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Antimicrobial Resistance in Nigeria and the One-Health Approach to Antimicrobial Stewardship: A Review

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ABSTRACT

Antimicrobial resistance (AMR) is the ability of microorganisms, such as bacteria, viruses, fungi, and parasites, to survive, thrive and even proliferate in the presence of chemical agents meant to destroy or slow down their rate of growth. According to a study conducted in 2022, approximately 5 million deaths occurred globally that are related to AMR. This is an astronomical increase from 1.27 million AMR related deaths reported by a study conducted in 2019. By 2050, this number has been projected to rise to 10,000,000 deaths annually. Since AMR has been seen to be an ecological problem it calls for a cooperative, interdisciplinary strategy including experts in environmental, animal, and human health called the One Health strategy. The misuse of antibiotics is clearly linked as a causal factor for the evolution of resistance. Modern medicine has even inadvertently accelerated this change even further by eradicating competitor organisms which were drug-susceptible, thus allowing resistant microorganisms to multiply and spread via natural selection. AMR is also significantly aided by the improper prescription of antibiotics. AMR is a serious public health issue globally an in Nigeria. Current statistics suggest that without taking measured steps the spectrum of antibiotics which will be available for treatment of infections will continue to reduce. Antimicrobial stewardship along with the one health approach are strategies which will help to ensure that AMR can be brought under control.

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Introduction

The World Health Organization (WHO) has identified antimicrobial resistance (AMR) as one of the top 10 worldwide public health challenges that humanity faces [1]. AMR is a public health concern that affects people, animals, and the environment. Antimicrobial resistance is the ability of microorganisms, such as bacteria, viruses, fungi, and parasites, to survive, thrive and even proliferate in the presence of chemical agents meant to destroy or slow down their rate of growth [2].

Antimicrobial resistant microorganisms cause infections are not only hard to cure, but they also carry a constant risk of serious prolonged sickness and possibly even death. Antibiotics, antifungals, antivirals, disinfectants, and food preservatives are a few examples of antimicrobial agents that many microorganisms have developed resistance to [3]. More often used than any other group of antimicrobials, are antibiotics which are a class of antimicrobials used primarily to treat bacterial infections [4].

AMR has a detrimental effect on the world economy as it causes increase in medical expenses, loss of productive man hours to illness and decrease in quality of life of victims. Moreover, treating drug-resistant infections may become very challenging and perhaps even become incurable. Studies have shown that both natural resistance and exposure to antibiotics contribute to the rise of AMR in microbes [5]. The abuse and misuse of antibiotics by people, in agriculture, clinical and vet medicine, are factors contributing to AMR. Even a simple activity such as animal transportation, if poorly carried out can facilitate the spread of antimicrobial-resistant microbes from animals to humans [5].

According to a recent study conducted in 2022, approximately 5 million deaths occurred globally that are related to AMR. This is an astronomical increase from 1.27 million AMR related deaths reported by a study conducted in 2019. By 2050, this number has been projected to rise to 10,000,000 deaths annually [6]. Recent studies reveal that Sub-Saharan Africa (SSA) and South Asia have the highest rates of AMR-related mortality (23.5 and 21.5 deaths per 100,000, respectively), as compared to other regions as seen in the Global Burden of Disease research. Western SSA had the highest mortality rate worldwide due to AMR, followed by Eastern, Central, and Southern SSA with 27.3 deaths per 100,000 people [7].

In Nigeria, AMR has been found to be directly responsible for 64,500 deaths and to be linked or associated with 263,400 deaths in 2019. Out of 204 nations, Nigeria is ranked as having the 19th-highest age-standardized mortality rate per 100,000 and this rate is linked to AMR (The Burden of Antimicrobial Resistance (AMR) in Nigeria.).

Definition of One Health Approach

Since AMR has been seen to be an ecological problem influenced by interactions between people, animals, and the environment, solving this issue calls for a cooperative, interdisciplinary strategy including experts in environmental, animal, and human health, a One Health strategy is required [9]. The term “One Health approach” refers to this multimodal strategy for combating AMR. One Health is described as “a cooperative endeavour involving

various health science professions, along with their associated disciplines and institutions, collaborating at local, national, and global levels" with the goal of achieving optimal well-being for people, domestic animals, wildlife, plants, and the environment [9]. This is especially important because of the difficulties caused by factors such as the growing human population, changing climate, increasing pollution, and the depletion of Earth's non-renewable resources [10].

