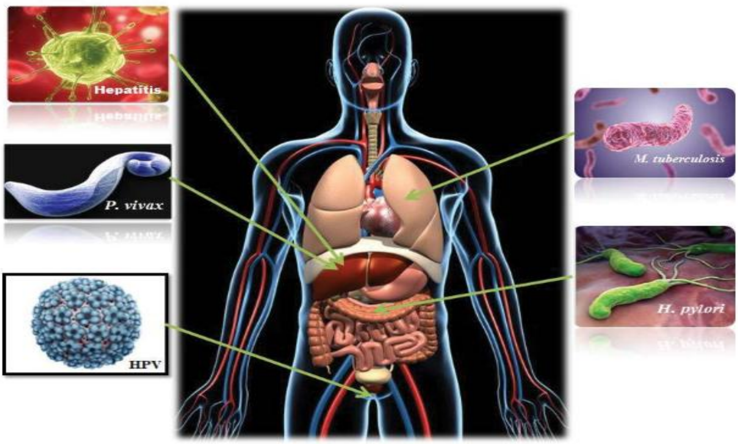

Figure 2: Common Human Pathogen and their Site of Action (Sarmah *et al*., 2018)

1.1.3.1 Unique Characteristic of Pathogenic Microorganisms

For a microorganism to be successful as a pathogen, certain characteristics also known as attributes of pathogenicity are necessary (Leitao, 2020). These characteristics include:

1. Ability to Adhere, Colonize and Invade Host Tissues: Pathogens must not just find a suitable host but a suitable environment within the host to survive and multiply. Some pathogens have host tropism and are highly specific for certain host species while others can infect a wide range of host species. Pathogens must and often possess structures with which they attach firmly to target host cells thereby facilitating colonization.

2. Immune System Evasion: As part of the struggle for survival, a pathogen must have strategies to circumvent or overcome the host's immune defences in order to establish disease.

3. Replication: Many pathogens replicate rapidly, leading to an exponential increase in their numbers within a very short time in the host as a result of which they overwhelm the host defence and cause disease.

4. Infectivity: Pathogens must have exit routes from an infected host as well as mechanisms to spread to new hosts.

5. Pathogenesis (Disease Causation): The presence of the pathogen should elicit tissue damage or the inhibition of important biological functions either directly or indirectly giving rise to disease symptoms. Some pathogens are able to cause diseases by producing molecules that cause damage to host cells and/or interfere with cellular functions. On the other hand, an aggressive immune response to the presence of the pathogen in the host can also cause malfunctions and cellular damage often attributable to the pathogen.

2.0 MECHANISMS OF PATHOGENESIS

Microbial pathogenesis is the process through which microbes initiates destruction in a host as a consequence of the interaction between the host and the pathogen. To cause disease, a pathogen must gain entry, colonize and adhere to tissue surfaces, overcome or evade the immune system and cause damage to host cells (Ribet and Cossart, 2015). Pathogens are usually distinct from the normal flora. The normal flora causes diseases only opportunistically if the immune system is weakened or if they are translocated to an unfamiliar site within the host body. In contrast, frank pathogens actively struggle with the immune system to cause diseases. In consonance with their nature, frank pathogens have well developed and sometimes uniquely specialized mechanisms for breaching immunological barriers and eliciting specific responses from the host organism that contribute to the survival and multiplication of the pathogen (Colella *et al*., 2023).

2.1 Microbial Entry

A pathogen's capacity to reach a site in the body conducive for its development and reproduction is a vital step in pathogenesis. Microbes can enter the body through several channels including the mouth (ingestion), nose (inhalation), urinary tract (urogenital system), skin (active or passive) and direct contact (eye, ear, and skin) (Zachary, 2017).

2.2 Colonization and Adhesion

After entry, colonization occurs when microbes adhere to host cell and/or other structures using specialized organelles (adhesins). Adhesion generally refers to the attachment of microbes to parts of the host's body and different pathogens use varieties of mechanisms to adhere to their host cells and tissues (Pizarro-Cerdá and Cossart, 2006).

Adhesins molecules usually occur on the surface of most pathogens and bind to specific receptors (glycoproteins) on host cells. Microbial organelles commonly used for this purpose include but are not limited to the fimbriae and flagella of bacteria, the cilia of protozoa and the capsid or membrane proteins of viruses. Protozoans can also use hooks and barbs for adhesion while spike proteins on viruses also enhance viral adhesion.

The production of glycocalyces (slime layers and capsules), with their high sugar and protein content, can also allow certain bacterial pathogens to attach to cells (Chahales and Thanassi, 2015).

When biofilms are formed, they can also act as adhesion factor. A biofilm is a community of bacteria joined together through the production of glycocalyx which allows the organisms to attach to a surface. This extra-polymeric substance not only allows for attachment but provides protection for the organisms as well.

2.3 Invasion

Once adhesion is successful, invasion can proceed. Invasion, which is a necessity in systemic infections, involves the dissemination of a pathogen from the site of infection/entry to other sites within the body. Pathogens may produce exoenzymes or toxins to serve as virulence factors that allow them to damage and spread past host biological barriers and then spread deeper into the body. In addition, pathogens may also produce virulence factors that are protective against the host's immune defences as they traverse the host body.

Intracellular pathogens are able to invade by entering the host's cells where they hide, reproduce and spread to adjacent cells. Some can only reproduce inside of host cells (obligate intracellular pathogens) and others can reproduce either inside or outside of host cells (facultatively intracellular pathogens). By entering the host cells, intracellular pathogens can evade the immune system while also exploiting the nutrients in the host cell to multiply and disseminate (Thakur *et al*., 2019).

Entry into a cell can occur by endocytosis, a cellular process where the pathogen is surrounded by the cell's plasma membrane. Host leukocytes, such as phagocytes and some other immune cells, actively endocytose pathogens in a process called phagocytosis (Cooper, 2000). Normally, phagocytosis is an immuno-protective mechanism that takes the pathogen into the host cell for its degradation by digestive enzymes. However, some intracellular pathogens have the ability to survive and multiply within phagocytes (Rosales and Uribe-Querol, 2017).

2.4 Evasion of Host's Immune system

Pathogens, especially bacteria and viruses have remarkable abilities to evade immune surveillance, a pivotal strategy for their survival within the host environment. This adaptive skillset plays a crucial role in the aftermath of their successful colonization of the host (Kahn et al., 2002; Finlay and McFadden, 2006). These immune evasion strategies include several meticulous steps, including inhibiting immune-related signalling pathways, concealing within various host cells, disrupting phagosomes, deactivating reactive oxygen species, and modulating the host's immune response by altering the molecular patterns on their outer surfaces (Van Avondt *et al*., 2015; Rana *et al*., 2023). These molecular modifications serve as camouflages that render pathogens less recognizable to the host's immune receptors thereby avoiding detection, persisting and thriving within the host's body (Finlay and McFadden, 2006).

The possession of these complex camouflage skills and meticulous invasive techniques by bacterial pathogens significantly hinders the development of innovative vaccines and novel treatments. Armed with these constantly evolving intelligent survival mechanisms, pathogens particularly bacteria are able to continually manipulate the host's immunity thereby constituting a formidable challenge that requires equally ingenious approaches to counter their shrewd strategies.

Some of the ingenious ways by which microorganisms circumvent the host’s immune responses and chemotherapy include but are not limited to the following:

- Interference with the production of the effector cells of the lymphoid lineages such as the “B” and “T” cells (*Listeria monocytogenes*).
- Destruction of protective antibodies such as the cleaving of the Fc portion of IgA by proteases (*Neisseria gonorrhoeae*)
- Production of capsule that prevents phagocytosis (the fungus *Cryptococcus neoformans* usually develop a thicker capsule upon entering the lungs).
- Resistance to lysis by lytic enzymes even after being phagocytosed by the host’s cells of inflammation (*Mycobacterium tuberculosis*)
- Enzymatic deactivation of antibiotics, efflux pump and the modification of target sites.
- The production of biofilm for communal protection (Many capsule-producing bacteria).
- Antigenic heterogeneity (Influenza and other viruses).
- Genetic dissemination of resistance (Most bacteria).

2.5 Production of toxins and enzymes

Many pathogens cause cellular and tissue damages by producing toxins. Toxins are biological molecules that harm living things by disrupting important biological functions in the host and are commonly associated with bacteria even though the origin may be viral in nature. Bacterial toxins are broadly grouped into two main types. The cell-associated toxins are known as **endotoxins** (bacterial lipopolysaccharide) while the extracellular diffusible toxins on the other hand are knowns as **exotoxins** (tetanospasmin and botulinum toxin) (Silbergleit *et al*., 2020). Some bacteria produce enzymes that break down tissue, allowing the infection to spread through tissues faster. Other bacteria produce enzymes that allow them to enter and/or pass through cells. Examples include collagenase, hyaluronidase, staphylokinase etc.

