“WHEN MICROBES SPEAK, THE WORLD LISTENS”

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By

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INTRODUCTION

Mr. Vice-Chancellor Sir, it is a profound honour to stand before you today as Professor of Microbiology to deliver the 422nd inaugural lecture at the Obafemi Awolowo University. This event marks not just a personal milestone, but an opportunity to celebrate the ubiquitous and astonishing microbes I have dedicated my life to understanding. When I was growing up as a pre-teen in Lagos, Nigeria, I dreamed of becoming a medical doctor to save lives after losing a younger sibling to a preventable childhood disease. However, I hit a bump in the road after secondary school when the University of Port-Harcourt, Nigeria, offered me admission to study botany instead of medicine. I accepted the offer, but with my heart still set on a career in human health.

My final year project on bacteria causing diseases in plants sparked my passion for microbiology. I appreciated that lives can be saved not only through medicine but also through other professions when thoughts are towards achieving positive changes. I realised that expertise in microbiology, specifically infectious diseases and public health microbiology, could lead to a career that would help me fulfil my childhood aspirations. After graduating with a B.Sc. degree in Botany from the University of Port-Harcourt, Nigeria, I furthered my graduate studies in microbiology. I received MSc and PhD degrees in Microbiology, as well as a Master of Public Health (MPH) degree from Obafemi Awolowo University, Ile-Ife, Nigeria. I joined the Department of Microbiology at this esteemed institution of learning as an Assistant Lecturer in 2008, where I progressed through the ranks to become a Professor in 2021.

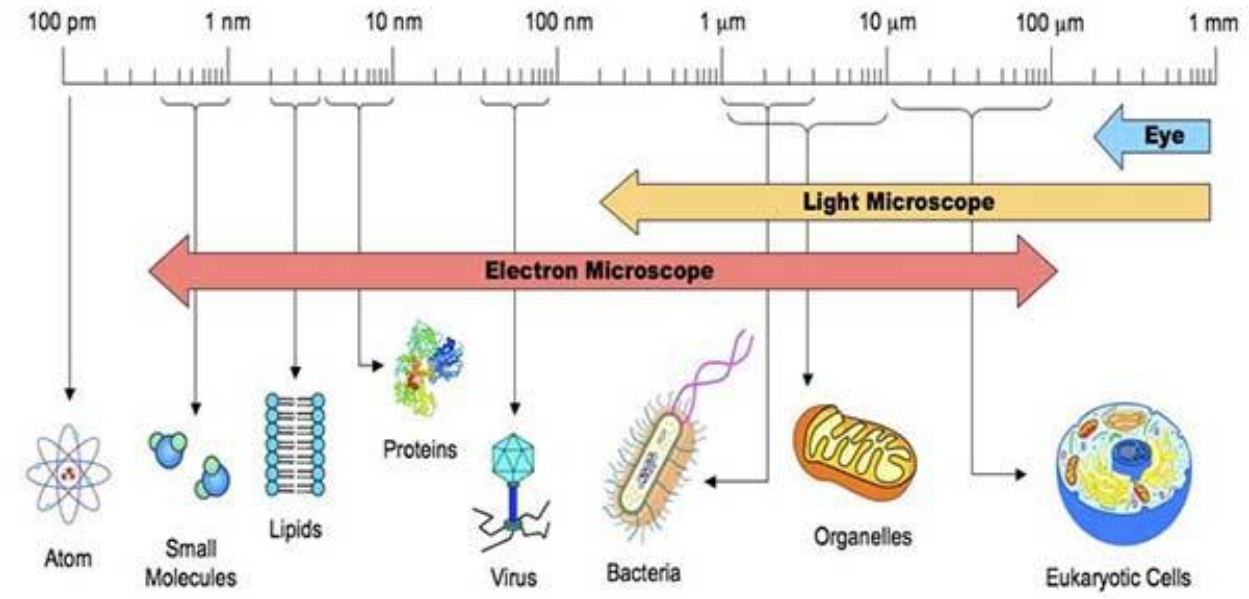
The title of today's lecture, "When Microbes Speak, the World Listens", highlights the profound impact that microorganisms have on global systems. It suggests that while microbes are invisible to the naked eye, their effects, whether in health, disease, ecosystems, or industry, are impossible to ignore. It signifies the moment we move beyond viewing microbes merely as passive subjects under the microscopes, as simple pathogens to be eradicated, or even as beneficial tools. It heralds an era where we recognise them as active communicators, engaged in a constant, intricate dialogue with each other (Xavier and Bassler, 2005) with their environment, and crucially, with us, humans. The lecture draws from more than two decades of my research endeavours, spanning medical and public health microbiology in Nigeria. I explored how listening to microbes shapes our survival, innovation, and responsibility.

The Invisible and Essential Microbes

"The Little Prince once said: It is only with the heart that one can see rightly; what is essential is invisible to the eye. As a child, I thought he was talking about love or friendship. As a microbiologist, I realised he was also describing the engine of our planet."- Antoine de Saint-Exupéry.

We live in a world dominated by the unseen. Microbes are minute living things that cannot be seen by the naked eye (Figure 1). They (including bacteria, viruses, fungi, actinomycetes, and archaea) comprise the oldest, most diverse, and most ubiquitous life forms on Earth. Microbes are the foundation of nature. Just because we cannot see them without a microscope does not mean they are not the most 'essential' players in our existence. Microbes are everywhere and very resilient living organisms that thrive in boiling hydrothermal vents (60^{o}C >400^{o}C), Antarctic (-80^{o}C), the dead sea (salinity at 33.7%), the soils beneath our feet while others such as root-

colonising bacteria and the flora in human guts take advantage of the abundant resources provided by higher organisms (Stark, 2010; Fierer *et al.*, 2016). For millennia, humanity perceived microbes only through their impacts (the spoilage of food, the spread of plague, the magic of fermentation). Today, we understand that microbes do communicate. They do so through biochemical signals, genetic exchanges, population dynamics, and ecological transformations. When microbes speak, they reveal secrets of health, disease, ecology, and evolution. It is our imperative as humans to listen to them.



Adapted (Urry *et al.,* 2020)

Figure 1: Comparative sizes of microbes and other biomolecules

I. THE DARK DISCOURSE: MICROBES AS ADVERSARIES

Antimicrobial Resistance (AMR): The cycle of infection, hospital and community shuttling

When microbial dialogue turns hostile, consequences are severe, and they cause harm to the host. The subset of microbes that cause disease via toxins, destroying cells, or triggering an immune response is referred to as pathogens. According to Nature Review Microbiology (2011), pathogens represent an extremely small fraction of less than 1% known to cause diseases in humans. Pathogenic microbes are treated with antimicrobial agents that inhibit or kill them through various modes of action. The nomenclature for antimicrobials is linked to the classification of the target microbes. For instance, antibiotics target bacteria, antifungals treat fungi, antivirals are used for viruses, etc. However, over time, pathogens have developed various mechanisms to counter the effect of these antimicrobial agents. Antimicrobial resistance (AMR) poses a major threat to human health. In 2019, bacterial-associated AMR alone was directly responsible for 1.27 million global deaths (ARC, 2022).

Antimicrobial resistance is microbial evolution in real-time. AMR in bacteria is the ability of the microbe to circumvent the inhibitory or killing ability of antibiotics. Achieving this goal results in multidrug resistance (MDR), characterised by resistance to three or more classes of antimicrobials; extensive drug resistance (XDR) occurs when the isolates are susceptible to only one or two classes, while pandrug resistance (PDR) is defined as resistance observed to all agents in all antimicrobial classes (Magiorakos *et al.,* 2012). Bacteria can acquire resistance traits through two main paths, which include vertical transmission, which occurs from mother to child (at birth or lactation) or spontaneously due to antibiotic exposure (Patangia *et al.,* 2022), and horizontal gene transfer (HGT) (Chiș *et al.,* 2022). HGT is the movement of genetic material

between bacteria via conjugation (direct contact), transformation (uptake of naked DNA), or transduction (virus-mediated) as shown (Figure 2).

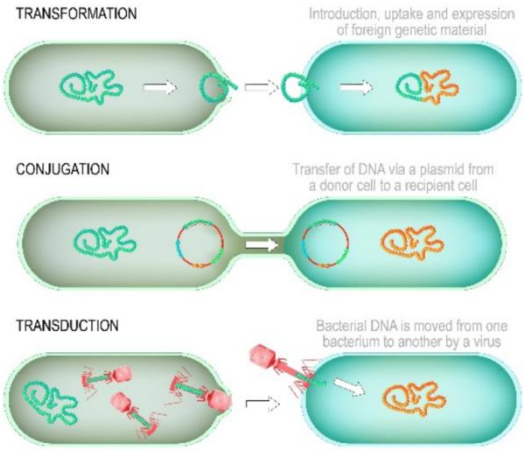


Figure 2: Mechanisms of horizontal gene transfer

Hospitals have been widely identified as an environment with high cases of AMR. The early colonisation by MDR organisms framed the neonatal skin as the first frontier in the battle against hospital-acquired infections (Ako-Nai *et al.,* 2001; 2002). However, the story of microbial resistance does not end at the skin's surface, nor in the first days of life. The same environmental and socio-economic pressures that shape the infant's microbiome continue to exert their force as the child grows. I was compelled to ask: what happens when these resistant commensals are replaced or joined by the world's most formidable paediatric pathogens? I turned attention to *Streptococcus pneumoniae*, a leading cause of pneumonia, sepsis, and meningitis, and a ruthless killer of children under five. In a study of 100 children under 5 years presenting at a clinic in Akure, we isolated and identified 16 encapsulated pneumococcal strains from the blood (Torimiro *et al.,* 2018). The picture that emerged was a sobering escalation of the resistance we

first documented on the neonates. The same drivers of resistance we observed on day one of life (environmental pressure, transmission dynamics) culminate in invasive, life-threatening infections by the age of five.

