OPEN ACCESS

Orapuh Journal

REVIEW ARTICLE

Journal of Oral & Public Health

Challenges of antimicrobial resistance in sub-Saharan Africa: The past, present, and future perspectives

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ARTICLE INFO

Received: *12 April 2024*
Accepted: *09 May 2024*
Published: *11 May 2024*

Keywords:
Antimicrobial, global burden, infections, resistance, sub-Sahara

Peer-Review: *Externally peer-reviewed*

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To cite:
Elijah, O. B., Umukoro, E. K., Moke, E. G., Igben, V. J. O., Arighwrode, O., Onakpoya, E. E., Dennis-Eboh, U., Ekuerhare, B. E. (2024). Challenges of antimicrobial resistance in sub-Saharan Africa: The past, present, and future perspectives. *Orapuh Journal, 5*(2), e1120. https://dx.doi.org/10.4314/orapj.v5i2.20

ISSN: *2644-3740*

Published by Orapuh, Inc. (info@orapuh.org)

Editor-in-Chief: Prof. V. E. Adamu
Engelhardt School of Global Health & Bioethics,
Euclid University (Pôle Universitaire Euclide)

ABSTRACT

Infectious diseases continue to be a major global problem in public health, accounting for millions of fatalities annually, despite a century of frequently successful preventative and control efforts. Antimicrobial resistance (AMR) and the appearance of novel diseases are both consequences of the rapid pace at which society, technology, and microbes are changing. It is projected that AMR was responsible for the deaths of 700,000 people around the world in 2014, making it one of the most significant threats to the world's public health. This essay points to the challenges of antimicrobial resistance in sub-Saharan Africa and its prospects. An online search was done on relevant published studies in PubMed, Scopus, Embase, and ResearchGate from the period 1992 to 2023, of which 61 were adapted for this article. The sub-Saharan Africa region, despite being the worst hit when it comes to infectious disease and, by proxy, antimicrobial resistance, can win the war in the long run.

INTRODUCTION

There have been three distinct periods in the evolution of bacterial infectious diseases: before the discovery of antibiotics, during their widespread use, and after the

establishment of antibiotic resistance. Because the most potent antibiotic classes are saved for use as a last resort in therapy when confronting a bacterial infection, this creates a risky but necessary situation for the patient. However, bacteria already possess mechanisms that render these classes ineffective (Balsalobre et al., 2014).

Infectious diseases continue to be a major global problem in public health, accounting for millions of fatalities annually, despite a century of frequently successful preventative and control efforts (Bloom & Cadarette, 2019; Omo-Aghoja et al., 2021; Baker et al., 2022; Zhang et al., 2023). Antimicrobial resistance and the appearance of novel diseases are both consequences of the rapid pace at which society, technology, and microbes are changing (Aslam et al., 2018; Antimicrobial Resistance Collaborators, 2022; Nwobodo et al., 2022). In the twenty-first century, food-borne illness and antibiotic resistance have become major issues (Cohen, 2000). Despite progress, infectious diseases continue to account for a disproportionately high number of fatalities (69%) in sub-Saharan Africa (SSA) (Young et al., 2009).

The discovery of effective antimicrobials ranks among medicine's greatest achievements of the last century (Sengupta et al, 2013). Total global use of antibiotics climbed by 65% between 2000 and 2015, from 21.1 to 34.8 billion daily specified doses, and is expected to increase even more by 2030 (Klein et al., 2018). Growing demand from low- and middle-income countries (LMIC) consumers was the primary factor in the expansion. Antibiotic use in many LMICs has caught up to, and in some cases even surpassed, that in high-income nations due to rising economies and improved access to medications (Belachew et al., 2021). Antibiotic use is on the rise across the board, but in Sub-Saharan Africa (SSA), an area with one of the greatest infectious disease burdens in the world, this trend may be even more pronounced than in other LMICs (Belachew et al., 2021). The close link between antibiotic overuse and the rise of antimicrobial resistance (AMR) has made the issue of antibiotic misuse a major public health concern (Belachew et al., 2021).