2.6 Host Damage (Disease)

Following invasion, successful multiplication of the pathogen usually leads to tissue damage. The damage can be described as local, focal, or systemic, depending on the extent of the host's tissues affected. A local infection is confined to a small area of the body, typically near the portal of entry. For example, a hair follicle infected by *Staphylococcus aureus* infection may result in a furuncle around the site of infection with the bacterium entirely contained to this small location. Other examples of local infections that is characterised by more extensive tissue involvement include urinary tract infections confined to the bladder or pneumonia confined to the lungs (Patterson, 1996).

In a focal infection, a localized pathogen, or the toxins it produces, can spread to a secondary location. For example, using a hard brush for cleaning the teeth can lead to an infection of the gum by a member of the normal oral microbiota; *Streptococcus*. These *Streptococcus* species may then gain access to the bloodstream and make their way to other locations in the body, resulting in a systemic infection.

When an infection becomes circulated throughout the body, it is called a systemic infection. For example, infection by the varicella-zoster virus characteristically occur through the upper respiratory tract but ultimately spreads around the body, giving rise to the symptomatic skin lesions associated with chickenpox (Ayoade, 2022). Since these lesions are not the original sites of infection, they are therefore clear manifestations of a systemic infection.

3.0 IMMUNE RESPONSES

An immune response is a physiological reaction that occurs for the purpose of defending against exogenous factors which include all microbial pathogens (Ahrend *et al.* 2025). Even harmless foreign agents such as pollen and food components can also trigger immune response. These special forms of immune response are classified as hypersensitivity or allergy (Summer *et al.,* 2024). A transplanted tissue or organ meant to save life as a medical intervention can provoke immune response leading to graft-versus-host disease. The nature of immune response can either be innate or adaptive but these two arms of immunity are always working together interdependently using humoral and cellular components to protect the host.

3.1 The Innate Immune Response: The body's first reaction to an invader is usually a very quick but non-specific response and is largely the same for any type of pathogen. Components of the innate immune response include physical barriers like the skin and mucous membranes, immune cells such as neutrophils, macrophages, and monocytes, and soluble factors including cytokines and complement (Summer *et al.,* 2024).

3.2 The Adaptive Immune Response: The adaptive arm of immunity on the other hand, is the body's immune response which is tailored in action and acts specifically against each antigen type. However, it takes longer time to activate the components involved but once activated, adaptive immunity keeps immunological memory of the antigen encountered. This arm of the immune system comprises the "B" and "T" cells. B cells are responsible for the production of antibodies also known as immunoglobulins (John *et al.*, 2024).

The first exposure of the host to a particular pathogen will lead to the activation of T cells and subsequently B cells that are tailor-made for the antigens on the pathogen and this process is called **primary** immune response. Memory T and B cells are also produced to mount a faster and more efficient secondary immune response in the event of a subsequent exposure to the same pathogen (John *et al.*, 2024). It is this understanding that gave rise to the development of vaccine which remains one of the best medical progress ever made by mankind.

Pathogens are recognized and detected via pattern recognition receptors (PRR) which recognises by identifying pathogen-associated molecular patterns (PAMPs). These are unique structural components of pathogens that are not found in the host's system. Examples of PAMPs include the peptidoglycan cell wall or lipopolysaccharides (LPS) of bacteria, both of which are never found in the human body (Wang *et al.,* 2024). Foreign pathogen that are able to bypass the physical barriers into a host are recognized by the PRRs on macrophages and other cells of inflammation leading to their phagocytosis, degradation and presentation to the specific arm of immunity.

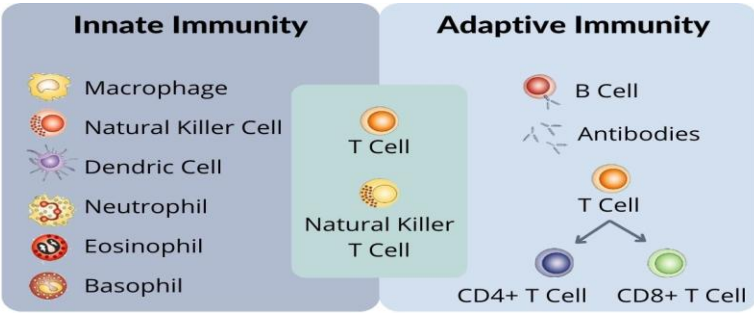

Figure 2: Innate and Adaptive Immunity

4.0 CHEMOTHERAPY

Chemotherapy as applied to infectious diseases denotes the clinical application of chemical drugs with antimicrobial activity to overcome microbial pathogens namely bacteria, viruses, parasites, fungi etc. (Mubeen *et al.*, 2021; Parija, 2023). These agents are developed based on their ability to exert toxicity selectively by inhibiting or completely destroying the growth of microbial pathogens with minimal or no harm at all to the host (Kuriyama *et al.*, 2014; Pancu *et al.*, 2021). These agents are characteristically designated antibacterial, antifungal, anthelmintic, antiprotozoal, and antiviral agents based on the type of microorganisms they target. The origin of modern chemotherapy can be traced to the work of Paul Ehrlich (1854–1915), the German scientist who pioneered the concept of targeted drug therapy (Zipfel and Skerka, 2022). Ehrlich conceptualised the possibility of an ideal chemical or molecule that he christened the "magic bullet" (Williams, 2009; Gradmann, 2011; Zipfel and Skerka, 2022). He hypothesised that the agent would selectively destroy pathogens without affecting the cells of the host (Kuriyama *et al.*, 2014). Ehrlich's foresight blew the first whistle that heralded the race for the development of chemotherapy and gave birth to the first conceptual framework for selective toxicity in the control of microbial pathogenicity. The first fruit of his proposition was reaped when Alexander Fleming accidentally discovered the first antibiotic called penicillin in 1928 officially marking the birth of the antibiotic era (Sharma and Kumar, 2024). What followed naturally was the development of other antibiotics, antiviral, antifungal, and antiparasitic drugs thereby expanding the scope of chemotherapy to cover other microbial groups (Bryan-Marrugo *et al.*, 2015; Zipfel and Skerka, 2022; Shapiro *et al.*, 2023).

4.1 Microbial Resistance to Chemotherapy

Microbial resistance is broadly defined as the ability of a microorganism to withstand the effects of a chemotherapeutic agent that was previously effective against it (Uddin *et al.*, 2021). Its history dates back to the initial discovery of the first antibiotics penicillin in 1928, with its widespread use soon leading to the emergence of organisms resistant to it (Ahmed *et al.*, 2024). Reygaert *et al.* (2018) noted that the introduction of antibiotics in the 1900's was thought to be the end of the war against microorganisms. However, it was soon discovered that these organisms have the innate capabilities to develop resistance against any antimicrobial agent. The phenomenon has today, escalated into a global public health crisis (Salam *et al.*, 2023), threatening the effectiveness of existing chemotherapeutic agents and demanding immediate attention (Akram *et al.*, 2023) without which the future of infectious disease management is doomed. The alarming rise of microbial resistance is primarily driven by the excessive and inappropriate use of antimicrobial agents across medicine, veterinary practice, and agriculture (Ahmed *et al.*, 2024).

The global spread of resistant microorganisms, genes, and gene determinants is one of the major challenges of the twenty-first century (Ekwanzala *et al.*, 2018). Microbial resistance has been termed a “Silent Pandemic” due to its insidious spread worldwide (Paneri and Sevta, 2023), emerging as a major global health problem that causes significant morbidity and mortality, with sub-Saharan Africa disproportionately affected (Moyo *et al.*, 2023).

Over the years, microorganisms have continually evolved resistance mechanisms to counteract chemotherapeutic agents, ensuring their survival and proliferation (Paneri and Sevta, 2023). These adaptive mechanisms include intrinsic structural defences, acquisition of resistance genes through horizontal gene transfer, biofilm formation, and targeted genetic mutations, all of which contribute to the neutralization of antimicrobial compounds (Smith *et al.*, 2023). In some microbe particularly in Gram-negative bacteria limiting the uptake of chemotherapeutic compounds is a key resistance mechanism, the outer membrane's lipopolysaccharide (LPS) layer serves as a permeability barrier. Microbe can also alter target sites of therapeutic compounds through mutations, reducing antimicrobial binding affinity, produce inactivating enzymes which hydrolyse and neutralize therapeutic compounds and use efflux pumps to actively expel antimicrobial agents.

