

Antibiotic-Resistant Bacteria Prevalence in the Environment of Poultry Farms

Badr Eldin Mostafa^{*}

Department of Microbiology, University of Malaya, Wilayah Persekutuan, Kuala Lumpur, Malaysia

ABOUT THE STUDY

Antibiotics are used in large amounts in veterinary medicine for therapeutic purposes as well as to increase animal husbandry production by serving as growth promoters and prophylaxis agents against developing diseases. The significance of the overuse and misuse of veterinary antibiotics is worrying, as it contributes to the increase in emergence and spread of Antibiotic-Resistant Bacteria (ARB) causing infections in both humans and animals.

Antibiotic usage patterns in animal husbandries vary across regions and countries. Noticeably, the quantity of antibiotics being sold in low and middle income countries is far greater than that in high income countries. Southeast Asia (SEA) is considered a hotspot area for Antibiotic Resistance (AMR), as it is a bloc of fast-developing and interconnected economies. SEA countries (Vietnam, Thailand, and Indonesia) have seen fast growth in the aquaculture and poultry production sectors in recent decades, accounting for 48% of the worldwide veterinary antibiotic market. Antibiotic prevention and therapy has become one of the most effective ways for these countries to avoid uncontrolled epidemic infections that threaten their economies.

Undoubtedly, animal husbandries are an important component in understanding the interplay of ARB between humans, animals and the environment. In summary, ARB diffuses between humans and animals through environmental sources. AMR can be transmitted from environmental bacteria to those that colonize humans and animals. This paper aims to assess the prevalence of Multiple Antibiotic Resistance (MAR) among environmental bacteria in poultry farms and to determine the risk contamination category of poultry by calculating the Multiple Antibiotic Resistance Index (MARI). The results provide preliminary findings on ARB distribution in the poultry environment, as this environment is one of the potential sources of ARB.

There were high levels of resistance to certain antibiotics, those commonly used for human health. Some of these antibiotics are classified by the WHO as critically important antibiotics. The resistance rates were substantially high for some of those antibiotics, especially ampicillin (79.3%), erythromycin (63.7%), linezolid (30.2%), rifampicin (23.1%), gentamicin (16.3%) and ciprofloxacin (15.4%). There was also a high level of resistance to antibiotics that are listed as highly important antibiotics in human medicine, including cefazolin (86.8%), fusidic acid (84.6%), clindamycin (65.5%), benzylpenicillin (51.9%) and trimethoprim-sulfamethoxazole (45.3%).

The resistance percentage, which was significantly higher in broiler farms and closed systems, may have influenced the presence of multi-antibiotic-resistant bacteria and increased the likelihood of contamination on farms. Other studies have shown that poultry type can influence the contamination and the presence of multi-antibiotic-resistant bacteria. This was further proven by the analysis in this study, which showed that 39.53% of the MARI values indicated high risk MARI and 14.48% were ambiguous. This MARI value distribution is alarming, as it shows that isolates originated from high-risk sources of contamination with antibiotics, which may increase the possibility of transfer of mobile antibiotic genes between bacteria.

Antibiotic usage in poultry farms, either directly or indirectly, could be one of the factors causing the increase in MAR, and there are always possibilities for various effects, including MAR in environmental bacteria as well as occupational-related risks.

Citation: Mostafa BE (2022) Antibiotic-Resistant Bacteria Prevalence in the Environment of Poultry Farms. Glob J Agric Health Sci. 11:133.

Copyright: © 2022 Mostafa BE. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Correspondence to: Badr Eldin Mostafa, Department of Microbiology, University of Malaya, Wilayah Persekutuan, Kuala Lumpur, Malaysia, E-mail: badmostafa@umu.edu.ma

Received: 02-May- 2022, Manuscript No. GJBAHS-22-17017; Editor assigned: 04-May-2022, PreQC No. GJBAHS-22-17017(PQ); Reviewed: 18-May-2022, QC No GJBAHS-22-17017; Revised: 25-May-2022, Manuscript No. GJBAHS-22-17017(R); Published: 02-Jun-2022. DOI: 10.35248/2319-5584.22.11.133.