Journal of Medical Genetics and Clinical Biology
Homepage : https://journal.antispublisher.id/index.php/JMGCB
Email : admin@antispublisher.com

e-ISSN : 3032-1085
JMGCB, Vol. 3, No. 2, February 2026
Page 200-209

What is the Antibiotic Resistance of Bacteria, Microbial Transmission, Mechanisms of Drug Resistance, and its Controls: A Mini Review

Ali Salman Jasim Al-Mamoor[1], Saja Salem Abdul Hassan Rasan[2], juman oday sabri[3], Halah Ali Abdulhussein Alsaleh[4], Lubna Abdulazeem[5]
[1]Al-Mustaqbal University, Iraq
[2]Islamic University - Al-Diwaniyah, Iraq
[3,4,5]University of Babylon, Iraq

Check for updates OPEN ACCESS

DOI : https://doi.org/10.61796/jmgcb.v3i2.1642

Sections Info

Article history:
Submitted: December 15, 2025
Final Revised: December 30, 2025
Accepted: January 12, 2026
Published: January 19, 2026

Keywords:
Antibiotics
Resistance
Antimicrobial
Superbugs
Efflux pumps

ABSTRACT

Objective: *The overuse and misuse of antibiotics in humans and agriculture is the main causes of antibiotic resistance, which occurs when bacteria evolve to survive antibiotics, making infections more difficult to treat, sometimes impossible, and potentially deadly.* ***Methods:*** *This study utilizes a review and analysis of existing literature on antibiotic resistance, focusing on the mechanisms by which bacteria evolve to survive antibiotics. Key techniques include the examination of molecular biology studies to identify bacterial resistance mechanisms such as drug inactivation, target modification, and efflux pumps. Additionally, observational data on human activity, including antibiotic misuse in both clinical and agricultural settings, are assessed to understand their role in accelerating the development of resistance. Case studies of "superbugs" like MRSA are also reviewed to demonstrate the clinical consequences of antibiotic resistance.* ***Results:*** *As a result, bacteria develop mechanisms like drug inactivation, target modification, or expulsion via efflux pumps, creating "superbugs" like MRSA.* ***Novelty:*** *Human activity speeds up this natural evolutionary process, which poses a serious danger to world health and necessitates careful antibiotic management and cleanliness.*

INTRODUCTION

Routes of microbial transmission

Microbial infections are the most prevalent in infectious diseases suffered by humans, and transmission pathways through which microbes can reach a susceptible host away from the source. This review is designed to define and elucidate the principal pathways of microbial transmission of infection and the significance of each pathway in disease spread, as well as outline how prevention measures limit transmission to protect public health [1].

For various kinds of germs, the routes vary – from person to person and in some cases through the air or other ways driven by the environment and human activity. An understanding of these routes of transmission is essential to the optimal control and management of preventing and managing infectious diseases at both the community level and healthcare settings [2].

RESEARCH METHOD

First, a direct transfer

The direct transfer of germs from someone who is sick to another person does not need an intermediary is direct transmission. This includes: Close contact, including

wounds, handshakes, and skin touches, and Respiratory droplets close: these are produced when someone coughs, sneezes, or speaks near you.

This route can make many infectious diseases more contagious, particularly in crowded areas [3].

Secondly, there is indirect transmission

Indirect transmission: This is through contaminated media that could be; Contaminated articles or surfaces, e.g., door handles, medical instruments, and Contaminated food and water. You can also get microbes from eating or drinking contaminated food. This road is often traveled in unsanitary conditions [4].

Third: Air transportation

People who are far from the source of infection can inhale germs that are suspended in the air for long periods of time within microscopic particles. This is known as airborne transmission. This pathway is regarded as one of the riskiest since it is difficult to manage, particularly in enclosed settings with inadequate ventilation [5].

