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A Review of The Superbug Crisis

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ABSTRACT:
A global public health concern with a substantial economic impact is antimicrobial resistance, which is the capacity of microorganisms to alter and adapt their behavior, rendering medications typically employed against them useless. The rise of drug-resistant infections, driven by the overuse and misuse of antibiotics in healthcare, agriculture, and other sectors, has led to the emergence of dangerous superbugs, such as MRSA and MDR-TB. These resistant bacteria evade traditional treatments through various mechanisms, including horizontal gene transfer, biofilm formation, and the production of resistance enzymes. Antimicrobial Resistance spreads primarily through human-to-human interaction and environmental sources, including contaminated water and food. Addressing this crisis requires a multifaceted approach, including antimicrobial stewardship, better hygiene practices, more effective infection control, and the development of new treatments. Artificial intelligence is emerging as a promising tool to identify resistance patterns and optimize treatment regimens, offering hope in the fight against AMR. Efforts to combat AMR must be collaborative, involving governments, healthcare providers, researchers, and communities to ensure sustainable solutions to this global health challenge.

Keywords: Superbug Crisis, Antibiotic resistance, and Artificial intelligence

1. INTRODUCTION

Drug-resistant bacterial infections already kill millions of people globally each year, low- and middle-income countries are responsible for almost 90% of direct deaths and more than 99.5% of AMR-related deaths among children under five. However, even wealthier countries face frightening statistics: 11,000 Italians are estimated to die each year from AMR [1]. Antimicrobial resistance occurs when microbes, including bacteria, fungi, parasites, and viruses, become resistant to antimicrobial drugs, like antibiotics, frequently used to treat these infections [2.]. The widespread problem is mostly ascribed to the consequences of excessive or careless use of antibiotics in various settings, primarily in clinical treatment, farming, animal medicine, emergencies, and the food chain [3]. Instead of being relegated to a future scenario, antimicrobial resistance, sometimes known as the "Silent Pandemic," requires prompt and effective intervention to reduce its incidence and prevalence [4]

Antimicrobial-resistant bacterial infections have become more common and more common in the twenty-first century, posing a latent pandemic danger to global public health and calling for immediate action [5.]. Any nation can experience antibiotic resistance, and people of any age or gender can be impacted. AMR is one of the greatest concerns to food security and global health in the current situation [6].

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Figure (1): The complex challenge of AMR

Numerous interconnected elements pertaining to agriculture and healthcare have an impact on the development and spread of AMR at the same time. Furthermore, it can be influenced by trade, finance, improper waste management, and medications, making AMR one of the most complex public health issues in the world [7]. The swift worldwide spread of antibiotic-resistant bacteria ("superbugs") has made drug-resistant diseases a critical and worrying global health threat, the World Health Organization considers antimicrobial resistance one of the biggest dangers to public health. MRSA (Methicillin-resistant Staphylococcus aureus), a well-known example of an early superbug, contributes significantly to global deaths caused by these resistant infections [1].

2. SUPERBUGS

Superbugs are bacteria and fungi that are no longer effectively killed by the drugs designed to treat them, in actuality, superbug-caused infections have little to no accessible treatment, the acronym ESKAPE highlights some of the most problematic superbugs, as shown in figure (2). Among the most widespread current threats are drug-resistant versions of these bacteria, including MRSA, CRE, CRKP, ESBL-producing Enterobacterales, VRE, and multidrug-resistant strains of *Pseudomonas aeruginosa* and *Acinetobacter*. Only after the extensive and prolonged usage of antibiotics to treat their ailments have multidrug-resistant bacteria surfaced. For instance, after decades of antitubercular medication treatment, *M. tuberculosis* evolved into MDR-TB, a significant superbug that is now widespread in both developing and underprivileged nations. [8] Superbugs can be also *Staphylococcus epidermidis*, *Clostridium difficile*, *Streptococcus pneumoniae*, *Burkholderia cepacia*, *Stenotrophomonas maltophilia*, *Campylobacter jejuni*, *Citrobacter freundii*, *Enterobacter*, *Haemophilus influenzae*, *Proteus mirabilis*, *Salmonella*, and *Serratia*).

