World Academy of Science, Engineering and Technology
International Journal of Environmental and Ecological Engineering
Vol:18, No:09, 2024

Microbial Phylogenetic Divergence between Surface-Water and Sedimentary Ecosystems Drove the Resistome Profiles

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Abstract : Antibiotic pollution and the evolution of antibiotic resistance genes (ARGs) are increasingly viewed as major threats to both ecosystem security and human health, and has drawn attention. This study investigated the fate of antibiotics in aqueous and sedimentary substrates and the impact of ecosystem shifts between water and sedimentary phases on resistome profiles. The findings indicated notable variations in the concentration and distribution patterns of antibiotics across various environmental phases. Based on the partition coefficient (Kd), the total antibiotic concentration was significantly greater in the surface water (1405.45 ng/L; 49.5%) compared to the suspended particulate matter (Kd =0.64; 892.59 ng/g; 31.4%) and sediment (Kd=0.4; 542.64 ng/g; 19.1%). However, the relative abundance of ARGs in surface water and sediment was disproportionate to the abundance of antibiotics concentration, and sediments were the predominant ARGs reservoirs. Phylogenetic divergence of the microbial communities between the surface water and the sedimentary ecosystems potentially played important roles in driving the ARGs profiles between the two distinctive ecosystems. ARGs of Clinical importance; including blaGES, MCR-7.1, ermB, tet(34), tet36, tetG-01, and sul2 were significantly increased in the surface water, while blaCTX-M-01, blaTEM, blaOXA10-01, blaVIM, tet(W/N/W), tetM02, and ermX were amplified in the sediments. cfxA was an endemic ARG in surface-water ecosystems while the endemic ARGs of the sedimentary ecosystems included aacC4, aadA9-02, blaCTX-M-04, blaIMP-01, blaIMP-02, bla-L1, penA, erm(36), ermC, ermT-01, msrA-01, pikR2, vgb-01, mexA, oprD, ttgB, and aac. These findings offer a valuable information for the identification of ARGs-specific high-risk reservoirs.

Keywords : antibiotic resistance genes, microbial diversity, suspended particulate matter, sediment, surface water
Conference Title : ICEES 2024 : International Conference on Environmental and Ecological Systems
Conference Location : Zurich, Switzerland
Conference Dates : September 16-17, 2024