Fourth: Transmission through living agents

Living things that spread bacteria from one diseased host to another are known as vectors. Examples of this include insects like flies and mosquitoes [Rodents: they might spread several diseases], In some regions that are connected to the existence of certain vectors, this route aids in the spread of illnesses [6].

Fifth: Becoming human from an animal

This kind of transmission is called zoonotic illness, and it occurs when bacteria are transferred from animals to people by direct contact, polluted environments, or unfit animal food. The vital connection between animal and human health is emphasised by this pathway [7].

Sixth: Is transmission from mother to fetus

During pregnancy, delivery, or nursing, some bacteria can be passed from an infected mother to the foetus, potentially causing health issues for the infant [8]. Resistance to antibiotics is a natural occurrence that is increased by misuse of antibiotics, but these are not the only causes. Therefore, the most important strategies to prevent from spreading this issue and protect public health include more prudent consumption of drugs, physicians' instructions, and designing new therapeutic methods [9].

The risk to human and animal health due to antimicrobial resistance is rising, which results from economic, environmental, and non-judicious use of drugs in a variety of ways. Enhanced health monitoring, public education campaigns, support of scientific research, and judicious use of antibiotics represent interrelated approaches that should be applied to the problem. To protect human health and a more secure, healthy future, antimicrobial resistance needs to be addressed as a one-health issue [10].

Tackling the complex problem of AMR needs a "top-down policy, regulation, and civilization" multi-layered platform. To accomplish this, the medical, veterinary, and environmental sectors will need to work together within a One Health framework. AWARENESS Raising public awareness and responsible use of antibiotics, as well as

innovation, are building blocks that can slow this threat to our health, the health of our children, and future generations [11], [12].

Microbes can spread in a variety of ways, which will depend on what type of bacterium it is and the setting, as well as how much hygiene you practice [13]. While personal hygiene, purified food and water, control of infection, and knowledge of sanitation are indispensable in combating contagious diseases, there is a need to understand the mechanisms for achieving these pathways when planning to prevent infectious-germ diseases. A crucial aspect of protecting the public health and mitigating disease transmission is control of channels for the dissemination of information [14], Fig. 1.

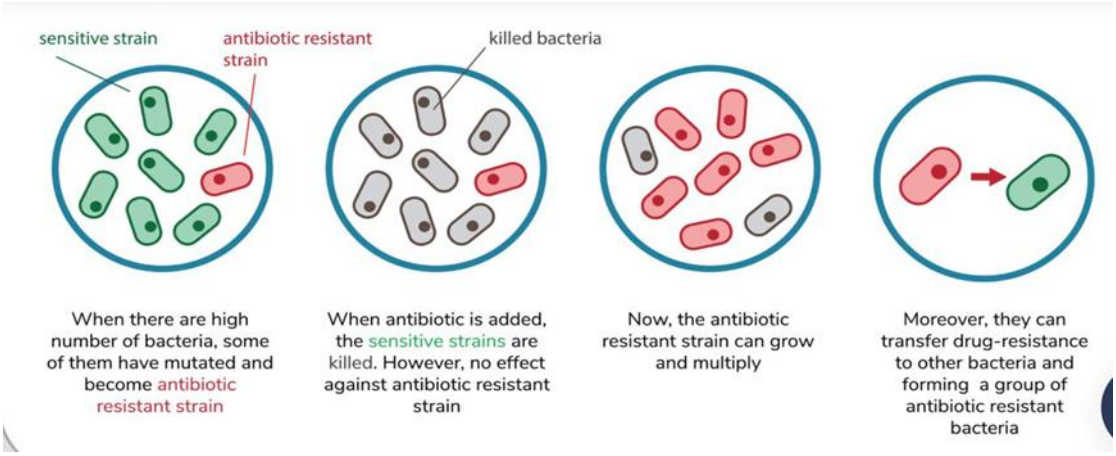

Figure 1. Antibiotic resistance, or how bacteria become resistant.

