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Epidemiological Analysis of Antibiotic Resistance

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Abstract: Oral microbiome antibiotic resistance presents major health problems globally, especially in poorer nations. The potential for the mouth cavity to act as a reservoir for resistant bacteria as a result of its frequent exposure to antibiotics poses a challenge to public health initiatives. A global problem that contributes to high morbidity and death in clinical settings is antibiotic resistance in bacterial pathogens. Gram-positive and gram-negative bacteria's multidrug resistance patterns have led to infections that are challenging or even impossible to cure with traditional antimicrobials. Broad range antibiotics are used extensively and mostly unnecessary since many healthcare facilities lack the ability to identify the underlying bacteria and their patterns of antibiotic sensitivity in patients with bacteremia and other serious infections. When combined with inadequate infection control measures, this approach has led to a sharp rise in developing resistance, which makes it simple for resistant germs to spread to other patients and the environment. Therefore, having access to current epidemiological data on antibiotic resistance in commonly encountered bacterial infections will be helpful in developing an efficient antimicrobial stewardship program in hospitals as well as in choosing empirical treatment approaches.

Keywords: Bloodstream infections, antimicrobial resistance, antimicrobial stewardship, multidrug resistance, infection-related fatalities, post-chemotherapy infections.

Introduction. A major global health concern that has a substantial impact on public health, particularly in developing nations, is antibiotic resistance. One significant area of concern is the oral microbiome, a complex ecosystem composed of numerous bacterial species that may act as a reservoir for antibiotic-resistant bacteria. Because the oral cavity is constantly exposed to the outside world and because antibiotics are used to treat dental and medical conditions, it is particularly vulnerable to the development and spread of resistant bacterial strains [1,2,3]. Over the past 20 years, multidrug resistance (MDR) in a variety of bacterial diseases has escalated to a pandemic level. According to the Centers for Disease Control and Prevention (CDC), at least 23,000 individuals in the US pass away from antibiotic-resistant diseases each year, which afflict over 2 million people annually. The estimated cost of healthcare is $20 billion, but missed productivity costs are much higher. According to a comparable British estimate, by 2050, the world economy might lose up to $100 trillion due to antimicrobial resistance, and 10 million people would die annually [4,5,6]. According to a recent study, a 30% decrease in the effectiveness of antibiotics for antibacterial prophylaxis during surgery and cancer chemotherapy might lead to an additional 120,000 surgical site infections and post-chemotherapy infections annually in the United States, as well as 6300 infection-related fatalities. Any bacterium can become resistant to antibiotics (AMR) while remaining susceptible to a wide range of other antibiotics, which enables effective clinical therapy. Most nosocomial infections in healthcare settings are caused by a specific group of bacteria that have recently been identified by the abbreviation ESKAPE [7,8]. *Enterococcus fecium, Staphylococcus aureus, Acinetobacter baumannii, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterobacter species* are all included in the term. Others, however, have challenged the acronym and the choice of these bacteria because it leaves out other enteric gram-negative pathogens, such as *Escherichia coli*, one of the most common bacterial agents that cause serious illnesses with important MDR pathways. A more suitable term, ESCAPE, has been suggested, in which "C" stands for *Clostridium difficile*, a significant nosocomial pathogen that can quickly develop an MDR phenotype, and "E" for *Enterobacteriaceae*, which includes all gram-negative enteric bacteria, such as *Proteus species, E. coli, K. pneumoniae* and *Enterobacter species* [9-13]. There are several risk factors that have been identified as contributing to elevated AMR rates, but the most important one is the improper and pervasive use of antibiotics. It has also been proposed that corruption and bad governance play a role in a nation's AMR levels. As a result, drug resistance monitoring of clinical isolates not only aids in our comprehension of the extent of bacterial evolution, but it also offers a prompt and efficient foundation for empirical anti-infective therapy and efficient hospital infection management. In order to give doctors a timely and efficient foundation upon which to empirically administer anti-infective medication and successfully manage nosocomial infections, we retrospectively analyze the drug resistance data of isolates from clinical patients [14,15,16].

The main purpose of the presented manuscript is to provide a brief literature on antibiotic resistance, which is becoming a serious global problem for medical practice, indicating the causes of its occurrence, risk factors and prevalence.

Relevance and necessity of the problem. Antibiotic resistance in bacterial pathogens is a worldwide issue that raises morbidity and mortality rates in therapeutic settings. The multidrug resistance patterns of both gram-positive and gram-negative bacteria have resulted in illnesses that are difficult or impossible to treat with conventional antimicrobials. Since many healthcare facilities are unable to identify the underlying bacteria and their patterns of antibiotic susceptibility in patients with bacteremia and other serious illnesses, broad range antibiotics are given frequently and mostly without need. This has led to a sharp rise in developing resistance, and when combined with inadequate infection control measures, resistant bacteria can spread quickly to other patients and the environment. Determining empirical treatment techniques and creating a successful antimicrobial stewardship program in hospitals would both benefit from the availability of current epidemiological data on antibiotic resistance in commonly encountered bacterial infections [4-12].

