

A Comprehensive Review of Multidrug-resistant microbes

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Abstract

The supreme danger to the life of humans is the microorganisms that are resistant to conventional drugs and cause several life-threatening diseases. Out of them, some are more terrifying as they are resistant to modern antibiotics and cause more complications than normal bacteria and other microorganisms. The resistance among various microbial species (infectious agents) to different antimicrobial drugs has emerged as a cause of public health threats all over the world at a terrifying rate. Due to the pacing advent of new resistance mechanisms and decrease in efficiency of treating common infectious diseases, it fails in microbial response to standard treatment, leading to prolonged illness, higher expenditures for health care, and an immense risk of death. Almost all the capable infecting agents (e.g., bacteria, fungi, viruses, and parasites) have employed high levels of multidrug resistance (MDR) with enhanced morbidity and mortality; thus, they are referred to as superbugs. although the development of MDR is a natural phenomenon, the inappropriate use of antimicrobial drugs, inadequate sanitary conditions, inappropriate food handling, and poor infection prevention, and control practices contribute to the emergence of and encourage the further spread of MDR. Considering the significance of MDR, to counter the problem we decided to find a solution for this threat and a study should be made to find a proper drug for combating the multidrug-resistant Bacteria.

Keywords

Multidrug resistance, immunodeficiency, Gene Transfer, Drug Efflux and Overexpression.

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I. Introduction

The evolution of microbial infections has increased dramatically in the last 20 years. Overuse of antimicrobial drugs in treating infections has led to the emergence of resistance among various strains of microorganisms. Multidrug resistance (MDR) is defined as the insensitivity or resistance of a microorganism to administered antimicrobial medicines, which are structurally unrelated and have different molecular targets, despite earlier sensitivity to them. These resistant microorganisms, like bacteria, fungi, viruses, and parasites, can combat the attack by antimicrobial drugs, leading to ineffective treatment and the persistence and spreading of infections, according to the World Health Organization (WHO).[1]

Although the development of MDR is a natural phenomenon, the rise in the number of immune-compromised conditions, such as HIV, diabetic patients, individuals who have undergone organ transplantation, and severe burn patients, makes the body an easy target for hospital-acquired infectious diseases, thereby contributing to the further spread of MDR. Studies from the WHO report have shown very high rates of resistance in bacteria such as *Escherichia coli* against antibiotics such as cephalosporin and fluoroquinolones, *Klebsiella pneumonia* against cephalosporin and carbapenems, *Staphylococcus aureus* against methicillin, *Streptococcus pneumoniae* against penicillin, Non-typhoidal *Salmonella* against fluoroquinolones, *Shigella* species against fluoroquinolones, *Neisseria gonorrhoea* against cephalosporin, and *Mycobacterium tuberculosis* against rifampicin, isoniazid, and fluoroquinolone, causing common infections, such as urinary tract infections, pneumonia, and bloodstream infections, and a high percentage of hospital-acquired infections. [2]

A limited number of antifungal drugs are available for the treatment of chronic fungal infections. Resistance to drugs such as polyene macrolides (amphotericin B), azole derivatives (ketoconazole, fluconazole, itraconazole, and voriconazole), DNA and RNA synthesis inhibitors (flucytosine), and 1,3- β -glucan synthase inhibitors (echinocandins) exists in isolates of *Candida spp.*, *Aspergillus spp.*, *Cryptococcus neoformans*, *Trichosporon beigellii*, *Scopulariopsis spp.*, and *Pseudallescheria boydii*. Prolonged drug exposure and nonstop viral replication result in the advent of various resistant strains and the persistence of infections despite therapy. This makes antiviral resistance a matter of concern in immune-compromised patients. [3]

Consequences of antiviral drug resistance were observed in immune-suppressed transplant recipients and oncology patients infected by either cytomegalovirus (CMV), herpes simplex virus (HSV), Varicella-zoster virus (VZV), human immunodeficiency virus (HIV), influenza A virus, hepatitis C (HCV), or hepatitis B virus (HBV). Parasitic multi-drug resistance has been analyzed in isolates of *Plasmodia*, *Leishmania*, *Entamoeba*, *Trichomonas vaginalis*, *schistosomes*, and *Toxoplasma gondii* against drugs such as chloroquine,

pyrimethamine, artemisinin, pentavalent antimonial, miltefosine, paromomycin, and amphotericin B as well as atovaquone and sulfadiazine. [4]

One of the most significant examples of a disease prone to MDR is malaria, caused by *Plasmodium falciparum*. Another protozoan parasite, *Entamoeba* spp., causes amoebiasis, which is also a major public health threat in many tropical and subtropical countries. Schistosomiasis is another global health threat considered like that of malaria and other chronic diseases. This review article emphasizes the significance of MDR, the various mechanisms contributing to its development, and the problems associated with MDR and its possible remedies.

