

AN EXAMINATION OF THE PRESENCE OF ANTIBIOTIC-RESISTANT GENES IN MUNICIPAL WATER SUPPLY SYSTEMS

Srimathi Bai V

Research Scholar

Department of Botany

NIILM University, Kaithal.

srimathibai@gmail.com

Dr. Nirmal Sharma

Research Guide

Department of Botany

NIILM University, Kaithal.

Abstract

Antibiotics are a brand-new category of pollution, and the rise of antibiotic resistance has created a worldwide health emergency. The distribution of drinking water and the purification of raw water are crucial functions of the urban water delivery system. The drinking water treatment system and the water distribution system will each be covered in this evaluation. Not all methods of water treatment can lower antibiotic resistance, according to prior studies. The network of the water supply also carries the potential danger of secondary contamination. This paper's study goal is to provide an overview of the prevalence and mechanism of antibiotic resistant genes (ARGs) and bacteria (ARBs) in the urban water supply system.

Introduction

Since their first discovery in 1928, antibiotics have been extensively employed in a variety of sectors [1]. However, owing to a lack of knowledge, individuals mistakenly assume that antibiotics work, which leads to an overuse of them. Data indicate a 35% rise in worldwide antibiotic usage between 2000 and 2010 [2]. According to studies, methicillin-resistant *Staphylococcus aureus* kills more Americans than emphysema, AIDS, and all other illnesses combined [3]. Nearly 75% of persons in the US receiving treatment for acute bronchitis are receiving unneeded antibiotics [1]. The World Health Organization has named antibiotic

resistance as the greatest danger to public health in the twenty-first century [4].

Antibiotic resistance, which has been identified as a new kind of pollutant, is enhanced by the misuse of antibiotics and may increase their residual quantity in the aquatic environment. Antibiotic resistance genes (ARGs) have now been discovered in a wide range of environmental media, including soil [9], sewage plants [5], livestock wastewater [6], surface water [7], drinking water [8], and livestock wastewater [9]. A significant amount of antibiotics are also released into the aquatic environment when wastewater containing feces is discharged into the water by the municipal sewage treatment facility [10]. Antibiotic resistance has now become a major issue for humanity as more and more ARGs are found in aquatic environments.

Additionally, the typical drinking water treatment method may not be able to completely eliminate ARGs and antibiotic resistant bacteria (ARB) from the water, and certain treatment units may potentially enhance their abundance [11]. Additionally, research has demonstrated that ARGs may be found in tap water, proving that the mechanism used to distribute drinking water is a significant source of pollution [12]. According to

domestic and international research, the presence and transmission mechanism of antibiotic resistance in urban water supply systems were examined in this article.

Mechanisms for the bacterial resistance to antibiotics and transfer of ARGs

The origin and mechanisms of antibiotic resistance

ARB relates to the bacterium's decreased sensitivity to the medicine with repeated contact with the antibiotic, which causes a decline in the treatment's effectiveness on the bacteria or even its ineffectiveness.

It is well acknowledged that the following four factors play a key role in the drug resistance mechanism of ARB. 1) Because certain bacteria's cell membrane permeability is relatively low or they lack the genes necessary to translate the target proteins that interact with antibiotics, some bacteria are innately resistant to many antibiotics [13]. 2) The bacteria pump out the antibiotic molecules that spread into the cell via the efflux pump on the cell membrane, lowering the concentration of antibiotics in the cell [13]. 3) Antibiotics are rendered inactive by enzymes produced by bacteria [14]. 4) A mutation in the target protein that interacts with antibiotics affects their affinity for the target protein, leading to bacterial resistance [15].

Transfer of ARGs

The molecular biology of bacterial antibiotic resistance involves the presence of internal drug resistance genes. The majority of the genes for resistance that bacteria carry are for both acquired and inborn resistance. Vertical gene transfer, as it is known in the former, is a technique used to ensure the passage of ARGs between intermediate parents and offspring [16]. HGT stands for horizontal gene transfer, which is the last one.

Several of the procedures described below may result in the major method of HGT, the transfer of genetic material across distinct species. 1) Conjugation, a procedure heavily reliant on mobile gene elements (MGEs) such plasmids, integrons, or transposons [17]. 2) Transformation, wherein bacteria absorb extracellular free DNA, create their own genetic material from it, and incorporate expression in vivo [18]. 3) Transduction, a technique that primarily employs bacteriophages to enable the horizontal transfer of resistance genes across viruses [19].