Antimicrobial resistance (AMR) is characterized as the capacity of microorganisms to persist and remain viable in the presence of antimicrobial agents (Abushaheen et al., 2020). The proliferation of antimicrobial resistance, the escalation of bacterial resistance to various antibiotics that are crucial for human pathogen management, and the dissemination of resistance from the relatively confined setting of medical facilities to the general populace, are increasingly recognized as a menace to the well-being of the public. The employment of antibiotics, regardless of whether it is for human, animal, plant, or food processing technology purposes, possesses the capacity to induce bacterial resistance at a certain juncture. Despite the increasing number of publications, there remains limited knowledge regarding the varying usage conditions that favour the preferential selection or limited selection of antibiotic-resistant bacteria. Once resistance has been established, it is not constrained by the boundaries of distinct ecological settings or nations (Acar & Rostel, 2001). It is projected that AMR was responsible for the deaths of 700,000 people around the world in 2014, making it one of the most significant threats to the world's public health. In addition to this, it has been anticipated that the number of deaths that can be attributed to it will reach 10 million by the year 2050 if actions are not taken to combat it (Sekyere & Asante, 2018).

In this review, an online search was done on relevant published studies in PubMed, Scopus, Embase, and ResearchGate from the period 1992 to 2023, of which 61 were adapted for this article. The keywords that directed our literature search were antimicrobial resistance, chemotherapy, sub-Saharan Africa, and bacterial infections.

CHALLENGES OF AMR IN SUB-SAHARAN AFRICA

The sub-Saharan region of the African continent refers to the geographical area located to the south of the Sahara Desert. The region comprises nations from Eastern, Western, Southern, and Central Africa. Sub-Saharan Africa is comprised of countries situated within this geographical region or those that have a portion of their land situated within this region. This geographic area, constituting a significant portion of the African continent, is widely acknowledged to carry the most substantial load of communicable illnesses on a worldwide scale. According to a study recently published in the Lancet, bacterial antimicrobial resistance (AMR) was responsible for an estimated 1.27 million deaths worldwide in 2019. The highest incidence of AMR-related deaths was observed in western sub-Saharan Africa, while Australasia had the

lowest number of deaths attributed to AMR (Godman et al., 2022).

Antimicrobial resistance (AMR) has had a significant negative impact on the prevalence of infectious diseases all over the world, with Sub-Saharan Africa being particularly hard hit. The World Health Organization (WHO) has classified it as a significant global health concern of the 21st century. In the year 2019, the sub-Saharan Africa (SSA) region exhibited the highest mortality rate (23.5 deaths per 100,000) which could be attributed to antimicrobial resistance (AMR) in comparison to other regions (Kariuki et al., 2022).

The impediment to antibiotic efficacy in healthcare is attributed to bacterial resistance to antibiotics, which is substantiated by substantial evidence indicating that the inappropriate use of antibiotics will ultimately lead to resistance development. Insufficient access to effective antibiotics diminishes the ability to prevent and treat health conditions that compromise immunity, such as HIV, cancer, surgical procedures, and diabetes (Ndihokubwayo et al., 2013).

One additional challenge pertains to the economic and financial implications imposed on individuals afflicted with infections caused by microorganisms that have acquired resistance to the antimicrobial agents employed in their therapy. Research conducted in nations with abundant resources has indicated that individuals afflicted with antibiotic-resistant bacterial infections exhibit elevated mortality rates, lengthier hospital stays, and increased healthcare expenditures in comparison to those with antibiotic-susceptible infections (Kariuki & Dougan, 2014).

Insufficient awareness is a significant obstacle to addressing the problem of antimicrobial resistance in the sub-Saharan African region. Residents who lack knowledge about antimicrobial stewardship and resistance, and the potential negative impact on future therapeutic outcomes, may engage in practices that contribute to the development of antimicrobial resistance. The study conducted by Babatola and co-workers in 2021 investigated the prescribing behaviour, knowledge, and perception of antimicrobial resistance and stewardship programs among physicians in Nigerian hospitals (Babatola et al., 2021). The findings revealed that a mere 28.2% of respondents, specifically 91 individuals, had prior knowledge of antibiotic stewardship (Babatola et al., 2021). In 2020, a nationwide survey was conducted in Nigeria to assess the level of public awareness regarding antimicrobial resistance, which involved the collection of samples from one state in each of the six geo-political zones in the country (Chukwu et al., 2020). Among the 482 participants who took part in this survey, it was found that while 272 (56.5%) of them were acquainted with the concept of "antibiotic resistance", only 40 (8.3%) demonstrated a satisfactory level of understanding of AMR (Chukwu et al., 2020).