Antimicrobial Stewardship (AMS)

Antimicrobial stewardship (AMS) initiatives are important initiatives which are to be used to achieve the one health objective. AMS uses evidence-based, multifaceted approaches to counteract the spread of AMR [11]. These approaches include AMR monitoring, education, and advice to promote prudent antibiotic use and enhance health outcomes. Although there is growing evidence that managing AMR requires a multidisciplinary approach, there is need to implement the usage of One Health and coordination of its initiatives and strategies to address AMR [12]. A recent comprehensive study revealed that coordinated AMS programme implementation strategies and practice are lacking across Africa [13]. As a result, further interventions is needed to enhance AMS nationwide using a multidisciplinary approach.

AMS initiatives were first used in hospital settings over 30 years ago, thus they have been well-established there. The integration of AMS programmes in primary health care (PHC) settings is less well-established due to obstacles such a lack of medical experts and limited treatment resources [14]. This is worrisome because in resource poor settings like SSA where AMR is growing, there is no concerted or coordinated effort for AMS at the primary health care level. The availability of almost any kind and class of antibiotics as an over the counter sale is worrisome and must be curbe [15].

Significance of Antimicrobial Stewardship

The appropriate choice of antimicrobial drugs, doses, delivery methods, and treatment duration are all important aspects of AMS [16]. Proper application of AMS will lower hospital length of stay, adverse medication events (such as antibiotic-associated diarrhoea and kidney toxicity), and other forms of health care expenses. AMS will also drastically slow down the growth and proliferation of multidrug-resistant organisms (MDROs) [12].

It is impossible to have successful AMS without the health and hospital administrators as well as vet professionals working together to identify and provide the required resources for its success. The only way to guarantee the success of AMS is for professionals from the fields of pharmacy, medicine, Infection control (IC), microbiology, public health, vet medicine and information technology to all worked together. The AMS goal is to establish an official, multidisciplinary teams that guarantee the appropriate use of antibiotics within the healthcare system across every level of provision of health care [17].

Interrelationship of Antimicrobial Resistance in Animals, Humans, and the Environment

Disease control measures are implemented when an individual, group or part of a population of humans, plants or animals is infected with a disease [18]. Antimicrobial medications are used to treat, manage, or shield plants, animals, and humans against infections of different types. It should come as no surprise that there is the employ and use of antibiotics for human, animal, and plants in similar ways [19]. For instance, streptomycin is used to treat or prevent infections in all areas of health care, including animal and human medicine as well as plant agriculture. As a result, antimicrobial resistance is a problem for both humans, animals and plants [20].

Unfortunately in Nigeria, there is the reckless and uncontrolled dispensing (at health centres, markets and even public transportation) and use of antimicrobials without the knowledge or input of qualified health professionals [21]. This has been a problem which has been around for a while and has even become exacerbated by recent economic downturns in Nigeria. Health professionals are seeking greener pastures away from the shores of the country and this is putting more pressure on an already belaboured health care system. The effect of all these problems are currently being seen and will worsen if the right steps are not taken.

Mechanisms of Antimicrobial Action

Different antimicrobial agents suppress the growth or eradicate microorganisms in different ways. Understanding the mechanisms by which antimicrobial agents operate is crucial for comprehending the development of AMR. The primary target of numerous antibiotics, including β-lactam and glycopeptides, is this physical barrier between the microorganism especially bacteria and their environment which is the case of bacteria is their cell wall [22]. Antibiotics that prevent the formation of bacterial cell walls include glycopeptides like vancomycin and teicoplanin, as well as β-lactams like penicillins, cephalosporins, carbapenems, and monobactams [23].