The 86% MDR on neonatal skin had evolved into 100% MDR in invasive pneumococci. This informed us that our treatment guidelines were failing and that our preventive strategies must be ruthlessly specific to our environment. We confirmed the presence of globally circulating serotypes 19F and 6B. However, a critical discovery was made: the invasive serotype 14 was documented in the study centre. This serotype is a notorious agent of childhood disease worldwide. We found a correlation between specific serotypes (such as 14 and 6B) and high resistance levels, emphasising that antibiotic pressure and serotype distribution shifts necessitate continuous surveillance, strict vaccine compliance, and locally informed response. The presence of serotype 14 is a sentinel event, a call for vigilant surveillance, and a stark reminder that our vaccines must be matched to the pathogens circulating in our communities. Unfortunately, local/indigenous strains have received inadequate attention in vaccine development.

My study on antibiotic resistance of clinical strains of *S. aureus* among different age groups in Ile-Ife showed a staggering 76.3% MDR out of the 172 clinical *S. aureus* isolates studied (Torimiro *et al.,* 2005). This was not just a few resistant pathogens; this was the dominant characteristic of the *S. aureus* population in our community (Ako-Nai *et al.,*1991; Torimiro *et al.,* 2013a; Adeyanju *et al,* 2022). It painted a picture of a pathogen that is increasingly shrugging off our first-line and second-line therapeutic defences. The analysis revealed a fascinating and

concerning pattern. Resistance was not uniform across all ages. Two key vulnerable groups were identified (the very young and the young adults).

Neonates (0-28 days) showed a slightly higher resistance profile compared to older children. This may translate directly into harder-to-treat infections when these infants fall ill. The most significant spike in resistance was observed in the adults 18-39 age group. This is the most economically active and socially mobile segment of our population. The study hypothesised that this higher exposure is linked to greater community interaction, self-medication practices, and possibly more frequent but incomplete antibiotic courses. This work taught me that the fight against antibiotic resistance cannot be confined to hospital wards. It is a battle being lost in the community, with the young and the economically active caught in the crossfire. We mapped resistance against age and moved from simply documenting a problem to understanding its transmission dynamics, providing the evidence base needed for targeted public health intervention (Torimiro *et al.,* 2005).

In my investigation of *S. aureus* in a peri-urban Nigerian community, the findings confirmed my gravest fears. From simple community-acquired infections like boils and skin abscesses, we isolated *S. aureus* strains with a shocking resistance profile. The central stark finding was that 85% of the community *S. aureus* isolates were multidrug-resistant (Torimiro and Torimiro 2012). Among the resistant strains, 50% were resistant to three classes, 5.9% showed resistance to six different classes, while 5 strains (12.5%) showed resistance to oxacillin (Table 1). This was not a minor issue; it was the dominant characteristic of the pathogen in our peri-urban community. The resistance crisis was not confined, but was ubiquitous. Our survey revealed that 75% of the

subjects had taken antibiotics before seeking hospital care. It was a watershed moment. It proved that the battlefield of AMR had expanded far beyond the hospital.

At this juncture, I sought to understand the primary weapon in the *S. aureus* arsenal: the production of β-lactamase (Torimiro *et al.,* 2013b). The analysis of 107 clinical isolates revealed β-lactamase production was not an exception, but the rule. A staggering 70.1% of all *S. aureus* strains were actively producing this enzyme, a scissor that cuts apart and deactivates penicillin-based antibiotics. β-lactamase production was significantly linked ($p < 0.05$) to resistance in three critical classes of drugs: Amoxicillin, Ceftriaxone, and Amoxicillin/Clavulanic acid (Augmentin), an antibiotic specifically engineered with a β-lactamase inhibitor to defend against this very enzyme. The failure of this last combination was particularly telling. It indicated that bacterial production of β-lactamase was so potent or of such a type that it could overwhelm our designed chemical defences. The problem extended beyond β-lactams. The study showed that 72% of the isolates were MDR. This demonstrated that once a strain had evolved the machinery for one type of resistance, it readily accumulated others, creating a perfect storm (that is, it becomes untreatable).

This episode in my research endeavours took me to the heart of the battle. I identified the enemy's master key (the β-lactamase enzyme) and proved it was being used to pick the locks on our most trusted medicines. The significant resistance to even our fortified drugs was a wake-up call. It taught us that we are not just fighting bacteria, but fighting against the powerful, selective force of our own antibiotic usage. This is not a problem that can be solved by new drugs alone. It is a behavioural and policy problem that requires a fundamental change in how we value and use these precious, life-saving molecules. Every unnecessary or uncompleted dose of amoxicillin or

ampicillin not only fails to treat one patient but also actively trains our collective microbial enemies, making them stronger for all of us.

Table 1: Antibiotic Resistance Profile of *S. aureus*

Antibiotic Class	Antibiotic	Susceptible n (%)	Resistant n (%)
Quinolones	Ciprofloxacin	40 (100%)	0 (0%)
	Ofloxacin	39 (97.5%)	1 (2.5%)
	Pefloxacin	38 (95%)	2 (5%)
βeta-lactams	Oxacillin	35 (87.5%)	5 (12.5%)
	Cloxacillin	28 (70%)	12 (30%)
	Amoxicillin	11 (27.5%)	29 (72.5%)
	Ceftriaxone	10 (25%)	30 (75%)
Aminoglycosides	Gentamicin	33 (82.5%)	7 (17.5%)
	Streptomycin	14 (35%)	26 (65%)
Other Classes	Chloramphenicol	30 (75%)	10 (25%)
	Erythromycin	26 (65%)	14 (35%)
	Cotrimoxazole	25 (62.5%)	15 (37.5%)
	Tetracycline	16 (40%)	24 (60%)

Torimiro and Torimiro 2012

In the hallowed halls of our hospitals, within the very places where we seek healing from surgical intervention, a silent and insidious war is being waged. It is a war not against a single pathogen, but against the relentless ingenuity of microbial evolution. My research into the antibiotic resistance profile of *S. aureus* strains isolated from surgical wounds uncovered a disturbing new front in this conflict, one that challenges established paradigms and demands an urgent, strategic response (Olutola *et al.,* 2016). The most disquieting finding of this study was the detection of Extended-Spectrum β-Lactamase (ESBL) production in these strains. β-

lactamase enzymes are the primary shields that *S. aureus* uses to defuse penicillin and cephalosporin antibiotics.

The discovery of the *Extended-Spectrum* variant is a game-changer. While well-documented in Gram-negative bacteria like *E. coli* and *Klebsiella*, their detection in *S. aureus* represents a dangerous horizontal gene transfer and a convergence of resistance mechanisms. These findings signal that *S. aureus* is not just strengthening its existing defences but is actively acquiring new, more powerful weapons from other bacterial families. This dramatically escalates the threat level, pushing us closer to the spectre of pan-drug-resistant infections. *S. aureus* is not only MDR but is now arming itself with the advanced weaponry of ESBLs, once the exclusive domain of Gram-negative bacteria. This transforms a surgical wound from a site of healing into a potential breeding ground for untreatable infections. It emphasised a brutal truth that shows the boundary between different classes of bacterial resistance is collapsing.

Probing deeper into this arsenal, I uncovered a chilling adaptive mechanism: the inducible β-lactamase. My research revealed that for many of these strains, exposure to β-lactam antibiotics (the very drugs designed to inhibit/kill them) does not merely select for resistant mutants; it actively triggers them to ramp up production of their resistance enzymes (Torimiro and Olutola, 2018). We demonstrated that the specific activity of β-lactamase increases linearly with the concentration of the antibiotic inducer. Think of it that the presence of cefoxitin or penicillin in the wound environment acts as a signal, commanding the bacterial cell to mass-produce the very enzyme that will destroy the drug. This is not passive resistance; it is an active, inducible defence system. Furthermore, we found that a significant reservoir of these armed strains exist not just in

the wounds themselves, but in the nasal cavities of the patients seeking care. The same sophisticated, inducible resistance was active in these colonising strains, turning the human body into a silent incubator for its own potential infection.

Yet, the most unsettling revelation was discovering that this advanced threat is extended to apparently healthy university students (Torimiro, 2018). Here, in the most routine of specimens, their urine, I found the same alarming pattern. I isolated Gram-negative bacilli from a significant majority of these asymptomatic individuals. Every single isolate was MDR, like their hospital counterparts. However, the critical finding was the presence of Extended-Spectrum β-Lactamase (ESBL) producers right here, in the community. These were not patients on lengthy antibiotic regimens; these were apparently healthy carriers. The ESBL-producing *E. coli* and *Klebsiella* sp. that I discovered displayed co-resistance to fluoroquinolones, aminoglycosides, and sulfonamides. This means the genetic machinery for ESBL is travelling with a suite of other classes of antibiotics, within a single bacterium.

We are facing a silent, community-wide colonisation by pan-resistant bacteria. The healthy individual is now an unwitting reservoir, carrying these pathogens in their urinary tract, ready to seed an untreatable infection after a simple medical procedure or a compromised immune system. This dynamic, responsive nature of resistance underscores a brutal truth. It confirms that the fire of resistance is no longer a controlled burn in our intensive care units (ICUs); it is a wildfire smouldering in our communities. Our strategies must now expand beyond hospital stewardship to encompass public health education, stringent regulation of antibiotic access, and a fundamental rethinking of our relationship with the microbial world. The boundary between

hospital and community has dissolved, and with it, the illusion that this crisis is someone else's problem.

Environmental Disruptors: Polluted Ecosystems

In the face of rising global food demand, aquaculture stands as a critical pillar for food security and a source of affordable animal protein. However, the sustainability of this vital sector is perpetually challenged by the threat of infectious diseases and environmental contamination. My investigation into the bacteriology and physico-chemical quality of freshwater earthen ponds stocking the African catfish (*Clarias gariepinus*) in Ile-Ife, Nigeria, provides critical insights with direct implications for fish health, food safety, and public health (Torimiro *et al*., 2014). The study revealed a diverse and concerning microbial ecosystem within these aquaculture environments.