Despite advancements in the collection and utilization of antimicrobial resistance (AMR) data about tuberculosis, HIV/AIDS, and malaria, there are still obstacles that need to be addressed. The primary obstacles include the absence of a comprehensive policy and plan to tackle antimicrobial resistance (AMR), inadequate regulatory capacity for medicines, and the prevalence of substandard or counterfeit antimicrobials. Additionally, there is a dearth of AMR surveillance strategies, insufficient laboratory capacity for AMR testing and reporting, a shortage of essential laboratory reagents and consumables, and limited quality assurance and control protocols. Numerous countries in the African Region encounter difficulties in safeguarding their populations against hazardous and substandard/counterfeit pharmaceuticals owing to resource constraints and the arduous task of overseeing medicine supply systems both domestically and internationally. Several African nations have failed to implement the prohibition on the utilization of oral artemisinin monotherapies for the management of uncomplicated malaria. This poses a significant threat to the advancement of artemisinin-based combination therapies (ACTs) due to the potential development of resistance (Ndihokubwayo et al., 2013).

FACTORS CONTRIBUTING TO THE PREVALENCE OF AMR IN SUB-SAHARAN AFRICA

The discovery of antimicrobial drugs is widely regarded as one of the most important advances made in contemporary medicine over the last 100 years (Sengupta et al., 2013). On the other hand, the sub-Saharan African region is home to several unusual elements that have emerged as significant contributors to the region's steadily increasing frequency of antibiotic resistance.

One of the challenges faced in the region pertains to the scarcity of dependable laboratories and research centres. Therapeutic protocols that rely on knowledge of the microbial cause and the pathogen's susceptibility to antimicrobial agents direct the empirical treatment of life-threatening infections. Tailoring therapy in the sub-Saharan African region is often unfeasible due to inadequate, reliable laboratory facilities with external quality assurance or collaborative surveillance, resulting in insufficient data about local susceptibility (Williams et al., 2018).

The pharmaceutical market in the region is inundated with substandard and counterfeit antimicrobial agents, posing a significant challenge. The issue stems from deficient regulatory frameworks, restricted domestic production capabilities, and insufficient quality control measures for antimicrobial agents. Additionally, there are apprehensions regarding the availability of skilled personnel and the level of collaboration among professional cohorts (Godman et al., 2022).

The prevalence of antimicrobial resistance in sub-Saharan Africa is exacerbated by the frequent prescription and dispensation of antibiotics, as well as inadequate diagnostic resources, inconsistent enforcement of regulations regarding non-prescription dispensation of antimicrobials, and the uneven availability of quality healthcare services (Williams et al., 2018; Moke et al., 2019; Godman et al., 2022).

MECHANISMS BY WHICH MICRO-ORGANISMS ACHIEVE AMR

There exist various antimicrobial agents, including antibiotics, disinfectants, and food preservatives, that are effective in combating microorganisms by impeding their growth, hindering their proliferation, or causing the death of the organisms (Abushaheen et al., 2020). The extended and extensive utilization of antibiotics has led to the emergence of antimicrobial resistance (AMR) among bacteria. The phenomenon of natural genetic evolution leading to antibiotic resistance has attained paradoxical proportions in the contemporary era. This has resulted in the emergence of antimicrobial resistance (AMR) as a significant health concern with potentially global ramifications, thereby underscoring the imperative of timely intervention (Abushaheen et al., 2020). Several mechanisms have been identified through which microorganisms acquire resistance. These include:

1. Target site modification

Certain strains of bacteria exhibit resistance to antimicrobial agents by altering their binding sites, thereby evading detection. The development of resistance to penicillin involves the mutation of the gene responsible for encoding penicillin-binding proteins (PBPs). These enzymes are typically located on the cytoplasmic membrane of bacterial cell walls and play a crucial role in the assembly and control of the final stages of cell wall building. As a result of this mutation, unique penicillin-binding proteins are expressed, such as the dominant PBP2a in *S. aureus*, which differs from the native PBPs (PBP1-4). This is particularly relevant in the context of MRSA. PBP2a exhibits reduced binding affinity towards β-lactam antibiotics and serves as a replacement for other PBPs, thereby facilitating the survival of *S. aureus* in the face of elevated levels of β-lactam drugs such as methicillin that target cell wall biosynthesis (Pucci & Dougherty, 2002; Santajit & Indrawattana, 2016). The peptidoglycan precursors' acyl-D-alanyl-D-alanine (acyl D-Ala-D-Ala) residues are targeted by glycopeptides to inhibit bacterial cell wall synthesis in methicillin-resistant Gram-positive organisms. The resistance of *Escherichia faecium* and *Escherichia faecalis* to glycopeptides such as vancomycin and teicoplanin can be enhanced by altering the peptidoglycan cross-link target from D-Ala-D-Ala to D-Ala-D-Lac or D-Ala-D-Ser. This alteration is facilitated by a complex gene cluster comprising Van-A, Van-B, Van-D, Van-C, Van-E, and Van-G (Giedraitiene et al., 2011; Santajit & Indrawattana, 2016).