1. Implication of MDR

The implications of multidrug resistance (MDR) are far-reaching and multifaceted, impacting various aspects of healthcare, public health, economics, and global health security. Here are the key implications.

Clinical Implications

Treatment Failures: MDR leads to higher rates of treatment failure because standard antibiotics become ineffective against resistant pathogens. This means that second- or third-line treatments, which may be less effective, more toxic, and more expensive, are needed.

Increased Mortality and Morbidity: Patients with MDR infections often have higher mortality rates due to limited options for effective treatment. These infections can also lead to severe complications and prolonged illness.

Prolonged Hospital Stays: Infections caused by MDR organisms often result in longer hospital stays for patients, as they require extended treatment and more intensive care.[5]

2. Economic Implications

Higher Healthcare Costs: Managing MDR infections is significantly more expensive due to the need for more expensive drugs, longer hospital stays, and additional diagnostic tests and treatments.

Loss of Productivity: Prolonged illness and higher mortality rates contribute to the loss of productivity and economic burden on families and society.

3. Public Health Implications

Increased Spread of Resistant Infections: MDR pathogens can spread more easily in communities and healthcare settings, leading to outbreaks that are difficult to control.

Compromised Medical Procedures: MDR undermines the effectiveness of routine medical procedures that rely on effective antibiotics, such as surgeries, cancer chemotherapy, and the care of premature infants.[6]

4. Scientific and Research Implications

Need for New Antibiotics: The rise of MDR highlights the urgent need for the development of new antibiotics and alternative treatments. However, the pipeline for new antibiotics is currently limited.

Investment in Research: Significant investment in research and development is required to understand the mechanisms of resistance and to develop new therapeutic strategies.[7]

5. Global Health Security Implications

Cross-Border Spread: MDR is a global issue, as resistant pathogens do not respect borders. International travel and trade can facilitate the spread of MDR organisms, making global surveillance and cooperation essential.

Bioterrorism Potential: There is a potential risk that MDR organisms could be used as biological weapons, posing a threat to national and international security.[8]

6. Ethical and Social Implications

Access to Effective Treatment: The emergence of MDR raises ethical concerns about equitable access to effective treatments, especially in low- and middle-income countries where healthcare resources may be limited.

Public Awareness and Education: Increasing public awareness and education about the risks of antibiotic misuse and the importance of adherence to prescribed treatments is critical in combating MDR.[9]

Risk Factors for Multidrug Resistance (MDR)

Multidrug resistance (MDR) is influenced by various risk factors that can be categorized into patient-related, healthcare-related, and societal factors. Understanding these risk factors is crucial for developing effective prevention and control strategies.

Patient-Related Factors

Previous Antibiotic Use: Patients who have recently used antibiotics, especially broad-spectrum antibiotics, are at a higher risk of developing or being infected with MDR organisms. Inappropriate or excessive use of antibiotics can result for resistant strains.

Underlying Medical Conditions: Patients with chronic illnesses such as diabetes, chronic kidney disease, or cancer, and those who are immunocompromised, are more susceptible to infections and may require frequent antibiotic treatments, increasing the risk of MDR.[10]

Hospitalization and ICU Stay: Prolonged hospital stays, especially in intensive care units (ICUs), expose patients to a higher risk of acquiring MDR infections due to the increased use of invasive devices and the high prevalence of resistant organisms in these settings.

Previous MDR Infections: A history of infection with MDR organisms increases the likelihood of future infections with similar resistant strains.[11]

Healthcare-Related Factors

Infection Control Practices: Inadequate infection control measures in healthcare facilities, such as poor hand hygiene, improper sterilization of medical equipment, and inadequate isolation of infected patients, can facilitate the spread of MDR organisms.[12]

Use of Invasive Devices: The use of medical devices such as catheters, ventilators, and central lines can introduce pathogens and provide a surface for biofilm formation, increasing the risk of MDR infections.[13]

Antibiotic Prescribing Practices: Overprescribing or inappropriate prescribing of antibiotics by healthcare providers, such as using antibiotics for viral infections or not following guidelines for dosage and duration, contributes significantly to the development of resistance.

Healthcare Worker Colonization: Healthcare workers who are colonized with MDR organisms can inadvertently transmit these pathogens to patients.[14]

Societal and Environmental Factors

Community Acquired Infections: The prevalence of MDR organisms in the community, including those associated with animal and food sources, can lead to the spread of resistant infections among the general population.[15]

Agricultural Antibiotic Use: The use of antibiotics in livestock and agriculture, often for growth promotion or disease prevention, contributes to the development and spread of MDR organisms through the food chain and environment.