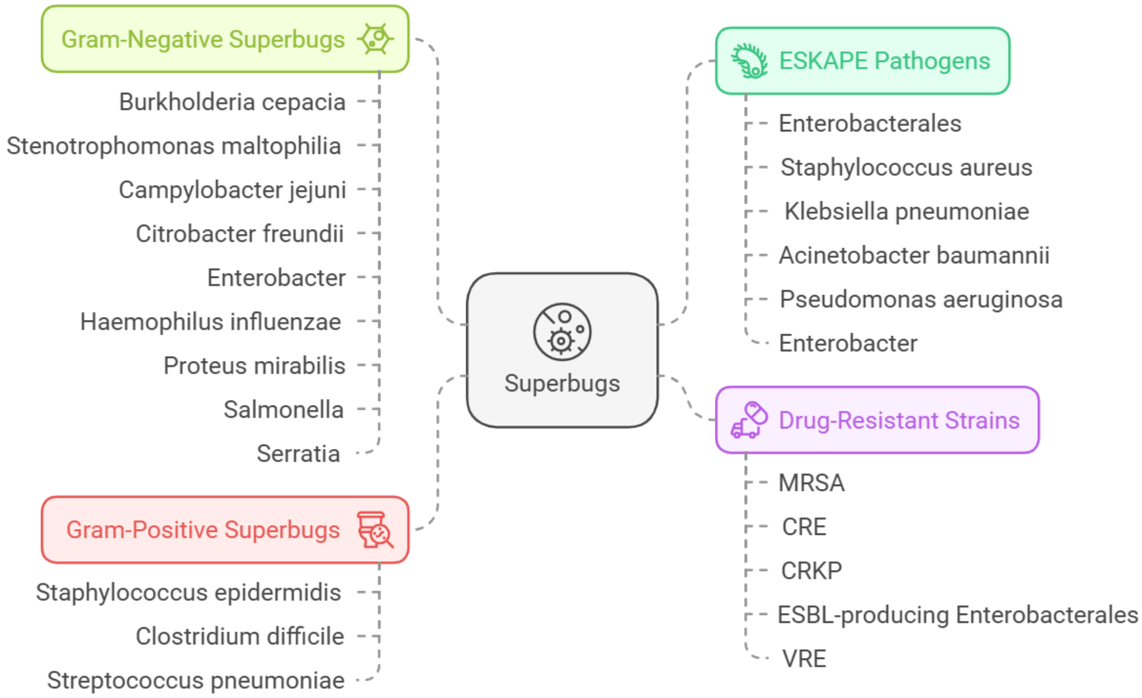

Figure (2): Superbugs bacteria

3. ANTIMICROBIAL RESISTANCE

Antimicrobial Resistance is caused by several factors, including natural selection, the overuse, and abuse of antibiotics, inadequate access to clean water and sanitation, and shoddy and fake medications [9], a partial antibiotic course and can also be caused by self-prescribing, using leftover antibiotics without a doctor's supervision, or prescribing medications for viral infections, also poor hygiene and inadequate sanitation lead to the spread of infectious diseases, which increases the need for antibiotics and eventually leads to resistance.

Lastly, poor-quality drugs can not have enough active ingredients or the right dosage, which could lead to ineffective treatment and the emergence of resistance. [10]. To resist the antibacterial effects of previously successful drugs used to cure ailments, microorganisms have evolved a variety of clever defense mechanisms. These defense mechanisms allow microbes to withstand the effects of antibiotics and other antimicrobial substances, frequently preventing or killing them. Bacteria and other parasites exhibit remarkable adaptability in circumventing the effects of antimicrobial drugs through a variety of strategies, including modifying their structure or employing specific metabolic pathways. These strategies can involve producing enzymes that break down or alter antibiotics, limiting drug entry into the cell, changing their metabolic processes, altering drug targets (like ribosomes), and using efflux pumps to expel antibiotics before they can reach effective concentrations [10;11]. Additionally, bacteria can form surface-bound colonies called biofilms, which have different levels of nutrition and have limited antibiotic penetration [12]. Bacteria can also gain resistance through horizontal gene transfer, acquiring resistance genes from neighboring cells or even different species [13]. This process, often facilitated by plasmids and other mobile genetic elements, allows the rapid spread of multi-drug resistance within microbial communities.