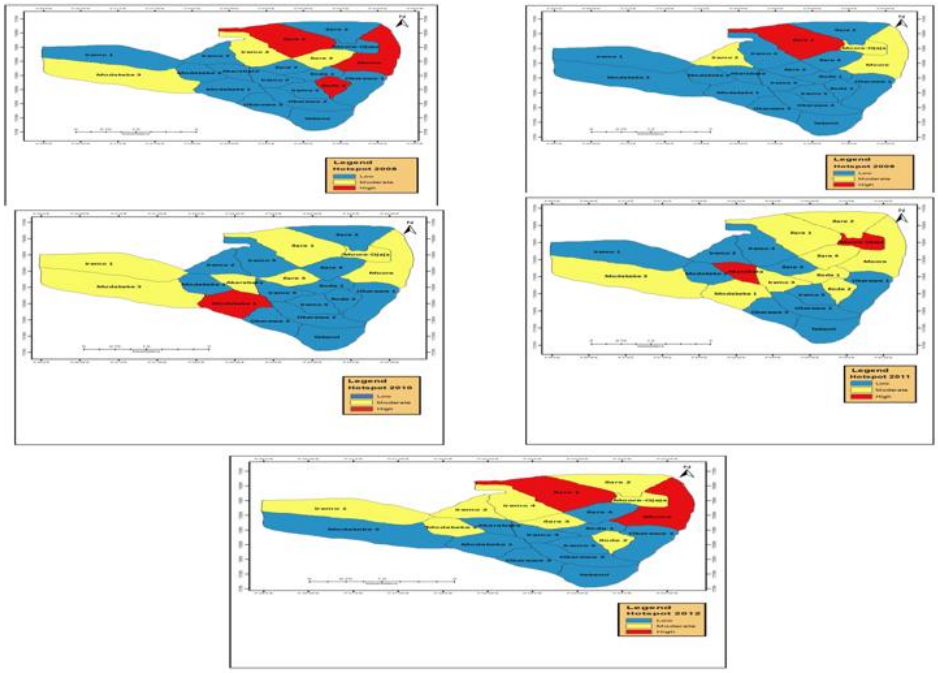
We identified a total of twenty-five bacterial isolates belonging to thirteen genera. Most alarmingly, these microbial consortia included potential pathogens such as *Aeromonas* sp., *Pseudomonas* sp., *E. coli*, *S. aureus*, and *Shigella* sp. The presence of *E. coli* and *Streptococcus faecalis* points strongly to faecal contamination. These are likely from the surrounding watershed, underscoring the interconnection of water quality and agricultural practice. Perhaps the most significant finding of this work was the high prevalence of multiple antibiotic resistance. A staggering 80% of the bacterial isolates exhibited resistance to multiple classes of antibiotic. This transforms these ponds from mere food production units into potential reservoirs and amplifiers of drug-resistant bacteria. When fish are harvested from such environments, they can become vectors, transmitting these resistant pathogens through the food chain to consumers, thereby

posing a silent but substantial threat to the clinical effectiveness of antibiotics in our communities.

From an environmental perspective, the physico-chemical parameters of the pond waters, including temperature, pH, and water hardness, were largely within acceptable limits for warm-water fish culture, indicating that basic water quality was not the primary stressor. However, we noted two critical issues. There was Low Dissolved Oxygen (DO) levels (0-4.8 mg/L), below the recommended standard, which can stress fish populations, making them more susceptible to disease. In addition, elevated phosphate levels indicate nutrient pollution that can drive eutrophication and destabilise the aquatic ecosystem. This research sounds a clear warning. Our fish ponds are not isolated systems; they are mirrors reflecting broader environmental and public health challenges. The coexistence of pathogenic bacteria and multidrug resistance in a food production system is a recipe for a public health crisis.

This threat is not confined to our aquaculture systems. The same narrative of contamination plays out in the very water that sustains the surrounding community of Ile-Ife. My research revealed a parallel public health crisis: the sources of water for domestic use themselves are reservoirs for a similar roster of pathogens (Torimiro *et al.,* 2020a). We mapped five years of retrospective hospital cases of Acute Gastroenteritis (AGE), and isolated bacterial pathogens from household domestic water of some of the cases. The families of bacteria (*Shigella*, *E. coli*, and *Salmonella*) were prevalent in drinking water, with all samples contaminated with faecal coliforms far above safe limits. Critically, geographical information systems (GIS) and spatial mapping pinpointed recurring disease hotspots in wards where communities relied heavily on shallow wells (Figure

3). The faecal contamination indicated in our fish ponds is the same contamination that drives outbreaks in the human population. The microbial voices from the ponds and the community wells are telling one story: environmental neglect fuels a cycle of infection that undermines both food security and human health.



Torimiro, Ogunbodede and Daramola (2020a)

Figure 3: Spatial pattern and AGE burden hotspots in Ile-Ife for 2008 -2012

This cycle of contamination extends directly from our water to our food. My research into cassava processing environments revealed a silent threat. I examined the presence of enterotoxigenic *Bacillus* species in Nigerian cassava processing environments, highlighting significant food safety concerns (Torimiro *et al.,* 2022). A majority of the *Bacillus* species (76%) were found to carry the *nhe*, *hbl*, and *bceT* enterotoxin genes. These bacteria produce

diarrhoeagenic toxins during their vegetative growth stage, which can contaminate cassava products and cause lethal foodborne outbreaks upon consumption (Figure 4).

A similar pattern of health risks of enterotoxin-producing *Bacillus* species was also found in fermentation effluents from maize and African locust bean (ALB) processing sites (Figure 5). This confirms that this threat is widespread in the fermentation of maize and African locust beans (Daramola *et al.,* 2025a). We found that over 40% of *Bacillus* isolates from fermentation waste sites carried genes including *nhe*, *hbl*, and *bceT*, potent for diarrheal toxins. Alarmingly, a third of them harboured multiple enterotoxins simultaneously. This shows that the indiscriminate disposal of fermentation effluents actively cultivates pathogens that can contaminate food. Thus, the narrative is clear and interconnected. From the contaminated fish pond and community well to the cassava yard and fermentation site, environmental neglect creates a unified crisis of microbial threats.

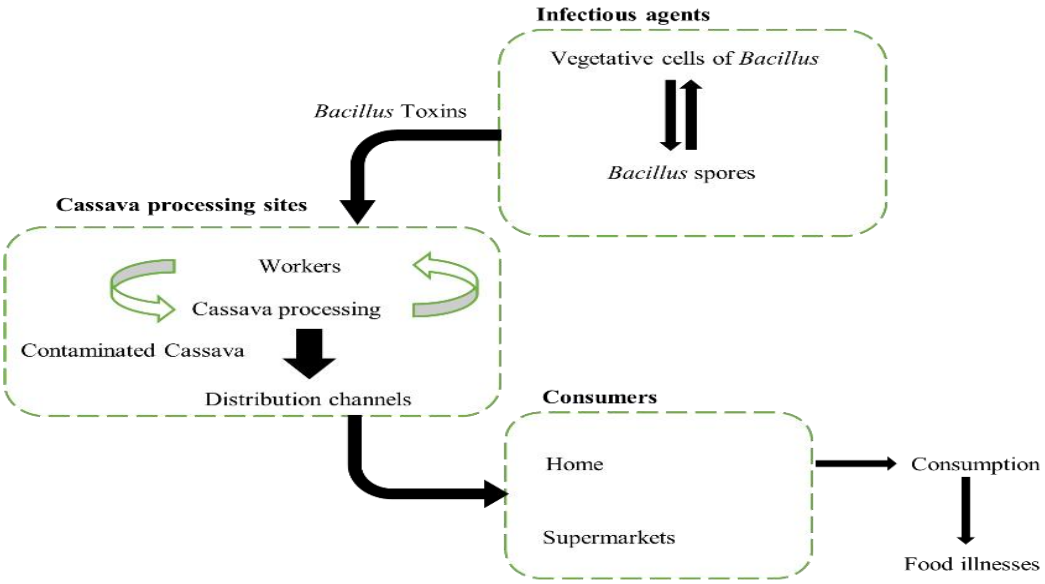


Figure 4: Schematic overview of enterotoxin transmission from cassava fermentation effluent to humans

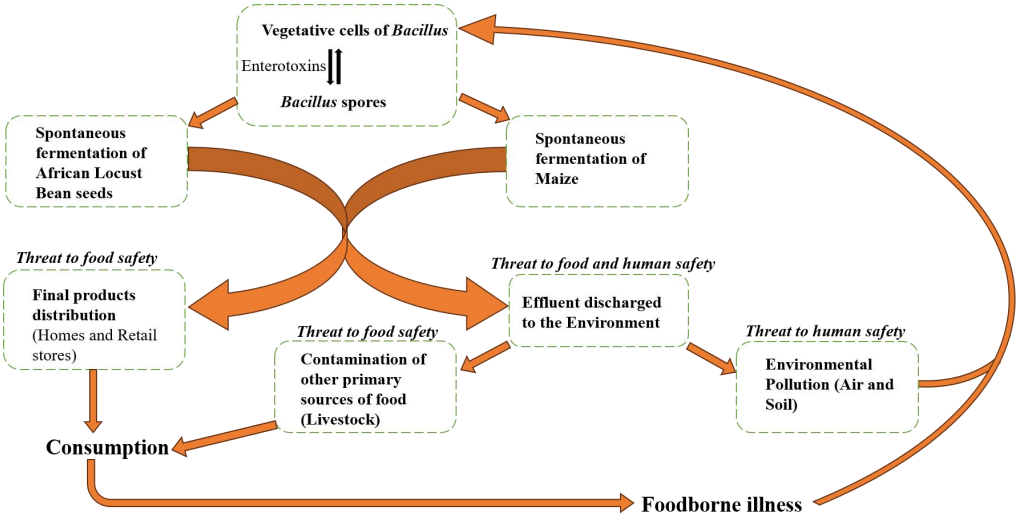


Figure 5: Schematic overview of enterotoxins transmission from maize and African locust bean seed fermentation effluents to humans

Even beyond microbial pathogens, environmental contamination from industrial activities can disrupt ecosystems and pose silent threats to human health. For instance, in a study conducted on soils around transformer installation sites in Nigeria, we found elevated levels of heavy metals like cadmium and lead (Akhigbe *et al.,* 2019a). The parallel study of the same transformer sites revealed elevated levels of radionuclides in oil-contaminated soils (Akhigbe *et al.,* 2019b). While total concentrations were often within regulatory/permissible limits, the critical finding was their high bioavailability (meaning humans could easily absorb them). Another study revealed that the presence of transformer oil in these contaminated sites altered the soil physicochemical parameters and soil quality (Akhigbe *et al.,* 2020). This introduced a substantial quantity of polycyclic aromatic hydrocarbons (PAHs) into the soils, thereby exposing the residents and workers to chronic health risks. The health risk assessment was stark: for children, the primary risk was from accidentally ingesting contaminated soil, with hazard levels indicating a significant probability of long-term health effects. This shows that the true danger lies not in

acute poisoning, but in the insidious, cumulative exposure that can occur even at low levels of contamination. It was a reminder that our environmental stewardship must extend to both biological and chemical fronts.