Global Travel and Migration: Increased international travel and migration can facilitate the spread of MDR organisms across borders, leading to global dissemination of resistant strains.[16]

Socioeconomic Factors: Limited access to healthcare, poor sanitation, and overcrowded living conditions can increase the risk of MDR infections, particularly in low- and middle-income countries.

Categorization of MDR

Multidrug resistance (MDR) can be categorized in various ways based on the type of microorganisms involved, the mechanism of resistance, and the clinical context. Here are the primary categories:

1. By Type of Microorganism

A. Bacterial MDR

Gram-Positive Bacteria: Examples include methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant Enterococci (VRE).[17]

Gram-Negative Bacteria: Examples include extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae, carbapenem-resistant Enterobacteriaceae (CRE), and multidrug-resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. [18]

B. Fungal MDR

Candida Species: *Candida auris* is a notable example of a multidrug-resistant fungus.

Aspergillus Species: Some strains are resistant to multiple antifungal agents.

C. Viral MDR

HIV: Multidrug-resistant HIV can result from mutations that confer resistance to multiple antiretroviral drugs.[19]

Influenza: Resistance to antiviral drugs like oseltamivir can occur in influenza viruses.

D. Parasitic MDR

Plasmodium falciparum: Some strains of this malaria-causing parasite are resistant to multiple antimalarial drugs.[20]

Leishmania Species: Resistance to antimonial drugs and other treatments can occur.[21]

2. By Mechanism of Resistance

A. Enzymatic Degradation

Beta-lactamases: Enzymes like ESBLs and carbapenemases break down beta-lactam antibiotics, rendering them ineffective.[22]

B. Target Modification

MRSA: The *mecA* gene alters penicillin-binding proteins, reducing the efficacy of beta-lactam antibiotics.

VRE: Modifications to the D-Ala-D-Ala target of vancomycin reduce drug binding.

C. Efflux Pumps

Pseudomonas aeruginosa: Utilizes efflux pumps to expel antibiotics, decreasing intracellular drug concentration.[23]

E. coli: Certain strains express efflux pumps that confer resistance to multiple antibiotic classes.

D. Reduced Permeability

Gram-Negative Bacteria: Modifications to porin channels in the cell membrane can decrease drug uptake.[24]

3. By Clinical Context

A. Hospital-Acquired Infections (HAIs)

Infections acquired in healthcare settings, often involve MDR pathogens like MRSA, CRE, and multidrug-resistant *Pseudomonas aeruginosa*. [25]

B. Community-Acquired Infections

MDR organisms cause infections in the general population, such as community-acquired MRSA (CA-MRSA). [26]

4. By Extent of Resistance

A. Multidrug-Resistant (MDR)

Resistant to at least one agent in three or more antimicrobial categories.

B. Extensively Drug-Resistant (XDR)

Resistant to at least one agent in all but two or fewer antimicrobial categories. [28]

C. Pan drug-Resistant (PDR)

Resistant to all agents in all antimicrobial categories.

Pathophysiology of MDR

The pathophysiology of multidrug resistance (MDR) involves complex biological mechanisms that allow microorganisms to survive exposure to multiple antimicrobial agents. Understanding these mechanisms is essential for developing strategies to combat MDR. Here are the main mechanisms by which bacteria, fungi, viruses, and parasites develop resistance: [29]

1. Genetic Mechanisms

A. Mutation

Spontaneous Mutations: Random genetic changes can lead to resistance. For example, mutations in genes encoding target proteins can reduce drug binding. [30]

Hypermutability: Some organisms have increased mutation rates, enhancing their ability to develop resistance. [31]

B. Horizontal Gene Transfer (HGT)

Conjugation: Transfer of plasmids carrying resistance genes between bacteria through direct contact.

Transformation: Uptake of free DNA fragments from the environment by a bacterium, which can include resistance genes. [32]

Transduction: Transfer of resistance genes between bacteria via bacteriophages (viruses that infect bacteria).

2. Biochemical Mechanisms

A. Enzymatic Degradation

Beta-Lactamases: Enzymes that hydrolyze the beta-lactam ring of antibiotics like penicillin and cephalosporins, rendering them ineffective. [33]

Extended-Spectrum Beta-Lactamases (ESBLs): Enzymes that confer resistance to a broader range of beta-lactam antibiotics, including third-generation cephalosporins. [34]

Carbapenemases: Enzymes that break down carbapenems, a class of last-resort antibiotics.

B. Modification of Target Sites

Altered Penicillin-Binding Proteins (PBPs): Modified PBPs reduce binding affinity for beta-lactam antibiotics, as seen in MRSA. [35]

Ribosomal Modifications: Mutations or methylation of ribosomal RNA can confer resistance to aminoglycosides and macrolides.