Over the past few decades, several microbes have developed AMR through various mechanisms [14]. Resistant to methicillin Because of horizontal gene transfer and changes in the mecA and mecC genes, Staphylococcus aureus is resistant to many medications, including methicillin [15]. Resistant to carbapenem by gaining carbapenemase genes, Enterobacteriaceae, including Escherichia coli and Klebsiella pneumoniae, have developed resistance to carbapenem medications [16]. *Acinetobacter baumannii*'s resistance to multiple antibiotics arises from a combination of mutations and the acquisition of resistance genes [17]. The alarming rise in these MDR microbial strains demonstrates how easily harmful bacteria, viruses, fungi, and protozoa can elude destruction by chemical agents.

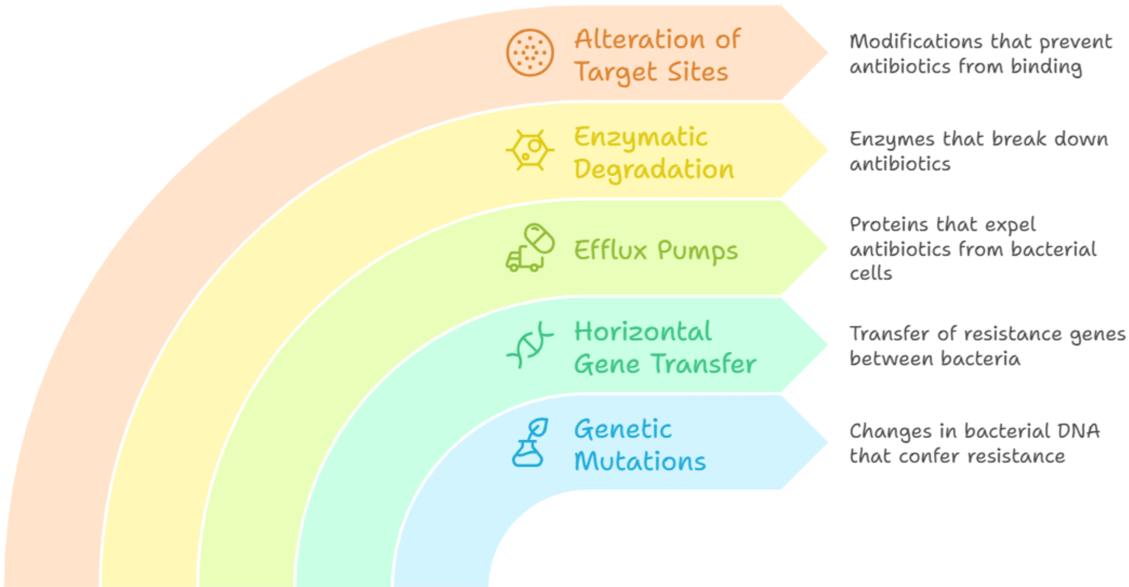

Figure (3): Mechanisms of antimicrobial resistance in bacteria

4. ROUTES OF TRANSMISSION OF AMR

Antimicrobial resistance primarily spreads through human-to-human interaction, both within and outside of healthcare settings, reservoirs where antimicrobial-resistant genes can proliferate and transfer include humans, animals, water, and the environment [18]. Specific hotspots, such as sludge, wastewater from urban treatment plants, and natural fertilizers, and transmission routes vary considerably depending on the bacterial species and resistance mechanisms involved [19]. One direct way that humans can acquire antimicrobial resistance from animals is by the ingestion of animal feed that has been treated with antibiotics [20]. Other typical modes of infection include direct animal-human contact and the use of food or water contaminated by feces [21].