Agricultural Spoilers: Postharvest Losses and Food Security

My exploration of microbes as adversaries extends beyond clinical settings and polluted environments into the very heart of our food supply. A compelling case is the silent crisis of postharvest losses, where microorganisms act as direct agricultural spoilers, undermining food security and economic stability. In a study on onion bulbs, a staple crop with over 2 million metric tons produced annually in Nigeria, we isolated and identified a community of bacteria and fungi from deteriorating onions, including *Staphylococcus* spp., *Flavobacterium* spp., *Bacillus* spp., and the fungus *Aspergillus fumigatus* (Torimiro *et al.,* 2020b).

Critically, the pathogenicity tests confirmed that these isolates were not merely passive bystanders but active agents of decay. When reintroduced to healthy onions, they caused significant soft rot, with *Flavobacterium* spp. producing the largest lesions (28 mm in diameter). This demonstrates a direct cause-and-effect relationship between these microbial contaminants and the rapid deterioration of a vital food crop. The implications are twofold: First, these spoilage organisms lead to massive economic and nutritional losses. Secondly, some microbes like *Staphylococcus* and *Bacillus* are known agents of foodborne illness, turning a food security issue into a direct public health threat. This research crystallises a critical challenge. Microbes are formidable adversaries in our agricultural systems, causing postharvest losses that exacerbate food insecurity and create a bridge for devastating pathogens to enter the human food chain.

II. THE POSITIVE DIALOGUE: MICROBES AS PARTNERS AND PIONEERS

Environmental Stewards: Bioremediation and Nutrient Cycling

Bioremediation is a sustainable technology that utilises the metabolic capabilities of microorganisms, plants, or their enzymes to degrade, detoxify, or accumulate environmental pollutants. By transforming hazardous substances such as heavy metals, petroleum hydrocarbons, and industrial waste materials into stable or non-toxic forms such as water and carbon dioxide, it offers a "green" alternative to invasive chemical or physical cleaning methods. This strategy can be applied *in situ* (treating contaminated soil or water at the site) or *ex situ* (through excavated materials). Its cost-effectiveness and ability to restore ecosystem health make it a vital tool for long-term environmental management and pollution control.

Mr. Vice-Chancellor Sir, if not for the iconic role of microbes as the earth's ultimate degraders/recyclers, we would all have been buried in a mass of dead organisms. Microbes speak by breaking down organic matter to its simplest form. In polluted soils and waterways, they degrade hydrocarbons (such as *Pseudomonas* in oil spills), fix nitrogen (*Rhizobia* in legume roots), enriching soils without synthetic fertilisers, and detoxify heavy metals via enzymatic transformation. Just as we fight microbes that degrade our health, we can partner with others to mitigate pollutants. The same microbial versatility that poses a threat in the clinic holds immense potential for environmental remediation and industrial innovation. We can transform environmental liabilities into valuable biological assets by understanding and directing this microbial power. While my work exposed the perils of microbial resistance in clinical settings,

my research adequately explores the remarkable utility of microbes, demonstrating how they can be harnessed to solve environmental challenges.

I have extensively researched the detoxification of cyanide using various enzymes. Cyanide is a potent toxin that inhibits cellular respiration. Strategically, enzymes serve as highly specific biological catalysts that accelerate the degradation of complex environmental pollutants into non-toxic or less harmful substances. Compared to whole microorganisms, isolated enzymes can function in extreme conditions where cellular life might struggle. Such as environments include those with high toxicity or fluctuating pH levels. By lowering the activation energy of chemical reactions, enzymes like oxidoreductases and hydrolases break down hydrocarbons, pesticides, and heavy metals. In my research, we explored 3-mercaptopyruvate sulfurtransferase (3-MST) from *Pseudomonas putida* KT12440, isolated from industrial effluent, for cyanide bioremediation (Adekunle *et al.,* 2017). The 3-MST enzyme provides a robust tool for remediating cyanide-contaminated industrial wastewaters. The enzyme facilitates detoxification by converting cyanide into thiocyanate, a significantly less toxic compound.

Optimal enzyme production occurred at 30°C and pH 9.0, utilising mannitol and casein as preferred carbon and nitrogen sources, respectively. Similarly, the enzyme beta-cyanoalanine synthase (β-CAS), isolated from *Pseudomonas straminea* in industrial effluents, serves as an important agent for the bioremediation of cyanide-polluted wastewaters (Okonji *et al.,* 2018). It facilitated detoxification by catalysing a reaction between toxic hydrogen cyanide and L-cysteine to produce β-cyanoalanine, a less harmful non-protein amino acid. These characteristics make it a robust candidate for treating industrial discharge from mining and steel sectors.

My exploration of microbial cyanide detoxification revealed enzyme rhodanese from *Bacillus cereus*, isolated from the toxic effluent of a steel smelting industry (Itakorode *et al.,* 2019). Where BCAS offers one pathway, rhodanese provides a complementary, robust mechanism. This enzyme functions as a precise molecular machine, efficiently converting the lethal cyanide into the less toxic thiocyanate. It is stable and highly active under the alkaline and warm conditions typical of industrial waste. Later, my team and I produced rhodanese from *Klebsiella oxytoca* JCM 1665 and immobilised the rhodanese on alginate-glutaraldehyde beads for cyanide bioremediation (Itakorode *et al.,* 2023). Rhodanese's biochemical stability makes it a viable tool for treating cyanide-contaminated water and protecting aquatic ecosystems.Together, BCAS and rhodanese exemplify a powerful principle: that for our most stubborn industrial poisons, microbes have already evolved precise, enzymatic solutions. This discovery is more than a biochemical characterisation; it represents a powerful blueprint for bioremediation. It shows that we can recruit and harness specific microbial enzymes as precise tools to neutralise industrial pollutants.

This principle progresses from molecular machines to entire microbial communities. Consider the challenge of spent engine oil. My research indicated that bacteria such as *Bacillus* and *Pseudomonas* are effective degraders (Yusuf *et al.,* 2021). However, this is achievable only when we provide their ideal conditions: the organic nutrient, casein, an alkaline pH (8-9), and warmth (35-45 °C). Thus, my role evolved from simply discovering these microbial allies to unlocking their full potential by mastering their environment. Building on this, I identified novel bacterial degraders like *Providencia stuartii* and *Bacillus pseudomycoides* in soils contaminated with

transformer oil (Torimiro *et al.,* 2020c). Through detailed analysis, we mapped their specific abilities to break down persistent hydrocarbons like alkyl-PAHs. This work reinforces a central theme that my role is not to invent solutions from scratch, but to discover and deploy the exquisite, pre-evolved tools that the microbial world provides. I am harnessing nature's own profound wisdom for a cleaner world, from enzymatic scalpels to entire degradative consortia.

Microbial Enzymes for Industrial Processes

In the quest for sustainable industrial processes, enzymes from microorganisms have emerged as powerful biocatalysts. Among these, pectinases, which are enzymes that break down the pectin in plant cell walls, hold a position of critical importance. They are the workhorses in industries ranging from fruit juice clarification and wine production to the treatment of industrial wastewater and the recycling of agricultural waste. The global demand for these enzymes is immense, yet a significant challenge remained: finding robust microbial strains that can produce high yields of pectinase under the usual harsh conditions of industrial processes, such as high temperatures and alkaline pH. Therefore, my study (Torimiro and Okonji, 2013) provided a comparative evaluation of pectinase production by three *Bacillus* species: *B. stearothermophilus*, *B. cereus*, and *B. subtilis*. These bacteria were isolated from agro-waste and put through a rigorous series of tests to determine their potential as industrial enzyme producers. *Bacillus stearothermophilus* emerged as the most promising industrial candidate. It combines the highest pectinase activity with the most robust physicochemical profile: exceptional thermostability at 60°C and optimal function at a moderate alkaline pH of 7.5.

In another study, we transformed deteriorating fruits, oranges, and grapefruits, a major source of postharvest waste, into valuable industrial resources. We examined pectinolytic activities of pectinase produced by some bacteria cultured from rotting oranges and grapefruits as a sustainable method to mitigate economic losses associated with food spoilage. I opened the door to more efficient, cost-effective, and environmentally friendly bioprocesses by identifying and characterising such robust microorganisms. Leveraging these microbially derived enzymes optimises food processing efficiency and reduces environmental waste, offering a biotechnological pathway to enhancing the circular economy (Torimiro *et al.,* 2019). These studies emphasise a powerful message that the solutions to many of our industrial challenges can be found in nature's own microbial arsenal. These works are not merely academic exercises, but tangible steps towards developing superior biocatalysts that can drive innovation in our food, textile, and waste management industries, ultimately contributing to a more sustainable future.