C. Efflux Pumps

Overexpression of Efflux Pumps: Proteins that actively transport antibiotics out of the cell, decreasing intracellular drug concentration. Common in *Pseudomonas aeruginosa* and *E. coli*. [36]

Multidrug Efflux Systems: Pumps that can expel a wide range of antibiotics, contributing to multidrug resistance.

D. Reduced Permeability

Porin Channel Modifications: Changes in the structure or expression of porin proteins in the bacterial outer membrane reduce antibiotic uptake. Notable in Gram-negative bacteria like *Klebsiella pneumoniae*. [37,38]

Biofilm Formation: Bacteria in biofilms are less accessible to antibiotics due to the protective extracellular matrix.

3. Adaptive Mechanisms

A. Phenotypic Plasticity

Dormancy and Persisted Cells: Some bacteria can enter a dormant state where they are metabolically inactive and less susceptible to antibiotics. [39,40]

Biofilm Production: Bacteria in biofilms exhibit altered growth rates and gene expression, providing resistance to antimicrobial agents. [41]

4. Specific Pathogen Examples

A. Methicillin-Resistant *Staphylococcus aureus* (MRSA)

Mechanism: Acquisition of the *mecA* gene encoding an altered PBP (PBP2a) with low affinity for beta-lactams. [42]

B. Carbapenem-Resistant *Enterobacteriaceae* (CRE)

Mechanism: Production of carbapenemases (e.g., KPC, NDM) that degrade carbapenem antibiotics. Often coupled with porin modifications and efflux pump overexpression. [43]

C. Multidrug-Resistant Tuberculosis (MDR-TB)

Mechanism: Mutations in genes encoding drug targets (e.g., *rpoB* for rifampicin resistance, *katG* for isoniazid resistance). [45]

Management of MDR

Managing multidrug resistance (MDR) is a complex challenge that requires a multifaceted approach involving prevention, monitoring, treatment, and education. Here are the key strategies and practices for effective management of MDR:

1. Prevention and Control

A. Infection Control Measures

Hand Hygiene: Rigorous handwashing practices among healthcare workers to prevent the spread of MDR organisms. [46]

Environmental Cleaning: Regular cleaning and disinfection of hospital surfaces and equipment.

Isolation Precautions: Isolating patients infected or colonized with MDR organisms to prevent cross-contamination. [47]

Screening and Surveillance: Routine screening for MDR organisms in high-risk areas, such as intensive care units (ICUs).

B. Vaccination

Immunization Programs: Vaccinating against preventable diseases reduces the need for antibiotics and lowers the risk of developing resistance. [48,49]

2. Antibiotic Stewardship

A. Rational Use of Antibiotics

Prescribing Guidelines: Adhering to evidence-based guidelines for antibiotic use to ensure appropriate selection, dosage, and duration. [50,51]

Review and De-escalation: Regularly reviewing antibiotic therapy and de-escalating to narrower-spectrum agents based on culture results and clinical response. [52]

Education and Training: Educating healthcare providers on the principles of antibiotic stewardship and the consequences of misuse. [53]

B. Surveillance and Monitoring

Resistance Patterns: Monitoring local and regional antibiotic resistance patterns to inform treatment guidelines and stewardship interventions. [54]

Antibiotic Usage: Tracking antibiotic prescribing and consumption to identify areas for improvement. [55]

3. Research and Development

A. New Antibiotics

Incentives for Development: Providing financial incentives and support for pharmaceutical companies to develop new antibiotics. [56]

Novel Therapies: Exploring alternative treatments, such as bacteriophage therapy, antimicrobial peptides, and immunotherapies. [57]

B. Diagnostic Tools

Rapid Diagnostics: Developing and implementing rapid diagnostic tests to quickly identify MDR organisms and guide appropriate therapy.[58]

4. Public and Professional Education

A. Awareness Campaigns

Public Education: Raising awareness about the dangers of antibiotic misuse and the importance of adhering to prescribed treatments.[59]

Professional Training: Providing ongoing education for healthcare workers on infection control, antibiotic stewardship, and the management of MDR infections.[60]

5. Global Collaboration

A. International Cooperation

Sharing Data: Collaborating on global surveillance of antibiotic resistance and sharing data to track the spread of MDR organisms.[61]

Joint Initiatives: Participating in international initiatives, such as the World Health Organization's Global Action Plan on Antimicrobial Resistance.[62]

B. Policy Development

National Strategies: Developing and implementing national action plans to combat antimicrobial resistance, including regulations on antibiotic use in healthcare and agriculture.

6. Treatment of MDR Infections

A. Combination Therapy

Using Multiple Drugs: Combining antibiotics with different mechanisms of action to enhance efficacy and prevent the emergence of resistance.[63]

Synergistic Combinations: Selecting combinations that work synergistically to improve outcomes.[64]

B. Individualized Therapy

Personalized Medicine: Tailoring antibiotic therapy based on the patient's specific infection and susceptibility profile.