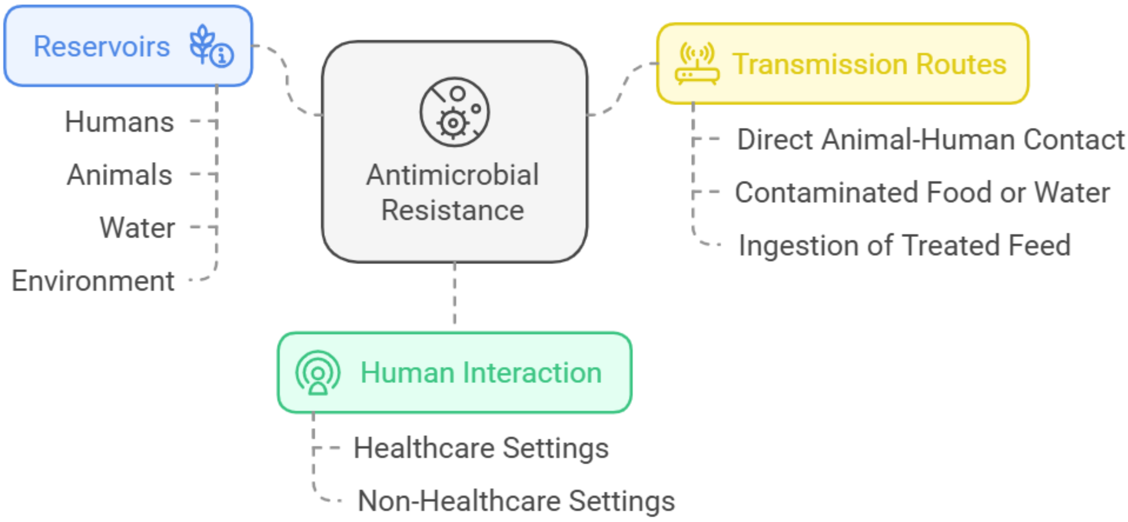

Figure (4): Sources and Routes of Transmission of AMR

5. COMBAT OF ANTIMICROBIAL RESISTANCE

Antimicrobial resistance combat by artificial intelligence is currently employed in some healthcare domains [22;23]. By quickly recognizing patterns in bacterial behavior and adjusting treatment plans accordingly, several published studies on artificial intelligence show how efficiently it prevents antibiotic resistance [24;25]. These developments have enormous potential for creating more individualized and efficient strategies to combat the threat that antibiotic-resistant microorganisms represent to world health. The advancement of machine learning and artificial intelligence (AI) techniques presents promising prospects for enhancing precision medicine and antimicrobial stewardship in response to the pressing AMR epidemic [26].