Madu *et al*. (2014) isolated *Bacillus licheniformis* from the cassava waste dump site. It was observed the microbe thrived in alkaline conditions (pH 9.0), operated optimally at a warm 40°C (reducing cooling costs), and achieved peak production in just 48 hours (a cost-effective timeline for potential industrial scale-up). In a breakthrough for sustainable science, we demonstrated that this bacterium did not need expensive, pure substrates. It could be fueled by agricultural waste (orange bagasse, banana peels, and plantain peels). This is the very essence of a circular bio-economy: converting waste into wealth. Thereafter, we embarked on a meticulous biochemical quest, using the classic techniques of protein science (ion-exchange and gel-filtration chromatography) to purify the pectinase from the complex soup of other proteins (Madu *et al.,* 2016). The result was a 10.5-fold purification, yielding a single, potent enzyme

with a specific activity of 9.47 U/mg. We had successfully isolated the precise molecular scissor we set out to find. A relatively compact enzyme of 38 kDa, ideal for diffusion and action, performing best at a pH of 9.0. It was not only highly active at 50°C but also exhibited remarkable stability, retaining most of its activity for over an hour at 45°C. It had a high affinity for its natural substrate, with a low Km for polygalacturonic acid, meaning it works efficiently even at low substrate concentrations. It retained significant activity in the presence of various preservatives and metal ions, suggesting it would not be easily deactivated in a complex industrial mixture. This embodies the complete journey of translational research: from environmental isolation to biochemical refinement.

III. THE HUMAN COUNTER-OFFENSIVE STRATEGIES AND SOLUTIONS

Combating Antimicrobial Resistance (AMR)

Mr. Vice-Chancellor Sir, in my quest to combat the escalating crisis of AMR, I not only looked to the future of drug discovery but also to the wisdom of ancient remedies. A few of my research projects have explored different approaches to combating AMR. This includes natural products, porphyrins, and nanomaterials as an eco-friendly alternative for developing potent bio-antibiotics.

Wound infections are one of the most common hospital-acquired infections, and it continues to be a challenging problem with AMR contributing as a significant cause of disease burden (Gottrup *et al.,* 2005). My research into the antibacterial efficacy of various (14) honey types from South Western Nigeria provides a compelling and scientifically validated alternative (Adeyemo *et al.,* 2017). Locally sourced honey was found to exhibit significant and broad-spectrum antibacterial activity against a panel of wound-associated bacteria. Notably among

them was the super dark-amber honey, which exhibited the highest potency, with a broad spectrum of activity that compared favourably to the standard antibiotic, streptomycin. Some of these honeys successfully inhibited pathogens such as *S. aureus, P. aeruginosa* and *E. coli* that were resistant to streptomycin. The antibacterial action was not due to a single compound but a combination of factors, including high sugar concentration, low pH, and the presence of naturally occurring hydrogen peroxide and phytochemicals. This multi-target mechanism makes it exceptionally difficult for bacteria to develop resistance. This work powerfully illustrates that part of the solution to the complex problem of AMR may lie in harnessing the sophisticated, natural defences found in our own environment.

Natural products such as essential oils (EOs) and honey offer multi-targeted mechanisms that make it difficult for bacteria to develop resistance compared to conventional monotherapy antibiotics. Essential oils are complex mixtures of volatile compounds (such as terpenes and phenols) that attack bacteria on multiple fronts. The lipophilic nature of EOs allows them to intercalate into the bacterial cell membrane. This increases permeability, leading to the leakage of critical intracellular components such as ATP and ions, eventually causing cell death (Burt, 2004). Some EOs can block bacterial efflux pump proteins that "pump out" antibiotics before they can work. When these pumps are disabled, EOs can restore the efficacy of traditional antibiotics. Additionally, EOs can disrupt bacterial communication (quorum sensing), which prevents the formation of protective biofilms and reduces the expression of virulence factors. In the face of devastating MDR clinical isolates (including methicillin-resistant *S. aureus* (MRSA) and resistant *E. coli* and *Klebsiella* spp.), we explored the essential oil from *Citrus aurantifolia* (Christm.) Swingle peels (Torimiro *et al.,* 2020d). Against a backdrop of total resistance to

multiple conventional antibiotics, the lime peel oil extracted via hydro-distillation with a 1% yield, exhibited excellent, broad-spectrum antibacterial activity at concentrations of 25%, 50%, and 100% v/v. It demonstrated potent inhibitory and bactericidal effects at remarkably low concentrations, 0.195% to 3.125% v/v.

Porphyrins are versatile macrocyclic compounds that combat antimicrobial resistance (AMR) primarily through their role as photosensitizers in antimicrobial photodynamic therapy (aPDT). In my study, I have used charged, neutral, free-base, and metallated porphyrins as photosensitizers to combat multidrug-resistant bacteria isolated from chronic wounds. While exploring neutral (TPP) and anionic (TPPS) porphyrins metallated with zinc, tin, and silver, it was observed that these compounds absorbed light, entered an excited state, and generated reactive oxygen species such as singlet oxygen and superoxide. The metallation and light exposure significantly enhanced antibacterial activity. Specifically, zinc-metallated anionic porphyrin (ZnTPPS) showed excellent biocidal action with an increased zone of inhibition when exposed to light (Table 2) effectively inhibiting *S. aureus*, *Klebsiella* sp., *Proteus* sp., and *E. coli* (Daramola *et al.,* 2021). This approach, known as antibacterial photodynamic therapy (APT), demonstrated a powerful paradigm where we can create effective, resistance-proof therapies for wound decontamination by strategically modifying natural compounds and combining them with light.

Table2: Antibacterial activity of free-base TPPS and MTPPS against the bacterial isolates (zone of inhibition in mm)

	TPPS		ZnTPPS		SnTPPS		AgTPPS		Streptomycin Sulphate
	Dark	Light	Dark	Light	Dark	Light	Dark	Light	
S.aureus	18 ± 0.8	18 ± 0.8	31 ± 1.4	33 ± 1.1	11 ± 0.0	15 ± 0.7	14 ± 0.7	15 ± 0.7	35 ± 1.4
Klebsiella sp.	20 ± 1.4	16 ± 0.6	30 ± 1.2	32 ± 0.7	0	17 ± 0.7	15 ± 2.8	17 ± 0.8	27 ± 2.8
Proteus sp.	0	0	23 ± 2.1	28 ± 0.7	0	0	0	0	27 ± 1.4
E.coli	33 ± 2.1	17 ± 0.7	26 ± 0.7	30 ± 1.4	13 ± 0.3	20 ± 0.7	14 ± 0.4	17 ± 0.7	35 ± 2.8

Daramola, Olajide, **Torimiro** and George (2021)

Free-base porphyrins often showed poor activity; their effectiveness significantly improved when complexed with metal ions, particularly zinc (Zn) and tin (Sn). Notably, anionic porphyrins (TPPS and TCPP series) were found to be effective like the cationic ones, challenging the assumption that only positively charged agents could successfully bind to negative bacterial cell walls (George *et al.,* 2022). To overcome challenges such as leaching and poor bacterial uptake, porphyrins were immobilized on chitosan (Figure 6), a biopolymer with inherent antimicrobial properties (George *et al.,* 2025). The silver-based composites, specifically C-AgTMPP and C-AgTHPP, were the most effective, eradicating all tested pathogens within 24 hours of light exposure with minimal bactericidal concentration (MBC) values as low as 1.25 µg/mL.

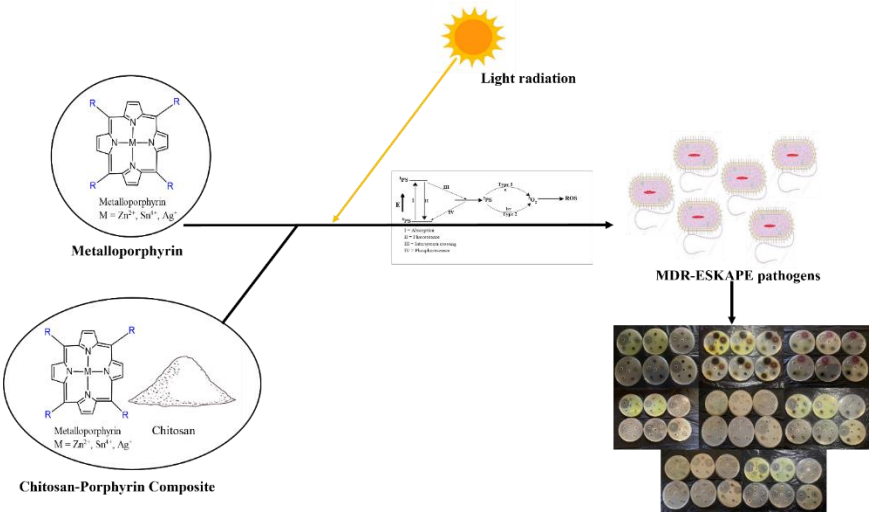


Figure 6: An overview of chitosan-porphyrin composite as photosensitizers in aPDT

My team and I also studied a complementary strategy using biosynthesised metallic nanoparticles and their composites for drug discovery. Nanotechnology offers a powerful shift from traditional antibiotics, which often fail due to specific bacterial mutations. By utilizing multiple, simultaneous mechanisms of action, nanomaterials make it significantly harder for pathogens to develop resistance. Unlike conventional drugs that target single metabolic pathways, nanomaterials overwhelm bacteria through physical and chemical disruption. Metal nanoparticles (Ag, Au, ZnO) physically damage the lipid bilayer, causing lethal leakage of cellular contents. Due to their size and transport mechanisms, certain nanocarriers can bypass the efflux pumps used by bacteria against traditional antibiotics.

Alayande *et al.* (2019) compared green-synthesized (using *Amaranthus spinosus* Linn. leaf extract) with traditional chemically synthesized zinc oxide (ZnO) nanoparticles and their potential to inhibit the growth of bacteria, specifically targeting *P. aeruginosa*, *Salmonella typhi*,

and *Shigella dysenteriae.* We observed that green-synthesized ZnO nanoparticles were more effective, demonstrating superior bactericidal properties due to complexation with plant phytochemicals such as tannins and flavonoids. These nanoparticles combat bacteria by disrupting cell membranes and inducing oxidative stress, which leads to cell growth inhibition and death. The plant's natural phytochemicals not only helped form the nanoparticles but also created a bioactive coating, enhancing their antimicrobial power. This demonstrates that green synthesis is more than an eco-friendly process, but a strategy to create smarter, more potent treatment against pathogenic bacteria.

