Urban recreational water – potential breeding ground for antibiotic resistant bacteria?

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The emergence of multidrug-resistant bacteria, or “superbugs,” has become an urgent and worldwide concern. Antibiotic-resistant bacteria (ARB) cause significant morbidity and mortality (O’Neill, 2016). It has been estimated that ARB cause at least 23,000 deaths annually in the United States alone and hundreds of thousands of deaths in developing countries (Bougnom and Piddock, 2017). Antibiotic resistance genes (ARGs) protect bacteria against common antimicrobial molecules through several mechanisms, such as membrane modification, efflux, target modification, and inactivation (Blair et al., 2015). ARGs are often shared and acquired using mobile gene elements, such as integrons and transposons on plasmids, thereby facilitating their propagation in the environment through horizontal gene transfer (HGT) (Bennett, 2008). The transmission of ARGs into bacteria may allow bacteria to become “superbugs” with resistance to multiple antibiotic drugs. ARGs and mobile gene elements, such as class 1 integron (intI1), are frequently used as indicators for anthropogenic contamination in the environment because they respond to specific stresses, such as antibiotic drugs, heavy metals, polycyclic aromatic hydrocarbons (PAHs), and other contaminants (Qiao et al., 2018; Chen et al., 2017; Riquelme et al., 2017; Ye et al., 2017; Jiang et al., 2018).

The aquatic environment is a suitable reservoir for both ARGs and bacterial pathogens (Luo et al., 2010; Li et al., 2015; Qiao et al., 2018; Meng et al., 2017; Ozkal et al., 2017). Although the presence of ARGs and pathogens has been studied in various water systems, including waste water, rivers, aquaculture, and drinking water, their presence in recreational water (Fig. 1) still remains poorly studied. Because urban recreational water is often used for leisure and relaxation, there is a potential public health risk arising from exposures to ARGs and pathogens in water. Therefore, it is of great importance to understand the occurrence of ARGs and pathogens in recreational water.

Dong et al. (2019) recently investigated the presence of ARGs, intI1, and bacterial pathogens in three urban recreational lakes of Beijing. A total of 24 water and sediment samples were collected at two separate locations of each lake and at two different time points (September and November). The prevalence and abundance of six ARGs, intI1, and five common bacterial pathogens were determined using quantitative polymerase chain reaction (qPCR). Six ARGs included those targeted against sulfonamides (sul1, sul2), tetracyclines (tetW, tetX), and β-lactams (blaTEM, blaSHV). Five pathogens, including Escherichia coli, Salmonella enterica, Aeromonas spp., Mycobacterium avium, and Pseudomonas aeruginosa, were detected. Total bacterial amount was also measured by determining the 16S rRNA genes using qPCR. The diversity of bacterial pathogen was measured by using next generation sequencing.

The ARGs sul1, sul2, blaTEM, and intI1 were detected in all samples; and tetX and tetW were identified in most of the samples. In contrast blaSHV was detected in a few samples. The concentration of ARGs ranged from 5 to 500,000 copies/mL in water and from 5.8 × 10^3 to 5.9 × 10^8 copies per gram of sediment (in dry weight). sul1 showed the highest level among the five detectable ARGs. The detection frequencies (75%–100%) were high for five detectable ARGs, indicating the prevalence of these resistance elements in all three recreational lakes.

The levels of Escherichia coli, Aeromonas spp., Mycobacterium avium, Pseudomonas aeruginosa and Salmonella enterica ranged from 10^3 to 10^5 copies/100 mL in water and from 10^4 to 10^6 copies/g sediment (dry weight). All five pathogens were detected in 25% of the samples, suggesting the pervasiveness of these pathogens in three recreational lakes. Sixty-eight genera of pathogens were further identified by using next generation sequencing, indicating the diversity of potential pathogens in urban recreational water.

The results of Dong et al. (2019) revealed the prevalence of ARGs and bacterial pathogens in urban recreational water. Although the absolute abundance of ARGs in recreational
water was slightly lower than or equal to that in urban rivers, the levels of ARGs in sediment were up to 2-fold higher than those in the urban rivers in Beijing, suggesting that ARG contaminations could be more severe in recreational lakes than in urban rivers. The level of Salmonella enterica in recreational water was not quantifiable, but more attention should be given to the occurrence of this pathogen, because a small number of this pathogen (15–100 CFU) is sufficient to cause infection and serious disease.

Dong et al. (2019) also found that the abundance of intI1 was significantly correlated with that of sul1 and tetX in both water and sediment. The abundances of intI1 and blaTEM in water were also significantly correlated. Therefore, the propagation of sul1, tetX, and blaTEM may be facilitated by intI1. intI1 is one of the most active integrons associated with the spread of ARGs and substantially contributes to the evolution and proliferation of multiple antibiotic resistant bacteria (Diehl and LaPara, 2010; Sanderson et al., 2016).

Overall, the findings of Dong et al. (2019) are important for understanding the occurrence and distribution of ARGs and bacteria pathogens in recreational water. The wide distribution and high abundance of ARGs and pathogens in recreational water warrants better monitoring and control of ARGs and pathogens and their propagation in recreational lakes to protect public health from associated risks.

REFERENCES


