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ANTIBIOTIC USE IN FOOD ANIMAL AND THE DEVELOPMENT OF ANTIBIOTIC RESISTANT BACTERIA

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Abstract: *Antibiotic resistance is a major issue that has been steadily increasing and spreading over the last decade. This review will briefly discuss the impact of antibiotic residues in food products, the mechanism of development of antibiotic resistance, and the transmission of resistance.*

Keywords: *Antibiotic resistance, antibiotic residue, food animals.*

Introduction.

Antibiotic resistance is a major issue that has been steadily increasing and spreading over the last decade. Overuse or serious misuse of antibiotics is the key underlying mechanism causing this problem. Antibiotics are still widely utilized, not just for the treatment of human diseases but also, to a large extent, in agriculture, cattle, and animal husbandry, despite this increasing worldwide concern. If the current situation continues, we may soon find ourselves in a post-antibiotic period where pharmaceuticals may be unable to treat even the most basic infections. This review will briefly discuss the impact of antibiotic residues in food products, the mechanism of development of antibiotic resistance, and the transmission of resistance.

Impact of antibiotic residue in food products.

Antibiotics pose a risk to human health in two ways: adverse drug reactions (ADR) and the possible prevalence of antibiotic resistance by exerting selective pressure on clinically important bacteria.

Allergies are one of the most serious side effects of antibiotics in food. Many antibiotics and medications might cause allergic responses. The majority of the information is about penicillin, aminoglycoside, and tetracycline hypersensitivity (Merve Bacanlı and Nurşen Başaran, 2019). Urticaria, angioneurotic edema, gastrointestinal responses, aplastic anemia, shock, and mortality are the frequent signs of allergic reactions (Solensky and Solensky, 2012). Antibiotics have yet to be studied for their long-term effects on human health (Merve Bacanlı and Nurşen Başaran, 2019).

Antibiotics with β -lactams are less harmful. However, it has been determined that they are to blame for the majority of antimicrobial-related allergic reactions in people (Davies and Davies, 2010).

Because of the transportable qualities of resistance, the most serious adverse consequence of antibiotic residues is the transmission of antibiotic resistant microorganisms to people. Diseases caused by antibiotic-resistant bacteria kill more individuals. Antibiotic-resistant bacteria are expected to kill more people than cancer by the year 2050 (Merve Bacanlı and Nurşen Başaran, 2019). The transmission could happen through the food chain or through animal handling (Merve Bacanlı and Nurşen Başaran, 2019).

From the above-mentioned studies and many other research articles, we can conclude that the main concern in the use of antibiotics for therapeutic and non-therapeutic purposes should be the risk of the development of antibiotic-resistant bacteria and their circulation in the eco-systems.

Mechanism of development of antimicrobial resistance.

Microorganisms have evolved sophisticated ways to avoid being destroyed by numerous harmful substances through a Darwinian selection process. Only a few antimicrobial medications (such as sulphonamides and fluoroquinolones) are entirely synthetic, as they are produced naturally by microorganisms such as environmental fungus and saprophytic bacteria (Alison H Holmes et al. 2016). The resistance acquired against β -lactam antimicrobial medications, in which the enzymes (β -lactamases) that inactivate these antibiotic compounds have lived for millions of years, is an example of a naturally occurring resistance mechanism that has had an influence on human health (Alison H Holmes et al. 2016).

Antibiotic resistance can arise through a variety of ways, including mutations in a bacterial cell's genome, changes in the proteome, the creation of bacterial cell contacts, and the horizontal gene transfer of plasmids (Shousha et al. 2015). Antibiotic resistance is also influenced by the microbiota of the human gut, particularly in hospitalized patients. (2018, San Millan) Antibiotic resistant genes in the gut microbiome can be horizontally transmitted from pathogenic species and exchanged amongst resident species (Merve Bacanlı and Nurşen Başaran, 2019). Conjugative plasmids are critical for the spread of resistance genes in the gut.

Antibiotic resistance mechanisms used by various microorganisms can be divided into two categories: (i) mechanisms with a genetic foundation for microbial resistance, and (ii) mechanisms with a mechanistic basis for antimicrobial resistance. Genetic resistance develops as a result of mutations that alter antimicrobial targets, decrease drug absorption, enhance chemical efflux, and alter metabolic pathways, as well as horizontal gene transfer via transformation, transduction, and conjugation (Avantika Mann et. Al 2021). Mechanistic resistance, on the other hand, arises when antimicrobial molecules are modified, chemicals are prevented from reaching antimicrobial targets, target sites are bypassed, and resistance is caused by global cell adaptation mechanisms (Jose et al., 2017).