β-lactam antibiotics have a structure that is similar to the the D-Ala-D-Ala dipeptide of a newly formed peptidoglycan layer. The β-lactam antibiotic is able to form covalent bonds with serine present on the active sites of bacteria cell wall synthesis and thus hinders the crosslinking of peptidoglycans during cell wall formation. By stopping the formation of this linkage , the microbial cell cannot sustain life and cell death will occur

Another mechanism of action of antimicrobials is the inhibition of protein synthesis. Due to the fact that the bacterial and eukaryotic ribosomes vary structurally, antibiotics are able to block protein synthesis, usually acting on the 30S or 50S subunits of the 70S bacterial ribosome, thereby preventing the bacterial ribosome from synthesising proteins. Cell development is either stopped or slowed down when protein synthesis is inhibited [25].

Tetracyclines, aminoglycosides, and macrolides are able to attach to the 30S subunit of proteins to prevent their production [26]. Upon entering the bacterial cell, these antimicrobial agents attach to the A-site of the ribosome's 30S subunit, causing a switch in translation from intra-helical to extra-helical. This leads to the formation of an erroneous mRNA tRNA pairing, which causes protein synthesis to be mistranslated thereby putting a stop to protein synthesis [26].

In the peptidyl transferase centre (PTC), amino acids are usually linked to produce a poly peptide chain which is usually the 50S subunit of the bacterial ribosome (Tirumalai, et al., 2021). A nascent peptide exit tunnel (NPET), which allows the polypeptide chain to escape from the ribosome is also present in the 50S subunit. Between the NPET and the PTC, the 50S subunit is binded to by chloramphenicol thereby blocking the addition of fresh polypeptides ad ultimately inhibiting the protein synthesis and production process [27].

Antimicrobial agents are also capable of inhibiting DNA synthesis in microbial cells. There are essential enzymes known as topoisomerases are needed for the production of new bacterial DNA in other for a bacteria to divide and proliferate [28]. The absence or inactivation of these enzymes will affect both positive and negative supercoiling, resulting in abnormal DNA structure. This abnormal DNA cannot unwind and replicate to form new DNA. Quinolone antibiotics work by attaching to topoisomerase IV or II, thereby changing the way DNA supercoils [29]. This causes double-stranded DNA to break down and ultimately results in cell death. This is an important mechanism which antibiotics use to destroy or inhibit the growth of bacteria [28].

The biosynthesis route that involves folate formation is another target for antibiotics as eukaryotic cells usually use mechanisms of active transport to absorb folate through DE novo synthesis [30].The class of sulphonamides have been shown to prevent bacteria from using para aminobenzoic acid (PABA) in the manufacturing of folates. Sulphonamides do this by working as competitive inhibitors and consume the folate present in the environment thereby denying bacteria of the use of this folate in their development. Sulphonamides are able to do this because they have a structure which is similar to PABA [31].

Mechanisms that Confer Antimicrobial Resistance in Microbe

Bacteria may display innate, acquired, or adaptive antibiotic resistance. There are many mechanisms that help bacteria to display resistance to many classes of antibiotics. The glycopeptide resistance that Gram-negative bacteria display for instance is as a result of the outer membrane's impermeability inside the bacterial cell envelope is an example of intrinsic resistance [32]. When a previously susceptible bacteria develops a resistance mechanism via mutation or the acquisition of additional genetic material from an external source (horizontal gene transfer), the resistance is referred to as acquired resistance. Three primary pathways are known to be involved in horizontal gene transfer and these pathways include transformation, transduction and conjugation [33].

Role of Genetic Elements in Antimicrobial Resistance in microbe

Transposons, integrons, insertion sequences, and pathogenicity islands (PAIs) are all genetic elements that can contribute to antimicrobial resistance (AMR) in bacterial isolates. There are different mechanisms and processes through which genetic elements are able to affect and confer AMR on bacteria isolates.

Transposons are mobile genetic elements and they move within the genome of bacteria and can also be transferred from bacteria to bacteria by plasmids. Transposons carry genes which encode for resistance and their ability to be transferred to other bacteria helps to propagate AMR [34]. The Tn1546 transposon is an example of a transposon found in vancomycin-resistant Enterococcus faecium (VRE) and carries the vanA gene that confers resistance to vancomycin (Nijhuis, et al., 2021). Tn4401 codes for the blaKPC gene, which confers resistance to carbapenem antibiotics in Klebsiella pneumoniae and Pseudomonas aeruginosa [35]. Tn3 is another transposon coding for genes resistant to β-lactams, aminoglycosides, and trimethoprim [36]. Lastly among the transposons to be discussed Tn916 carried the tet(M) gene, and confers resistance to tetracycline [37].