A multimodal strategy that includes measures to optimize the use of antimicrobials through stewardship programs and evidence-based prescribing guidelines, improve infection prevention and control, and develop novel antimicrobial agents is needed to control and curtail microbial resistance (Capuozzo *et al*., 2024; Dikkatwar *et al*., 2024). In addition, systematic monitoring of antibiotic usage and the global implementation of standardized practices are essential to curb misuse and slow the emergence of resistance.

5.0. THE MICROBIAL PUSH

5.1 Diseases in History

Human history has largely been shaped by diseases caused by microbial pathogens by determining the nature and distribution of human population, influencing socioeconomic order and accelerating scientific development during times of peace and wars.

5.1.1 The Plague of Justinian

The Plague of Justinian was an outbreak that affected the Byzantine Empire from 541 to 542 AD. The disease, which was probably a form of bubonic plague, is thought to have originated in Egypt and spread through trade routes to Constantinople. The disease as we now know today, was caused by *Yersinia pestis*, carried by fleas. The Byzantine Empire was quickly overwhelmed by the disease, which caused fever, vomiting, and painful swellings in the lymph nodes. As the death toll rose, city leaders imposed a strict quarantine, closing all ports and prohibiting travels in and out of the city (Flemming, 2023). However, these measures failed to contain the outbreak, and the plague eventually spread throughout the empire. It is estimated that somewhere between 30% and 50% of the population, up to 50 million people, perished before the disease finally ran its course. Emperor Justinian himself was reported to have contracted and suffer the disease but luckily survived (Mordecai *et al*., 2019; Singh and Tyagi, 2024).

5.1.2 The Black Death

The Black Death is perhaps one of the most famous pandemics in history. This outbreak of bubonic plague occurred in Europe from 1346 to 1353 and killed an estimated 25 million people, nearly one-third of Europe's population as at that time (Boyd, 2022). It was also caused by the bacterium *Yersinia pestis.* However, during these times, little was known about the aetiology of the disease or how to treat it effectively leading to one of the most devastating outbreaks in human history (Dias, 2024).

The Black Death had a profound impact on Europe, both socially and economically. It also ushered in a new era of medical science, as researchers began to study the disease to find a possible cure in a **push me and I push you,** manner (Boyd, 2022).

5.1.3 The Plague in Modern Times

Plague is classified as a re-emerging infectious disease by the World Health Organization (WHO). Between 2010 and 2015, there were an estimated 3,248 cases of plague, with 584 fatalities worldwide (Parums, 2025). Most of those cases occurred in the Democratic Republic of the Congo, Madagascar, and Peru. Despite its reputation as a medieval disease, the plague is still a threat in the modern world. Although now relatively rare, it still causes significant morbidity and mortality in epidemic settings. Consequently, it is important that preventive measures are put in place (Mostafavi *et al.,* 2025).

5.1.4 Syphilis

In 1494, the world was introduced to a new and deadly disease: syphilis. Often referred to as "the great pox," syphilis is caused by the bacteria *Treponema pallidum* and is characterized by painful sores, fever, and eventual death (Zbar, 2022). Other symptoms of syphilis include rashes and muscle aches. If left untreated, syphilis can lead to deformities, dementia, and death.

The disease first appeared in Europe following the colonization of the Americas, and it quickly spread through the population. Over the next few centuries, syphilis would kill more than 50,000 people. however, with the current advances in medicine, syphilis is now easily treatable with antibiotics. Despite this, the disease remains a serious global health concern, with approximately 12 million new cases occurring yearly (Zbar, 2022).

5.1.5 Tuberculosis

Tuberculosis, popularly called TB, is an ancient disease that first appeared in humans thousands of years ago. It is believed to be one of the oldest diseases that afflicted mankind (Waksman, 2021). Tuberculosis is caused by the bacterium, *Mycobacterium tuberculosis,* which is spread through the air when people cough or sneeze. The earliest documented outbreak of tuberculosis dated back to 1500 AD, and has since claimed millions of lives over the years. The most famous victim of tuberculosis was probably Queen Elizabeth I, who died of the disease in 1603, though yet a subject of dissension among historians. However, it was not until the 19th century that tuberculosis became a true pandemic (Mussie, 2023).

In the past few hundred years, tuberculosis has been largely controlled due to advances in medicine and public health. In 1815, the causative bacterium was described by a physician named Georges Cuvier and in 1882, Robert Koch established its person to person transmission. Fortunately, there are now effective treatments for tuberculosis through a cocktail of drugs which must be taken for an extended period but are helpful for persons affected by this deadly disease (Waksman, 2021).

5.1.6 Smallpox

The history of smallpox is highly controversial, comprising false starts, dead ends, and blind alleys. It was among the most dreaded diseases in ancient times because of the role of smallpox epidemics in the collapse of civilizations (Bonhomme, 2025). Believed to have started originally in Africa or Asia from where it then spread to Europe and the Americas through trade and travel, the first outbreak was reported to have occurred in the 13th century in China before becoming global (Berche, 2022).

Transmission is through contact with infected people or objects and it can also be airborne though rarely. *Variola major* is the causative virus and the symptoms include fever, severe body aches, and a unique rash that ultimately transforms into lesions and scabs. The outcome is usually fatal, and survivors were often left with defacing scars as sequelae (Berche, 2022).

It was especially devastating to native populations who lack anti-smallpox immunity with the outbreaks and devastating epidemics occurring intermittently throughout history. It was believed that small pox killed an estimated 300 million people in the 20th century alone. However, due to a massive global vaccination effort launched in the 1960s, the disease is considered eradicated from the human population since 1977 (Bonhomme, 2025).

5.1.7 Yellow Fever

Before the turn of the nineteenth century, another deadly disease later identified as yellow fever began to spread throughout the colonies of North America. The disease which is transmitted through mosquitoes is usually accompanied with fever, vomiting, and jaundice often leading to death without adequate medical intervention. In some cases, patients also bleed from their nose and mouth. Between 1793 and 1798, approximately 25,000 people living within this colonies died from what is now referred to as "The American Plague." A leading physician at the time, Benjamin Rush attributed the cause of yellow fever to "miasma," or bad air underscoring the level of ignorance about the disease at the time (Tuells *et al.,* 2022).

In the early nineteenth century, the disease transmission was greatly controlled through proper sanitation and enhanced mosquito control measures. Yellow fever, however, remains a significant public health challenge in many parts of the world today with sporadic outbreaks of the disease still being reported in parts of Africa and Latin America (Bonhomme, 2025).

5.1.8 The Seven Cholera Pandemics

Cholera, a waterborne disease has caused seven major pandemics over the past 200 years. Cholera is transmitted through contaminated food or drinks and is associated with symptoms such as vomiting, severe watery diarrhoea and dehydration. Successful management of the disease involves rehydration with fluids and electrolytes. Cholera transmission is preventable through improved sanitation and provision of clean water to people living in areas of endemicity (Muzembo *et al*., 2022).

5.1.9 Influenza Pandemics

Influenza viruses have afflicted humans repeatedly for centuries. The first recorded influenza pandemic occurred in 1510, and several outbreaks have occurred ever since. The transmission is inherently difficult to contain, because the virus is airborne and spreads rapidly through human interaction. These viruses are highly mutative and are notorious for having several antigenic forms which makes immunological recognition and memory difficult during different outbreaks. As a result, influenza pandemics can cause widespread illness sporadically. Flu pandemics are often mild in comparison to other major diseases but on occasions, they can be as equally deadly, as was observed with the 1918 Spanish flu and COVID-19 (Dias, 2024).

5.1.10 Ebola

Ebola virus disease is a deadly haemorrhagic fever that was first detected in 1976 in Sudan and the Democratic Republic of Congo. Since then, it has caused several thousands of deaths and 29 epidemics (Hanić and Mitić, 2022). Ebola virus affects humans and other primates and the disease spreads mainly within Africa in communities lacking adequately functional healthcare systems. The virus is spread through contact with bodily fluids and symptoms include fever, diarrhoea, and bleeding. There is no known specific cure for Ebola, but early diagnosis and syndromic management can improve the outcome (Hanić and Mitić, 2022).