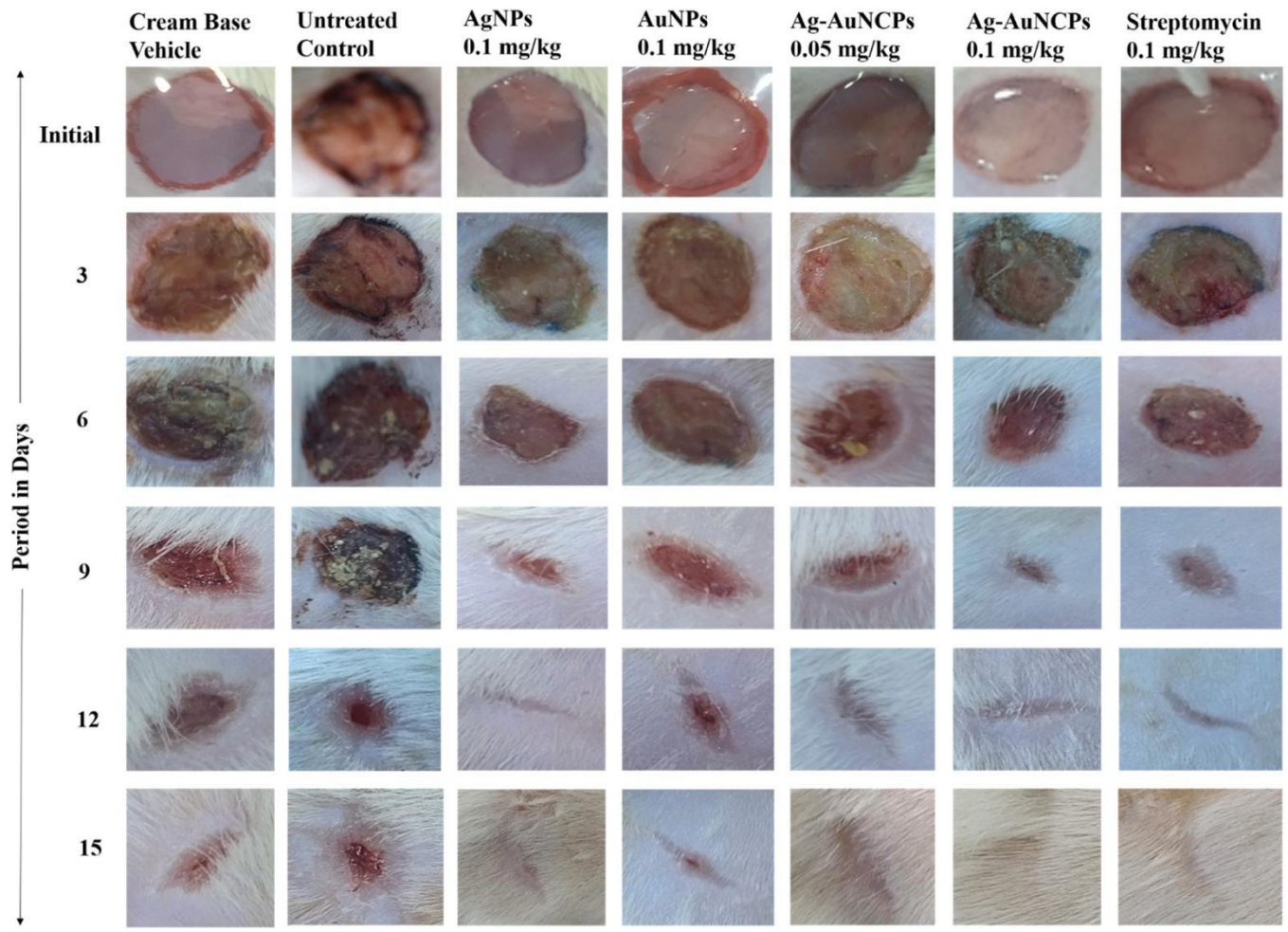
The biogenic production of silver nanoparticles (AgNPs) was explored (Omole *et al.,* 2024) as well as gold nanoparticles (AuNPs) for the treatment of multidrug-resistant (MDR) bacteria found in chronic wounds (Omole *et al.,* 2025a) using *Lysinibacillus fusiformis* isolated from the soil. These bacteria act as natural stabilising and reducing agents, offering a less toxic alternative to conventional antibiotics, demonstrating broad-spectrum efficacy against *Pseudomonas aeruginosa*, *Proteus mirabilis*, and *Enterobacter hormaechei*. To further address the challenge of multidrug-resistant (MDR) bacteria in chronic wounds, bimetallic silver-gold nanocomposites (Ag-Au NCPs) were synthesised using the cell biomass of *Lysinibacillus fusiformis* (Omole *et al.,* 2025b).

The biological "green" synthesis of Ag-Au NCPs demonstrated enhanced antibacterial efficacy against the tested MDR pathogens, including *P. aeruginosa* and *E. hormaechei,* with a potent bactericidal effect. These nanocomposites overcame resistance mechanisms such as biofilm formation and efflux systems by providing a high surface-area-to-volume ratio, which facilitated

superior adsorption and interaction with bacterial cells. This success with nanotherapeutics, alongside the photodynamic approach, showcases a versatile and powerful toolkit for combating complex wound infections.

My research took a critical translational step forward when these nanoparticles and nanocomposites were incorporated into oil-in-water creams (Omole *et al.,* 2025c). This is a formulation chosen for its superior skin absorption and penetration. In a rigorous *in vivo* study using an MDR *P. aeruginosa*-infected excision wound model in Wistar rats, the bionanoformulated creams demonstrated remarkable tissue-regenerating capabilities. The most striking finding was the rate of wound closure (Figure 7). The bimetallic silver-gold nanocomposites (Ag-AuNCPs) cream achieved complete regeneration of infected tissues in just 11 days, outperforming both silver nanoparticles (13 days) and gold nanoparticles (15 days), and even showing a favourable comparison to a standard streptomycin cream.

Critically, histopathological analysis confirmed this was true regeneration, with restored skin structures like collagen fibres, hair follicles, and glands. We found that the mechanism involves reversing the pathogen's oxidative stress by boosting antioxidant enzymes and reducing lipid peroxidation. Importantly, these creams showed no adverse effects on liver or kidney function. This work provides a dual-action therapeutic strategy that simultaneously eradicates resistant pathogens and actively promotes the regeneration of functional tissue. Additionally, this work offers a promising blueprint for overcoming the global challenge of AMR, particularly in the context of chronic wound care. It paves the way for future clinical trials aimed at bringing these solutions from the laboratory to the bedside.



Omole, **Torimiro,** Adeyemi, Saravanan, and Ganesh (2025c)

Figure 7. Contraction in Wounds Infected with MDR *P. aeruginosa*

IV. LISTENING INTENTLY: SCIENTIFIC TOOLS FOR MICROBIAL DIALOGUE

To navigate this complex relationship, from harnessing their benefits to countering their threats, we must learn to listen. This section explores the sophisticated scientific tools that allow us to decode the microbial dialogue, translating their silent language into actionable knowledge.

Decoding Resistance: From Phenotypes to Genes

To truly overcome AMR, we must move beyond what we see in a Petri dish and understand the genetic blueprint behind it. This is the critical work of decoding resistance, from its visible phenotype to the very genes that orchestrate its power. In my study (Torimiro and Torimiro, 2012), I specifically hunted for the community-associated methicillin-resistant *S. aureus* (CAMRSA) strains that were resistant to last-line beta-lactam antibiotics like methicillin and oxacillin. Phenotypically, we found that 12.5% of the isolates were resistant to oxacillin. Genetically, however, the picture was more complex and intriguing. The gold-standard *mecA* gene, which confers methicillin resistance, was detected in only one of the five phenotypically resistant strains. This discrepancy suggested the presence of other, perhaps novel, resistance mechanisms in our local strains. It emphasises the need for local molecular surveillance and warns against relying solely on genetic tests developed for the Western strains.

My initial research efforts had painted two alarming, yet seemingly separate, pictures: one of MDR *S. aureus* thriving within our hospitals (Torimiro *et al.,* 2005), and another of equally resistant strains circulating in our community (Torimiro and Torimiro, 2012). This led to a critical and complex question: Were these two distinct, or were they intimately connected? Were we seeing separate fires, or was one sparking the other? To answer this, I employed Sodium

Dodecyl Sulphate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) to analyse the whole-cell protein profiles of these strains (Torimiro *et al.,* 2013a).

A unique molecular fingerprint for each bacterial isolate was obtained, and it allowed us to observe their deep-seated relatedness. This was the "smoking gun" which provided compelling evidence that the strict boundary between hospital and community strains was porous. This chapter in our research was a detective story. We found the same fingerprints at the two crime scenes (the hospital and the community). It proved that the resistant pathogens in our clinics and in our homes are not strangers to one another; they are kin. They trade places, they share strengths. This discovery taught us a humbling lesson that we cannot defend our hospitals without also protecting our community, and we cannot safeguard our community without securing our hospitals. The line between them is an illusion, and our fight against resistance must be as interconnected as the pathogens we seek to defeat.

A comprehensive study on the local epidemiology of nosocomial *S. aureus* in a Nigerian teaching hospital deepened this story (Adeyanju *et al.,* 2022). We found that 19% of patients were already colonised with *S. aureus* on admission, a hidden reservoir of potential infection. Molecular genotyping provided the definitive link: in over 57% of hospital-acquired infections, the culprit was genetically identical to the strain the patient carried in their own nose upon arrival. This was the ultimate "inside job", proving the community strain was the source of the hospital infection. These strains were not just resistant (61.7% were MDR), they were also virulent. A significant portion carried potent toxins like Panton-Valentine Leukocidin (PVL). So, the boundary is not just porous; it is non-existent. The same clones, armed with both resistance and

virulence, circulate between our communities and our hospitals. This demands an integrated defence, protecting both fronts simultaneously, because the threat is the same.