2. Reduced intracellular drug accumulation

The equilibrium between a microorganism's ability to take in antibiotics and rid itself of them is a major factor in determining how responsive the organism will be to a particular treatment (Santajit & Indrawattana, 2016). Therefore, one technique that bacteria adopt to acquire resistance to antibiotics is to lessen the amount of the drug that can pass through the bacterial cell membrane.

Some of the mechanisms that bacteria use to accomplish this goal are as follows:

(1) a decrease in the number of protein channels (porins) on the bacterial outer membrane, which in

turn reduces the amount of drug that can enter the bacteria.

(2) the existence of efflux pumps, which in turn reduces the amount of drug that can collect within the cells.

Porins are a type of protein that facilitates the transfer of hydrophilic substances, including antibiotics, across the bacterial cell membrane. These proteins create channels, also referred to as water-filled pores, on the outer membrane of bacteria (Nikaido, 1992). Consequently, a decrease in the quantity of porins located in the outer membrane of bacteria leads to a reduction in the influx of drugs into the bacterial cell, thereby promoting resistance. *Pseudomonas aeruginosa* serves as an illustration, as a decline in the quantity of OprD porin protein in *P. aeruginosa* leads to a decline in drug influx into the cell, thereby enabling the bacterium to acquire resistance to imipenem (Fukuoka et al., 1993).

Proteins located on the membrane that facilitate the export of antibiotics from the cell and uphold their reduced intracellular levels are commonly referred to as "efflux pumps" (Giedraitiene et al., 2011). Bacterial strains that express these proteins exhibit an elevated capacity to eliminate antibiotics from the intracellular compartment (or the inter-membrane space in Gram-negative bacteria) by actively extruding the drug molecules from the cell at a rapid pace. Consequently, the drug concentrations fail to attain a threshold level that can trigger a bactericidal or bacteriostatic effect (Santajit & Indrawattana, 2016). Multidrug resistance is often attributed to the efficient pumping of a wide range of antibiotics by most efflux pumps, which are known to be multidrug transporters (Sun et al., 2014). Five distinct superfamilies of efflux pumps have been identified and characterized. These comprise:

- The ATP-binding cassette (ABC) family
- The small multidrug resistance family
- The major facilitator's family
- The resistance-nodulation-division (RND) family
- The multidrug and toxic compound extrusion family.

Two of these efflux pumps, namely MexAB-OprM and MexCD-OprJ, are accountable for resistance to at least three primary classes of antibiotics. These antibiotic classes include carbapenems, fluoroquinolones, and aminoglycosides. *P. aeruginosa* strains that overexpress the MexXY-OprM gene are resistant to aminoglycosides, fluoroquinolones, and some antipseudomonal cephalosporins, according to several studies. In addition to this, a significant number of clinical *P. aeruginosa* isolates also exhibit MexCD-OprJ and MexEF-OprN (Schweizer, 2003; Vaez et al., 2014; Santajit & Indrawattana, 2016). Additionally, it has been observed that the prevalence of strains that overproduce these efflux pumps has increased in clinical isolates of both *Enterobacter aerogenes* and *K. pneumoniae*. The overexpression of the AcrAB efflux pump in conjunction with the decreased production of porins distinguishes the imipenem-resistant *E. aerogenes* MDR strains. These bacteria have an efflux pump that also expels other antibiotics that are not connected, such as fluoroquinolones, tetracycline, and chloramphenicol (Nikaido & Pagès, 2012).