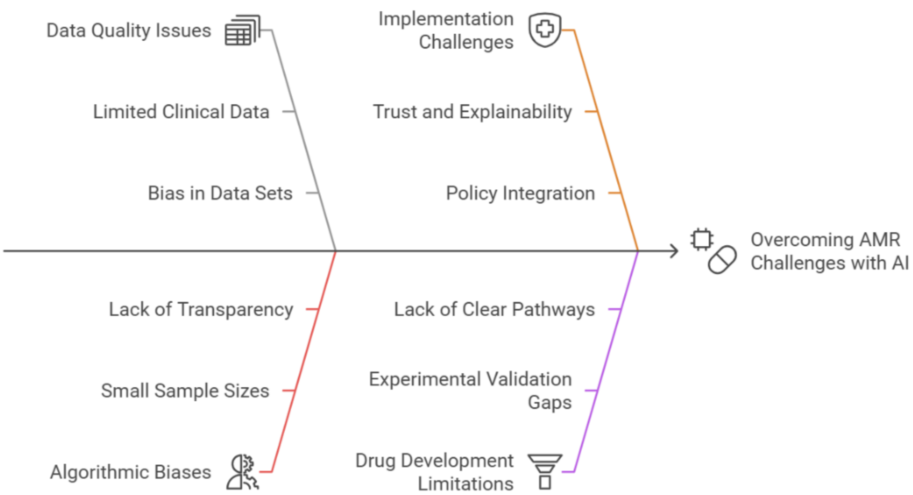

Figure (5): Artificial intelligence in combating AMR

6. DRIVERS OF ANTIMICROBIAL RESISTANCE

Four main categories of factors cause antimicrobial resistance, environmental factors such as population density, overcrowding, rapid disease spread, poor sanitation, ineffective infection control programs, and widespread agricultural antibiotic use; drug-related factors such as substandard drugs and over-the-counter availability of antibiotics; patient-related factors including self-medication, lack of education, and misconceptions about antibiotic use; and physician-related factors. (27)