5.1.11 The AIDS Pandemic

In 1981, a new disease later identified as HIV/AIDS was first reported among the gay community in the United States from where it quickly spread to other countries. The AIDS pandemic has since become a global health challenge (Culshaw, 2023). Even though, not as deadly as some preceding pandemics, it has caused an estimated 35 million deaths worldwide and still counting. The disease has had very profound impact on the global economy and has also spotlighted the social gradient in healthcare access and disease as well as the stigma surrounding sexually transmitted infections. Given the great deal of fear and misunderstanding that surrounded the transmission of the disease at the initial stage, the importance of education and awareness in disease prevention and control was once again underscored (Culshaw, 2023).

Figure 2: Timeline of Pandemics in Human History (Hazel, 2022).

5.2 Factors That Aid the Microbial Push

5.2.1. Migratory and Behavioural Changes

- Migration Due to Urbanization leads to high population density which overstretches social facilities and outpaces infrastructure and in turn create overcrowding and poor sanitation. The spread of respiratory and enteric diseases like tuberculosis and cholera are common.
- Population Movement as a result of natural disaster such as conflict, famine, earthquake etc. create artificial settlements with significant risk for infections.
- Behavioural changes such as intravenous drug use, risky feeding habits and dangerous sexual practices encourages the spread of HIV/AIDS and Hepatitis C.

5.2.2. Climatic and Environmental Changes

- Encroachment on forest and other reserved areas for human benefits facilitates human-vectors contact leading to zoonotic diseases like Ebola, Nipah virus, and Lyme disease. More than 60% of emerging diseases are of animal origin mostly through increased contact with wildlife or livestock.
- Climate Change, global warming and altered rainfall patterns has extended the range and availability of vectors (e.g., mosquitoes and ticks) taking diseases like Dengue, Malaria, and Zika to new geographic areas.
- Human progress such as dam construction and irrigation systems is helping to create breeding grounds for vectors of Rift Valley fever and Schistosomiasis.

5.2.3. International Movement and Trade

- Mobility across the globe through air travel allows an infected person to spread diseases across the globe within 24 hours especially during the asymptomatic stages. SARS and COVID-19 are good examples in this category.
- Trade and Shipping leading to the consumption of sea foods is helping to internationalise hitherto localised parasites.

5.2.4. Technological Advancements

- Advanced medical procedures such as transplants, transfusions and the use of invasive and immunosuppressive processes in disease management (e.g. catheters, steroidal drugs) are creating new opportunities for infections.
- Globalised food production system can result large-scale transmission of diseases as a result of a single contamination event as seen with *E. coli* O157:H7 outbreaks.

5.2.5. Microbial Evolution and Change

- The uncontrolled application of pesticides and antibiotics in humans and livestock has continued to create a dangerous pool of hardy and drug-resistant microbial strains thereby renewing the threat from pathogens such as MDR-TB and MRSA.
- Mutation events among pathogens leading to the emergence and re-emergence of serotypes different from the immunologically recognized serotypes and/or treatable serotypes. This is very

common among viruses especially the RNA viruses because of their high mutation rate e.g. reassortment (e.g., Influenza A), or recombination to evade the human immune system or adapt to new hosts.

5.2.6. Inadequate Preventative Measures

- Decreasing vaccination coverage due antivaccination advocacies or the disruption of immunization programs due to natural or political causes reverses progress in controlling diseases like measles, polio, and diphtheria.
- Inexistent, un-developing and insufficient health infrastructure (diagnostic capabilities) to support infectious diseases surveillance. Poor sanitation, lack of clean water, and failing vector control programs allow "old" diseases like cholera to resurge.

6.0 THE HUMAN PUSHBACK

The history of human advancement in medical sciences is a story of how man transformed from being a mere defenseless victim of myriad microbial onslaughts through being a reactive fighter to subsequently becoming an active agent of change using the instrumentality of knowledge and collaboration.

6.1 OUR CONTRIBUTIONS

6.1.1 Disease Surveillance

Diseases do not occur randomly but rather in patterns that reflect the operation of underlying events called risk factors. Risk factors enable the occurrence and sustenance of diseases within populations. Epidemiological studies are vital for understanding risk factors, diseases outbreaks, monitoring trends and enabling sustainable, targeted and evidence-based public health policies. Robust disease surveillance remains the cornerstone of any genuine public health effort. The detection of emerging pathogens and epidemics, determination of the true burden of diseases and clear information on the pattern as well as the underlying factors upon which diseases thrive are only possible through surveillance.

Prevalence of Hepatitis B Virus among Women Attending Antenatal Clinic in the General Hospital, Minna, Niger State.
Adabara, N, U., Ajala, O. O., Momohjimoh, A., Hashimu, Z. & Agabi, A. Y. V.
This study was carried out to determine the prevalence of hepatitis B infection among women attending antenatal clinic in General Hospital, Minna, Niger state.
Blood samples were collected from 200 subjects and analysed using in vitro diagnostic strip designed for the qualitative determination of Hepatitis B Surface Antigen (HBsAg) in human serum. Thirteen (6.5%) out of the 200 subjects investigated were found to be positive for hepatitis B infection. On the basis of age, the distribution of HBV infection among the subjects revealed that the age group 20-29 has the highest rate of infection of 10.3% followed in descending order by 40-49 (4.5%), 30-39 (4.2%) and 10-19 (0.0%). Infection rate was found to be related to the low level of awareness and the poor standard of living observed among the subjects. The study therefore highlights the need for increased awareness, provision of drugs and immunization in the study area.
Prevalence of hepatitis B virus infections among blood donors in Federal Capital Territory, Abuja, Nigeria Ezeonu, C. M., Garba, S. A., Adabara, N. U., & Kuta, F. A.
This study determined the prevalence of HBV infection among 550 blood donors aged 18 to 60 years from selected hospitals and blood transfusion centres within the Federal Capital Territory, Nigeria, using hepatitis B surface antigen (HBsAg) rapid diagnostic test (RDT) kit and Enzyme linked Immuno-sorbent Assay (ELISA). Representative positive and negative samples for RDT and ELISA were tested by both conventional and real-time polymerase chain reaction (PCR) assay. Forty-nine (8.9%) and 14 (2.8%) out of the 550 blood donors tested positive for HBsAg with the RDT and ELISA respectively. Replacement donors had higher prevalence rate of the HBV infection than voluntary donors. The highest prevalence of HBV infection was recorded among the 30–39 year age group. The difference in the rate of infection between the males and the females was not statistically significant ($p>0.05$). A perfect agreement between RDT and PCR and fair agreement between ELISA and PCR

were observed. This study reports a high prevalence of hepatitis B virus infections among blood donors in Abuja, Nigeria which underscores the need for proper screening of blood for transfusion to completely eliminate the incidence of transfusion transmitted HBV infections.

Prevalence of Intestinal Protozoan Parasites Infection Among Primary School Pupils in Bosso Local Government Area, Niger State, Nigeria.

Mohammed, Y., Aliyu, M., Dabo, N. T., Adabara, N. U., Otone, B. & Ige, A. O

The study was carried out to determine the prevalence of *Entamoeba histolytica* and *Giardia lamblia* among primary school pupils in four communities of Bosso Local Government Area in Niger State, Nigeria. Stool samples from 250 pupils were collected and examined for *Entamoeba histolytica* and *Giardia lamblia* using formol-ether concentration technique. Out of the 250 samples analysed, 115 (46%) for either *Entamoeba histolytica* or *Giardia lamblia* or both. Ninety (36.0%) subjects were positive for *Giardia lamblia* while 46 (18.4%) subjects had *Entamoeba histolytica*. Single species infection was seen in 78 (67.8%) of the infected pupils whereas 47 (40.9%) were infected with both parasites. The age group (9-10) years had the highest rates of infection of 14 (21.5%) and 37 (56.9%) for *G. Lamblia* and *E. histolytica* respectively. Males had the highest rate of infection (53.5%) compared to the females with (46.3%). Poverty, ignorance and poor environmental sanitation were factors found to be associated with the high prevalence rates recorded.

Seroprevalence of Hepatitis B Virus Among Students of Federal University of Technology Minna, Niger State, Nigeria.

Adabara, N. U., Yusuf, K. A., Kuta, F. A., Zakari, H., Adedeji, S. A., Abdulsalam, R. & Garba, S. A.

This study determined the seroprevalence of hepatitis B virus surface antigen (HBSAg) among students of Federal University of Technology Minna, Nigeria. Blood samples were collected from a total of one thousand (1000) students and screened using the one step Hepatitis B surface antigen test strip (Diaspot HBSAg). The screening revealed that 43 (4.30%) subjects out of the total 1000 screened were positive for HBSAg. The age distribution of HBV infection among the subjects showed that age group 17-20 years had 1 (0.3%) positive out of the 322 subjects screened, 21-24 years had 31 (8.1%) positive out of the 381 screened while 25-28 years had 11 (3.97%) positive out of the 297 subjects screened. The gender distribution of HBV infection revealed prevalence rates of 3.0% and 5.5% for the males and the females respectively. No significant difference was observed in the distribution of HBV infection with respect to age and gender in the study area ($p<0.05$). The result of this study suggests a declining trend in the prevalence of hepatitis B virus infection in the study area, but however underscores the need for a renewed campaign on the essence of vaccination against HBV.

