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Investigation of drinking water bacterial community through high-throughput sequencing

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Delivery of safe and pathogen-free drinking water is crucial to public health. However, there exist challenges to the maintenance of the sterility of drinking water throughout the drinking water distribution systems (DWDS). Microbial growth in DWDS, such as growth of opportunistic pathogenic microorganisms, can lead to severe health problems in consumers (Berry et al., 2006; Brettar and Hofle, 2006; Lu et al., 2014; Zhang et al., 2015). Therefore, the impact of different factors on the drinking water biofilm bacterial community in DWDS merits investigation to provide information and insight into the development of effective control measures (Fig. 1).

In the past, culture-based methods or direct counting methods have been the major strategies for the investigation of the microbial community (Liu et al., 2013). Lehtola et al. (2004) investigated the biofilm bacterial community on different pipe materials (copper and plastic) by various methods such as heterotrophic plate count, lipid biomarker, and fluorescence staining. The results showed that biofilm formation was slower in copper pipes than in plastic pipes. Moreover, pipe materials also influenced the microbial and Gram-negative bacteria community structure in biofilms and drinking water. A recent study also confirmed that microbial community was affected by pipe materials (Liu et al., 2014). However, these methods have a limitation in identifying different bacterial cells in the sample.

The bacteria are usually identified as groups rather than single species.

Recently, due to advances in molecular biology, there is an increasing body of research on the bacterial community in DWDS using high-throughput sequencing techniques. With the use of molecular-based methods, the richness and diversity of biofilm bacterial community can be better assessed (Luo et al., 2015; Tian et al., 2015; Wei et al., 2015; Zhang et al., 2014; Yu et al., 2014). Among these molecular-based methods, 16S rRNA sequencing was commonly applied. Williams et al. (2004) compared the diversity of drinking water bacteria in chlorinated and chloraminated distributed water. The major species of the bacterial community was α -proteobacteria under these two disinfectants, but the use of disinfectants affected the bacterial population dynamics. A recent study demonstrated that disinfectant type and dosage affected the bacteria community (Mi et al., 2015). *Proteobacteria* was the predominating species in chloraminated drinking water biofilms, while *Firmicutes* prevailed in chlorinated and unchlorinated biofilms. Different studies also reported the impact of different factors on the bacterial diversity and population by 16S rRNA sequencing, such as distance from source (Vaz-Moreira et al., 2013), water age and pipe materials (Wang et al., 2014), hydraulic regimes (Douterelo et al., 2013), and quality of feeding water (Sun et al., 2014; Wu et al., 2015). Since the bacteria can be identified down to the species level, the change of bacterial population and diversity by different factors were clearly revealed by the high-throughput sequencing coupled with different statistical analysis, such as cluster analysis (Williams et al., 2004), principal component analysis (Vaz-Moreira et al., 2013), and calculation of different indices (Douterelo et al., 2013).

There are several possible uses of high-throughput sequencing in the investigation of bacterial communities in DWDS (Mi et al., 2015). Although there is plenty of research on the bacterial communities in DWDS, the link between drinking water and

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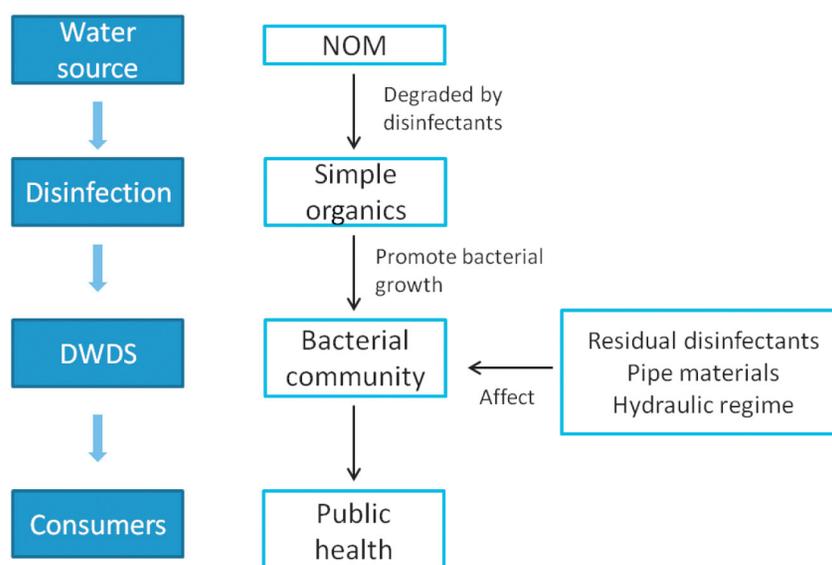


Fig. 1 – Factors that affect drinking water bacterial communities during the delivery to consumers. DWDS: drinking water distribution systems; NOM: natural organic matter.

human health is seldom studied. High-throughput sequencing can also be applied to investigate the bacterial communities in human gastrointestinal (GI) tracts (Rajilic-Stojanovic et al., 2007), which play an important role in human health. Microorganisms in drinking water sources may colonize in GI tracts and this phenomenon may pose a potential health risk to consumers. Lee et al. (2010) compared the bacterial communities in drinking water and germ-free GI tracts by high-throughput sequencing. Through phylogenetic analysis, a close relation between the two communities was observed, indicating that bacteria in drinking water would affect the GI bacterial community. However, there is a lack of studies to demonstrate the impact of drinking water bacterial communities on human GI bacterial communities.

Another perspective is the study on the impact of natural organic matter (NOM) degradation on bacterial communities. The presence of NOM in source water is very common. Sunlight irradiation or addition of disinfectants in drinking water source can degrade NOM into simple organics, such as low-molecular-weight organic acid (Brinkmann et al., 2003; Yavich et al., 2004; Swietlik et al., 2009). These simple organics can be assimilated by microorganisms to promote their growth (Hammes et al., 2007). Nevertheless, the effect of these simple organic acids on the overall bacterial community in DWDS is still unclear. Moreover, the quality and quantity of the formation of simple organics by different disinfectants vary (Swietlik et al., 2009). The differences in the composition of organic acids by different disinfectants may favour the growth of different types of bacteria, subsequently affecting the bacterial communities. By the use of high-throughput sequencing, the change of bacterial diversity and richness by the different disinfectants in the presence of NOM can be further revealed.

Moreover, most of the abovementioned studies were conducted in experimental setup or distribution simulators, which may have different bacterial communities compared to

real DWDS. Roeder et al. (2010) showed that the long-term presence of disinfectants has great influence on the drinking water biofilm communities, possibly due to the selective pressure on microorganisms by the disinfectants. Therefore, investigation of how different factors, especially the disinfectants, affect the bacterial communities in real drinking water and DWDS would provide more realistic information for better control of water quality.

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