3. Formation of biofilm

Biofilms are intricate assemblages of microorganisms that reside as a thin stratum on biotic or abiotic surfaces, embedded within a framework of extracellular polymeric substances that are synthesized by the biofilms. The microorganisms present in the biofilm exhibit interactions with both the surrounding environment and with one another. The primary constituent of the matrix is secreted extracellular polymeric substances, which primarily comprise polysaccharides, proteins, lipids, and extracellular DNA from microorganisms (Sharma et al., 2014; Santajit & Indrawattana, 2016). The process of biofilm formation involves three fundamental steps. The initial stage involves adhesion, whereby cells contact a surface and subsequently attach to the designated location. The subsequent stage involves the progression and development of microorganisms, whereby they initiate the production of exopolysaccharide that forms the matrix, and subsequently advance from micro colonies to multi-layered cell clusters. The ultimate phase in this process is characterized by detachment, which can be categorized into two distinct forms: active and passive. The process of active detachment is instigated by the bacteria themselves, through mechanisms such as quorum sensing and enzymatic degradation of the biofilm matrix. Passive detachment, on the other hand, is a result of external factors

such as fluid shear, scraping, and human intervention (Laverty et al., 2014).

One could posit that the primary factors contributing to antimicrobial resistance are not the conventional mechanisms of drug resistance, such as target site modification, efflux pumps, or enzymatic degradation. The biofilm matrix is hypothesized to serve as a physical and biochemical barrier that creates an environment conducive to the reduction of drug efficacy. This may be attributed to factors such as reduced oxygen levels, altered pH, limited water availability, and increased levels of CO_2. Eliminating bacteria through conventional antibiotics is challenging under such circumstances. In addition, in instances of limited nutrient availability, bacteria may develop a heightened tolerance to antibiotics. The complete restoration of susceptibility in bacteria extracted from the biofilms and cultured in broth suggests that phenotypic rather than genotypic factors may be to blame for the observed increased antibiotic resistance of cells located in the deeper strata of a biofilm. The prevalent microorganisms detected in biofilms within healthcare facilities are *S. aureus, P. aeruginosa, A. baumannii*, and *K. pneumonia* (Del Pozo & Patel, 2007; Høiby et al., 2010).

THE PAST

History of Antibiotics

In the 19th century, pneumonia, tuberculosis, diarrhoea, and diphtheria were widely recognized as primary contributors to mortality among both children and adults (Zaffiri et al., 2012). Although Semmelweis (1818–1865) and Lister (1827–1922) introduced antisepsis in 1867, hospital and post-surgical infections caused by gram-positive bacteria continued to be a prevalent cause of mortality. Until the implementation of antimicrobial chemotherapy, which became instrumental in reducing surgical infection rates from 40% to 2% (Zaffiri et al., 2012).

To combat *Treponema pallidum*, the bacterium that causes syphilis, Paul Ehrlich introduced the arsenic-based medication Salvarsan in 1909. The discovery established the fundamental basis for the subsequent advancement of antimicrobial agents. The discovery of penicillin by Alexander Flemming in 1928, however, marked a significant milestone in the development of antimicrobial drugs. This drug became available for clinical use in 1946 and remains in use today as a therapeutic agent. The discovery of penicillin was considered a remarkable feat of modern science, as it demonstrated the ability to effectively treat a wide range of infections caused by staphylococci and streptococci. Considering the reality that these two pathogens were responsible for the highest incidence of documented infections then, it is understandable why the revelation of this discovery brought about a sense of relief (Kourkouta et al., 2018).

Origin/History of Antimicrobial Resistance

The precise genesis of genes that confer antimicrobial resistance remains uncertain. However, it is widely posited that environmental microorganisms, including those that naturally synthesize antimicrobial agents, represent significant primary reservoirs. It has been hypothesized that the resistance gene was transferred from the antibiotic-producing organisms to the surrounding microorganisms, enabling them to survive and flourish in a hostile environment. The theory is buttressed by the significant genetic and biochemical resemblances observed between resistance determinants originating from antibiotic-producing organisms and certain crucial and prevalent resistance genes detected in both gram-negative and gram-positive bacteria (Aarestrup, 2005).