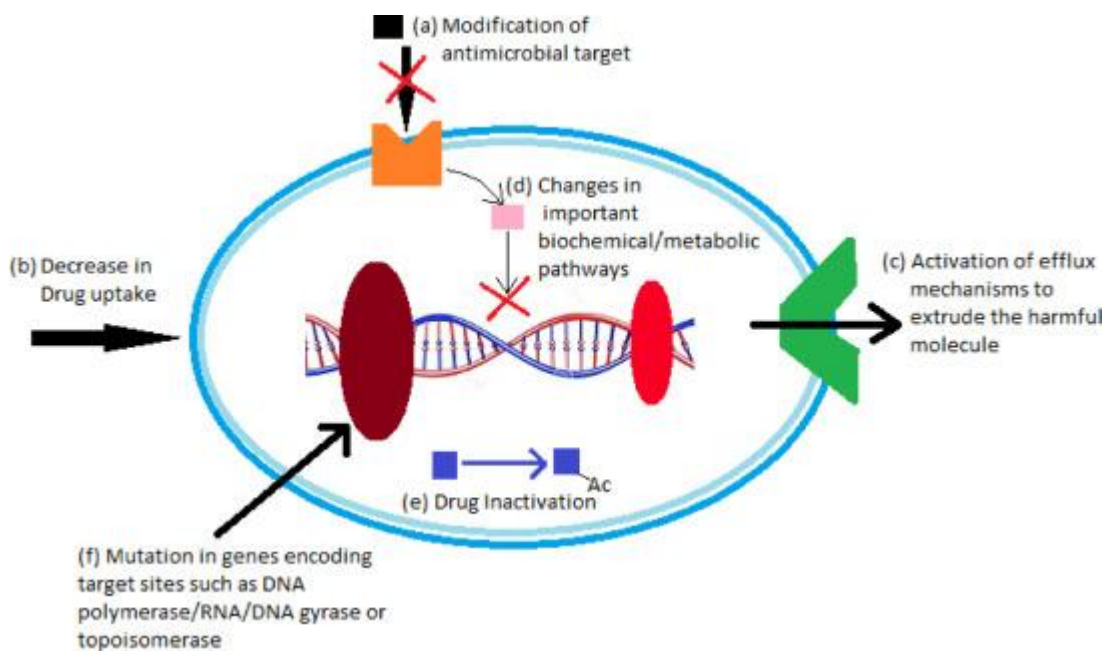


Fig.1. Antibiotic resistance mechanisms used by microorganisms (bacteria) (Avantika Mann et. Al 2021)

Transmission of resistance.

ABR can spread through direct or indirect contact throughout the food chain. Direct contact occurs when humans are exposed to animals and biological substances (such as blood, urine, feces, milk, saliva, and sperm), and it facilitates the spread of resistant germs from one host to another (Founou et al., 2016), through aquaculture and with manure-contaminated habitats, and in particular the environment plays a crucial role since it can act as a reservoir for antibiotic resistance genes (Economou et al., 2015). Workers who are exposed to antibiotic-resistant bacteria on the job, such as veterinarians, farmers, abattoir workers, and food handlers, as well as those who come into direct touch with them, are at a greater risk of becoming colonized or infected (Marshall and Levy, 2011). Exposed employees and their families are increasingly recognized as a plausible pathway for antibiotic-resistant bacteria and ARGs to enter the community and health-care settings, where further exchanges and the procurement of resistance mechanisms are obvious. Moreover, the coexistence of these elements with harmful bacteria in many habitats, including the human gut, may lead to the emergence of resistant strains. (Marshall and Levy, 2011).

Furthermore, humans may be exposed to antibiotic-resistant bacteria and ARGs indirectly through interaction with or ingesting contaminated food products (e.g., meat, eggs, milk, and dairy products). This indirect spread across the food chain is a more advanced and more complicated route (Founou et al., 2016). Acar and Moulin (2006) and Marshall and Levy (2011) found comparable or clonally interrelated antibiotic-resistant bacteria and ARGs of animal source in humans without occupational contact, implying that they were transferred through food consumption and/or handling.

According to Padungtod et al. (2008), the public health hazard is commonly associated with both the direct and indirect transmission of antibiotic-resistant bacteria and ARGs in developing countries, where inadequate biosafety and food

safety procedures are practiced farm-to-fork and where close humans to animals and the environment interact, whereas EFSA and ECDC (2015) noted that the indirect spread appears to be more frequent in developed countries as antibiotic-resistant bacteria and ARGs from the farm are maintained in the food product to reach the final consumers.

Although the immediate threat of antibiotic-resistant foodborne pathogens is more obvious, the transfer of antimicrobial resistance features through the genetic pool housed in bacteria, bacteriophages, or DNA fragments is likely the most dangerous circumstance (Economou et al. 2015). Horizontal gene transfer, which is how most bacteria transfer antibiotic resistance genes, can happen in any matrix. Nonetheless, it is more likely in dietary categories with high microbial cell counts (fermented, minimally processed, or raw foods) (Rossi et al., 2014).

To sum up, bacteria that have antibiotic resistance genes, independent of pathogenicity, can pose an indirect public health risk by expanding the existing genetic pool of resistance (Economou et al. 2015).

Conclusion.

ABR is a worldwide public health challenge that is significantly influenced by antibiotic use in food animals. The subtherapeutic use of antibiotics for a long time as a growth promoter, its improper use in human medicine, and in agriculture are factors that contribute to the development of antibiotic resistant bacteria. Furthermore, several studies show that the use of antimicrobials on farms or feedlots contributes to the problem of antimicrobial resistance and its spread in the environment. As a result, knowledge of the mechanisms of development of resistant bacteria and ARG, as well as their transmission between bacteria and the environment, is essential to confront the situation.

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ВЛИЯНИЕ ГЛИФОСАТА В КОРМАХ НА ЗООТЕХНИЧЕСКИЕ ПОКАЗАТЕЛИ СЕЛЬСКОХОЗЯЙСТВЕННОЙ ПТИЦЫ

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Аннотация. В статье приводятся результаты эксперимента по влиянию на организм сельскохозяйственной птицы глифосата, широко применяемого гербицида, в корме. Полученные данные позволяют предположить о возможном антибактериальном эффекте глифосата, однако необходимы дальнейшие лабораторные изыскания.

Ключевые слова: птицеводство, глифосаты, кормление, токсичность.

Введение. На сегодняшний день широкое обсуждение ведётся вокруг наиболее широко применяемой основы гербицидов в мировом сельском хозяйстве – глифосата. Глифосат является активным компонентом системных гербицидов, используемых в сельском хозяйстве уже порядка 50 лет. Он