Relative Bacteriological Assessment of Public Borehole and Well Water in Bosso Town, North-Central Nigeria

Adabara, N. U., Mawak, J.D., Momohjimoh, A., Bala, J.D., Abdulrahaman, A.A., Oyedum, U.M. & Jagaba, A.

This study was carried out to determine the relative bacteriological quality of borehole and well water supplies within Bosso town. Twenty (20) water samples comprising 10 each of borehole and well samples were aseptically collected from Bosso Town and analyzed using membrane filtration technique. The results showed that most (60.0%) of the water samples from the boreholes sources except the samples from Rafin-Yashi, Maikunkele, F.U.T Minna, Tudun Fulani, contained coliform counts below 10cfu/100ml while the majority (90.0%) of the well water sampled had coliform counts above 10cfu/100ml. The organisms isolated included species of *Escherichia, Pseudomonas, Streptococcus, Staphylococcus, Salmonella, Shigella, Clostridium, Bacillus, Yersinia* and *Serratia*. *E. coli* had the highest frequency of occurrence (25%) followed in descending order by *Staphylococcus aureus* (8.3%), *Salmonella* sp (8.3%), *Pseudomonas aeruginosa* (8.3%), *Bacillus subtilis* (8.3%), *Clostridium* sp (6.7%), *Streptococcus feacalis* (6.7%), *Shigella* sp (6.7%), *Streptococcus pyogenes* (5%), *Klebsiella* sp (5%), *Proteus vulgaris* (5%), *Yersinia* sp (3.3%) and *Serratia* sp (3.3%). This study reveals that both well water and borehole water samples were contaminated with greater contamination observed with well water. This highlights the need for a continuous assessment of the quality of public water supply and intervention measures to prevent outbreak of water-borne diseases.

The Risk of Transfusion Transmitted Malaria and The Need for Malaria Screening of Blood Donors in Abuja, Nigeria

Ezeonu, C. M., Adabara, N. U., Garba, S. A., Kuta, F. A., Ewa, E. E., Oloruntoba, P. O. & Atureta, Z.

This study investigated the prevalence of malaria among 550 blood donors aged 18 to 60 years from blood bank units of some selected hospitals in Federal Capital Territory (FCT), Abuja, using gold standard microscopy for malaria parasite detection. Two hundred and fifty-two (45.8%) donors were positive for malaria parasites. Replacement donors had higher prevalence rate of malaria compared to voluntary donors. The distribution of infection on the basis of age revealed the highest prevalence rate of malaria among the 20- 29yrs age group. The rate of infection among the males and the females was not significantly different ($p>0.05$). No association was observed between the blood group types and the rate of malaria infection ($p > 0.05$). A high prevalence of malaria parasitaemia was observed among blood donors in FCT, Abuja, Nigeria in this study. The need for improved blood banking and the introduction of malaria screening as part of routine screening for blood donation and the provision of modern blood screening equipment within healthcare facilities are highly advocated.

6.1.2 Molecular Epidemiology

Serotypes surveillance represents and still remains one of the most challenging aspects in the fight against microbial pathogens. The ability of the microbial pathogen to change its form significantly undermines every prevention and control effort. It ruins the several years of efforts and resources put into the development of vaccines by enabling vaccine escape antigenic changes and reverses the successes associated with the discovery of antimicrobials through target alteration. The end results are usually antimicrobial resistance, vaccine failure and increased virulence in form of serotypes replacement.

Prevalence and Molecular Characterization of *Helicobacter pylori* Isolated from Subjects Attending Selected Hospitals in Nasarawa State.

Audu, S. L., Adabara, N. U., Kuta, F. A., Kabiru, A. Y., Enejiyon, S. O., & Adedeji, S. A.

This study determined the prevalence and molecular characteristics of *H. pylori* in Akwanga and Keffi, Nassarawa State. The presence of *H. pylori* in stool samples collected from 200 subjects (100 each from General Hospital Akwanga and Federal Medical Centre Keffi) was detected using rapid test kit while the bacterial DNA was extracted using standard methods. This was followed by DNA amplification using PCR, gel electrophoresis of the amplicons, sequence analysis and multiple sequence alignment. Eighteen (9.00%) out of the 200 samples analysed were found to be positive for H. pylori. The highest prevalence (3.00%) was recorded among the 26-30 years age group while the age group 6 – 10 years had no infection at all. The males had higher prevalence of infection (5.50%) compared to the females (3.50%). The rate of infection was found to be higher among rural dwellers (5.50%), those that take stream/river (4.50%) and those that use pit latrine toilet facility (5.50%) compared with those using water closet (3.55). The molecular result showed that *H. pylori* strain G-Mx-2003-108 was detected in the selected hospital each having 500 base pair. The result of this study has shown that the circulating strain of *H. pylori* in Nasarawa state is *H. pylori* strain G-Mx-2003-108. The carriage rate of *H. pylori* in the study area underscores the need for public enlightenment and provision of public sanitary facilities.

Molecular Characterization of Human Papilloma Virus from Women Attending Selected Hospitals Abuja, Nigeria.

Aondona, P. Y., Kuta, F. A., Abalaka, M. E. & Adabara, N. U.

This study identified the strains of HPV among women attending selected hospitals in the Federal Capital Territory, Abuja, Nigeria where cervical swab samples were randomly collected from 501 women. Structured questionnaires were administered to the women, after an informed consent had been obtained from the women. Cervical swabs were collected from the cervix and DNA was obtained by extraction. PCR method was done using consensus primer sets MY09/MY11 and

GP5+/GP6+. HPV DNA sequencing was done using Sanger Method. The HPV types identified were HPV 6 (6.67%), HPV 16 (13.33%), HPV 18 (13.33%), HPV 58 (13.33%), HPV 70 (33.33%), HPV 72 (6.67%) and HPV 81 (13.33%). The most prevalent type identified was HPV type 70. High risk type identified included HPV16, 18 and 58. Based on the results there is a need to increase the level of surveillance on females at risk of cervical cancer in this environment, since significant proportion of highly oncogenic strains with a high tendency to transform into malignancy were observed in this study. The results from this study also contributed to the epidemiological data on the distribution of HPV within this region.

Epidemiology and Molecular Identification of Rotavirus Strains Associated with Gastroenteritis in Children in Niger State.

Kuta, F.A., Uba, A., Nimzing, L., Damisa, D., & Adabara, N.U.

The study was conducted to determine the genetic diversity of the rotaviruses associated with gastroenteritis in children in Niger State. A total of 150 stool samples were collected from diarrheic children (0 – 5 yrs.) in four hospitals (Minna, Bida, Suleja and Kontagora) in Niger State. The stool samples were screened for rotavirus, using Enzyme linked Immunosorbent assay (ELISA). Eight stool samples were positive (5.33%). The prevalence of the disease according to sex of the children was as follows; male (4%) and female (1.33%). The prevalence of gastroenteritis according to water source was distributed as follows; pipe borne (2%), bore hole (1.33%), and river/stream (2%). The prevalence of rotavirus gastroenteritis among children according to the breast feeding was as follows; exclusively breastfed children had (2%) and those breastfed only recorded (3.33%). Molecular identification of the virus revealed the presence of the following genotypes: P6 (22%), G1 (22%), G2 (33%), and G8 (22%) in the study area.

6.1.3 Antimicrobial Resistance Surveillance

Antimicrobial resistance (AMR) stands out as one of the biggest threats to the management and control of infectious diseases that afflict humanity today. Antimicrobial resistance surveillance is indispensable to the early detection and tracking of the emergence and spread of resistant microbes. In addition, it provides guidance for clinical treatment decision-making as well as form the bedrock for public health policies for controlling the problem.

The Prevalence and Antibiotic Susceptibility Pattern of *Salmonella* Typhi among Patients Attending a Military Hospital in Minna, Nigeria.

Adabara, N.U., Ezugwu, B. U., Momojimoh, A., Madzu, A., Hashimu, Z. & Damisa, D.

