DOI: https:/doi.org/10.56981/M0000241

Intl. J. Med. Sci. 2022; 2(4) 01-04

International Journal of Medical Sciences
E. ISSN: 2961-3019
journal homepage: www.mespj.com/ijms

Document heading

ANTIMICROBIAL RESISTANCE

"Ecological features influencing the progress and expansion of antibiotic resistance" (Article Review)

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Article Info.

Article history:
Received 01 September 2022
Revised 15 October 2022
Accepted 04 December 2022

Keywords:
Antibiotic resistance
Ecological features

How to cite:
Sara Saad Abdulameer, Kawther Mohammed Radah Ali, Alaa Khalid Ali Alabbasi. Antimicrobial resistance. Intl J Med Sci. 2022;2(4):01-04. https:/doi.org/10.56981/M0000241.

ABSTRACT

Antibiotic resistance has been one of the main negative reasons for obstructing antibiotic entrance into the human body. This has become the reason for a huge number of illnesses and deaths worldwide. The study has focused on reviewing an article that concerns the topic of Ecological features influencing the progress and expansion of antibiotic resistance. The paper has reviewed a research article that several researchers on the development of antibiotic-resistant genes have executed. The study's main aim is to investigate the microbes that resist the antibiotic to combat the harmful bacteria responsible for resisting antibiotics to fight against harmful bacteria.

INTRODUCTION

The presence of antibiotic microbes in the environment is one of the beneficial factors that can combat harmful bacteria in living beings and the environment. There is recently becoming a threat in the globe as the resistance of antibiotics, and its widespread is the reason for the increased amount of healthcare crisis. The paper will review a research paper by several researchers who have executed a project on the environmental features responsible for the progress and expansion of antibiotic resistance. The main aim of the research is to investigate the resistant bacteria that resist antibiotics to combat harmful bacteria. The paper will comment on and analyze the steps taken by the researchers to incorporate models to carry out the investigation. To support the aspects presented by the article, this study will also refer to some authentic articles presented by other researchers on the relevant topic. The paper will review the reason for antibiotic resistance in the environment and elaborate on the origins of the resisting genes. The paper will elaborate on the mobilization of resistant factors into mobile genetic elements.

The study will present a piece of detailed information about the antibiotic residues that interact with the human microbiome.

DISCUSSION

Resistance to antibiotics and their widespread is responsible for the emergence of healthcare crises among humans and animals on Earth. The paper aims to review an article regarding antibiotic resistance in the environment caused by resistant "bacteria and pathogens". The main research gap lies in the environmental process leading towards resistance bacteria, which is considered "environmental dispersal barriers". The researchers have executed research to implement effective models regarding how the resistance bacteria emerge, mobilize, transform and are dispersed in the environment. An attempt has been made to define the environmental and evolutionary ecological features responsible for the growth of resistant bacteria and their transmission. Enlistment of the resistant genes emerges continuously, but it has been found that most of the genes do not lead to the emergence of resistant features in the development of bacteria. It only happens once, and if there is pressure for selection for managing them [3]. The article, which will be the main focus of this study, has investigated the conditions under which preventive measures must be taken and how the ecological features lead to antibiotic resistance. Additionally, it has been recollected from the paper that the resistance barriers are not only present to reduce risks but also can help to prevent resistant pathogens and genes by reaching towards the human.

The researchers have opined that antibiotic resistance is responsible for the increased number of deaths per year, and it has been increasing, which is recognized by the World Health Organisation. They have considered it to be a major threat to the globe. In this case, researchers from another article have opined that Antibiotic resistance is a traditional and one of the mounting problems. They have considered the resistome to be dynamic, and the causes of resistome include "overgrowth of population, increased migration in the globe, much more usage of antibiotics in clinics and animal production, selection pressure, poor sanitation, exposure of wildlife and poor sewerage system of disposal" [1]. Treatment of antibiotics is one of the important approaches in modern treatment that is used to combat infections. The period between 1930 to 1960 has been considered to be the golden era that has given rise to numerous antibiotics. This research has been discontinued as it has become impossible for the researchers to maintain the pace of the discovery of antibiotics to counterattack emerging resistant pathogens. Tenacious failure to invent or enhance new antibiotics and non-judicious usage are the main actors intertwined with antibiotic resistance growth [1]. In the past years, the role played by the environment as an important source, and distribution route of resistance has been recognized increasingly [3]. There needs to be more knowledge under which situation the ecology generates resistance development that makes mitigation of the development of mobile resistant features. Different authors, in this case, have highlighted the requirement to undertake a different perspective on antibiotic resistance, including its effect on humans, animals and the exterior environment. The article has provided the concept regarding the factors responsible for affecting the emergence, deployment, distribution and management of antibiotic resistance genes in the environment. The researchers have tried to provide accommodations for both environmental and evolutionary aspects. However, it has no attempt to present research on the ecological dimension of antibiotic resistance that harms living beings. They have decided to present basic concepts with ambiguous meanings in different pieces of literature. The researchers have followed an operational definition of resistance of genes defined by Martinez, Coque and Baquero. It defines that “a strain is resistant against an antibiotic if the minimal inhibitory concentration of the antibiotic is higher than for confirming parental wild type strain” [5]. They have also opined that "the gene which is known as resistance gene allows the bacterium to withstand a higher antibiotic concentration". The researchers have defined resistant genes as ones that have not been given importance previously as having resisting features. It has become much more difficult to elaborate on environmental emergence and depend on a different perspective of researchers when the potential of the resisting gene is positive. The article has considered the emergence of a resistance factor that helps

provide operational resistance. The article has measured a gene that has undergone deployment when it appears on a "mobile genetic element", including a "plasmid, integron or transposon".