Environmental risks of ARGs

Resistance genes are spread by a cyclical mechanism that is simple to accumulate in the human body (Fig. 1) [20]. When surface runoff and rains scour into soil, rivers, lakes, or groundwater, they contaminate the aquatic environment with a huge number of resistant bacteria that are present in animal feces from farms. Through horizontal gene transfer, the resistance genes from these resistant bacteria may be inherited by native environmental microorganisms. The resistance gene will also eventually reach the human body via the food chain in the carnivorous products offered by the cattle and poultry industries, and the resistance gene in the soil may also be passed on to the plant and ultimately enter the human body through the food chain [21]. When human feces enter a sewage treatment facility, the resistance genes they carry are not entirely eliminated. After being cleaned up by the sewage treatment facility, the sewage is released into the river, which serves as a water supply for the water treatment facility before entering the human body.

ARGs will build up in the human body,

making human cells more resistant to drugs and posing a severe danger to ecological security and public health. Both pathogenicity and multiple drug resistance are present in pathogenic bacteria when they acquire multiple resistance genes. Superbugs with the NDM-1 gene were discovered in humans for the first time in New Delhi, India, in 2010, which sparked concern throughout the globe [22]. Superbugs may simultaneously acquire resistance to a number of antibiotic medications, rendering them incurable and causing human mortality. In other words, we need to come up with a practical method for getting ARGs out of the environment.

Surface water

Although some resistance genes may be eliminated during the sewage treatment plant's treatment process, a significant amount of them are still released into the surface water with the effluent. By assessing the water and sediment samples of the Haihe River in China, Luo et al. have quantitatively investigated the presence of ARGs in surface water. The findings showed that the concentrations of Sul1 and Sul2 in sediments were substantially higher than those in water [23]. Zhang et al. had comparable results. In Jiangsu Province, China, they found and measured the levels of class 1 integronase genes as well as the tetracycline resistance genes tetA and tetC in diverse aquatic environments. Their research revealed that the amount of ARGs in lake sediments was much greater than in water samples [24]. Additionally, ARG-contaminated surface water may cause ARGs to appear in cattle, endangering human health and polluting the food chain [5].

Groundwater

ARGs started to appear in groundwater as

a result of sewage tank and soil penetration in animal farms. Tetracycline resistance gene was found in groundwater by Koike et al. Their research revealed that the widespread dispersion of ARGs in groundwater was significantly influenced by the exudation of animal manure [25]. Another study conducted in the US found that groundwater samples taken close to a pig farm had *Enterococcus* spp. that was resistant to four different antibiotics. This is consistent with other research showing that groundwater may contain ARGs [26].

Removal of ARGs in drinking water treatment

Coagulation sedimentation and filtration

In water treatment facilities, the main handling methods employed are coagulation, precipitation, filtration, and disinfection. They are designed to clean the water by removing colloids, suspended particles, and pollutants while lowering its chrominance and turbidity [27].

Recently, Li et al. conducted study on the removal of ARGs during the coagulation process. The results suggest that when employing FeCl₃ or perfluorinated compound (PFC) in municipal wastewater treatment facilities to remove ARGs, conventional pollutants including dissolved organic carbon (DOC) and dissolved ammonia nitrogen can also be efficiently eliminated.

The pH, temperature, and turbidity of raw water differ greatly from those of wastewater treatment facilities, and the coagulants used in each have different characteristics. These differences are well recognised. In the water treatment plant, the removal of resistance genes by coagulation and sedimentation will differ slightly. In this area, it is still unusual to uncover related studies, which points to a

possible trend for the future [29].

Filtration is a critical stage in the purification of water. The filter has accumulated the greatest biological material, and horizontal gene transfer is most probable there. According to Xu et al., two separate types of resistance genes were found to have decreased after treatment by the filtration unit in the water treatment facility. On the other hand, after sand filtration, the relative abundance of most resistance genes increased [30]. Guo et al. come to the same conclusion. Their team found that tetracycline resistance genes (tet A and tet O) had increased after sand filtration [11]. Although certain organic matter and suspended particles may be effectively removed from water by filtration, it is difficult to ensure biosafety. A hot field of research at the moment may be the factors behind the increase in the absolute quantity of resistance genes in filter effluent.

