Freshwater Viral Metagenome Reveals Novel Phage-borne Antibiotic Resistance Genes

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Abstract

Antibiotic-resistant bacteria are a threat to global health. One concern is that bacteria will pass antibiotic resistance genes (ARGs) to each other through horizontal gene transfer. A new study identified a novel source of ARGs in the environment. Bacteriophages are viruses that replicate inside bacteria, where they can incorporate bacterial genome fragments into phage capsids, allowing them to transfer those fragments to future hosts. Using metagenomics, researchers screened viral genes from an urban river for ARGs. They discovered 25 ARGs originating from bacteriophage genomes. Four genes were predicted to encode novel, functionally active beta-lactamases, conferring resistance to a variety of antibiotics. The results demonstrate that although present at low abundance, bacteriophages actively contribute functional ARGs to the freshwater metagenome, suggesting that they should be considered as a potential ARG dissemination route and included in ARG monitoring systems.