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# DISTRIBUTION AND RELATIONSHIP BETWEEN ANTIBIOTIC RESISTANCE GENES AND HEAVY METALS IN SURFACE SEDIMENTS OF TAIHU LAKE, CHINA

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The use of antibiotics accelerates the development of antibiotic resistance genes (ARGs) and bacteria which pose health risks to both humans and animals. Research has proved that increasing antibiotic resistance (AR) results from overuse of antibiotics in medicine, therapeutic and nontherapeutic applications in agriculture. Heavy metals, pharmaceuticals, and other wastes released into the environment can significantly influence environmental antibiotic resistance (AR). Over the years, Taihu Lake has become one useful site as it receives discharge from various sources mainly industrial pollution and aquaculture; antibiotics are used sparingly in medicine and agriculture. Within this context, 22 antibiotic resistance genes were quantified, to analyze and know their physicochemical characteristics and 10 heavy metals at seven sites, mainly to determine the distribution and relationship of antibiotic resistance genes and heavy metals in surface sediments along Taihu Lake located in the Yangtze Delta, owing to the rapid development of industry, agriculture, and fishery production. Significant correlations ( $p < 0.05$ ) were found between sediment ARGs level, especially for tetracycline and sulfonamides (e.g., tet(A), tet(D), tet(E), tet(O), sull, sulll, int-1) and specific heavy metals in the lake. In the surface sediments, heavy metals had a close relation to the resistance genes, but their interaction was abated with an increase in depth. For most of the heavy metals, the concentration of elements in the top sediments was higher than that in other depths. All ARGs tested were detected in the collected samples except tetJ, tetK, tetL, tetQ, tetS, tetX and tetY. They had a trend which inferred a statistically significant increase and then decreases in the relative abundance of these ARGs (normalised to 16SrRNA genes) with increasing depth. This study revealed that tetA, tetO, TEM, OXY, int-1, sull and sulll were universal in surface sediments with high abundance, indicating that these genes deserve more attention in future work.

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