Integrons are genetic elements which express gene cassettes and allow bacteria to acquire and express resistance genes. Integrons can also be found on plasmids and continue to accumulate multiple resistance genes over time [38]. Class 1 integrons are some of the most common integrons and are found in Escherichia coli and Klebsiella pneumonia [39]. Class 1 integrons have genes that code for resistance to a wide variety of antibiotics such as β-lactams, aminoglycosides, and quinolones. Class two integrons are associated with multidrug resistance and can be found in isolates such as Salmonella spp. and Pseudomonas aeruginosa [40]. Class 3 integrons are not very popular but can still be found in Klebsiella pneumoniae and Enterobacter spp [41]. SXT element is another unique type of integron which is a composite of a transposon and an integrin. SXT element can be found in Vibrio cholerae and confers resistance to antibiotics such as sulfamethoxazole, trimethoprim, and chloramphenicol [31].

Insertion sequences are short segments of DNA which can move around the genome and cause disruptions. Examples of insertion sequences include ISCR1 element which confers resistance on bacteria such as Pseudomonas aeruginosa and Acinetobacter baumanni [42]. Other types of insertion sequences include IS26 which is present in many bacterial populations and IS6110 associated with Mycobacterium tuberculosis [43].

Pathogenicity Islands (PAIs) are large genomic regions which have clusters of virulence genes which play roles in the pathogenicity of bacteria [44]. Example of PAIs include SPI-1 and SPI-2 pathogenicity islands found in Salmonella enterica with genes coding for virulence factors and antibiotic resistance [45]. Vibrio Pathogenicity Island 1 (VPI-1), is another prominent pathogenicity island found in Vibrio cholerae, and contains genes that help in cholera toxin production [46]. The High-Pathogenicity Island (HPI) is another PAI found in Yersinia pestis, and carries genes encoding for the type III secretion system [44].

Mechanisms of Antimicrobial Resistance

There are four main mechanisms of antimicrobial resistance: (1) limiting drug uptake, (2) modifying drug targets, (3) inactivating drugs, and (4) actively expelling drugs. Acquired resistance mechanisms include modifications to drug targets, drug inactivation, and drug efflux. Limiting uptake, drug inactivation, and drug efflux are examples of intrinsic resistance mechanisms.

Limiting Drug Uptake

The limiting of entry of antimicrobial agents into microbial cells is an effective way of conferring resistance. The limiting of drug uptake occurs through many mechanism one of which is the reduction in the permeability of cell membranes. Some bacteria can develop a thicker cell wall and outer membrane which can then act of barriers to the uptake of antimicrobial drugs [47].

Modifying Drug Targets

Another mechanism of AMR involves altering or modifying the molecular targets of antimicrobial drugs, and this renders the drug ineffective. This alteration can be done by genetic mutation Microorganisms may acquire mutations in the genes encoding the drug target, resulting in structural changes that prevent the drug from binding effectively (Abushaheen, et al., 2020). Enzymatic modification is another way theta bacteria can modify drug targets. For example Methicillin-resistant Staphylococcus aureus (MRSA) strains produce a modified penicillin-binding protein (PBP2a) that has reduced affinity for β-lactam antibiotics, such as methicillin, rendering them ineffective in inhibiting cell wall synthesis [48].

Inactivating Drugs

Bacteria develops resistance by producing enzymes which work to inactivate antimicrobial drugs and neutralize them. This is possible by the modification and degradation of the drug molecule. Some bacteria possess enzymes such as β-lactamases that hydrolyze β-lactam antibiotics, rendering them inactive. Extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae hydrolyze β-lactam antibiotics, including penicillins and cephalosporins, thereby rendering them ineffective in treating infections caused by these bacteria [49].

Actively Expelling Drugs

The efflux pumps are critical components of bacterial cells that play a key role in their survival by actively pumping out various toxic compounds, including antibiotics and other antimicrobial agents. These pumps are classified into five main families based on their structure and energy source [50].