Global antimicrobial resistance epidemiology. The World Health Organization (WHO) stated in its global report on surveillance in AMR that AMR in a variety of infectious pathogens has grown to be a significant public health issue and that the 21st century may see a post-antibiotic era. WHO reported extremely high rates of resistance for both community-acquired (CA) and health-care associated (HCA) infections, despite the fact that many countries around the world lacked guidelines for methodology and had serious surveillance gaps. According to the statistics, reports of fluoroquinolone resistance in E. coli have been made in five of the six WHO global regions and 92 of the 194 member nations [1,4,5,6]. Similarly, 86 member states and 5 regions reported third-generation cephalosporin resistance, which is most likely caused by an extended-spectrum cephalosporinase. Comparable numbers were observed for methicillin resistance in S. aureus and third-generation cephalosporin or carbapenem resistance in *K. pneumoniae*. Antibiotic-resistant bacteria have become much more common over the past ten years, according to other significant epidemiological surveillance networks, such as those in the US (The National Healthcare Safety Network, or NHSN at the CDC) and Europe (such as the European Antimicrobial Resistance Surveillance Network, or EARS-Net, and the Central Asian and Eastern European Surveillance of Antimicrobial Resistance, or CAESAR). Below is a summary of their data on the various bacterial species that can cause bacteremia in various healthcare environments. Additionally, there is an online tool that displays the current rates of antibiotic resistance and use in different nations on an interactive map. The data is updated as new information becomes available [1,8,11, 12, 13].

Halting the spread of newly developed antibiotic resistance. The primary cause of new and expanding resistance is the use of antibiotics by both humans and animals, the latter for prophylactic and growth-promoting purposes. Antibiotic resistance may arise as a result of environmental antibiotic pollution, which also establishes a reservoir for genes that cause antibiotic resistance. However, it has been repeatedly demonstrated that resistance is pervasive in both community and hospital settings in areas with significant consumption. Emerging resistance is a complex issue that will necessitate numerous, well-coordinated efforts from different stakeholders in order to prevent and control [11,12,13]. Essential components of an antibiotic stewardship program at the hospital level include developing and implementing efficient point-of-care and rapid diagnostic tests, educating and promoting the responsible use of antibiotics, creating efficient surveillance systems to track resistance, and putting in place efficient infection control programs. Even at hospitals in the industrialized world, these programs are desperately required and may not be available [1, 3, 14, 15].

Mathematical model. The model is intended to explain the transmission dynamics of any one of various bacterial species, such as Staphylococcus species, Enterococcus species, Escherichia coli, Klebsiella pneumoniae, and Enterobacter, that frequently live in or on human skin, respiratory passages, or digestive tracts. These and other components of the typical human flora can cause symptomatic and even fatal infections, despite their largely commensal nature. In hospitals, these germs are spread by direct patient contact, institutional environment pollution, or unintentional assistance from human vectors (such as healthcare workers, or HCWs) (18–20). When antibiotics are used for treatment or prevention, the bacteria are constantly in contact with them [16-20]. These species are a source of antibiotic-resistant plasmids, which are horizontally transferred between bacterial strains and species and account for a large portion of multiple drug resistance in pathogenic bacteria. They also present a danger of opportunistic infection. The dynamics of a single bacterial species' transmission are taken into account in A, together with the use of two antimicrobial medicines known as drug 1 and drug 2. The single bacterial species in question is referred to as "bacteria" from here on. The model's structure is comparable to earlier compartmental models. The main distinction between this model and the majority of its predecessors is that in this model, the bacterial species of interest has already infected some or all of the individuals that enter the institution [21,22].

Discussion. *S. aureus* was the most often found Gram-positive bacterium in this investigation, followed by *E. faecalis, S. epidermidis* and *S. hemolyticus.* Vancomycin may be clinically appropriate for the treatment of severe infections in MRSA and MR coagulase-negative Staphylococcus, as no VR strains were found. *E. Coli, K. pneumoniae* and P. aeruginosa were the top three Gram-negative bacteria found. According to the monitoring data, *Enterobacterales bacteria* continue to be a major contributor to serious patient infections while having a high sensitivity rate (>90.0%) to carbapenem antimicrobial medications. Additionally, the research demonstrated that P. aeruginosa continues to exhibit a high sensitivity rate (>85.0%) to antimicrobial medications that include aminoglycosides. The prevalence of antimicrobial resistance, especially the MDR phenotype, is rising among nosocomial and clinically significant community infections [1,2,3,5,7]. Antimicrobials with a wider spectrum of activity are being used empirically more often as resistance rates rise in a particular setting out of concern that delaying the start of effective antimicrobial therapy could increase mortality, particularly in patients with substantial underlying illnesses and immunosuppression. A vicious cycle resulting in a surge in resistance isolates could be caused by such a strategy [14,15,16]. In addition to helping to minimize resistance, a good understanding of the local epidemiology of resistance may be crucial in creating antimicrobial stewardship strategies that work. In addition to identifying frequent bacterial species and their resistance patterns across various specimen types, the study makes the case for improved infection prevention and control strategies in hospitals as well as more sensible antibiotic use. Additionally, the paper advocates for more research to enhance the surveillance system and shows how surveillance data may be used to educate clinical practice and policymaking [17,18,19,20].

Conclusions. Antimicrobial resistance is common and on the rise, especially in nosocomial and clinically significant community infections with MDR phenotype. Antimicrobials with a wider spectrum of activity are being used empirically more often as resistance rates rise in a particular setting out of concern that delaying the start of effective antimicrobial therapy could increase mortality, particularly in patients with severe underlying diseases and immunosuppression. Such an approach could result in a vicious cycle that increases the number of resistant isolates. Having a solid understanding of the local epidemiology of resistance may help reduce resistance and play a big part in creating antimicrobial stewardship strategies that work.

Common bacterial species and their resistance patterns in various specimen types were found in the study, which also highlights the need for improved infection prevention and control procedures in hospitals as well as more sensible antibiotic use. The report also urges more research to enhance the surveillance system and shows how valuable surveillance data is for guiding clinical practice and policymaking.

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