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Antibiotics resistance genes in the environment, risk factors and control: A review

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ABSTRACT

Antibiotics resistance represents a global threat affecting human, animal and environment. Incorrect and over use of antibiotics in medicine, animal husbandry and agriculture leading to the continuous discharge of residual antibiotics into the environment which promote the spread of resistance genes. This review focus on antibiotics resistant genes, risk factors associated with its spread in the environment and control measurements. Environmental pollution, poor hygiene and untreated waste were characterized as major risk factors in the proliferation of antibiotic-resistant strain. Resistance can arise through genetic mutation or acquisition of new genetic material which can transfer between bacteria through genetic exchange that facilitate the spread of resistance pathogens. Strict management strategies especially promising drug combination, stewardship programs should be applied to increase antibiotic efficacy for treatment bacterial infections.

Keywords: Antibiotics, Resistant genes, Bacteria, Environment, Risk factors, Control measurements.

Introduction

Antibiotics are natural metabolic products or their derivatives produced by bacteria, fungi or Actinomycetes with killing or inhibiting growth of other competing microorganisms (Pandey. and Kumar, 2015). Since their discovery in the 20th century, these agents can be used in treatment of diseases and livestock farming (Hao *et al.*, 2014; Bacanli *et al.*, 2019; Hutchings *et al.*, 2019). Resistance to antibiotics is a global health problem with emergence of multi-drug resistant (MDR) strains can cause million deaths annually involving the dissemination of bacteria or their genes between human, animals and environments (Larsson and Flach, 2022). Human infections by antibiotics resistant bacteria resulting in delayed, inadequate or even failed patient outcomes particularly in hospital nosocomial infections (Tacconelli, 2006; Blair *et al.*, 2015). Diverse antibiotics resistance genes (ARGs) are identified in accordance with class of antibiotics to which they confer resistance, these included: (tet) for tetracycline, (erm) for macrolides, (bla) for β-lactams, (sul) for sulfonamides, (fca) for fluoroquinolone, (aac) for aminoglycosides, (van) for vancomycin, (mcr) for colistin and (mdr) for multidrug (He *et al.*, 2020; Jian *et al.*, 2021). Resistance can be arisen from mutation in the genome of bacteria or uptake of new genetic materials through genetic exchange, these changes allow bacteria to grow and survive in the environments even antibiotic is present (Larsson and Flach, 2022).

Antibiotics exert their effects on bacterial cell by the following mechanisms: inhibition of cell wall synthesis, inhibition of nucleic acid synthesis, block protein synthesis, interaction with cell membrane permeability, antibiotics inhibit folic acid synthesis (Haddad *et al.*, 2024). The persistent misuse and overuse of antibiotics in human and animal husbandry, agriculture played a significant role in promoting emergence and selection of antibiotics resistance (Ahmed *et al.*, 2024) .

This review summarized on antibiotics and ARGs that spread in the environments which create a great risk for human and animal health, studying risk factors and control measurements.

Environmental Risk Factors Affect the Spread of Antibiotics Resistance Genes: Environmental risk factors contribute to development and spread of antibiotic-resistant bacteria and antibiotics resistant genes, these include: poor hygiene, transmission of antibiotics resistant in clinical setting, in proper disposal of untreated waste for human and animal, use of antibiotics in aquaculture, agriculture and animal farming can promote spread of such resistance (Adenaya *et al*., 2025). There are different ways for antibiotics entry into the environment which affect human health and ecology, the main ways are water bodies and soil (Qiu *et al*., 2016; Ugbo *et al*., 2025). Exposure of human to antibiotics resistant bacteria and their genes in aquatic environment create a critical setting for spread and transmission of antibiotic resistance. *bla*NDM-1 gene was detected among carbapenem-resistant *Klebsiella pneumoniae* in Al-Hillah River water**,** Babylon Province, Iraq (Almarasini *et al*., 2020; Abbas,2021). Another study carried out in China documented that feces of human and livestock contained 57.6% and 42.6% of medical and veterinary antimicrobials residues, respectively (Chen *et al*., 2020).

Polyaromatic hydrocarbons are other factor affecting the spread of antibiotic resistance genes. A study detected high prevalence of ARGs for high quantity of antibiotics classes like: aminoglycosides, sulfonamide, tetracyclines, floroquinolones and ampicillin in polyaromatic hydrocarbons polluted areas. (Maurya *et al*., 2021).

Control Measurements for Resistance to Antibiotics: Antibiotics resistance in the environment can be controlled by reducing antibiotics resistant bacteria and their genes entry into the environment:

1-Appropriate drug use and stewardship programs: Correct use of antibiotics and antibiotic stewardship programs and refining can reduce antibiotic exposure, and thus lower the prevalence of antibiotic resistance in the environment.

2- Combination and alternative therapeutic strategies: Combination of two drugs or more have great therapeutic effect than their individual alone. Alternative strategies are required for treatment bacterial infections that represent effective way to control critical threat due to drug resistant pathogens. Alternative treatment options include: vaccination, phage therapy, Quorum sensing inhibition (Singh and Kim, 2025).

2-1-Drug combination therapy: Monotherapy by antibiotics can cause continuous emergence of resistance to available agent, so combination therapy is more effective such as combination of aminoglycosides with other antibiotics exhibit a synergistic antibacterial effect (Khanna, 2023).

2-2-Drug combination with inhibitors: One of the most common resistant mechanism of bacteria to antibiotics is the enzymatic inactivation of beta-lactam antibiotics by beta-lactamases. Other resistant mechanism is changing cell membrane permeability and efflux pump. Targeting this pathway to block evolution of resistance. Inhibitors of beta-lactamases are important to increase the effectiveness of beta-lactam antibiotics and prevent resistant (Tamma and Villagas, 2017; Gurello and MacDougall, 2023; Khanna, 2023). Clavulanate, sulbactam, vaborbactam, relebactam, tazobactam and avibactam are examples of beta-lactamase inhibitors which combined with beta lactam drug in combination with beta-lactam drugs to enhance the efficacy of drug (Letourneau and Calderwood, 2020).

3- Other anti- pathogenic techniques: like antimicrobial peptides (e.g., Bacteriocins, diptericins, microcins, defensins, ceprocins, Cathelcidins, etc.) are considered as efficient alternatives methods as compared to conventional antimicrobials in combating drug-resistant diseases caused by bacteria ((Singh and Kim, 2025).

Conclusions

Disease prevention is the most efficient strategy to control infections, then reducing the emergence of drug-resistant isolates. Exposure of bacteria to antibiotics in environment speed the evolution of resistant strains. Resistance transferred easily from one bacterium to another by genetic exchange. So strong strategies must be applied to limit the spread of resistant pathogens. Increased hygienic measures in hospitals, stewardship program, drug combination to enhance the effectiveness of the drug, alternative therapy to treat bacterial diseases are needed.

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