

Antibiotic Contamination: A Global Environment Issue

Jincai Ma¹ and Guangshu Zhai^{2*}

¹College of Natural Resources and Environmental Sciences, Jilin University, Changchun 130012, P.R. China

²Department of Civil and Environmental Engineering and IIHR Hydroscience and Engineering, The University of Iowa, Iowa City, IA 52242, USA

*Corresponding author: Guangshu Zhai, Department of Civil and Environmental Engineering and IIHR Hydroscience and Engineering, The University of Iowa, Iowa City, IA 52242, USA, Tel: 319335-5866; E-mail: zhai-guangshu@uiowa.edu

Rec date: Jul 26, 2014, Acc date: Jul 28, 2014, Pub date: Aug 01, 2014

Copyright: © 2014 Zhai G, et al. 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.

Editorial

The term antibiotic was firstly used by Nobel laureate Selman Waksman to describe microbial substances antagonistic to the growth of other microbes. It is now well accepted that antibiotic denotes any organic chemical that inhibits or kills microbes by specific interactions with bacterial targets, regardless of the source of the particular compounds, i.e. antibiotics could be from either natural or anthropogenic sources. Since their first introduction in clinical applications, antibiotics have saved countless lives, and made the majority of infectious diseases under control. However, the large scale production and use (especially overuse and misuse) of antibiotics in clinical and veterinary medicine, agriculture, aquaculture, and horticulture has released significant amount of antibiotics into the environment, and antibiotic contamination has been recognized as a worldwide phenomenon [1]. Recent research has showed that antibiotic concentration in wastewater, soil, and sediment was in the range from µg/kg to mg/kg. More importantly, the antibiotics in the environment generally resist to biodegradation due to their antimicrobial nature so that antibiotics have been classified as emerging pseudo-persistent organic pollutants for their continual input into the environment and permanent presence.

The main source of antibiotic contamination is wastewater from antibiotic manufacturer, large scale animal feeding operations, households, and hospitals. How to eliminate the antibiotic residue in various wastes is critical to minimize potential environmental contamination and the ecological health risk caused by antibiotic pollution. Due to their antimicrobial and persistence features, antibiotics generally cannot be efficiently removed by traditional methods applied in wastewater treatment plants, which include both physiochemical methods, e.g. coagulation, flocculation, sedimentation, and filtering, and biological processes, e.g. activated sludge and anaerobic digestion. In contrast, newly developed physico-chemical techniques including oxidation and advanced oxidation processes, such as chlorination, ozonation, fenton and photo-fenton reactions, photolysis, and photo-catalysis, can overcome the disadvantages of the biological methods, and have shown their success in remediation of antibiotics contamination in wastewater [2].

Unlike the other conventional organic pollutants, e.g. polychlorinated biphenyls (PCBs), antibiotics not only deteriorate environment quality, but also result in the appearance and rapid spread of resistant bacteria in the environment [3]. Therefore, antibiotic contamination be of increasing concern among general public, government officials, and scientists about potential ecological and public health risks [4]. We can imagine that the research on antibiotic contamination will continue to be a hot topic among scientific

communities. The future research on antibiotics might focus on the following areas:

Novel techniques for degradation of antibiotics. Although some promising technologies are available, their disadvantages are obvious, e.g. slow degradation rates, high cost on maintenance, and unstable performance. Further efforts might focus on improving the available techniques and continuous development of new techniques for antibiotic elimination in environment. Since each technique has its own strength and drawback, a combination of different techniques in one treatment process might be the ultimate solution for antibiotic decontamination in the environment.

New analytical protocols for antibiotic residue and their metabolites determination and quantification. Those analytical methods are great tools for survey of antibiotic contamination at spatial and temporal levels, construction of models for elucidating degradation pathway, identification of intermediate products that might be used as biomarkers for environmental monitoring, and assessment of the effectiveness of a remediation process.

Evaluation of ecological and health risk associated with antibiotic and antibiotic resistance. In addition to detect antibiotic residue in the environment, identification and quantification of antibiotic resistance genes are also important work that needs to be focused on. Because of the availability of omic- and meta-omics technologies and low cost of next generation sequencing techniques, it is possible to investigate the abundance and diversity of bacteria resisting antibiotics and antibiotic resistance genes in those bacteria, and to compare the distribution of such bacteria and genes at local, regional, and global scales[5]. In addition, with the aid of modern bioinformatics tools, people might achieve a better understanding of the transfer and evolution of antibiotic genes in the environment, and interpret the data in an ecological point of view [6].

References

1. Zhang T, Li B (2011) Occurrence, Transformation, and Fate of Antibiotics in Municipal Wastewater Treatment Plants. *Critical Rev Environl Sci Tech* 41: 951-998.
2. Homem V, Santos L (2011) Degradation and removal methods of antibiotics from aqueous matrices--a review. *J Environ Manage* 92: 2304-2347.
3. Neu HC (1992) The crisis in antibiotic resistance. *Science* 257: 1064-1073.
4. Davies J, Davies D (2010) Origins and evolution of antibiotic resistance. *Microbiol Mol Biol Rev* 74: 417-433.
5. Zhu Y, Johnson TA, Su J, Qiao M, Guo G, et al. (2013) Diverse and abundant antibiotic resistance genes in Chinese swine farms. *Proc Natl Acad Sci U S A* 110: 3435-3440.

6. Forsberg KJ, Reyes A, Wang B, Selleck EM, Sommer MOA, et al. (2012) The shared antibiotic resistome of soil bacteria and human pathogens. *Science* 337: 1107-11.