



Co-occurrence of antibiotics, antimicrobial resistance genes and wastewater indicators in surface waters near Bangkok, Thailand: Characterization, Distribution & Controls

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Aquatic pollution from emerging contaminants, including antibiotics and antimicrobial resistance (AMR) genes, is an important environmental concern particularly pertinent in megacities such as Bangkok, Thailand, impacted by rapid urbanization and massive water demand. Using a suite of environmental and hydrogeochemical tracers including inorganics and organics, nutrients, metal(loids), select antibiotics and AMR genes [1, 2], we characterize the distribution and spatial patterns of a range of contaminants in a ~ 150 km transect of the Chao Phraya River Basin in Thailand capturing areas both upstream and downstream of Bangkok. A range of antibiotics and AMR genes were identified in parts of the transect and downstream trends are investigated. Co-occurrence between selected antibiotics and AMR genes was not statistically significant, although other significant hydrogeochemical relationships (*e.g.* between pH and selected AMR genes) were observed, suggesting complex controls and selection pressures. Comparisons are made with the types and concentrations of similar compounds detected in other major river and groundwater systems near other rapidly developing cities in South Asia (*e.g.* Patna, India) [3-5]. This work highlights the added interpretive value of a comprehensive range of analytes and provides insight on the potential co-occurrence of antibiotics, antimicrobial resistance genes and wastewater indicators that may be observed in surface waters in such settings.

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