Disinfection

The primary types of disinfection techniques now in use include UV, ozone, chlorination, and chloramine disinfection. The most popular disinfection techniques are chlorination disinfection and UV disinfection. After chlorine treatment, Munir et al. found that the amount of ARGs did not substantially reduce [31]. UV disinfection is a physical procedure as opposed to chlorination disinfection, and because to the specificity of UV radiation, it is efficient at inactivating resistance genes [32]. According to some researchers, UV light may render resistance genes in DNA incapable of being converted, lowering the possibility of resistance genes spreading horizontally. The concentration of resistance genes might be decreased following UV disinfection, according to research by McKinney et al., but a 4-

orders-of-magnitude UV treatment was required to inactivate the resistance genes [33]. In recent years, some researchers have suggested that the inclusion of Ag-TiO₂ composite nanomaterials may also significantly increase the effectiveness of UV disinfection [32]. They also suggested that the combination of TiO₂ nanoparticles with near ultraviolet light might boost the efficiency of eliminating resistance genes.

Spread of ARGs in water-supply pipeline

Even though the ARG was much reduced in finished water after source water treatment, it was still present in tap water before entering the water delivery network. It has been shown that the absolute abundance of ARGs in the water supply network's effluent is much greater than that in the network's influent [12, 34]. For instance, according to study by Xu et al., there is a possibility of ARGs contaminating the water supply network because of the considerable rise in the absolute abundance of ARGs, particularly -lactam ARGs, in the effluent of the water supply network [30].

In the water supply network, the biofilm on the pipe walls may encourage the expression of certain genes. A biofilm will still build on the pipe wall even if there are just a few microorganisms in the network of pipes [29]. The bacteria adhering to the biofilm may take up the resistance gene from the water supply network, or the resistance gene may be horizontally transferred from the resistant bacteria in the drinking water carried by the pipe network to the local bacteria attached to the biofilm. Therefore, during the transport of water via pipes, secondary microbial contamination may occur.

There may be a health danger from the secondary contamination in the pipe

network, which has not gotten enough attention. The study of resistance genes in the global and Chinese water supply networks is still in its early stages.

Conclusion

The occurrence of ARGs in urban water supply systems has been extensively researched in the literature. There hasn't been a clear explanation of how ARGs are removed during the regular water treatment procedure, however. Additionally, the systems for distributing water might act as a breeding ground for ARGs. The biofilm and its impact on the enrichment of ARGs and ARB have recently attracted a lot of study attention. Research and development of the most trustworthy, cost-efficient, and efficient method to remove ARGs are urgently needed to ensure the biosafety of drinking water. In light of the analyses indicated above, we would like to provide a number of ideas and recommendations about ARGs.

1) In order to assess their ecological health concerns and provide a theoretical foundation for the prevention of resistance gene pollution, it is essential to examine the kinds and horizontal movement of many resistance genes in the environment as soon as feasible. 2) Drinking water treatment plants are not only a crucial location for resistance genes, but also the means by which they may be eliminated. In the future, we must concentrate on the impact of resistance genes being removed by a new set of water treatment procedures. 3) The primary focus of future study will also be the secondary contamination of the pipe network. To regulate the content of ARGs entering the building pipeline system, necessary disinfection procedures should be implemented at the conclusion of the pipe

network.

A complete study is still required to explore the removal and spread of ARGs in urban water supply systems with more quantitative data, which would help eliminate the danger they provide to public safety. Overall, there is currently little research on ARGs.