RESULTS AND DISCUSSION

Mechanisms of drug resistance acquisition among bacteria

One of the central health problems facing civilization right now is antibiotic resistance, in which many infectious diseases no longer respond to treatment, lengthening and adding to illness, and elevating death rates. This is what happens when bacteria gain the ability to resist and multiply even in the presence of antibiotics that are supposed to kill them. Several pathways have been identified that are involved in this resistance, e.g., genetic, biochemical, and behavioral ones [15].

First: Genetic mutations

During the multiplication of bacteria, random genetic changes take place. Some of these changes can change the structure of proteins or enzymes that antibiotics target, making it impossible for the medication to attach to or have an impact on the bacterium. germs with the resistant mutation live and proliferate when the antibiotic is applied, but susceptible germs perish [16].

Second: Horizontal transfer of genes

In addition to mutations, bacteria may also exchange genes with one another through a process called horizontal transfer, the most significant of which are:

- Bacterial conjugation: the process by which resistance genes are passed from one bacteria to another using plasmids.

- Transformation: The process by which bacteria take up resistance genes found in their surroundings.
- Phage transfer: the transmission of genes by bacterial viruses.

These processes aid in the rapid spread of drug resistance across many bacterial species [16].

Third: Enzyme synthesis that renders the antibody inactive

Certain bacteria create enzymes, such as those that break down specific medication types, that can deactivate or break down antibiotics before they can start working. Consequently, the medication becomes ineffective and is unable to eradicate the infection [17].

Fourth: Reducing drug permeability or expelling it from the cell

Bacteria may alter the structure of their cell wall or membrane, reducing the entry of antibiotics. Some bacteria also possess special pumps that rapidly expel the drug from the cell before it can take effect [18].

Fifth: Shifting the influence's position

Sometimes bacteria alter the drug's target (such as ribosomes or essential enzymes), making it impossible for the antibiotic to recognize or attach to it while the bacteria carry on with their regular activities [19], Fig. 2.

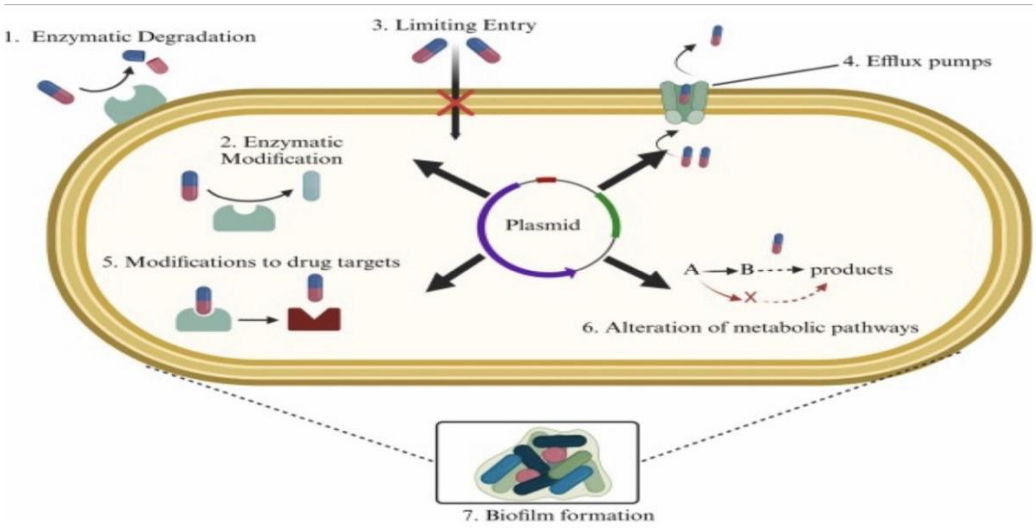

Figure 2. Mechanisms of bacterial resistance.