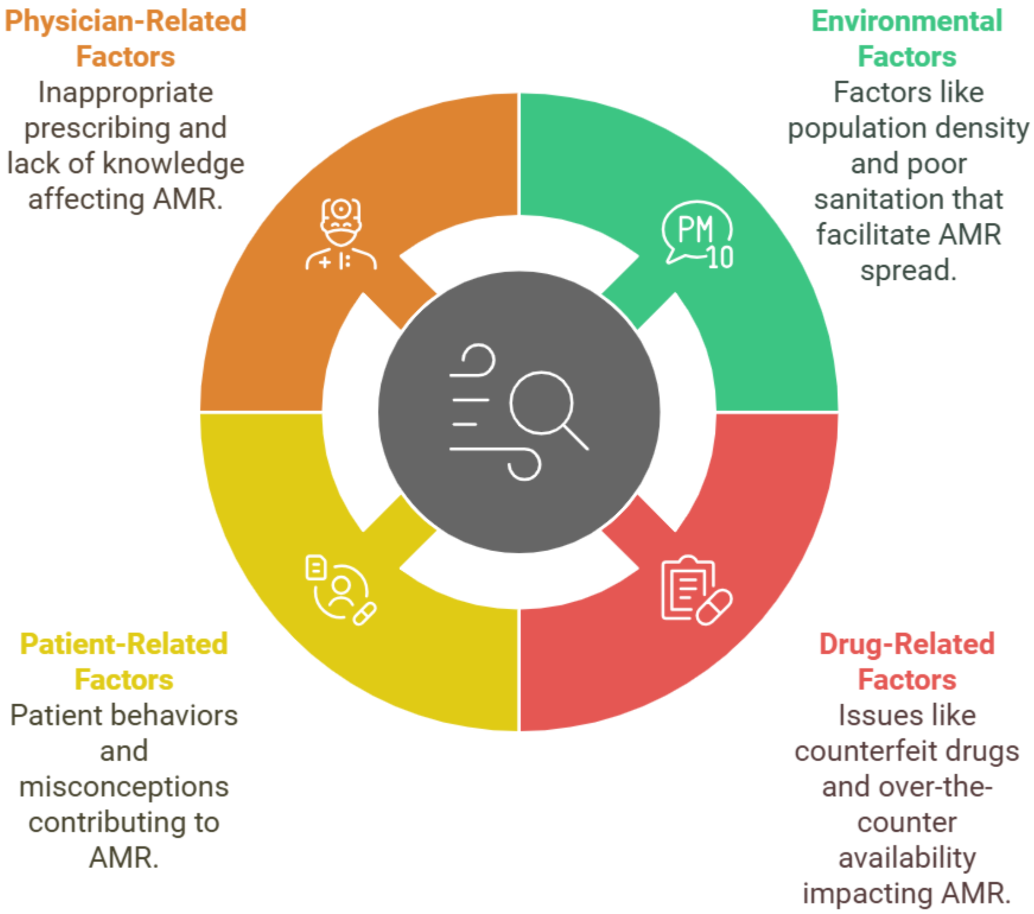

Figure (6): Drivers of antimicrobial resistance

7. STRATEGIES OF ADDRESS AMR

The top priorities of the strategy are appropriate hospital hygiene through antimicrobial stewardship, patient education, antibiotic therapy compliance, reasonable antibiotic prescribing, and the limited use of preventive antibiotics [28]. Accurate antimicrobial profiling for targeted antibiotic therapy and the development and accessibility of rapid diagnostic technologies are crucial in combating AMR and a five-point strategic plan such as increasing awareness and understanding of AMR; strengthening knowledge through surveillance and research; reducing infections through improved hygiene, sanitation, and infection prevention; optimize the use of antimicrobials in human and animal health; and encourage investment in new medicines, diagnostic tools, and vaccines.

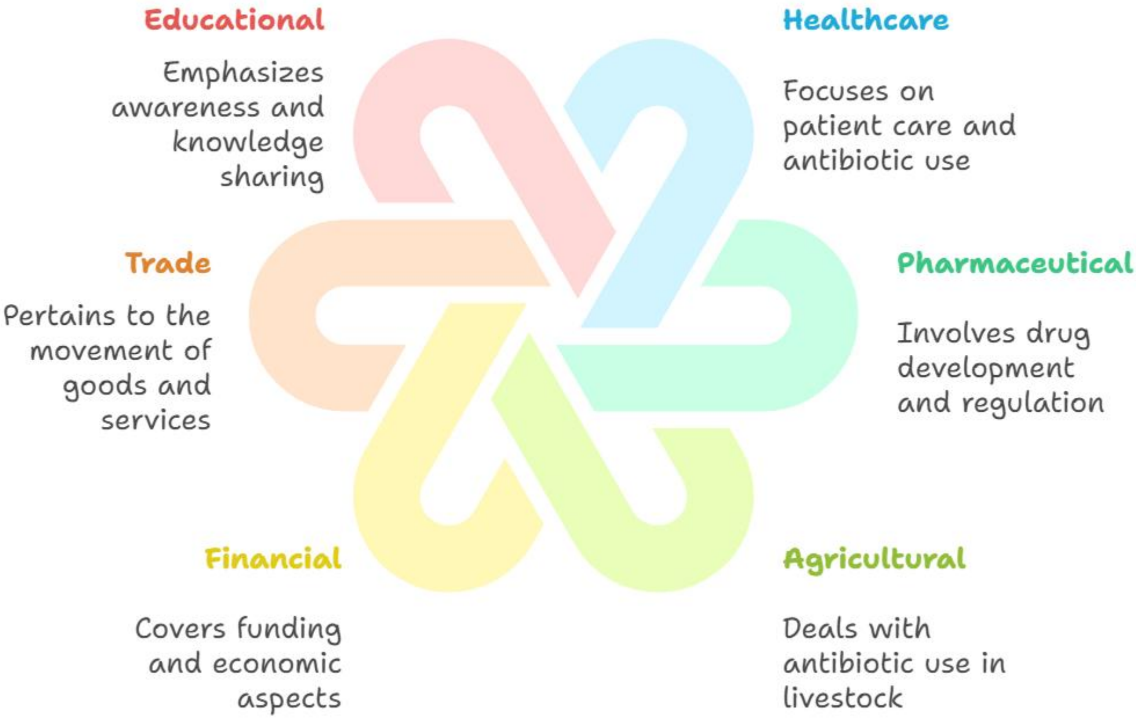

Figure (6): Strategies to Address Antimicrobial Resistance

8. CONCLUSION

Antimicrobial resistance is an urgent and complex issue that demands immediate and coordinated global action. The unchecked rise of drug-resistant infections threatens to undo decades of medical advancements, with significant consequences for public health, food security, and economic stability. Effective strategies to combat AMR must encompass a comprehensive approach that includes stricter regulations on antibiotic use, improved sanitation and infection control measures, better access to quality healthcare, and public education. Additionally, innovative technologies, such as artificial intelligence, hold great potential in detecting resistance early and tailoring treatment strategies. While the challenge is formidable, global cooperation and a commitment to long-term, sustainable practices can reduce the impact of AMR and safeguard public health for future generations.