This study investigated the antibiotic sensitivity pattern of *Salmonella* Typhi isolated from blood specimen. One hundred blood samples were collected from suspected typhoid fever patients in 31 Artillery Brigade Medical Centre, Minna, and were analyzed for *S.* Typhi while antibiotic sensitivity testing was done Kirby-Bauer method. Sixty (60.0%) samples out of the total 100 were positive for bacterial growth. The organisms isolated include *Salmonella* Typhi; 45 (75.0%), *Shigella*; 6 (10.0%), *E. coli*; 3 (5.0%), *Klebsiella*; 3 (5.0%), *Enterobacter*; 2 (3.3%), and *Citrobacter*; 1 (1.7%). Result of the sensitivity test showed that the isolates were resistant to all the antibiotics; ceftriaxone, cefuroxime, amoxicillin, ampicillin, ciprofloxacin, and augmentin, which are the drug of choice routinely used in the study area for the treatment of typhoid fever. They were however sensitive to chloramphenicol and ofloxacin, which, unfortunately, are not used in this study area for the treatment of typhoid fever. There appear to be multiple drug resistant (MDR) strain of *S.* Typhi in the study area. These may be as a result of overdependence or uncontrolled use of the few available antibiotics and/or inaccurate or inconclusive diagnosis resulting in the development and spread of resistant strains of *S.* Typhi. The study highlights the need for a strong collaboration between the physicians and the laboratory in the choice of antibiotics for the treatment of bacterial diseases in order to discourage the development of resistant strain of bacterial pathogen. A national antibiotic policy is also strongly advocated.

Study of Antibiotics Resistance in Bacteria Isolated from Retailed Eggshell in Three Major Markets in Minna, Nigeria

Adabara, N. U., Amarachi, C. E., Adedeji, A. S., Usman, A., Maude, A. M., Sadiq, F. U., Oloruntoba, F. P. & Kuta, F.A.

This study isolated, identified and determined the Antibiogram of bacteria isolates from eggshell of eggs obtained from three major markets in Minna, Nigeria. A total of ten (10) duplicate egg samples were purchased from egg retailers. The egg samples were analysed for the enumeration and isolation of bacteria. The isolated bacteria were identified using biochemical methods. Antibiotic susceptibility test to prescribed commercially available antibiotic discs was also investigated. The total viable bacteria count (TVBC) ranged from 1.38×104 - 2.52×104 cfu/mL while the total coliform count (TCC) ranged from 8.5×103 - 2.02×104 CFU/mL. *Escherichia coli* (9.1%), *Streptococcus pyogenes* (4.5%), *Enterococcus* sp. (4.5%), *Shigella* sp. (13.6%), *Salmonella* sp. (13.6%), *Staphylococcus aureus* (36.4%), *Clostridium* sp. (9.1%) and *Neisseria* sp. (9.1%) were isolated and identified from eggshells. Gram positive bacteria showed highest sensitivity to gentamycin (100%) however, resist cloxacillin, ceftadizime and erythromycin (100%). Similarly, there was no ciprofloxacin resistant Gram-negative bacteria though *E. coli, Salmonella* sp. and *Shigella* sp. isolated from eggshells were resistant to augmentin and amoxicillin. Further analysis of result revealed that all the isolated bacteria from eggshells were multidrug resistant except *Neisseria* sp. with multidrug resistant index greater than 0.2. The fact that these antibiotic resistant bacteria can be transferred to humans is of public health concern. Therefore, stringent use of public health regulations for cleaning eggs before retailing is advocated.

Detection of Extended Spectrum Beta-Lactamase Producing *Escherichia coli* from Urinary Tract Infection in General Hospital, Minna

Adabara, N. U., Bakinde, N. D., Enejiyon, S. O., Salami, T. & Iorzua, D.

This study determined the production of ESBL among *Escherichia coli* isolated from the urinary tracts of subjects attending General Hospital, Minna, Nigeria. One hundred and fifty (150) urine samples were collected from subjects and cultured on CLED agar for the isolation of *E. coli.* Antibiotic susceptibility testing was done using Kirby Bauer disk diffusion method, while the phenotypic identification of ESBL producing strains was carried out using double disk synergy test. All results were interpreted based on Clinical and Laboratory Standards Institute guidelines. In all, 26 (17.33%) out of the 150 urine samples cultured had *E. coli;* out of which 23 (88.5%) were subsequently found to be ESBL producers. Among the *E. coli* isolates, high rates of antibiotic-resistance were observed against nalidixic acid (100%), cefdinir (88.4%), cefotaxime (84.6%) and cefpodoxime (84.6%), while remarkable sensitivity to tarivid (46.1%), ciprofloxacin (38.4%) and gentamicin (34.6%) was also detected. This study has established the involvement of ESBL-producing *E. coli* in urinary tract infections in the study area. Rational prescription of antibiotics against pathogens generally is highly recommended to halt the spread of resistance.

Prevalence of Multidrug Resistance Genes in Escherichia Coli Isolates from Patients Attending Four Hospitals in Minna, Nigeria

Oloruntoba, F. P., Adabara, N. U., Adedeji, A, S., Kuta, F. A. & Ezeonu, C. M.

This study determined the prevalence, antibiotic susceptibility and resistance genes among multidrug resistant *Escherichia coli* isolates from diarrheic patients in four hospitals within Minna, Nigeria. Stool samples from one hundred and seven (107) diarrheic patients were collected and analysed to check for *E. coli* using spread plate techniques. The resistance pattern of the *E. coli* isolates to ten (10) antibiotics using disc diffusion techniques was determined. Five isolates with multidrug resistant index ≥ 0.5 were screened for antibacterial resistant genes (Tn3bla, GyrA, ParC, aadA2 and Sul1) using polymerase chain reaction. Seventy (70) samples representing 65.4% were *E. coli* positive while fifty-five (55) were resistant to at least one antibiotic. The highest level of resistance was against ampicillin (38.57%) while the least was against cefalexin (4.29%). Multidrug resistant isolates were 58.7% (41/70), while 28.6% (20/70) were resistant to three or more antibiotics. The result of the molecular characterization identified the five multidrug resistant isolates to be *E. coli* strain RAD34, *E. coli* strain CUSMBN2, *E. coli* strain CAU3471, and *E. coli* strain BYPFP. *Tn3bla/GyrA/ParC* resistant genes were detected in all the five isolates. *E. coli* isolate RAD34, *E. coli* strain CUSMBN2, *E. coli* strain CAU3471 and *E. coli* strain BYPFP possessed *Sul1* gene. However, *E. coli* strain BYPFP, *E. coli* strain CAU3471 and *E. coli* strain CUSMBN2 had *aadA2* gene. The result of this study established the active circulation of *Tn3bla, GyrA, ParC*, *aadA2* and *Sul1* resistant genes among *E. coli* in the study area.

6.1.4 Antimicrobial Activities of Natural Products

Given the rising global crisis of antimicrobial resistance (AMR), as a result of which existing antibiotics are becoming less and less effective by the day, the need for newer drugs against microbial pathogens has never been more urgent. Fortunately, plants contain a vast array of complex bioactive compounds with antimicrobial activities that have not been fully explored. The screening of plants for their antimicrobial activities is a critical research direction driven primarily by the need to address antimicrobial resistance as well as widen the option for the clinical management and control of infectious diseases.

Phytochemical and antibacterial Studies of Root Extracts of Euphorbia heterophylla on some Enteric Bacteria

Oyedum, U. M., Kuta, F. A. & Adabara, N. U.

Four enteric organisms namely; Salmonella Typhi, Shigella flexneri, E. coli, and Proetus vulgaris were determined. The isolates were subjected to antimicrobial susceptibility test using agar diffusion technique. Phytochemistry of the Euphorbia heterophylla crude extracts revealed the presence of flavonoids, alkaloids, saponins, tannins, and cardiac glycosides. Methanolic and aqueous extracts produced clear zones of inhibition at concentration ranging from 50 to 200mg/ml. in vivo antimicrobial assay revealed that the mice treated with the crude methanolic and aqueous extracts after being infected with the various test organisms survived and showed only minute pathological effects. On the other hand, untreated mice (control) died after 48hours of inoculation with the isolates (Salmonella Typhi, Shigella flexneri, E. coli, and Proetus vulgaris). Euphorbia heterophylla crude extracts especially its methanolic and aqueous extracts could be potential sources for the treatment of diseases associated with enteric organisms such as Salmonella Typhi, Shigella flexneri, E. coli, and Proetus vulgaris. Further studies should be directed towards isolation and characterization of the active compounds in the crude extracts.