The impact of antimicrobial resistance on human and animal populations

Antimicrobial resistance (AMR) is one of the most formidable global public health and environmental challenges with consequences directly influencing human and animal health, as well as the health systems and economies [20]. This paper aims to outline the impact of AMR on human and animal populations, demonstrate how the two are connected, while emphasizing that a holistic approach must be taken in addressing this problem [21].

Antibiotics, widely used in human and veterinary medicine, have revolutionized the practice of infectious disease control. Nevertheless, the excessive or inappropriate use

of these medicines has led to the development of resistant bacteria, challenging their validity. Since AMR can cross over to affect humans, animals, and the environment, it is a global health issue [22].

First, how human health is impacted by antibiotic resistance

Antibiotic resistance affects humans in several ways, the most important of which are as follows:

1. Medical treatment failure: As for some infections, there can be (in some cases) no cure or a very difficult-to-treat and chronic condition.
2. Increased death rates: People with resistant infections may have a greater chance of dying, and this is particularly true among children and the elderly.
3. More costly medicine: Patients require other, more expensive drugs and longer hospital stays.
4. Risk to modern medicine: Surgery, cancer care, and organ transplants all require antibiotics to prevent infections [23].

Two, the effects of antibiotic resistance on animal health

Animals are also impacted by antimicrobial resistance, especially pets and farm animals:

1. Rise in animal illnesses: Bacterial infections become harder to combat, leading to the death of animals or decreased production.
2. Losses of livestock: Resistance has an impact on the dairy and meat industry by decreasing milk/meat production, and increasing cost of treatment.
3. Human transmission: Humans can get resistant bacteria from animals through food, close contact, or the environment [24].

Third: The human-animal relationship (One Health approach)

AMR is a reflection of the One Health approach that highlights the interconnectedness of diseases from animals, the environment, and humans. The extensive use of antibiotics in animal farming has given rise to the emergence of antibiotic-resistant bacteria that also affect humans, and traces of a variety of drugs impregnate water environments as well, these species of resistance being disseminated through our environment [25].

Fourth: The effects on society and the economy

The effects of antimicrobial resistance extend beyond health problems, including: • An increased burden on healthcare systems.

- There is a risk to food security due to the decrease in animal productivity.
- Negative effects on economic development, especially in developing countries.
- The increasing health discrepancy across populations is due to unequal access to proper medicines [26], [27].

Challenges in addressing antimicrobial resistance

Antimicrobial resistance (AMR) has been identified as one of the most critical global health challenges of the twenty-first century, posing a threat to the effectiveness of medical treatments and reversing progress made in combating infectious diseases. This

study aims to assess the most important barriers against international initiatives to decrease AMR, focusing on scientific, medical, legal, and economic aspects [28].

Millions of people have been saved by antimicrobials, but during the process, resistant bacteria have rapidly evolved. Due to its multifactorial etiology and the interaction of variables, this issue is dangerous in nature and demands complex solutions that may integrate public health, research science, as well as health policy [29], Fig.3.

Figure 3. Bacteria are developing new ways to resist antibiotics.

First, scientific and medical difficulties

1. The fast evolution of microorganisms: Bacteria and other microbes form new resistance much faster than new drugs can be developed, due to their enormous potential for adaptation through mutations and gene transfer [30].
2. Few other treatment options: With no effective antibiotics for several resistant diseases, doctors are simply unable to treat them.
3. Poorly diagnosed: Misdiagnosis could cause an unnecessary use of antibiotics, which would generate resistance.

Second: Obstacles related to the application of antibiotics

- Overuse and misuse: This might involve failing to complete a course of treatment, taking antibiotics at inappropriate dosages, or being prescribed with no medical need.
- In agriculture and animal husbandry: The broad utilization of antibiotics for preventative or growth-promoting purposes is another driver for the rise of resistance.
- Free access to drugs: In several countries, antibiotics are sold over-the-counter without a prescription, leading to increased abuse [31].

Third: Research and economic difficulties

1. Insufficient investment in the development of new drugs: Pharmaceutical companies have financial challenges as a result of the low economic return compared to chronic treatments.