REFERENCES

[1] WHO. Ten threats to global health in 2019". spotlight/ten-threats-to-global- health-in-2019

[2] Lim, J.-S. Chai, W.-X. Ser, A. Van Haeren, Y.-H. Lim, T. Raja, J.-B. Foo, S. Hamzah, R. Sellappans, H.Y. Yow. (2024). Novel drug candidates against antibiotic-resistant microorganisms: A review, Iran J. Basic Med. Sci. 27, 134–150. https://doi.org/10.22038/IJBMS.2023.71672.15593.

[3] Asghar, A. Khalid, Z. Baqar, N. Hussain, M.Z. Saleem, Sairash, K. Rizwan. (2024).An insight into emerging trends to control the threats of antimicrobial resistance (AMR): an address to public health risks, Arch. Microbiol 206 , 72, https:// doi.org/10.1007/s00203-023-03800-9

[4] Founou, A.J. Blocker, M. Noubom, C. Tsayem, S.P. Choukem, M.Van Dongen, L.L. Founou. (2021). The COVID-19 pandemic: A threat to antimicrobial resistance containment, Futur Sci. OA 7 (2021) FSO736. doi: 10.2144/fsoa-2021-0012

[5] Read, A.F.; Woods, R.J. Antibiotic resistance management. Evol. Med. Public Health 2014, 2014, 147.

[6] Samreen; Ahmad, I.; Malak, H.A.; Abulreesh, H.H. Environmental antimicrobial resistance and its drivers: A potential threat to public health. J. Glob. Antimicrob. Resist. 2021, 27, 101–111.

[7] Kaur, N.; Prasad, R.; Varma, A. Prevalence and antibiotic susceptibility pattern of methicillin resistant staphylococcus aureus intertiary care hospitals. Biotechnol. J. Int. 2014, 4, 228–235.

[8] Parmanik, A.; Das, S.; Kar, B.; Bose, A.; Dwivedi, G.R.; Pandey, M.M. Current Treatment Strategies Against Multidrug-Resistant Bacteria: A Review. Curr. Microbiol. 2022, 79, 388.

[9] Endale, M. Mathewos, D. Abdeta, Potential Causes of Spread of Antimicrobial Resistance and Preventive Measures in One Health Perspective-A Review, Infect. Drug Resist 16 (2023) 7515–7545, https://doi.org/10.2147/IDR.S428837.

[10] Chiş, L.L. Rus, C. Morgovan, A.M. Arseniu, A. Frum, A.L. Vonica-ţincu, F. G. Gligor, M.L. Mureşan, C.M. Dobrea, Microbial Resistance to Antibiotics and Effective Antibiotherapy, Biomedicines 10 (2022) 1121, https://doi.org/ 10.3390/biomedicines10051121.

[11] Mohanty, S. Pachpute, R.P. Yadav, Mechanism of drug resistance in bacteria: efflux pump modulation for designing of new antibiotic enhancers, Folia Microbiol. (Praha) 66 (2021) 727–739.

[12] Uru´en, G. Chopo ommassen, R.C. Mainar-Jaime, J. Arenas, Biofilms as promoters of bacterial antibiotic resistance and tolerance, Antibiotics 10 (1) (2021) 36, https://doi.org/10.3390/antibiotics10010003.

[13] Weisberg, J.H. Chang, Mobile Genetic Element Flexibility as an Underlying Principle to Bacterial Evolution, Annu. Rev. Microbiol 77 (2023) 603–624, https://doi.org/10.1146/annurev-micro-032521-022006.

[14] van Duin, D.L. Paterson, Multidrug-Resistant Bacteria in the Community: An Update, Infect. Dis. Clin. North Am 34 (2020) 709–722, https://doi.org/10.1016/ j.idc.2020.08.002.

[15] Peacock, G.K. Paterson, Mechanisms of methicillin resistance in

Staphylococcus aureus, Annu. Rev. Biochem. 84 (2015) 577–601, https://doi. org/10.1146/annurev-biochem-060614-034516.