Harnessing Microbial "Voices" for Innovation

Once we learn to listen, we can begin to collaborate. This involves connecting the unique chemistries and capabilities of microbes and turning their ancient voices into powerful new tools for food security, medicine, and industry. A striking example is found in my work on *Bacillus subtilis*, where its natural biochemistry was harnessed not to fight it, but to collaborate with it (Omole *et al.,* 2018). We directed this common soil bacterium to perform a remarkable feat for the green synthesis of silver nanoparticles. I did not stop at synthesis, but engineered these microbial nanoparticles into a brilliant, colorimetric sensor for a seemingly intractable problem (the postharvest spoilage of fruit).

As a banana spoils, it releases specific volatile compounds. The bacterial nanoparticles, acting as a sentinel, detect this compound and undergo a vivid colour change (from reddish-brown to transparent), providing a clear, visual early-warning system. This is innovation born from conversation: we listened to the microbe's synthetic capability, and we listened to the fruit's chemical cry for help, connecting them to create a simple, powerful tool to combat food loss. This is the promise of harnessing microbial voices. I transformed their ancient chemistry into modern sustainable solutions that protect our health, our environment, and our food security.

Beyond preservation of food using bacteria metabolites, one of the key approaches I have explored was "modern diagnostics" utilising bacteria and bacteria-mediated material as

"biosensors" to detect foodborne pathogens and their toxins in real-time. In the detection of food pathogens, bio-receptors (also known as bio-recognition elements) serve as the critical sensing component of nanotechnology-based biosensors. These bioreceptors are highly specific and sensitive, ensuring that the sensor only reacts to the intended pathogen, even in complex food matrices. Their primary importance lies in their ability to distinctly identify and bind to specific target analytes (Daramola *et al.,* 2022a).

These analyte-bio-receptor complexes are designed to trigger a signal, often a visual colour change when using chromogenic substrates, that can be easily read by transducers or the naked eye. This approach enables real-time, visual-aided results, which are essential for monitoring food quality and safety without the long wait times of traditional culture methods. Some commonly explored bio-receptors, include enzymes, chromogenic substrates, biopolymers, antibodies, nucleic acids (aptamers, peptide nucleic acid), bio-mimic substances, and many more.

One significant approach is the affinity capture, which employs functionalised (bioconjugated) bacteria-synthesised nanoparticles as a hook to selectively isolate foodborne pathogens from complex matrices. These bacterial strains reduce metal salts into nanoparticles, which are then coated with high-affinity ligands. The introduction of these bioconjugated nanoparticles to food samples initiates their specific binding to surface antigens of target bacteria, such as *E. coli*, *Salmonella*, and *Listeria,* among others. This step concentrates the pathogens and removes interfering substances, significantly enhancing the sensitivity of downstream detection methods. It represents a sustainable, cost-effective alternative to traditional chemical synthesis for rapid food safety diagnostics.

As part of my research work, the affinity capture of diarrhoeagenic *Escherichia coli* (DEC) pathotypes was achieved using a novel nanocomposite of poly-L-lysine (PLL) and silver nanoparticles (AgNPs) (Daramola *et al.,* 2022b). The AgNPs were biosynthesised using the bacterium *Bacillus subtilis*, offering an eco-friendly production route. The capture mechanism relies on electrostatic interaction. The positively charged amino acid terminals of the PLL-AgNPs bind to the negatively charged O-antigen regions of the *E. coli* lipopolysaccharide layer (Figure 8). This interaction triggers a visible colorimetric change from reddish-brown to colourless with brown precipitates, allowing for rapid optical detection within two hours of interaction. The binding affinity varies between pathotypes, with the strongest adhesion observed in Shiga toxin and Enteroaggregative *E. coli* (Daramola *et al.,* 2022b).

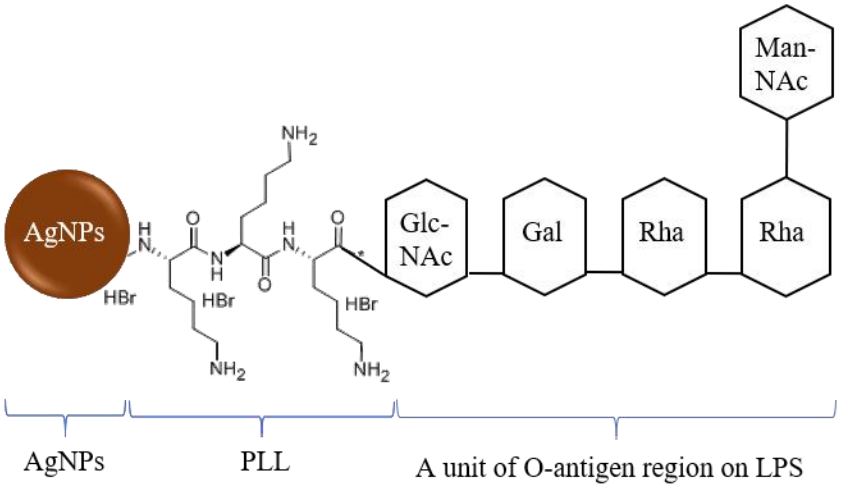


Figure 8: Affinity capture of enteric bacterial pathogens using functionalized silver nanoparticles

Subsequently, I engineered *Bacillus subtilis* to synthesise iron oxide and gold nanoparticles, which were assembled into nanocomposites (Fe_3O_4-AuNCs) (Daramola *et al.,* 2024). These nanoparticles were functionalised with ligands ethylenediaminetetraacetic acid (EDTA) and polymers (polyethylenimine - PEI and polyethylene glycol- PEG) to enhance their binding capabilities. The capture mechanism relies on electrostatic interaction, where the positively charged functionalized nanocomposites bind to the negatively charged outer membranes (lipopolysaccharides) and cell walls (teichoic acid) that resulted in a highly selective system that can efficiently capture bacteria like *Salmonella* typhimirium and *Bacillus cereus* that are major causes of gastrointestinal infection (Daramola *et al.,* 2025b). The affinity capture process resulted in the formation of large, heavy complexes that self-precipitate, enabling the rapid detection of the pathogens (Figure 9).

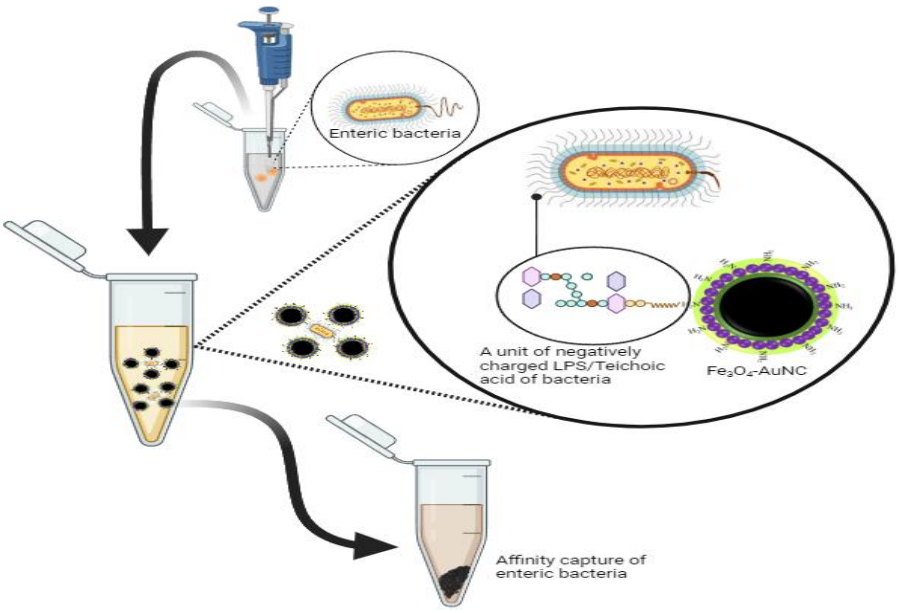


Figure 9: Affinity capture of foodborne bacterial pathogens using functionalized iron-gold nanocomposites

I have also developed a novel colorimetric biosensor using *Bacillus subtilis* to biosynthesize iron oxide (Fe_3O_4) and gold (Au) nanoparticles. These nanoparticles were combined into a nanocomposite (Fe_3O_4-AuNCs), capped with EDTA, and linked using polymers such as PEI or PEG. The nanocomposites were functionalised with different chromogens, 2-Nitrophenyl- α-D-glucopyranoside (2-NPGP), urea, and Triphenyl Tetrazolium Chloride (TTC) to detect enteric pathogens. The TTC-functionalised Fe_3O_4-AuNCs linked by PEI successfully detected *S. typhimirium* and *E. coli*, showing an intense red colour change within 2 and 6 hours, respectively (Figure 10). Additionally, 2-NPGP-functionalised composites provided a light, pale colour specifically for *S. aureus* (Daramola *et al.,* 2025c). This transforms complex detection into a simple, visual alarm, showcasing the power of microbial synthesis for practical food safety.