2. High research and development costs: Developing a new antibiotic is a costly, time-consuming, and sometimes unsuccessful procedure.
3. Inequality in treatment access: Low-income countries lack access to modern diagnostic instruments and effective antibiotics [32], [33].

Fourth: Issues with legislation and regulations

1. Health policy deficiencies: Inadequate national antimicrobial resistance plans are implemented in some nations.
2. Absence of monitoring systems: Making evidence-based decisions is challenging in the absence of reliable data on resistance trends.
3. Inadequate international collaboration: Because antimicrobial resistance is transboundary, efforts are limited by the absence of international cooperation [34].

Fifth: Awareness and social issues

1. Low community awareness: Many individuals are unaware of the risks associated with antibiotic abuse.
2. Unhealthy practices include trading prescriptions or putting medications away for later use.
3. Myths: The notion that medications can treat any illness, including viral ones [35], [36], [37].

Controls of Antibiotic Resistance

It is possible to combat antimicrobial resistance by controlling antibiotic resistance. They include enhancing sanitation and hygiene, implementing infection control strategies to stop the spread of resistant bacteria, creating new antimicrobials that bacteria are not resistant to, and strengthening conservation initiatives to preserve the efficacy of both new and old antimicrobials [38], [39], [40], [41]. cautious use of antibiotics, support vaccinations and their substitutes, and encourage quick and innovative diagnostics to cut down on needless and empirical antimicrobial treatment [42], [43].

CONCLUSION

Fundamental Finding : Antimicrobial resistance, because the processes protecting its survival, even in the absence of selective pressure from antibiotic usage, are not fully understood, the establishment of antimicrobial resistance may be unavoidable in the evolutionary process. **Implication :** By controlling and monitoring the use of antibiotics, providing farmers and animal owners with expert guidance, and working with the human healthcare industry, veterinary services, including veterinarians and veterinary paraprofessionals, play a critical role in combating antimicrobial resistance. This highlights the importance of a coordinated approach across sectors to reduce the spread of resistance. **Limitation :** Despite ongoing efforts, the full understanding of resistance mechanisms remains elusive, and the inevitability of resistance development poses a significant challenge. This limits the immediate effectiveness of existing strategies to combat resistance. **Future Research :** Developing innovative tactics to counter this danger requires a thorough grasp of the resistance mechanisms. We must be aware that germs will become resistant to both new and old antibiotics, which is a reality of evolution. As

a result, research on the mechanisms of resistance and efforts to produce new antibiotics should be persistent and robust. This is most likely a protracted "war" against organisms that are highly capable of adaptability and survival.

REFERENCES

[1] K. J. Aldred, R. J. Kerns, and N. Osheroff, "Mechanism of quinolone action and resistance," *Biochemistry*, vol. 53, no. 10, pp. 1565–1573, 2014.

[2] C. Costelloe, C. Metcalfe, A. Lovering, D. Mant, and A. D. Hay, "Effect of antibiotic prescribing in primary care on antimicrobial resistance in individual patients: A systematic review and meta-analysis," *BMJ*, vol. 340, 2010.

[3] L. Fernández and R. E. W. Hancock, "Adaptive and mutational resistance: Role of porins and efflux pumps in drug resistance," *Clin. Microbiol. Rev.*, vol. 25, no. 4, pp. 661–681, 2010.

[4] A. H. Holmes *et al.*, "Understanding the mechanisms and drivers of antimicrobial resistance," *Lancet*, vol. 387, no. 10014, pp. 176–187, 2016.

[5] H. Hao *et al.*, "Benefits and risks of antimicrobial use in food-producing animals," *Front. Microbiol.*, vol. 5, p. 288, 2014.

[6] H. K. Allen *et al.*, "Call of the wild: Antibiotic resistance genes in natural environments," *Nat. Rev. Microbiol.*, vol. 8, no. 4, pp. 251–259, 2010.