References

1. Fauci A S and Marston H D 2014 *J. Amer. Med. Assoc.* 311 1853
2. Van Boeckel T P, Gandra S, Ashok A, Caudron Q, Grenfell B T, Levin S A and Laxminarayan R 2014 *Lancet Infect. Dis.* 14 742
3. Spellberg B, Blaser M, Guidos R J, Boucher H W, Bradley J S, Eisenstein B I, Gerding D, Lynfield R, Reller L B, Rex J, Schwartz D, Septimus E, Tenover F C and Gilbert D N 2011 *Clin. Infect. Dis.* 52 S397
4. Zhang Q, Jin R and Tian G 2018 *Appl. Microbiol. Biotechnol.* 102 8261
5. Amos G C A, Zhang L, Hawkey P M, Gaze W H and Wellington E M 2014 *Vet. Microbiol.* 171 6. 441
7. Ge L, van Asseldonk M A P M, Valeeva N I, Hennen W H G J and Bergevoet R H N 2014 *NJAS Wageningen J. Life Sci.* 70/71 1
9. Sidhu J P S, Tiehm A and Stoll C 2012 *Environ. Sci. Technol.* 46 9716
10. Huerta B, Marti E, Gros M, Lopez P, Pompeo M, Armengol J, Barcelo D, Balcazar J L,
11. Rodríguez-Mozaz S and Marce R 2013 *Sci. Total Environ.* 456/457 161
12. Chen P, Chaoqi C and Li X 2018 *Front. Environ. Sci. Eng.* 12 5
13. Ye Z L, Deng Y, Lou Y, Ye X and Chen S 2018 *Front. Environ. Sci. Eng.* 12 7
14. Guo X, Li J, Yang F, Yang J and Yin D 2014 *Sci. Total Environ.* 493 626
15. Xi C, Zhang Y, Marrs C F, Ye W, Simon C, Foxman B and Nriagu J 2009 *Appl. Environ. Microbiol.* 75 5714
17. Nikaido H 1994 *Science* 264 382
18. Allen H K, Donato J, Wang H H, Cloud-Hansen K A, Davies J and Handelsman J 2010 *Nature Rev. Microbiol.* 8 251
19. Tuomanen E and Charpentier E 2000 *Microbes Infect.* 2 1864

20. Dodd M C 2012 *J. Environ. Monitor.* 14 1754
21. Bouwer E J and Ehlers L J 1999 *Water Sci. Technol.* 39 163
22. Zhang X X, Zhang T and Fang H H P 2009 *Appl. Microbiol. Biotechnol.* 82 397
23. Ochman H, Lawrence J G and Groisman E A 2000 *Nature* 405 299
24. Wellington E M, Boxall A B, Cross P, Feil E J, Gaze W H, Hawkey P M, Johnson-Rollings AS, Jones D L, Lee N M, Otten W, Thomas C M and Williams A P 2013 *Lancet Infect. Dis.* 13 155
25. Cho J I, Joo I S, Choi J H, Jung K H, Choi E J, Han M K, Jeong S J, Son N R, Lee S H and Hwang I G 2013 *Food Sci. Biotechnol.* 22 161
26. Walsh T R, Weeks J, Livermore D M and Toleman M A 2011 *Lancet Infect. Dis.* 11 355
27. Luo Y, Mao D, Rysz M, Zhou Q, Zhang H, Xu L and Alvarez P J J 2010 *Environ. Sci. Technol.*
28. Zhang X, Wu B, Zhang Y, Zhang T, Yang L, Fang H H P, Ford T and Cheng S 2009 *Ecotoxicol.* 18 652
29. Koike S, Krapac I G, Oliver H D, Yannarell A C, Chee-Sanford J C, Aminov R I and Mackie R I 2007 *Appl. Environ. Microbiol.* 73 4813
30. Sapkota A R, Curriero F C, Gibson K E and Schwab K J 2007 *Environ. Health Perspect.* 115 1040
31. Zainal-Abideen M, Aris A, Yusof F, Abdul-Majid Z, Selamat A and Omar S I 2012 *Water Sci. Technol.* 65 496
32. Li N, Sheng G P, Lu Y Z, Zeng R J and Yu H Q 2017 *Water Res.* 111 204
33. Tan Q, Li W, Zhang J, Zhou W, Chen J, Li Y and Ma J 2019 *Front. Environ. Sci. Eng.* 13 36
34. Xu L, Ouyang W, Qian Y, Su C, Su J and Chen H 2016 *Environ. Pollut.* 213 119
35. Xagorarakis I, Wong K and Munir M 2011 *Water Res.* 45 681
36. Shao S, Hu Y, Cheng J and Chen Y 2018 *Critical Rev. Biotechnol.* 38 1195
37. McKinney C W and Pruden A 2012 *Environ. Sci. Technol.* 46 13393
38. Su H C, Liu Y S, Pan C G, Chen J, He L Y and Ying G G 2018 *Sci. Total Environ.* 616/617 453