The phenomenon of antimicrobial resistance can be viewed through an evolutionary lens, whereby continued exposure to antimicrobial agents leads to the natural selection of microorganisms that possess resistance traits (Silbergeld et al, 2008). Bacterial organisms have undergone evolutionary adaptations in response to naturally occurring antimicrobial agents. Antimicrobial agents commonly utilized in clinical medicine are derivatives of substances synthesized by various organisms, including Streptomyces, Bacillus, Penicillium, and Cephalosporin. The acceleration of global resistance development has been attributed to the exploitation of these agents by humans. The significance of healthcare settings in the proliferation and dissemination of resistant bacteria is evident. However, the identification of many resistant infections in a hospital does not necessarily indicate that the origin of resistance is exclusive to the 4 walls of a hospital. The significance of community origins as sources of pathogen transmission in the clinical setting is increasingly being acknowledged. The study of methicillin-resistant Staphylococcus aureus (MRSA) provides a

paradigm for reorienting research efforts toward the origins of emerging infections. This shift in focus highlights the significance of exploring non-hospital factors that contribute to antimicrobial resistance (Silbergeld et al., 2008).

An illustrative instance pertains to the correlation between the utilization of antimicrobial agents in the field of animal husbandry, and the emergence of antimicrobial resistance. Over 50% of antimicrobial utilization is linked to the manufacturing of livestock for food. Globally, significant quantities of antimicrobial agents are utilized to promote growth and prophylaxis, with comparatively lesser amounts being used for therapeutic purposes (Aarestrup, 1999). The utilization of antimicrobial agents has the potential to promote the proliferation of resistance genes in non-pathogenic bacteria. These genes may subsequently be transmitted to various pathogenic bacterial species, thereby conferring acquired resistance (Aarestrup, 1999).

The Fight Against Antimicrobial Resistance

Historically, the primary focus of combating multi-resistant microorganisms has been directed toward gram-positive bacteria, with pharmaceutical companies investing in the development of novel drugs to combat these organisms. Sadly, the escalating issue of gram-negative resistance has not kept pace with the identification of antibiotics for managing infections caused by these microorganisms, leading to a significant proportion of intractable infections and the emergence of a disconcerting outlook (Balsalobre et al., 2014).

PRESENT APPROACHES

Infections that are associated with antibacterial resistance are known to increase morbidity, mortality, and the expense of treatment, and they may also place individuals in the community at a higher risk of contracting an infection (Kariuki & Dougan, 2014). Resistance to first-line antibacterial medicines is typically addressed using second- and third-line antibacterial drugs in high-income nations where the burden of infectious illnesses is generally minor. However, individuals with antibacterial-resistant infections might not be able to get or afford effective second-line treatments in underdeveloped nations with a high burden of infectious diseases. Poor sanitation, unstable water sources, civil unrest, and an increase in the population of immune-compromised persons, such as those living with HIV, in Sub-Saharan Africa (SSA), all contribute to the rapid spread of infections with increased resistance. Because of the insufficient resources available for disease detection and monitoring, the burden of illnesses caused by treatable bacterial infections, their unique causes, and the knowledge of antibacterial resistance are not well understood throughout the majority of SSA. As a result, the ability to lessen the effects of these illnesses is significantly restricted (Kariuki & Dougan, 2014).

Joint External Evaluations (JEEs) are an effective tool for assessing a nation's capacity to manage global health hazards, as they offer a standardized set of metrics for benchmarking all countries. In 2020, a study was conducted to assess the level of antimicrobial resistance (AMR) readiness in sub-Saharan African countries. The study involved a comparison of the Joint External Evaluation (JEE) scores of various countries in the region, with a focus on identifying the position of AMR in other JEE categories. The findings of the study revealed that although significant efforts are required to align AMR with other areas such as immunization, there exist countries and regions that have successfully executed AMR control initiatives (Elton et al., 2020). The difference between the mean SSA AMR preparedness score and the SSA JEE preparedness score shows that most SSA countries have not given AMR significant priority in comparison to other sub-areas. The absence of an AMR National Action Plan in most countries indicates a potential deficiency in a targeted and cohesive approach, despite some countries reporting efforts to develop and execute such plans, which represents a favourable advancement in the battle against AMR. The category of 'Antimicrobial Stewardship' displays the lowest mean score among the AMR categories, indicating that it requires the most significant improvement in JEE score to achieve alignment with the other categories. Directing attention towards antimicrobial stewardship has the potential to enhance the AMR preparedness ratings of nations and align AMR with other sub-domains, such as immunization. One could posit that the magnitude of the issue of antimicrobial resistance (AMR) may not be commensurate with that of other public health concerns. However, the absence of a comprehensive system of national surveillance makes it arduous to accurately ascertain the actual scope of the issue (Elton et al., 2020).