[7] K. Akata, T. Muratani, K. Yatera, K. Naito, and T. Noguchi, "Induction of plasmid-lactamase DHA β-lactams in Enterobacteriaceae," *PLoS One*, vol. 14, no. 7, e0218589, 2019.

[8] S. Bansal, P. Bajaj, S. Pandey, and V. Tandon, "Topoisomerases: Resistance versus sensitivity, how far we can go," *Med. Res. Rev.*, vol. 37, no. 2, pp. 404–438, 2017.

[9] A. Bharadwaj *et al.*, "Multidrug-resistant bacteria: Their mechanism of action and prophylaxis," *BioMed Res. Int.*, vol. 2022, Art. no. 5419874, 2022.

[10] J. M. A. Blair *et al.*, "Molecular mechanisms of antibiotic resistance," *Nat. Rev. Microbiol.*, vol. 13, pp. 42–51, 2015.

[11] M. E. Böhm *et al.*, "Discovery of a novel integron-borne aminoglycoside resistance gene present in clinical pathogens by screening environmental bacterial communities," *Microbiome*, vol. 8, no. 1, pp. 1–11, 2020.

[12] Z. Breijyeh, B. Jubeh, and R. Karaman, "Resistance of gram-negative bacteria to current antibacterial agents and approaches to resolve it," *Molecules*, vol. 25, no. 6, p. 1340, 2020.

[13] A. Checcucci *et al.*, "Exploring the animal waste resistome: The spread of antimicrobial resistance genes through the use of livestock manure," *Front. Microbiol.*, vol. 11, p. 1416, 2020.

[14] F. Hemmati *et al.*, "Quorum quenching: A potential target for antipseudomonal therapy," *Infect. Drug Resist.*, vol. 13, pp. 2989–3005, 2020.

[15] M. P. Motley, K. Banerjee, and B. C. Fries, "Monoclonal antibody-based therapies for bacterial infections," *Curr. Opin. Infect. Dis.*, vol. 32, pp. 210–216, 2019.

[16] G. Subramaniam and M. Girish, "Antibiotic resistance—A cause for reemergence of infections," *Indian J. Pediatr.*, vol. 87, pp. 937–944, 2020.

[17] European Centre for Disease Prevention and Control, "Antimicrobial resistance in the EU/EEA (EARS-Net): Annual epidemiological report 2019," 2020.

[18] D. Matzov, A. Bashan, and A. Yonath, "A bright future for antibiotics?" *Annu. Rev. Biochem.*, vol. 86, pp. 567–583, 2017.

[19] G. Haidar *et al.*, "Ceftolozane-tazobactam for the treatment of multidrug-resistant *Pseudomonas aeruginosa* infections," *Clin. Infect. Dis.*, vol. 65, pp. 110–120, 2017.

[20] P. A. Fraile-Ribot *et al.*, "Mechanisms leading to in vivo ceftolozane/tazobactam resistance