- ATP-binding cassette (ABC) family or ABC transporters which utilize energy from ATP hydrolysis to actively pump substrates across the cell membrane (Wang et al., 2021). Examples include the P-glycoprotein (P-gp) in humans which is involved in drug resistance in cancer cells and pumps out chemotherapeutic drugs, such as doxorubicin and paclitaxel [51].

- Multidrug and toxic compound extrusion (MATE) family have MATE transporters that use proton motive force (PMF) generated by the movement of protons across the cell membrane to drive substrate efflux [52]. Examples include NorM in Vibrio parahaemolyticus which confers resistance to multiple antibiotics such as norfloxacin and ethidium bromide [53].

- Small multidrug resistance (SMR) family code for SMR transporters which are small membrane proteins that use the PMF to actively export substrates out of the cell. Examples include the QacA/B in Staphylococcus aureus [54].

- Major facilitator superfamily (MFS) code for MFS transporters and they facilitate the passive transport of substrates across the membrane driven by the electrochemical gradient [55]. Example of the MFS transporters include the tetracycline efflux pump TetA in Escherichia coli which confers resistance to tetracycline antibiotics by actively pumping them out of the cell [56].

- Resistance-nodulation-cell division (RND) family code for RND transporters which utilize the PMF and proton gradient across the cell envelope to drive substrate efflux. Example include the AcrAB-TolC in E. coli which is an RND efflux pump complex involved in resistance to a broad range of antibiotics, including β-lactams, fluoroquinolones, and tetracyclines [57].

Selected Multi-drug Resistant Bacteria of Public Health Interest

Enterococcus

Multidrug resistance has arisen in these organisms from various acquired resistance mechanisms. High levels of resistance to aminoglycosides (by enzymatic breakdown), vancomycin (by modifications in peptidoglycan production; known as VRE), and beta-lactams (by beta-lactamase enzymes and modified binding proteins) have been recorded among strains of Enterococcus sp [58]. For Enterococcus infections ampicillin is still the preferred as a medication with efficacy. However, there are currently few alternatives for treating systemic Enterococcus infections that are showing Multi drug resistance such as linezolid, daptomycin, and tigecycline [59].

MRSA (Methicillin-Resistant Staphylococcus Aureus)

This types of Staphylococcus aureus usually possesses the mecA gene, which codes for a structural alteration in penicillin-binding protein 2a (PBP2a), in order to be classified as MRSA [48]. Due to this modification, beta-lactam antibiotics are unable to attach to the cell walls of these bacteria. Due to the fact that methicillin plates are unstable, it is uncommon to do laboratory testing for S aureus sensitivity to methicillin. Instead, except for a few noteworthy cases, ceftaroline resistant strains that show resistance to oxacillin typically exhibit resistance to all beta-lactam antibiotics as well [60].

Extended-Spectrum Beta-Lactamase (ESBL) Organisms

It has been discovered that many gram-negative bacterial species produce beta-lactamase, which confers acquired resistance to beta-lactam antibiotics [61]. By hydrolysing the beta-lactam ring of the drug, this enzyme renders its antibacterial effects ineffective. Before penicillin was used medicinally, in 1940, a penicillinase was found in E. coli, and this was the first beta-lactamase to be isolated [62]. With time, new substances were created to fend off the effects of this enzyme, such as broad-spectrum cephalosporins. As was to be expected, the use of these antibiotics caused resistance to drugs with a wider range of action, which gave birth to the ESBL enzyme.

Presently, P aeruginosa and several Enterobacteriaceae species include more than 150 ESBLs. For infections that produce ESBL, carbapenems continue to be the preferred medication [63]. Ipenem-cilastatin, doripenem, meropenem, and ertapenem are among the beta-lactam antibiotics in this subclass. With the exception of ertapenem, which is ineffective against Pseudomonas or Acinetobacter, all of these medications have shown promise against ESBLs

Carbapenemase Resistant Organisms

The most widely used spectrum of antibiotics on the market are the carbapenems [65]. They are a good option for treating a variety of resistant gram-negative nosocomial infections. Acinetobacter and carbapenem-resistant Enterobacteriaceae (CRE) are linked to 1,100 fatalities and hospital admissions annually in studies done recently [66]. Other potential species that produce carbapenemase include E. coli, P. aeruginosa, and K pneumoniae. Patients with ESBL E coli or K pneumoniae-associated bacteremia who received piperacillin-tazobactam treatment as opposed to carbapenem had a greater 30-day death rate [67].