Therapeutic Drug Monitoring: Monitoring drug levels to ensure optimal dosing and minimize toxicity.[65]

7. Innovative Approaches

A. Phage Therapy

Bacteriophages: Using viruses that specifically target and kill bacteria as an alternative to traditional antibiotics.[66]

Combination with Antibiotics: Combining phages with antibiotics to enhance antibacterial efficacy.[67]

B. Antimicrobial Peptides

Natural and Synthetic Peptides: Developing peptides that have antimicrobial properties and can serve as alternatives or adjuncts to antibiotics.

C. Immunotherapy Boosting Host Defenses: Using treatments that enhance the patient's immune system to fight infections more effectively.[68]

II. Conclusion

The rapid increase of severe systemic infections and the spread of resistant microorganisms are indisputable facts. The limited effectiveness of existing antimicrobial drugs requires the continuous development of new drugs. It is also important to implement awareness programs to promote their appropriate use to regain control over diseases. Multidrug resistance (MDR) is a natural phenomenon that poses a serious threat to public health worldwide. Global cooperation is necessary to combat MDR. Pathogens tend to develop various resistance mechanisms to survive adverse conditions. Improved knowledge of the molecular mechanisms that control MDR should aid in the development of new therapies to combat these persistent infections. Additionally, it will help to deepen our understanding of the pathobiology of microbial organisms. The threat of multidrug-resistant microbes cannot be underestimated. These harmful microorganisms pose a real danger to all living beings, and urgent action is necessary to mitigate the potential risks. It is our collective responsibility to take appropriate measures to combat this threat and safeguard our health and well-being.

References

- [1]. A. C. Hurt, "The epidemiology and spread of drug resistant human influenza viruses," *Current Opinion in Virology*, vol. 8, pp. 22–29, 2014.
- [2]. Agniswamy, J.; Kneller, D.W.; Ghosh, A.K.; Weber, I.T., Novel HIV PR inhibitors with C4-substituted bis-THF and bis-fluorobenzyl target the two active site mutations of highly drug resistant mutant PR(S17). *Biochem. Biophys. Res. Commun.*, 56, pp. 30–35, 2021.
- [3]. Antimicrobial Resistance Global Report on Surveillance, World Health Organization, Geneva, Switzerland, 2014.
- [4]. B. Ullman, "Multidrug resistance and P-glycoproteins in parasitic protozoa," *Journal of Bioenergetics and Biomembranes*, vol. 27, no. 1, pp. 77–84, 1995.
- [5]. C. A. Muzny and J. R. Schwebke, "The clinical spectrum of *Trichomonas vaginalis* infection and management challenges," *Sexually*