[16] Baroud, I. Dandache, G.F. Araj, R. Wakim, S. Kanj, Z. Kanafani, M. Khairallah, A. Sabra, M. Shehab, G. Dbaibo, G.M. Matar, Underlying mechanisms of carbapenem resistance in extended-spectrum β-lactamase-producing Klebsiella pneumoniae and Escherichia coli isolates at a tertiary care centre in Lebanon: role of OXA-48 and NDM-1 carbapenemases. Int J Antimicrob Agents.2013 Jan;41(1):75-9. doi: 10.1016/j.ijantimicag.2012.08.010.

[17] Kyriakidis, E. Vasileiou, Z.D. Pana, A. Tragiannidis, Acinetobacter baumannii antibiotic resistance mechanisms, Pathogens 10 (2021) 373, https://doi.org/ 10.3390/pathogens10030373.

[18] Godijk, N.G.; Bootsma, M.C.J.; Bonten, M.J.M. Transmission routes of antibiotic resistant bacteria: A systematic review. BMCInfect. Dis. 2022, 22, 482.

[19] Krzemi ́nski, P.; Markiewicz, Z.; Popowska, M. Entry Routes of Antibiotics and Antimicrobial Resistance in the Environment. In Antibiotics and Antimicrobial Resistance Genes: Environmental Occurrence and Treatment Technologies; Hashmi, M.Z., Ed.; Springer International Publishing: Cham, Germany, 2020; pp. 1–26.

[20] Costa, P.M.; Loureiro, L.; Matos, A.J. Transfer of multidrug-resistant bacteria between intermingled ecological niches: The interface between humans, animals and the environment. Int. J. Environ. Res. Public Health 2013, 10, 278–294.

[21] Landers, T.F.; Cohe**n,** B.; Wittum, T.E.; Larson, E.L. A review of antibiotic use in food animals: Perspective, policy, and potential.Public Health Rep. 2012, 127, 4–22.

[22] Ahmed, S.K.Artificial intelligence in nursing: Current trends, possibilities and pitfalls, J. Med. Surgery, Public Heal 3 (2024) 100072

[23] Ahmed, S. Hussein, D. Chandran, M.R. Islam, K. Dhama, the role of digital health in revolutionizing healthcare delivery and improving health outcomes in conflict zones, 20552076231218160, Digit. Heal 9 (2023), https://doi.org/ 10.1177/2055207623121815

[24] Lau,H.J. Lim, S.C. Foo, H.S. Tan, The role of artificial intelligence in the battle against antimicrobial-resistant bacteria, Curr. Genet 67 (2021) 421–429.

[25] Gulumbe, U.A. Haruna, J. Almazan, I.H. Ibrahim, A.A. Faggo, A.Y. Bazata, Combating the menace of antimicrobial resistance in Africa: A review on stewardship, surveillance and diagnostic strategies, Biol. Proced. Online 24 (2022) 1–13.

[26] Marra, P. Nori, B.J. Langford, T. Kobayashi, G. Bearman, Brave new world: Leveraging artificial intelligence for advancing healthcare epidemiology, infection prevention, and antimicrobial stewardship, Infect. Control Hosp. Epidemiol 44 (2023) 1909–1912.

[27] Abushaheen, M.A.; Muzaheed; Fatani, A.J.; Alosaimi, M.; Mansy, W.; George, M.; Acharya, S.; Rathod, S.; Divakar, D.D.; Jhugroo,C.; et al. antimicrobial resistance, mechanisms and its clinical significance. Dis. A-Mon. DM 2020, 66, 100971.

[28] Majumder, M.A.A.; Rahman, S.; Cohall, D.; Bharatha, A.; Singh, K.; Haque, M.; Gittens-St Hilaire, M. Antimicrobial Stewardship: Fighting Antimicrobial Resistance and Protecting Global Public Health. Infect. Drug Resist. 2020, 13, 4713–4738.