The article has also elaborated on the origins of the resistant genes, and it has been recollected that novel antibiotic-resistant factors can grow and develop anywhere. Surprisingly, the number of bacterial cells on the globe has been found at about 1030—a thousand billion billion billion. These bacterial cells provide enormous genetic variability and chances for more transformations, reorganizing and horizontal transfer of a gene. Thus, new resistant factors appear regularly, and the researchers could never detect the huge majority of the events. The article has elaborated on several reasons resistant genes do not submerge pathogens. The novel resisting genes are the paper's main focus unless any selection pressure is found to manage them from resisting antibiotics.

Further, suppose the negligible fitness cost for the resistant factor is found to be low. In that case, it might only become permanently established in the bacterial population if a positive selection of pressure is found. The pressure of selection might be weaker until and unless it is present in the way the resistant factor might be retained. The overuse of antibiotics leads to the huge spread of antibiotic resistance that poses much more health risks to humans [2]. The overuse of antibiotics in huge amounts might possess a robust selection pressure on human and ecological bacterial systems, as reported by the National Academics of Sciences and Medicine [6]. The antibiotics that emerge in the bacterial system might cause genetic or mutational alterations in sensitive bacteria. As a result, it allows the bacteria to live and further increase as antibiotic-resistant bacteria that has the potential to transmit antibiotic-resilient genes. The genetic elements that are mobile, including microbes such as "plasmids, prophages and integrons", might further increase the distribution and promotion of genetic recombination of antibiotic-resistant genes by transforming them. In this case, the researchers have opined that antibiotic-resistant genes are considered to be emerging environmental pollutants [2].

The mobilization of the resistant factors has been elaborated on in the paper. Just like the novel resistant factors, resistant genes have the potential to be mobilized anywhere. The resistant factors that have been currently mobilized onto a mobile genetic element are mainly intertwined with the increased fitness costs, related to the burden of keeping more than one copy of a similar gene and the hardness of managing the expression control of the gene on a mobile element. According to the researchers, "Resistance genes with considerably lower fitness costs may, of course, be recruited to mobile genetic elements, and sub-inhibitory concentrations of an antibiotic could then suffice to select for carriage of them". It is very significant to consider the fact that resistant genes have emerged in a setting of rivalry and collaboration within different species. Some of the resistant genes might have made use of antibiotics as combatting agents. As a result, both the known and the novel resistance determinants can be chosen naturally if they confer a competitive benefit against antibiotic producers. It might also allow the hosting bacteria to live in higher concentrations of an antibiotic microbe that is produced by them. Such is the natural selecting procedure that helps to preserve an ecological pool of resistant genes but indirectly to further establishes the resistant genes in pathogens as it might deploy resistant factors. Antibiotic resistance has become one of the most critical factors that lead to harm to human health, and the emergence of antibiotic resistance has contributed globally too. The contributors generally include – a) Unavailability of investigation of resistance development. b) Availability of poor-quality antibiotics, c) misuse of the clinical products d) easy availability of antibiotics at a huge rate [4].

The researchers have opined that as antibiotics have been used recently, hazard valuations of human experience to antibiotic resistance in the atmosphere have attracted much more attention. The human health risk valuations are to make an estimation of the probable illness and death that is caused by the infection transmitted and connected with antibiotic-resistant genes, and it includes four types of elements: "hazard identification, exposure assessment, dose-response assessment, and risk characterization". The research has focused on presenting a holistic view of health risk valuations of the antibiotic residues in the atmosphere, which is based on antibiotic-resistant genes. This aspect presented by the paper can be a very informative and valuable article for the researchers in order to execute further

research. A piece detailed information about the antibiotic residues that make interaction with the human microbiome has been presented in the study. The microbiome consists of a huge number of diverse microorganisms that inhabit the body of human beings. If an individual intakes antibiotic residue from the atmosphere daily, then a huge amount of it might enter into the human gastrointestinal tract, in which nearly 800 to 1000 several bacterial species and much more than 7000 different strains are inhabiting. The microbes that stay in the tract have 95% of them as beneficial bacteria and the leftovers are harmful bacteria and opportunistic pathogens. The presence of antibiotics has been found in water surface too and in wastewater. Through their presence in water, it can directly enter into the body of human beings easily and inhabit in the human intestinal tract. It is also present in air, dust, soil, food, egg and meat, milk, vegetables, grains, fish and shrimps. The report of the antibiotic resistant genes that is present in the mentioned sources have been elaborated in the article with authentic references. Further, the paper has commented upon the risks that might emerge and how dangerous can it be and its effect on human exposure to antibiotic-resistant in the environment.

CONCLUSION

The article that has been chosen to make a review has presented the presence of antibiotic resistance genes that has been responsible for resisting the advantages of antibiotic in the environment. The presence of the harmful antibiotic resistance gene has been a huge global threat and spreading of it has become the concern of the researchers. This study is a review article that has reviewed an article concerning the growth environmental features that are responsible for the progress and expansion of antibiotic resistance. The paper has analyzed and commented the steps that has been possessed by the researchers to implement the models of execute the required investigation. The paper has reviewed the causes for the antibiotic resistance and has elaborated on the source of resisting genes. The mobilization of the resistant factors into mobile genetic element has been elaborated in the paper.

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