- Transmitted Infections, vol. 89, no. 6, pp. 423–425, 2013.
- [6]. C. Doliwa, S. Escotte-Binet, D. Aubert et al., “Sulfadiazine resistance in *Toxoplasma gondii*: no involvement of overexpression or polymorphisms in genes of therapeutic targets and ABC transporters,” *Parasite*, vol. 20, no. 19, pp. 1–6, 2013.
 - [7]. C. P. Wu, S. Ohnuma, and S. V. Ambudkar, “Discovering natural product modulators to overcome multidrug resistance in cancer chemotherapy,” *Current Pharmaceutical Biotechnology*, vol. 12, no. 4, pp. 609–620, 2011.
 - [8]. C. R. Lee, I. H. Cho, B. C. Jeong, and S. H. Lee, “Strategies to minimize antibiotic resistance,” *International Journal of Environmental Research and Public Health*, vol. 10, no. 9, pp. 4274–4304, 2013.
 - [9]. D. Bansal, N. Malla, and R. C. Mahajan, “Drug resistance in amoebiasis,” *Indian Journal of Medical Research*, vol. 123, no. 2, pp. 115–118, 2006.
 - [10]. D. Bansal, R. Sehgal, Y. Chawla, N. Malla, and R. C. Mahajan, “Multidrug resistance in amoebiasis patients,” *Indian Journal of Medical Research*, vol. 124, no. 2, pp. 189–194, 2006.
 - [11]. D. C. McFadden, S. Tomavo, E. A. Berry, and J. C. Boothroyd, “Characterization of cytochrome b from *Toxoplasma gondii* and Q(o) domain mutations as a mechanism of atovaquone-resistance,” *Molecular and Biochemical Parasitology*, vol. 108, no. 1, pp. 1–12, 2000.
 - [12]. Dworzack DL., Aminoglycosides: Mechanisms of action and resistance. In: *The Aminoglycoside Antibiotics: A Guide to Therapy*. CRC Press, pp. 23–44, 2019.
 - [13]. E. Orozco, C. López, C. Gómez et al., “Multidrug resistance in the protozoan parasite *Entamoeba histolytica*,” *Parasitology International*, vol. 51, no. 4, pp. 353–359, 2002.
 - [14]. F. C. Tenover, “Mechanisms of antimicrobial resistance in bacteria,” *The American Journal of Medicine*, vol. 119, no. 6, pp. S3–S10, 2006.
 - [15]. Fulfager, A.D. Yadav, K.S., Understanding the implications of co-delivering therapeutic agents in a nanocarrier to combat multidrug resistance (MDR) in breast cancer. *J. Drug Deliv. Sci. Technol.*, 62, pp. 102–105, 2021.
 - [16]. G. I. Olasehinde, O. Ojuronbe, A. O. Adeyeba et al., “In vitro studies on the sensitivity pattern of *Plasmodium falciparum* to anti-malarial drugs and local herbal extracts,” *Malaria Journal*, vol. 13, article 63, 2014.
 - [17]. G. S. Chethana, K. R. Hari Venkatesh, F. Mirzaei, and S. M. Gopinath, “Review on multidrug resistant bacteria and its implication in medical sciences,” *Journal of Biological Scientific Opinion*, vol. 1, no. 1, pp. 32–37, 2013.
 - [18]. Garcia, E. Ly, N. Diep, J.K. Rao, G.G., Moving from point-based analysis to systems-based modeling: Integration of knowledge to address antimicrobial resistance against MDR bacteria. *Clin. Pharmacol. Ther.*, 110, pp. 1196–1206, 2021.
 - [19]. Georgopapadakou, N.H., Penicillin-binding proteins and bacterial resistance to β -lactams. *Antimicrob Agents Chemother*, 37(10), pp. 2045–2053, 1993.
 - [20]. H. Nikaido, “Multidrug resistance in bacteria,” *Annual Review of Biochemistry*, vol. 78, pp. 119–146, 2009.
 - [21]. Hoiby, N. Bjarnsholt, T. Givskov, M. Molin, S. Ciofy, O., Antibiotic resistance of bacterial biofilms. *Int. J. Antimicrob. Agents*, 35, pp. 322–332, 2010.
 - [22]. J. Fishbain and A. Y. Peleg, “Treatment of *Acinetobacter* infections,” *Clinical Infectious Diseases*, vol. 51, no. 1, pp. 79–84, 2010.
 - [23]. J. Loeffler and D. A. Stevens, “Antifungal drug resistance,” *Clinical Infectious Diseases*, vol. 36, no. 1, pp. S31–S41, 2003.
 - [24]. J. Suppiah, R. M. Zain, S. H. Nawi, N. Bahari, and Z. Saat, “Drug-resistance associated mutations in polymerase (p) gene of hepatitis B virus isolated from Malaysian HBV carriers,” *Hepatitis Monthly*, vol. 14, no. 1, Article ID e13173, 7 pages, 2014.
