Characteristics of Bacterial Communities in Biological Filters of Full-Scale Drinking Water Treatment Plants

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Introduction

Biological filtration refers to the process of removing both particulate matter and biodegradable organic matter (BOM) from water [1]. Biological filters can remove organic compounds through the fixed biofilm that develops on various media such as sand, anthracite, granular activated carbon (GAC), or membranes [2]. The biologically active rapid filter and the biological activated carbon (BAC) filter have been widely used for decades in drinking water treatment plants [1–5]. The rapid filter is usually filled with sand or anthracite, and is considered the most economical way to remove particles and BOM with the same filter unit [1]. However, many previous studies have demonstrated that the BAC filter is a more appropriate process to remove BOM than the rapid filter [4, 5]. Generally, the combination of ozonation and GAC filter is referred to as the BAC process [3]. Ozonation converts high-molecular-weight refractory organic matter into low-molecular-weight BOM, and this increased BOM can be effectively removed by the bacteria attached to the BAC filter [1, 4, 6–8].

Biological filtration has many advantages for drinking water treatments. First of all, it is important to increase the biostability of drinking water by reducing the quantity of BOM which can cause bacterial regrowth in distribution systems [1, 3–5]. It can reduce the disinfection by-product formation, and improve the water quality for human consumption. Biological filters have the additional advantage of treating pathogens, and reducing the disinfection by-products which are detrimental to human health [3].

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The taxonomic and functional characteristics of bacterial communities in the pre-chlorinated rapid filters and ozonated biological activated carbon (BAC) filters were compared using Illumina MiSeq sequencing of the 16S rRNA gene and community-level physiological profiling (CLPP) based on sole-carbon-source utilization patterns. Both the rapid filters and BAC filters were dominated by Rhizobiales within α-proteobacteria, but other abundant orders and genera were significantly different in both types of filter. Firmicutes were abundant only in the intermediate chlorinated rapid filter, while Acidobacteria were abundant only in the BAC filters. Bacterial communities in the rapid filter showed high utilization of carbohydrates, while those in the BAC filters showed high utilization of polymers and carboxylic acids. These different characteristics of the bacterial communities could be related to the different substrates in the influents, filling materials, and residual disinfectants. Chlorination and ozonation inactivated the existing bacteria in the influent and formed different bacterial communities, which could be resistant to the oxidants and effectively utilize different substrates produced by the oxidant, including Phreatobacter in the rapid filters and Hyphomicrobium in the BAC filters. Bradyrhizobium and Leptothrix, which could utilize compounds adsorbed on the GAC, were abundant in the BAC filters. Ozonation increased taxonomic diversity but decreased functional diversity of the bacterial communities in the BAC filters. This study provides some new insights into the effects of oxidation processes and filling materials on the bacterial community structure in the biological filters of drinking water treatment plants.

Keywords: Bacterial community, substrate utilization, rapid filter, biological activated carbon filter, biological filter, drinking water
(DBPs) precursors and chlorine demand, which can help to maintain stable residual chlorine in the distribution system [1, 3]. Biological filtration can also remove various biodegradable micropollutants including taste and odor compounds [1–3, 9]. Furthermore, an active biofilm can extend the lifetime of a GAC filter by bio-regeneration [3].

However, there is a lack of information about which microorganisms are involved in the functions [2]. It is necessary to identify the attached microorganisms and characterize the microbial communities of various biological filters in order to determine the role of microorganisms and enhance the removal of biodegradable contaminants. Especially, the change of microbial community in the biological filters after the oxidation process is important to produce biologically stable drinking water in full-scale water treatment plants. Bacteria have a unique substrate preference [10, 11], so the change of microbial composition in biological filters can result in removal of different BOM in water. Both chlorination and ozonation can increase the BOM concentration, but they can produce different kinds of substrates [8, 12, 13]. Without the dominance of bacteria utilizing new substrates produced by those oxidants, biological filters cannot effectively remove the increased BOM, which can cause bacterial regrowth in the distribution system [14, 15]. In addition, understanding the microbial community in a biological filter is useful in terms of public health because the biofilm in a biological filter can be a source of microbial contamination in the distribution systems [16]. It is also possible to screen pathogenic or disinfection resistant microorganisms and adopt appropriate measures to control them in advance [17, 18].

Recently, many researchers have used molecular biological methods to evaluate microbial community structures in the aquatic ecosystem. In particular, next-generation sequencing (NGS) is a culture independent and high-throughput method of analyzing the structure of an entire microbial community [10, 19, 20]. In addition, community-level physiological profiling (CLPP) based on sole-carbon-source utilization (SCSU) patterns has deepened understanding of the metabolic ability and functional characteristics of microbial communities [21]. In this study, therefore, Illumina MiSeq sequencing of the 16S rRNA gene and CLPP were used to investigate the characteristics of bacterial communities attached to the biological filters in full-scale drinking water treatment plants.

The main purposes of this study were 1) to compare the differences in the taxonomic and functional characteristics of bacterial communities in rapid filters and BAC filters which received pre-chlorinated water and ozonated water, respectively; 2) to investigate the relationship between the taxonomic composition and substrate utilization patterns of bacterial communities; and 3) to elucidate how the different oxidation processes, i.e., chlorination vs ozonation, effect on the bacterial communities of biological filters.

Materials and Methods

Study Sites and Sampling

This study was conducted at three, full-scale water treatment plants (WTPs) in Seoul, South Korea (Fig. 1). All three WTPs use the surface water of the Han River as source water, and consist of conventional and advanced water treatment processes. The conventional treatment includes pre-chlorination, coagulation-sedimentation, and rapid filtration; whereas the advanced treatment includes ozonation and BAC filtration, and post-chlorination finally follows the advanced treatment. Pre-chlorination was applied at the intake of the raw water, and ozone was added after the rapid filters of the WTPs. Intermediate chlorine was added after sedimentation only at WTP2. The rapid filters of WTP1 and WTP3 are filled with sand, while WTP2 has a dual media (anthracite/sand) rapid filter. The BAC filters are filled with coal-based granular activated carbon (GAC), and the empty bed contact time (EBCT) is 15 min. The detailed design and

![Fig. 1. Flow diagram of processes in the three drinking water treatment plants.](PAC (poly aluminium chloride): coagulant)