Antibacterial Activities and Synergistic Effect of The Bioactive Compounds of Selected Medicinal Plants Against Diarrhoea-Causing Pathogens

Saadu, M., Adabara, N. U., Kuta, F. A., Muhammed, H. L. & Wuna, M. M.

In this study, the antimicrobial properties and toxicological effects of *Anogeissus leiocarpus* and *Khaya senegalensis*, two traditional medicinal plants from West Africa, were investigated against diarrhoea-causing pathogens. Cold maceration was used to prepare extracts from the plants. *Anogeissus leiocarpus* yielded 22.87g of extract, while *Khaya senegalensis* yielded 13.94g. Both plant crude extracts exhibited varying degrees of antibacterial activity against *Vibrio cholerae*, *Klebsiella pneumoniae*, and *Salmonella* sp. at different concentrations. *A. leiocarpus* and *K. senegalensis* showed the highest antibacterial activity, with significantly higher zones of inhibition at all concentrations against all test organisms. The Minimum Inhibitory Concentration (MIC) for A. leiocarpus ranged from 0.10 to 0.96 mg/mL, while the Minimum Bactericidal Concentration (MBC) ranged from 0.10 to 1.09 mg/mL. For *K. senegalensis*, MIC ranged from 0.96 to 1.80 mg/mL, and MBC ranged from 1.02 to 1.92 mg/mL. Fractionation of the most active crude extracts resulted in the highest yields in the n-Hexane fractions for both *A. leiocarpus* and *K. senegalensis*. Significant differences were observed in the antibacterial activity of these fractions. *K. senegalensis* fractions and *A. leiocarpus* n-Hexane fraction showed the highest activity against *V. cholerae*, while the ethyl acetate fraction of *K. senegalensis* exhibited significant activity against *K. pneumoniae*. The aqueous fraction of *A. leiocarpus* displayed the highest activity against *Salmonella* sp., whereas none of the *K. senegalensis* fractions were active against *Salmonella* sp. Antibacterial activity of *K. senegalensis* ethyl acetate and *A. leiocarpus* n-Hexane and aqueous column chromatography fractions against the test organisms was concentration dependent, with the highest antimicrobial activity observed at 200 mg/mL concentration. Importantly, there were no significant differences in the body weights of experimental animals across all groups. In conclusion, *A. leiocarpus* and *K. senegalensis* extracts and their fractions demonstrated promising antimicrobial properties against diarrhoea-causing pathogens. These findings support

their traditional medicinal use in West Africa and suggest their potential as natural remedies for combating bacterial infections.

Antifungal Activities of *Vernonia amygdalina* Crude Extracts and Fractions against Strain1161, P37005 and RM1000

Owoyale, A. D. M., Galadimma, M., Daniyan, S. Y. & Adabara, N. U.

This study determined the antifungal activities of the crude extracts and fractions of *Vernonia amygdalina* against strain 1161, P37005 and RM1000. *Vernonia amygdalina* leaves were extracted by the reflux extraction protocol which was done in a successive method. This study also analysed quantitatively the phytochemical that were present in the crude leaf extracts of *Vernonia amygdalina*. The study identified the presence of tannin, flavonoid, alkaloids, saponin and phenols. The three strains used in this study were tested for their susceptibility, However, activity of the crude extract was assayed at a varying concentration of 40, 60, 80 and 100 mg/ml. The methanol leaf extract (MLE) at a concentration of 100mg/ml showed the highest zones of inhibition 15.33± 1.23 mm against strain 1161(isolate S5). The result of the minimum inhibitory concentration (MIC) and minimum fungicidal concentration showed for active crude extracts were 12.5 mg/ml and 50 mg/ml presented for the n- hexane crude extract against strain 1161(IsolateS5). The value for the methanol crude extract were 12.5 mg/ml and 50 mg/ml against strain 1161 (Isolate: S5). Furthermore, the value of 12.5 mg/ml and 100mg/ml were showed for n- hexane crude extract against P37005 (isolate: B4) However, the antifungal activity of the fractions against the strains were determined at concentrations of 5mg/ml and 10mg/ml. The various fractions of *Vernonia amygdalina* showed inhibitory activity against all the strains.16.00± 0.0mm was the highest value that was presented for n-hexane fraction of *Vernonia amygalina* against strain 1161 and P37005. The result of the minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) for active fractions (F1) are 12.5 mg/ml and 25 mg/ml showed for n- hexane fraction of *Vernonia amygdalina* against strain P37005(Isolate B4). The value of 12.5 mg/ml and 25 mg/ml were showed for n- hexane fraction (F4) of *Vernonia amygdalina* against strain 1161 (isolate: S5). Fraction (F4) showed 3.125 mg/ml and 6.25 mg/ml against strain P37005 (isolate: B4). The methanol fraction (F1) showed values of 3.125 mg/ml and 25 mg/ml respectively against strain RM1000(isolate B2). Fraction F6 had values of 3.125 mg/ml and 6.25 mg/ml against strain P37005 (isolate: B4). It can be deduced from this study that the n- hexane and methanol crude extracts showed a significant result than the ethyl acetate crude extracts. Furthermore, there was inhibitory activity for the n-hexane, ethyl acetate and methanol fractions against all the tested strains.

6.1.5 Immunity Surveillance

Antibodies are unique among biomarkers in their ability to identify persons with protective immunity to vaccine-preventable diseases and to measure past exposure to diverse pathogens (Arnold *et al*., 2018) thereby making it the best marker for measuring seroconversion and ultimately the successes of vaccination programmes.

Assessment of Maternofoetal Transfer of Anti-tetanus Immunoglobulin G in Jos University Teaching Hospital (JUTH), Jos.

Adabara, N. U., Kandakai-Olukemi, Y. T., Enenebeaku, M. N. O. & Daru, P. H.

This study evaluated the coverage efficacy of the tetanus immunization programme in Jos University Teaching Hospital (JUTH), Nigeria and certain factors that affect the efficiency of maternofoetal transfer of tetanus toxoid (TT) IgG antibodies. Sera from 43 mother-baby pairs selected randomly in JUTH were investigated for TT IgG antibodies using enzyme linked immune-sorbent assay (ELISA) technique. TT IgG antibodies were detected in 36 and 38 mothers and babies respectively. Thirty-six (83.7%) and 38 (88.4%) mothers and babies respectively were found to be seropositive (equivalent to or greater than 0.151IU/ml of TT IgG antibodies). Three (7.0%) seronegative mothers had seropositive babies. One (2.3%) seropositive mother had a seronegative baby. A highly significant correlation was observed between maternal and foetal TT IgG antibodies level (r=0.905). Twenty-one (58.3%) of the 36 seropositive mothers had concentrations lower than their respective babies. The ratio of the mean concentrations of the TT IgG antibodies of cord blood to maternal blood (C/M ratio) was less than one. Maternofoetal transfer of TT IgG antibodies was found to be unrelated to the baby's gender, weight and the mode of delivery. The study underscores the need to improve on the current immunization programme in JUTH and for further studies to understand how maternal characteristics affect the maternofoetal transfer of TT IgG antibodies in JUTH.

Detection of Immunoglobulin G to Poliovirus in Children 5-10 Years Old in Minna, Nigeria

Enejiyon, S. O., Wuna, M. M., Babayi, H. & Adabara, N. U.

In the Minna, data on the seroprevalence rate of antibodies to poliovirus serotypes which can be used to determine children's immune status and the vaccine efficacy against poliomyelitis is sparse. This study aim was to detect immunoglobulin G to poliovirus in children aged 5-10 years old in Minna, Nigeria. About 2 mL of blood was collected by venepuncture from 91 children selected randomly from various health care facilities across Minna. Blood samples were centrifuged to obtain the sera. The detection of poliovirus specific immunoglobulin G (IgG) was done using polyclonal Enzyme linked immunosorbent assay (ELISA) detection test kits. In this study, all the children had detectable level of antibodies, 85 (93.4%) children consisting of 49 (53.8%) males and 36 (39.6%) females showed protective level of antibodies (seropositive). Seropositivity rate of 96.8% (30/31), 94.0% (31/33) and 88.9% (24/27) was recorded among children aged 9-10, 7-8 and 5-6 years old respectively. About 74.7% (68/91) of the participants were weak responder (concentration of antibodies <50 U/mL) to the vaccines received with low seroconversion rates while 6.6% (6/91) of the children had sub-protective level of antibodies (seronegative). Age, sex, parents' occupation, mothers' educational status and drinking water source had no significant association ($p>0.05$) with seroprevalence rates while fathers' educational status showed significant statistical association with seroprevalence rate ($p<0.05$). High seropositivity was recorded in this study, nation-wide seroprevalence is recommended to comprehensively evaluate the progress made so far in sustaining polio-free status.