development," *J. Antimicrob. Chemother.*, vol. 73, pp. 658–663, 2018.
[21] Z. Hamzaoui *et al.*, "Role of OmpK35 and OmpK36 alteration and bla genes in carbapenem resistance," *Int. J. Antimicrob. Agents*, vol. 52, pp. 898–905, 2018.
[22] N. Atac *et al.*, "Role of AcrAB-TolC efflux pumps on quinolone resistance of *E. coli* ST131," *Curr. Microbiol.*, vol. 75, pp. 1661–1666, 2018.
[23] G. Morroni *et al.*, "High rate of ceftobiprole resistance among MRSA isolates," *Antimicrob. Agents Chemother.*, vol. 62, 2018.
[24] L. Poirel *et al.*, "High rate of association of 16S rRNA methylases and carbapenemases," *Antimicrob. Agents Chemother.*, vol. 62, 2018.
[25] X. Wang *et al.*, "Emergence of a novel mobile colistin resistance gene mcr-8," *Emerg. Microbes Infect.*, vol. 7, p. 122, 2018.
[26] J. K. Bender *et al.*, "Emergence of transferable resistance gene optrA," *Int. J. Antimicrob. Agents*, vol. 52, pp. 819–827, 2018.
[27] M. Kussmann *et al.*, "Emergence of dalbavancin-induced non-susceptible *S. aureus*," *Emerg. Microbes Infect.*, vol. 7, p. 202, 2018.
[28] A. H. Holmes *et al.*, "Understanding the mechanisms and drivers of antimicrobial resistance," *Lancet*, vol. 49, no. 7, pp. 2680–2684, 2016.
[29] R. Moutafchieva and D. Mladenov, "Antimicrobial resistance: Review," *Trakia J. Sci.*, vol. 18, no. 4, pp. 401–404, 2020.
[30] M. E. Böhm *et al.*, "Discovery of a novel integron-borne aminoglycoside resistance gene," *Microbiome*, vol. 8, no. 1, pp. 1–11, 2020.
[31] A. Checcucci *et al.*, "Exploring the animal waste resistome," *Front. Microbiol.*, vol. 11, p. 1416, 2020.
[32] B. Das *et al.*, "Antibiotic resistance in *Vibrio cholerae*," *Vaccine*, vol. 38, no. 1, pp. A83–A92, 2020.
[33] T. Gil-Gil, J. L. Martínez, and P. Blanco, "Mechanisms of antimicrobial resistance in *Stenotrophomonas maltophilia*," *Expert Rev. Anti Infect. Ther.*, vol. 18, no. 4, pp. 335–347, 2020.
[34] T. H. Hasan and R. A. Al-Harmoosh, "Mechanisms of antibiotics resistance in bacteria," *Syst. Rev. Pharm.*, vol. 11, no. 6, pp. 817–823, 2020.
[35] S. A. Khan *et al.*, "Antimicrobial resistance via food chain," *BMC Vet. Res.*, vol. 16, p. 302, 2020.
[36] K. Kitagawa *et al.*, "Use of oral cephalosporins and quinolones and resistance," *Spinal Cord*, vol. 58, pp. 705–710, 2020.
[37] O. Lomovskaya *et al.*, "Impact of intrinsic resistance mechanisms on QPX7728," *Antimicrob. Agents Chemother.*, vol. 64, no. 6, e00552-20, 2020.
[38] O. Schwengers *et al.*, "Platon: Identification of bacterial plasmid contigs," *Microb. Genomics*, vol. 6, 2020.
[39] S. A. Shaikh *et al.*, "From drug target to leads," *Curr. Pharm. Des.*, vol. 13, no. 34, pp. 3454–3470, 2007.
[40] L. K. Sharkey and A. J. O'Neill, "Molecular mechanisms of antibiotic resistance," in *Bacterial Resistance to Antibiotics*, Wiley-Blackwell, 2019, pp. 27–50.
[41] O. Makarewicz *et al.*, "Antibiotic resistance in pulmonary infections," in *Anti-Infectives and the Lung*, ERS Monograph, 2017.
[42] M. R. Meini, L. I. Llarrull, and A. J. Vila, "Catalytic mechanism of metallo-lactamases," *FEBS Lett.*, vol. 589, no. 22, pp. 3419–3432, 2015.
[43] K. I. Mohr, "History of antibiotics research," *Curr. Top. Microbiol. Immunol.*, vol. 398, pp. 237–272, 2016.

Ali Salman Jasim Al-Mamoor
Al-Mustaqbal University, Iraq

Saja Salem Abdul Hassan Rasan
Islamic University - Al-Diwaniyah, Iraq

Juman Oday Sabri
University of Babylon, Iraq

Halah Ali Abdulhussein Alsaleh
University of Babylon, Iraq

Lubna Abdulazeem
University of Babylon, Iraq