

Environmental Dimension of Antimicrobial Resistance

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Received: September 03, 2021

Published: January 01, 2022

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Antibiotic resistance and other genes are ubiquitously present in nature. Most of the genes for resistance are encoded and originate in bacteria from the natural environment like beta lactamases and fluoroquinolone genes etc. This rapid evolution and concomitant spread of these new antibiotic resistant genes have been enhanced by modern human activity and its effects on the homeostasis in environmental milieu. Environmental vectors, such as bacteria and its genomic diversity, present in soil and water bodies need elaborate studies to ascertain their role and mechanism and for resistance risk management. Policy needs to be augmented to adopt and for facilitating decreasing the risk of spread of these resistant genes from environmental sources to humans and animals through wastes, indiscriminate killing, antimicrobial treatment of poultry and livestock, water sewage effluent supply, food supply, all of which contribute to the risk of introducing antibiotic resistant bacteria and other pathogens in the environment. The holistic and interdisciplinary study must include improved waste management containing antibiotic waste products and antibiotic resistant genes.

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