Pseudomonas Aeruginosa

Pseudomonas has a membrane permeability that is intrinsically. relatively low, up to about 100 times lower than that of E. coli [68]. The way fluoroquinolones work to combat bacteria is by specifically targeting enzymes that are involved in the replication of DNA. Pseudomonas sp has developed beta-lactam resistance as a result of its ability to cause enzymatic drug inactivation, overexpression of it efflux pumps genes, and changes in penicillin-binding proteins [69]. Studies have shown that Pseudomonas resistance is more likely to arise when the bacterium is exposed to antipseudomonal beta-lactam antibiotics more often. Every extra day of antipseudomonal beta-lactam medication was linked to a 4% higher chance of developing resistance after a 60-day follow-up, study was done [69].

The role of Humans in the Increase in Antimicrobial Resistance in Microorganism

Worldwide, antibiotics are either overused or abused despite constant warnings from health organisations regarding medication misuse. The misuse of antibiotics is clearly linked as a causal factor for the evolution of resistance [70]. Modern medicine has even inadvertently accelerated this change even further by eradicating competitor organisms which were drug-susceptible, thus allowing resistant microorganisms to multiply and spread via natural selection.

Antimicrobial resistance is also significantly aided by the improper prescription of antibiotics. According to a 2016 research, 50% of patients got antibiotics at least once while they were hospitalised, and the total usage of antibiotics did not vary between 2006 and 2012 [71]. The World Health Organisation has warned repeatedly about the dire shortage of new medicines needed to address the growing problem of antibiotic resistance [72]. Therefore, the care of drug-resistant tuberculosis patients, gram-negative bacteria causing UTIs, pneumonia, and other illnesses caused by 12 pathogens recognised by the WHO has been put in jeopardy due to the lack of therapeutic choices. Furthermore, as the elderly and children have weakened immune systems and are thus more vulnerable to infections, a shortage of new medications may potentially be fatal for these groups within the human population.

Trends of Antimicrobial Resistance in Nigeria

AMR has continued to pose a serious problem to human health and clinical medicine in SSA and Nigeria in particular. The AMR scourge is high in SSA due to poverty, high burden of infection and poor regulation of the use of antibiotics and other antimicrobials. There is also the obvious dearth of viable alternatives to the use of antibiotics thereby compounding an already serious issue [7].

AMR continues to cause morbidity and mortality among the general public, increasing cost of healthcare while reducing the quality of life of patients suffering from its effect. A serious reason for the increase in AMR in Nigeria is the prescribing habits among primary health care workers and other health workers with prescribing rates of some antibiotics being as high as 72% for amoxicillin and 70% for ampicillin/cloxacillin according to a study done by Manga et al. There is also serious uninformed abuse of antibiotics by prescribing them for all sorts of unconfirmed and undiagnosed ailments such as typhoid fever, vaginal discharges fresh trauma wounds, unspecified diarrhoea and even common cold [73].

Even at secondary and tertiary health facilities there is high prevalence of AMR among clinical isolates. In a study to determine the prevalence of AMR among clinical isolates to third-generation cephalosporins, bacterial isolates such as Staphylococcus aureus, Escherichia coli, Staphylococcus spp., Enterococcus spp. and Klebsiella pneumoniae all showed high multidrug resistance to antibiotics from different classes [74]. The most prevalent isolates consistently showing resistance to various classes of antibiotics in Nigeria include Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa and Klebsiella pneumonia. Methicillin resistant S. aureus (MRSA) for an example is at an all-time high accounting for nearly about 40 % of AMR reported in isolates in Nigeria in 2020 [75].

