Determining Bacterial Antibiotic Resistance and Heavy Metal Tolerance in Clinical and Environmental Settings: Local Action of Global Importance

Shyamapada Mandal*

Laboratory of Microbiology and Experimental Medicine, Department of Zoology, University of Gour Banga, Malda, India

*Corresponding Author: Shyamapada Mandal, Laboratory of Microbiology and Experimental Medicine, Department of Zoology, University of Gour Banga, Malda, India.

Received: December 08, 2019; Published: January 21, 2020

The antibiotics, which are still the gold standard therapeutics against a large number of bacterial infections, and the heavy metals, which are in use in various anthropogenic activities, remain the two universal categories of environmental pollutants, and are unsafe to public health and biological safety [1]. As such, the use, misuse and overuse of antibiotics leads to the emergence and spread of multidrug resistant organisms (MDROs) [2], in different environmental settings, such as the water bodies, including sewages that act as mixing vessels for effluents from hospitals, agricultural field and domestic activities, on one side. The metal ions, on the other side, aid in the process of global emergence of MDROs in environmental and clinical settings too, thus sustaining the heavy metal tolerance in association with co-selection of bacterial antibiotic resistance [3,4].

The bacterial antibiotic resistances in the current clinical settings developed a great hindrance threatening the efficacies of almost all available antibiotics, amongst mainly the gram-negative pathogens: the ESKAPE as well the top listed WHO priority pathogens, such as *Escherichia coli, Acinetobacter baumannii, Pseudomonas aeruginosa* and *Klebsiella pneumoniae*, and the gram-positive: *Staphylococcus aureus*, members also [5-8]. Moreover, the aquatic bacteria [9-11], constituted the potential human pathogens, as well as the 'ESKAPE' (*Enterococcus faecalis, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Escherichia coli*) pathogens, which represent a severe threat of emerging inoperable MDROs infections to humans.

Acquaintance with the local status of antibiotic resistance among potential pathogenic bacteria, in different settings is thus, crucial in combating bacterial antibiotic resistances. As the studies suggest, the bacterial MAR (multiple antibiotic resistance) indices might be of help in identifying the source of fecal contamination as well as to categorize the health risk contaminated niches, the clinical bacteria as well as the environmentally isolated bacteria of clinical relevance might be used as important tools in detecting and monitoring antibiotic (and heavy metal) pollution in given niches [11-13]. Moreover, the studies demonstrated the occurrence of plasmid, encoding multiple antibiotic and heavy metal co-resistances, among gram-negative bacteria from river and sewage, which potentially act as the source of dissemination of pathogenic bacteria and the bacterial antibiotic resistances [9-11,14], impacting the environmental as well as human health in this part of the globe, requiring public awareness on the issues of misuse and/or overuse of antibiotics, in our part of the globe. Such findings, therefore, suggest for a prioritizing research on antibiotic resistances among bacteria, mainly the 'ESKAPE' group of pathogens, for incessant public health scrutinizing activities in clinical and community settings, and among environmental bacteria as well, in order to tackle the emergence of multiple antibiotic resistant pathogenic bacteria, locally as well as globally.

Bibliography

- 1. Zhu YG., et al. "Diverse and abundant antibiotic resistance genes in Chinese swine farms". Proceeding of the National Academy of Sciences, USA 110 (2013): 3435-3440.
- 2. Sommer MOA., *et al.* "The human microbiome harbors a diverse reservoir of antibiotic resistance genes". *Virulence* 1 (2010): 299-303.

Citation: Shyamapada Mandal. "Determining Bacterial Antibiotic Resistance and Heavy Metal Tolerance in Clinical and Environmental Settings: Local Action of Global Importance". *EC Microbiology* 16.2 (2020): 01-02.

Determining Bacterial Antibiotic Resistance and Heavy Metal Tolerance in Clinical and Environmental Settings: Local Action of Global Importance

- 3. Eze E., *et al.* "Association of metal tolerance with multidrug resistance among bacteria isolated from sewage". *Journal of Rural and Tropical Public Health* 8 (2006): 25-29.
- 4. Baker-Austin C., *et al.* "Co-selection of antibiotic and metal resistance". *Trends in Microbiology* 14 (2006): 176-186.
- 5. Wright CD. "The antibiotic resistome: the nexus of chemical and genetic diversity". Nature Reviews 5 (2007): 175-186.
- 6. Tacconelli E., *et al.* "Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis". *Lancet Infectious Diseases* 18 (2018): 318-327.
- 7. Rice LB. "Federal funding for the study of antimicrobial resistance in nosocomial pathogens: no ESKAPE". *Journal of Infectious Diseases* 197 (2008): 1079-1081.
- 8. World Health Organization. "WHO Traditional Medicine Strategy, Geneva". WHO (2002).
- 9. Das SN., *et al.* "Plasmid mediated antibiotic and heavy metal co-resistance in bacterial isolates from Mahananda River Water (Malda, India)". *Translational Medicine* 6 (2016): 185.
- 10. Das SN., *et al.* "Detection of mercury and cadmium resistance among multiple antibiotic resistant enteric bacteria from municipal sewage water in Malda, India". *International Research Journal of Pharmacy* 9.9 (2018): 171-176.
- 11. Das SN., *et al.* "Heavy metal tolerance in association with plasmid mediated multiple antibiotic resistances among clinical bacterial isolates, India". *Bioscience Biotechnology Research Communications* 11 (2018): 612-618.
- 12. Nandi S., *et al.* "Bacteriological profiling of commercially available eye cosmetics and their antibiotic susceptibility pattern". *Translational Biomedicine* 7 (2016): 1-8.
- 13. Tambekar DH., *et al.* "MAR indexing to discriminate the source of faecal contamination in drinking water". *Nature Environment and Pollution Technology* 4 (2005): 525-528.
- 14. Luo G., *et al.* "Antibiotic resistance genes and correlations with microbial community and metal resistance genes in full-scale biogas reactors as revealed by metagenomic analysis". *Environmental Science and Technology* 51 (2017): 4069-4080.

Volume 16 Issue 2 February 2020 ©All rights reserved by Shyamapada Mandal.

Citation: Shyamapada Mandal. "Determining Bacterial Antibiotic Resistance and Heavy Metal Tolerance in Clinical and Environmental Settings: Local Action of Global Importance". *EC Microbiology* 16.2 (2020): 01-02.

02