FUTURE PERSPECTIVES

In light of the aforementioned challenges about the factors believed to be responsible for the substantial burden of antimicrobial resistance (AMR) in the sub-Saharan African region, the implementation of the following measures, policies, and actions has the potential to effectively combat and establish a favourable environment for success against AMR in the sub-Saharan African region and globally.

Development and establishment of comprehensive national and regional policies and plans to fight, prevent, and manage AMR are just one of the many possible ways to try and curb the menace of AMR in the sub-Saharan Africa region (Leung et al., 2011; WHO, 2011; Ndihokubwayo et al., 2013; Chukwu et al, 2020). While these as well as other measures such as building clinical laboratory capacity and improving AMR surveillance would contribute greatly to improving the outcome of the fight against AMR in the region, the need exists for looking more into other scientifically inclined measures in a bid to achieve this feat (Gulumbe et al., 2022).

Research studies have highlighted scientific approaches that could contribute to the fight against AMR; one of those being the use of technology to facilitate drug development and discovery (Atanosov et al., 2012; Ayon, 2023). This entails exploring and exploiting technology in aiding the identification of new or novel sources of naturally occurring antibiotics. An example of this is the *iChip platform* which facilitates the screening of natural products from previously unculturable soil organisms by mimicking their native environment, thereby resulting in the development of antibiotic compound(s) with novel mechanisms of action (Atanosov et al., 2012; Ling et al., 2015; Marston et al., 2016; Dzobo, 2022; Ayon, 2023).

Another scientific approach that could contribute to the fight against AMR is the development of vaccines that are capable of conferring immunity against bacterial infections and/or diseases. Although according to the study, this is still in the works, it however looks promising as it can deployed among target populations that are at risk of infections, for prophylactic use (Peltola, 2000; Dagan & Klugman, 2008; Marston et al., 2016; Alghamdi, 2021; Micoli et al., 2021).

Manipulating microbial communities to counteract resistant infections is yet another promising scientific strategy that could prove effective in the fight against AMR (Fabijan et al., 2023; Shree et al., 2023). It involves the use of bacteriophages and viruses that are highly pathogen-specific in their "cidal" action, to treat bacterial infections. An example is the use of *Bdellovibrio* and *Micavibrio* bacteria that parasitize gram-negative pathogens to treat infections caused by these pathogens (Marston et al., 2016; Bonfiglio et al., 2020; Bratanis et al., 2020).

Exploiting and targeting factors such as toxins, secretion systems, adhesins, iron acquisition systems, biofilm formation, quorum-sensing pathways, and others that contribute to pathogen's virulence, as novel therapeutic targets, could help combat AMR; as it will reduce the pathogenicity of the pathogen, allow enough time for the host's cell to clear the bacterial infection from its system, while in the same breath preserving the host's microbiota (Marston et al., 2016; Annunziato, 2019; Murugaiyan et al., 2022).

CONCLUSIONS

The sub-Saharan Africa region, despite being the worst hit when it comes to infectious disease and, by proxy, antimicrobial resistance, can win the war in the long run. By implementing the various policies as discussed above, among other proffered solutions and scientific strategies, the huge burden of morbidity and mortality borne by the region on account of AMR can be drastically reduced to the barest minimum.

Multi-resistant bacteria pose a serious threat to the general public's health, necessitating a coordinated and comprehensive response. This reaction must not exclude veterinary professionals, agricultural experts, or members of the media. Feeding the network of unified information with the data that is available from all of the participants' fields allows us to reduce selective pressure, surpass challenges in the development of new drugs, implement an effective management therapy, and redirect the additional costs to an alternative program that supports resistance, which means that in the future we may be able to keep antimicrobial susceptibility trends at a level that we can cope with.

Acknowledgments: We would like to thank all the authors whose works have enriched this study.

Author contribution statement: EOB, UEK, MEG, IVJ, AO, OEE, DEU, and EBE substantially contributed to the conception, design, drafting, interpretation of the relevant literature, and analysis of the review article of the work. EOB, UEK, MEG, and IVJ have been involved in writing and acquisition of data or revising the review article for intellectual content. All authors agreed and confirmed the manuscript for publication.

Ethical Approval: Not applicable

Conflicts of Interest: None declared.

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