 - [25]. J. W. Bennett, J. L. Robertson, D. R. Hospenthal et al., “Impact of extended spectrum beta-lactamase producing *Klebsiella pneumoniae* infections in severely burned patients,” *Journal of the American College of Surgeons*, vol. 211, no. 3, pp. 391–399, 2010.
 - [26]. K. J. Cortez and F. Maldarelli, “Clinical management of HIV drug resistance,” *Viruses*, vol. 3, no. 4, pp. 347–378, 2011.
 - [27]. K. Nagamune, S. N. J. Moreno, and L. D. Sibley, “Artemisinin-resistant mutants of *Toxoplasma gondii* have altered calcium homeostasis,” *Antimicrobial Agents and Chemotherapy*, vol. 51, no. 11, pp. 3816–3823, 2007.
 - [28]. K. W. Hamilton and N. O. Fishman, “Antimicrobial stewardship interventions: thinking inside and outside the box,” *Infectious Disease Clinics of North America*, vol. 28, no. 2, pp. 301–313, 2014.
 - [29]. Khunweeraphong, N. Kuchler, K., Multidrug resistance in mammals and fungi—From MDR to PDR: A rocky road from atomic structures to transport mechanisms. *Int. J. Mol. Sci.*, 22, pp. 1–31, 2021.
 - [30]. Knight, G.M. Glover, R.E. McQuaid, C.F. Oлару, I.D. Gallandat, K. Leclerc, Q.J. Fuller, N.M. Willcocks, S.J. Hasan, R. van Kleef, E., Antimicrobial resistance and COVID-19: Intersections and implications. *Elife*, 10, pp. 1502–1510, 2021.
 - [31]. Kotra, L.P. Haddad, J. Mobashery, S., Aminoglycosides: perspectives on mechanisms of action and resistance and strategies to counter resistance. *Antimicrob Agents Chemother*, 44(12), pp. 3249–3256, 2000.
 - [32]. L. Qi and J. Cui, “A schistosomiasis model with praziquantel resistance,” *Discrete Dynamics in Nature and Society*, vol. 2013, Article ID 945767, 13 pages, 2013.
 - [33]. L. Rodero, E. Mellado, A. C. Rodriguez et al., “G484S amino acid substitution in lanosterol 14- α demethylase (ERG11) is related to fluconazole resistance in a recurrent *Cryptococcus neoformans* clinical isolate,” *Antimicrobial Agents and Chemotherapy*, vol. 47, no. 11, pp. 3653–3656, 2003.
 - [34]. L. Strasfeld and S. Chou, “Antiviral drug resistance: mechanisms and clinical implications,” *Infectious Disease Clinics of North America*, vol. 24, no. 2, pp. 413–437, 2010.
 - [35]. Lermينياux, N.A. Cameron, A.D.S., Horizontal transfer of antibiotic resistance genes in clinical environments. *Can. J. Microbiol.*, 65, pp. 34–44, 2019.
 - [36]. Lobie, T.A. Roba, A.A. Booth, J.A. Kristiansen, K.I. Aseffa, A. Skarstad, K. Bjørås, M., Antimicrobial resistance: A challenge awaiting the post-COVID-19 era. *Int. J. Infect. Dis.*, 111, pp. 322–325, 2021.
 - [37]. M. Ouellette, D. Légaré, and B. Papadopolou, “Multidrug resistance and ABC transporters in parasitic protozoa,” *Journal of Molecular Microbiology and Biotechnology*, vol. 3, no. 2, pp. 201–206, 2001.
 - [38]. M. Cuenca-Estrella, A. Gomez-Lopez, E. Mellado, M. J. Buitrago, A. Monzón, and J. L. Rodriguez-Tudela, “*Scopulariopsis brevicaulis*, a fungal pathogen resistant to broad-spectrum antifungal agents,” *Antimicrobial Agents and Chemotherapy*, vol. 47, no. 7, pp. 2339–2341, 2003.
 - [39]. M. N. Alekshun and S. B. Levy, “Molecular mechanisms of antibacterial multidrug resistance,” *Cell*, vol. 128, no. 6, pp. 1037–1050, 2007.
 - [40]. M. Vanaerschot, F. Dumetz, S. Roy, A. Ponte-Sucre, J. Arevalo, and J. C. Dujardin, “Treatment failure in leishmaniasis: drug-resistance or another (epi-) phenotype?” *Expert Review of Anti-Infective Therapy*, vol. 12, no. 8, pp. 937–946, 2014.
 - [41]. McKeegan, K.S. Borges-Walmsley, M.I. Walmsley, A.R., Microbial and viral drug resistance mechanisms. *Trends Microbiol.*, 10, pp. 8–14, 2002.
 - [42]. Migliori, G.B. Tiberi, S. Zumla, A. Petersen, E. Chakaya, J.M. Wejse, C. Muñoz Torrico, M. Duarte, R. Affenaar, J.W. Schaaf, H.S., MDR/XDR-TB management of patients and contacts: Challenges facing the new decade. The 2020 clinical update by the

