

Swimming in Resistance Genes: Ecological Drivers of Antibiotic Resistance in Freshwater Lakes

Ester Eckert

CNR, Verbania, Italy

Freshwater environments serve as both reservoirs and conduits for antibiotic resistance genes. On one hand, these habitats naturally harbor a diverse genetic pool of resistance traits, which can evolve to counteract both current and future antibiotics. On the other hand, human activities—such as widespread antibiotic use in medicine and agriculture—introduce resistant bacteria into water systems, leading to genetic pollution from wastewater effluents. Notably, resistance genes can transfer from allochthonous bacteria to autochthonous microbes, where they may persist for decades.

This dynamic exchange, between the high-antibiotic pressure of clinical settings and the relatively low-pressure, highly diverse conditions of freshwater environments, creates a fascinating cycle of bacterial genetic evolution. In our recent studies, we focused on understanding the contamination, spread, diversity, and long-term persistence of antibiotic resistance genes in sub-alpine freshwater ecosystems. By tracking gene diversity and the composition of flexible genomic islands across a gradient of freshwater bodies with varying levels of human impact, we aimed to quantify the influence of treated wastewater on resistance gene distribution.

To explore the persistence of these genes, we studied the role of ecological interactions, water chemistry, and human pollution in shaping the resistome (the collection of antibiotic resistance genes in a community) and their horizontal transfer. While human pollution plays a significant role in the occurrence of resistance genes, ecological interactions and environmental parameters primarily modulate the actual composition of the antibiotic resistance gene pool in freshwater systems.