A study carried out by Afolayan et al., isolated Klebsiella pneumonia from 3 antimicrobial-resistance (AMR) sentinel surveillance sites which were tertiary hospitals in south-western Nigeria. Results of the study showed that majority of the 134 isolates sampled within the study were closely related to globally spread multi drug resistant strains of this organism. About 72% of the isolates in this study carried dfrA14, tetD, qnrS, oqxAB and blaCTX_M-15 genes which conferred resistance to different classes of antibiotics on these isolates. This confirms that even clinical isolates in Nigeria are showing very high AMR [76].

Veterinary use of antibiotics is not left out as it presents its own unique addition to the AMR problem. A retrospective study conducted in Nsukka, Enugu state Nigeria showed that from 2013 to 2017, 47.74% of a total case load files of 4851, had antibiotics prescribed. There was also an increase in overall antibiotics use from 85.49% to 91.63% of all the clients attended to within the veterinary teaching hospital [77]. This are antibiotics which will find their way into domestic pets, livestock, poultry and other forms of animal husbandry thereby increasing AMR in both the commensal and pathogenic isolates present in these animals [78]. Going by the interactions between animals and humans there will be cross exchange of resistance organisms helping to even exacerbate further the AMR scourge.

One Health Antimicrobial Resistance and Antimicrobial Stewardship; the Way Forward

In other to chart a course forward to reduce or eradicate AMR, it is important to understand the true state of things and then create a strategy and plans to make things better. Awareness of AMR and the harm it is causing is very important. A study conducted by Chukwu et al showed that from 358 responses to questionnaires in this study, 50.3% agreed that prescribing behaviour was at the root cause of AMR as a problem, while 49.2% has very good knowledge of what AMR was. These statistics for knowledge of AMR in this study are fair enough but there is need for serious health education and campaigns to increase awareness among the general public to perhaps 80 to 90% within the next ten years [79].

The idea of prescribing and using antibiotics to be “on the safe side” as admitted to by respondents within this study must be discouraged and stopped forthwith. Delayed antibiotics prescription strategy which is a strategy where a qualified heath professional prescribes an antibiotic for a patient to be used at a later date if symptoms do not improve is certainly a strategy which should be encouraged and adopted across all levels of healthcare [80]. Prescribing authorities must also be careful and key into this strategy and seek more knowledge as a study conducted by Babatola et al, insists that only about 28 % of physicians had heard of AMS and yet 67.2 % of these physicians were prescribing antibiotics on a daily basis in their clinical practice [81].

Patients on the other hand also have the poor habit of taking antibiotics without prescription, or those who even have prescriptions, refusing to complete their dose after the abating of symptoms as has been revealed in a national survey study conducted by Chukwu et al., [82]. Unfortunately, within this study, 76.6% of the respondents believed that they were powerless to stop the spread of AMR. This is an unhealthy opinion to have and health care professionals must engage in campaigns to educate the general public, not only of the scourge of AMR but the fact that it can be overcome with AMS.

To integrate the one health approach as a strategy to lower AMR in Nigeria, it is important to study the interactions between humans, animals, wildlife and the environment. The use of certain antibiotics across board by both clinicians and veterinary doctors to treat ailments in humans and animals must be discouraged as this practice is exacerbating the issue at hand. Microorganisms

keep circulating around man, animals, plants and the environment and the unregulated use of antibiotics will worsen an already bad situation [83].

The over use of third-generation cephalosporins and fluoroquinolones, both in animal husbandry and human health care must be controlled and eve reversed. There must also be sustained health campaigns to improve sanitation, personal hygiene and infection control in Nigeria. On the side of government, there may be the need to create an office or a unit at federal, state and local government ministries of health to tackle this menace of AMR. These offices or units can come up with programs and policies which could be implemented to improve AMS and reduce AMR [84-89].

Conclusion

AMR is a serious public health issue globally an in Nigeria. Current statistics suggest that without taking measured steps the spectrum of antibiotics which will be available for treatment of infections will continue to reduce. Antimicrobial stewardship along with the one health approach are strategies which will help to ensure that AMR can be brought under control. There is need to improve the awareness of the general public to the scourge of AMR and the collaboration of government, academia, health care professionals and the general public is essential to stem the tide of the scourge of AMR.

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