6.1.6 Vaccine Stability

The impact of the stability of vaccines on the success of immunization programmes worldwide cannot be overemphasised. A major concern is whether vaccines still remain potent after going through the distribution channel especially in tropical developing nations where the infrastructure to prevent excursion outside the cold chain is either absent or grossly inadequate. It is therefore critically important to clearly define the stability characteristics of any vaccine by producing a protocol that can easily determine the quality of any vaccine at any point in time.

Preliminary Investigation into the Thermostability Potential of Salmovac Vaccine Developed using Local Strains of Salmonella in Nigeria.

Adabara, N.U., Emeje, M.O., Garba, S.A., Galadima, M., Abubakar, A., & Kuta, F. A.

Vaccine instability caused by exposure to high temperature causes the wastage of large quantities of vaccines supplied worldwide particularly in developing countries with adverse effects on immunization programmes. In this study, the effects of storage temperature and the period of storage on the potency of the Salmovac Typhoid Fever Vaccine developed using local strains of Salmonella were studied. Three different batches of the vaccine were produced and stored at (40°C) for three months. Differential scanning calorimetry and animal challenge potency test in mice were used to determine the thermal stability and potency of the vaccine while the pH of the vaccine was determined using a pH meter. The temperature of onset of melting (T_o) of the vaccines was observed to increase after the first month of storage. At the conclusion of the three months study, all the three batches of the samples were observed to have T_o values that were higher than their initial values. The enthalpy of melting (ΔH) of the vaccine samples was also found to be high ranging from 457.181 to 681.119 J(g*K). In the potency test, all the vaccinated mice were protected against the intraperitoneal injection (challenge) of 10^6 colony forming units per 0.5mls of combined organisms (*Salmonella typhi*, *Salmonella paratyphi* A, *Salmonella Paratyphi* B, *Salmonella paratyphi* C) in comparison to the control group. The pH of the vaccines decreased consistently as the period of storage increases. The present study shows that the Salmovac vaccine has a high potential for thermostability.

6.2 Ongoing and Future Research Endeavours

1. Molecular Epidemiology of Human Infections in North-Central Nigeria
2. Development of Compounds for the Inhibition of Pathogen Specific Molecules
3. In-Silico and In-Vitro Study on Antimicrobial Activities of Plant Extracts Against Antimicrobial Resistance Encoding Genes

4. Seroprevalence of Immunity to Common Vaccine Preventable Diseases
5. Vaccinology

7.1 CONCLUSION

Mr Vice Chancellor Sir and distinguished ladies and gentlemen, the requirements for the total eradication of all pathogens are gargantuan while the opportunity is ironically faced with myriad of challenges. The eexperience from smallpox, the only disease that has been successfully eradicated globally, revealed that an all-inclusive global effort, potent vaccines, and a total absence of animal reservoir are required. This will mean a world where immunization coverage is not obstructed by either political or biological challenges, a world where there are no longer animal reservoirs for any pathogen at all. Unfortunately, all of these requirements are impossible to meet for all pathogens, both now and in the future. Many pathogens either have animal reservoirs or are genetically unstable continuously giving rise to the emergence of hitherto unknown serotypes unaccounted for in existing vaccines and/or drugs.

Permit me therefore Mr. Vice Chancellor to conclude, perhaps sadly, that infectious diseases are always going to be part of our world. While it is possible to completely eradicate certain pathogens, many others have come to stay and will remain until the end of time. The best bet for humanity will continue to be the prevention of transmission and the treatment of established cases.

7.2 RECOMMENDATIONS

Mr. Vice Chancellor Sir, it is clear from the foregoing that the total eradication of all infectious diseases is not a possibility and our best bet is to mitigate their destructive effect on human life. The following recommendations are hereby offered:

Individual

- Maintenance of healthy habits such as avoiding interactions that spread illnesses, responsible antibiotic use, health literacy, maintaining hand hygiene and respiratory etiquettes.
- Safe handling and preparation of food before consumption, control of diseases vectors and the use of clean and safe water.

- Seeking knowledge about personal and environmental health maintenance

Universities

- Inclusion of preventive initiatives into the curriculum of General Studies Courses
- Investment in molecular biology

Research Funders (Donor Agencies)

- Support Funding of basic researches in the Sciences even though they may not lead directly to products

Government

- Provision of improved infrastructure such as sanitation and water treatment systems.
- Ensure equitable access to healthcare.
- Investment in drugs and vaccines researches and high-tech laboratories
- Public health enlightenment campaigns to enhance health literacy among citizens.
- Investment in infectious diseases surveillance through collaborations between universities and health agencies.

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A Brief Profile of the Inaugural Lecturer

Professor Nasiru Usman Adabara was born on Wednesday 20th July, 1977 in Okeneba in Okene Local Government Area then in Kwara State but now Kogi State, Nigeria, to the family of Mall. Usman Umoru Adabara and Mallama Maryam Ahmed. At the age of six in 1983, he was enrolled in the Local Government Education Authority (LGEA) Nurul Islamic Primary School, Ahache Okene from where he had his First School Leaving Certificate (FSLC) in 1988. He was admitted on the Kwara State Government scholarship into the Government College Makurdi in Benue State in 1989 and went on to have his Senior Secondary School Certificate of Education (SSSCE) in 1994. He proceeded to the University of Jos in Plateau State where he bagged his BSc and MSc in Microbiology and Medical Microbiology in 2003 and 2009 respectively. The freshly graduated Nasiru Adabara was posted for National Youth Service Corps scheme to Adamawa State, Nigeria where he served as secondary school teacher at the Elkanemi College of Islamic Theology in Yola South Local Government Area from 2003 to 2004.

Prof. Nasiru Usman Adabara started his working life following his appointment by the Kogi State Government under His Excellency Alh Ibrahim Idris as the Supervisory Councillor of Finance for the Okene Local Government Area in January 2007. He served in this capacity up till august 2008 before joining the services of the Federal University of Technology, Minna as an Assistant Lecturer in the Department of Microbiology on the 1st of September, 2008.

After lecturing for close to two years, Prof. Nasiru Adabara started his Doctor of Philosophy (PhD) programme in Medical Microbiology (Immunology) under the renowned Immunologist and Vaccinologist Professor Samuel Alimi Garba at the Federal University of Technology, Minna (FUTM) Nigeria in 2010. He successfully completed the programme and graduated with a Doctor of Philosophy in Medical Microbiology with special interest in vaccine development and stability in 2015.

Having been employed as an Assistant Lecturer, Professor Nasiru Adabara climbed through the academic ladder from Lecturer II (2009), Lecturer I (2012), Senior Lecturer (2015), Associate Professor (2018) and finally became a Professor in the year 2021.

As an academic staff, Professor Nasiru Adabara has held many positions of responsibility within the University at various times. Such positions include Level Adviser, Departmental SIWES Officer, Departmental Examination

Officer, Departmental Project Coordinator, Departmental Postgraduate Coordinator, Deputy Dean of the School of Life Sciences and Head of the Department of Microbiology (2017-2020). He was elected the Dean of the School of Life Sciences in April 2025 and has been serving in that capacity.

He is a member of many professional bodies including the Science Association of Nigeria (SAN), Nigerian Society for Microbiology (NSM), American Society of Microbiology (ASM) and Biotechnology Society of Nigeria (BSN).

In the course of his lecturing service with the Federal University of Technology, Minna, Professor Nasiru Usman Adabara has supervised over fifty undergraduate projects, more than twenty Master's theses and ten PhD students. He is an external examiner to many Universities including Abdullahi Fodio University of Science and Technology, Aliero, Bayero University, Kano, Joseph Sarwuan Tarka University, Makurdi, Nile University of Nigeria, Abuja, University of Jos, Modibbo Adama University, Yola at either undergraduate or postgraduate levels. Professor Adabara has also served in several NUC adhoc committees either as chairman or member for the resource verification and accreditation of microbiology and related programmes. He has been involved in professorial assessment.

In 2013, Professor Adabara was at the international Vaccine Institute, Seoul, South Korea while still undergoing his PhD programme under the sponsorship of the World Bank STEP-B programme for a training in vaccinology. He was also at the Mount Kenya University, Thika, Kenya in 2025 under the sponsorship of the African Centre of Excellence for Mycotoxins and Food Safety for a training in microbiological techniques and molecular biology. He has attended and presented papers at local and international conferences. He has over sixty scholarly publications in reputable Journals.

Professor Nasiru Usman Adabara is married with children.

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