- Global Tuberculosis Network. *Int. J. Infect. Dis.*, 92, pp. 15–25, 2020.
- [43]. Musso, M. Mosti, S. Gualano, G. Mencarini, P. Urso, R. Ghirga, P. Del Nonno, F. Goletti, D. Palmieri, F., Hepatitis C virus infection: A challenge in the complex management of two cases of multidrug-resistant tuberculosis. *BMC Infect. Dis.*, 19, pp. 1–4, 2019.
- [44]. N. S. Lurain and S. Chou, “Antiviral drug resistance of human cytomegalovirus,” *Clinical Microbiology Reviews*, vol. 23, no. 4, pp. 689–712, 2010.
- [45]. Nikaido H., “Multidrug resistance in bacteria,” *Annual Review of Biochemistry*, 78, pp. 119–146, 2009.
- [46]. Ohannessian, R. Bénet, T. Argaud, L. Guérin, C. Guichon, C. Piriou, V., Heat map for data visualization in infection control epidemiology: An application describing the relationship between hospital-acquired infections, Simplified Acute Physiological Score II, and length of stay in adult intensive care units. *Am J Infect Control*, 45(7), pp. 746–759, 2017.
- [47]. P. B. Bloland, Drug Resistance in Malaria, World Health Organization, 2001.
- [48]. P. G. Fallon and M. J. Doenhoff, “Drug-resistant schistosomiasis: resistance to praziquantel and oxamniquine induced in *Schistosoma mansoni* in mice is drug specific,” *The American Journal of Tropical Medicine and Hygiene*, vol. 51, no. 1, pp. 83–88, 1994.
- [49]. P. Wutzler, “Antiviral therapy of herpes simplex and varicella-zoster virus infections,” *Intervirology*, vol. 40, no. 5-6, pp. 343–356, 1997.
- [50]. Pelfrene, E. Botgros, R. Cavaleri M., Antimicrobial multidrug resistance in the era of COVID-19: a forgotten plight? *Antimicrobial resistance & infection control*, 10(1), pp. 1-6, 2021.
- [51]. Prasad, R. Goffeau, A., Yeast ATP-binding cassette transporters conferring multidrug resistance. *Annu. Rev. Microbiol.*, 66, pp. 39–63, 2012.
- [52]. R. C. Owens Jr., “Antimicrobial stewardship: concepts and strategies in the 21st century,” *Diagnostic Microbiology and Infectious Disease*, vol. 61, no. 1, pp. 110–128, 2008.
- [53]. R. M. Greenberg, “New approaches for understanding mechanisms of drug resistance in schistosomes,” *Parasitology*, vol. 140, no. 12, pp. 1534–1546, 2013.
- [54]. R. W. Moehring and D. J. Anderson, “Antimicrobial stewardship as part of the infection prevention effort,” *Current Infectious Disease Reports*, vol. 14, no. 6, pp. 592–600, 2012.
- [55]. S. Dzidic, J. Suskovic, and B. Kos, “Antibiotic resistance mechanisms in bacteria: biochemical and genetic aspects,” *Food Technology and Biotechnology*, vol. 46, no. 1, pp. 11–21, 2008.
- [56]. S. J. Howard and M. C. Arendrup, “Acquired antifungal drug resistance in *Aspergillus fumigatus*: epidemiology and detection,” *Medical Mycology*, vol. 49, no. 1, pp. S90–S95, 2011.
- [57]. S. Khalilzadeh, M. R. Bolloorsaz, A. Safavi, P. Farnia, and A. A. Velayati, “Primary and acquired drug resistance in childhood tuberculosis,” *Eastern Mediterranean Health Journal*, vol. 12, no. 6, pp. 909–914, 2006.
- [58]. S. Kunjachan, B. Rychlik, G. Storm, F. Kiessling, and T. Lammers, “Multidrug resistance: physiological principles and nanomedical solutions,” *Advanced Drug Delivery Reviews*, vol. 65, no. 13-14, pp. 1852–1865, 2013.
- [59]. S. M. Marks, J. Flood, B. Seaworth et al., “Treatment practices, outcomes, and costs of multidrug-resistant and extensively drug-resistant tuberculosis, United States, 2005–2007,” *Emerging Infectious Diseases*, vol. 20, no. 5, pp. 812–821, 2014.
- [60]. S. Margeridon-Thermet and R. W. Shafer, “Comparison of the mechanisms of drug resistance among HIV, hepatitis B, and hepatitis C,” *Viruses*, vol. 2, no. 12, pp. 2696–2739, 2010.
- [61]. S. Mohapatra, “Drug resistance in leishmaniasis: newer developments,” *Tropical Parasitology*, vol. 4, no. 1, pp. 4–9, 2014.
- [62]. Song, X. Liu, P. Liu, X. Wang, Y. Wei, H. Zhang, J. Yu, L. Yan, X. He, Z., Dealing with MDR bacteria and biofilm in the post-antibiotic era: Application of antimicrobial peptides-based nano-formulation. *Mater. Sci. Eng. C Mater. Biol. Appl.*, 128, pp. 112–118, 2021.
- [63]. V. Singh, “Antimicrobial resistance,” in *Microbial Pathogens and Strategies for Combating Them: Science, Technology and Education*, vol. 1, pp. 291–296, Formatex Research Center, 2013.
- [64]. Verweij, P.E. Chowdhary, A. Melchers, W.J. Meis, J.F., Azole resistance in *Aspergillus fumigatus*: Can we retain the clinical use of mold-active antifungal azoles? *Clin. Infect. Dis.* 62, pp. 362–368, 2016.
- [65]. World Health Organization, “Antimicrobial resistance,” 2014.
- [66]. X. He, S. Li, and S. G. Kaminskyj, “Using *Aspergillus nidulans* to identify antifungal drug resistance mutations,” *Eukaryotic Cell*, vol. 13, no. 2, pp. 288–294, 2013.
- [67]. X. Z. Li and H. Nikaido, “Efflux-mediated drug resistance in bacteria: an update,” *Drugs*, vol. 69, no. 12, pp. 1555–1623, 2009.
- [68]. Z. Yang, C. Li, M. Miao et al., “Multidrug-resistant genotypes of *Plasmodium falciparum*, Myanmar,” *Emerging Infectious Diseases*, vol. 17, no. 3, pp. 498–501, 2011.