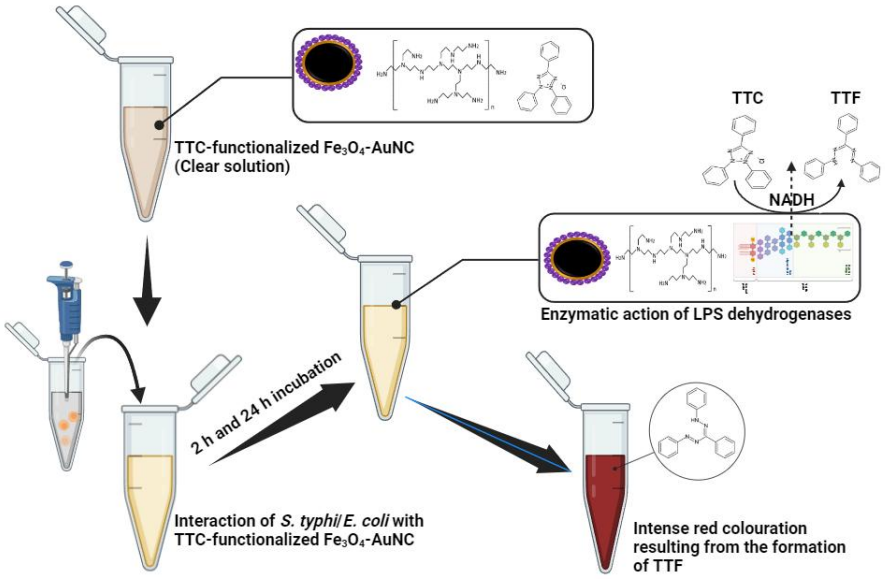


Figure 10: Colorimetric detection of *Salmonella* Typhimurium and *Escherichia coli* using functionalized iron-gold nanocomposites

We can partner with bacteria, fungi, and algae, using them to synthesise sustainable nanoparticles. These particles could be biofunctionalised to create powerful consortia that can tackle pollution with incredible precision. In a comprehensive review, this very synergy was explored (Torimiro *et al.,* 2021). For example, biofunctionalised magnetic iron oxide or silver nanoparticles effectively degrade persistent organic pollutants such as hydrocarbons and industrial dyes. Later, in the study that involved the use of soil bacteria from a metal workshop to biosynthesise iron oxide nanoparticles (IONPs), specific soil bacteria, including *Bacillus* and *Klebsiella* species, were found to possess high iron tolerance and the ability to bio-reduce iron salts into iron oxide nanoparticles (IONPs). The bacteria possessed specific genes (*fhu* and *suf*) that are likely responsible for their iron-reducing capabilities (Daramola *et al.,* 2023). This research offers insights into utilising bacteria for the eco-friendly production of IONPs, with potential applications in nanobioremediation. Therefore, it transforms our microbial partners from simple indicators of harm into active, empowered environmental healers, capable of restoring our soil and water from the inside out.

Quadruple Innovations Using Microbes as Nano-Biofactories

Mr. Vice-Chancellor Sir, in my quest to address pressing human challenges, I have harnessed the potential of microbes. I have four patents for innovations to boost human survival in food safety/security and drug discovery. Over 200,000 people die each year from food and waterborne illnesses in Nigeria (Onyeaka *et al.,* 2021). The presence of several pathogens, which include *B. cereus*, *Vibrio* spp., *Shigella* spp., *Salmonella* spp., *Salmonella typhimurium*, *K. pneumoniae, Enterococcus* spp., *Enterobacter* spp., *Micrococcus* spp., *Clostridium septicum, E. coli, and Staphylococcus* spp., has been well documented in food and water. Moreso, with increasing

AMR, strategic innovation into research and development for novel vaccines, diagnostics, and medicine is a priority as well as prevention of infections, which may result in inappropriate use of antimicrobials (WHO 2023).

Patent 1: Green synthesis of silver nanoparticles for optical detection of *Escherichia coli.* This innovation aids visual colour change and optical approach for the detection of *E. coli* pathotypes in water using coated silver nanoparticles (AgNPs) produced from a bacterium. The patent with number NG/PT/NC/2019/3865 is a form of solution-based biosensor that is used for the rapid detection of *E. coli*, the causal agent of diarrhoea. In contaminated water samples, 92% reduction in detection time as compared to available conventional methods was observed. It is very useful for rapid detection of the *E. coli* pathotypes in water and thereby preventing water- borne infections.

Patent 2: Biosynthesised silver nanoparticles as a biosensor for timely detection of postharvest fruit deterioration with patent number NG/PT/NC/2020/4628. This innovation presents a safe use of nanotechnology to combat food insecurity with the colorimetric detection of the onset of postharvest deterioration in fruit using bacterial-synthesized silver nanoparticles (AgNPs). This silver nanoparticle-based biosensor detects the early release of gas metabolites from deteriorating fruit, ten days before spoilage is visible to the naked eye. This innovation has the advantage of cutting down the losses from post-harvest deterioration of fruits, promotes food security, prevents environmental pollution, and reduces the severity of the health hazards caused by fruit spoilage.

Patent 3: An oil-in-water nanoformulated cream of bacterial-synthesized silver and gold nanocomposites for the treatment of multidrug- resistant chronic wound infection with patent number F/PT/NC/2023/9469. The nanoformulated cream has antibacterial activities that could increase wound tensile strength, hasten wound contraction, and allow epithelialisation and collagen synthesis to occur rapidly in chronic wound infections without adverse effect on liver and kidney functions.

Patent 4: Increasing food and water threats call for a need to accommodate an all-inclusive approach to disease prevention, detection, surveillance, assessments, and monitoring of pathogens in food and water before consumption. Building on the achievement in patent 1, additional foodborne pathogen *S. typhimirum* was included for detection. A nano-biosensor tool was designed for timely colorimetric detection of *S. typhimurium* and *E. coli* in water using a functionalised iron oxide-gold nanocomposite comprising the complexation of iron oxide nanoparticles, gold nanoparticles, ethylenediaminetetraacetic acid, polyethyleneimine, and 2,3,5,-triphenyl tetrazolium chloride (TTC) with number NG/PT/NC/O/2025/18855. These nanosentinels are incredibly sensitive, detecting as few as 2 bacterial cells per millilitre, and can be deployed on simple paper strips for rapid, on-site use.

The four patents contained an academic capacity building component that led to the award of MSc and PhD degrees under my supervision in the Department of Microbiology at the Obafemi Awolowo University to Drs. Oluwafemi B. Daramola and Richard K. Omole, who are now academic staff members at the Osun State University, Osogbo, Osun State.

V. THE WAY FORWARD: A PACT WITH THE MICROBIAL WORLD

One Health Approach

The health of humans, animals, and the environment is inextricably linked through a continuous cycle of microbial exchange and AMR. The same resistant genes found in hospital pathogens are present in community-acquired infections, fish ponds, and other environmental sites. To address this, the following interconnected actions are critically needed. In terms of surveillance, I recommend that a national One Health surveillance network that genetically tracks resistant pathogens and resistance genes across human clinics, veterinary settings, agricultural sites (like fish ponds and fermentation yards), and water sources should be established. This will allow for early warning of emerging threats and source attribution for outbreaks, moving from reactive to proactive containment. With respect to stewardship, a strict ban on the non-prescription sale of antibiotics for human and animal use should be enforced in Nigeria. Concurrently, the use of rapid, affordable diagnostic tests at the point-of-care to guide appropriate antibiotic prescribing should be invested in and promoted. This will preserve the efficacy of life-saving drugs.

As regards sanitation, I recommend that regulations to protect water sources (like community wells and aquaculture ponds) from faecal and industrial runoff should be implemented and enforced. Public health campaigns should be launched while providing adequate support for artisanal food processors to adopt safe waste disposal methods. Securing these critical nodes in the environment-food-water nexus is fundamental to breaking the cycle of infection that undermines both food security and human health. In addition, we must accelerate the pipeline for novel antimicrobials and alternative therapies, for our current arsenal is being systematically

dismantled. It is of utmost importance to note that microbes possess the ‘codes’ to unlock the armouries for new medicines, cleanse the earth, grow more food and sustain global systems.

Integrating Biorisk Management into Microbial Science Education

Mr. Vice-Chancellor Sir, permit me to give a short narrative of my personal experience with a laboratory- acquired infection (LAI). During my doctoral research, working on AMR *S. aureus* isolated from the hospital and community, I had a LAI caused by *S. aureus* that took 12 months to treat after several medical interventions. I was lucky to have survived this infection but others might not be that lucky. My stumbling into biosafety and biosecurity is not by chance but from this real-life encounter. Biosafety is the prevention of accidental exposure to pathogens, while Biosecurity is the prevention of intentional misuse of pathogens. Both are the core components of Biorisk Management.

Microbial science does not exist in a vacuum; it is deeply intertwined with the community. In regions where infectious diseases and antimicrobial resistance (AMR) are prevalent, the laboratory acts as a sentinel. In the modern laboratory landscape, technical proficiency in isolation and characterisation is no longer sufficient. Therefore, we must shift our educational paradigm from how to handle microbes to how to manage the risks they pose. The teaching of microbial science without biorisk management (BRM) is like teaching someone to drive a high-performance vehicle without mentioning the brakes. It is not just about safety; it is about professional competence. As we face global challenges from emerging zoonotic threats, pandemics, and the silent crawl of antimicrobial resistance, the laboratory is no longer an isolated room but a node in a global network of health and security.

The reality is that technical skills must be matched by risk-management skills. To foster a resilient culture of biosafety and biosecurity it is recommended that institutions must replace reactive compliance-based training with a 'cradle- to- grave' educational framework that embeds biorisk management into every stage of a scientist's development from undergraduate studies to laboratory leadership. This approach weaves the pillars of risk assessment, mitigation and performance directly into existing life science curricula through practical, scenario-based problem-solving and peer audits. This framework transforms responsible science into an intuitive lifelong professional identity capable of adapting to rapidly evolving biotechnologies by cultivating a 'just culture' that encourages open reporting of near misses and prioritises proactive bioethics. In fact, embedding BRM into Microbial Science curricula is a fundamental pillar of scientific excellence. It ensures that as we listen to what microbes speak, we are prepared to respond safely, securely, and ethically.

VI. CONCLUSION: AN ETERNAL CONVERSATION

This brings me to the core philosophical shift embedded in my title. "When Microbes Speak, the world Listens" implies a move away from the paradigm of conquest (Man versus Microbe) towards one of conversation and understanding. We need to move from a wartime footing to a diplomatic one. We are deeply embedded participants in a microbial world. We evolved with them, because of them. Our health, our environment, and our very future depend on the quality of this ongoing dialogue. My research, along with that of my brilliant colleagues and students here at Obafemi Awolowo University, Ile-Ife, Nigeria and around the world, is dedicated to deepening this conversation. We are developing sharper tools to listen. We are striving to understand the nuances of dialect in different environments. We are exploring how to intervene

thoughtfully, respectfully, and effectively when the conversation turns harmful. The microbes are speaking. They have always been speaking. It is time we listen; with humility, with curiosity, and with the unwavering commitment to translate their whispers into knowledge that heals our bodies, protects our planet, and illuminates the fundamental processes of life itself. In their speech lies the health of our children, the fertility of our soils, the clarity of our waters, and the resilience of our future. I close with three imperatives: look at the microscopic world with renewed wonder; listen to the message they carry for our survival; and leap into a future where we lead with science, biosafety, and biosecurity.

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