Process Biochemistry 48 (2013) 312–316

Contents lists available at SciVerse ScienceDirect

Process Biochemistry

journal homepage: www.elsevier.com/locate/procbio

Short communication

Changes of biomass and bacterial communities in biological activated carbon filters for drinking water treatment

Xiaobin Liao[a], Chao Chen[a], Zhao Wang[b], Rui Wan[b], Chih-Hsiang Chang[b], Xiaojian Zhang[a], Shuguang Xie[b,*]

[a] School of Environment, Tsinghua University, Beijing 100084, China
[b] College of Environmental Sciences and Engineering, The Key Laboratory of Water and Sediment Sciences (Ministry of Education), Peking University, Beijing 100871, China

ARTICLE INFO

Article history:
Received 23 October 2012
Received in revised form 8 December 2012
Accepted 23 December 2012
Available online 3 January 2013

Keywords:
Microbial community
Drinking water
Alphaproteobacteria
Sphingomonas
Biofiltration
Biodegradation

ABSTRACT

Biological activated carbon (BAC) filtration can usually perform well in removal of biodegradable organic compounds in drinking waters. In this study, a pilot-scale down-flow BAC filtration system was constructed for treatment of ozonated waters. The changes of biomass concentration and bacterial community in the BAC filters with contact time and service time were characterized using phospholipid fatty acid (PLFA) analysis and 16S rRNA gene clone library analysis, respectively. The operational results indicated the BAC filtration system could effectively remove dissolved organic carbon (DOC) and assimilable organic carbon (AOC). Biomass concentration decreased with contact time, but showed only a slight change with service time. Contact time and service time could affect the microbial community structure. *Alphaproteobacteria* was the largest bacterial group and might have important links with the DOC and AOC removal. This work might provide some new insights into microbial community and biological process in the drinking water biofilters.

1. Introduction

Due to the deterioration of surface water quality, the upgrading of the conventional treatment process (coagulation–flocculation, sedimentation, rapid sand filtration, and disinfection) has aroused increasing attention by drinking water producers in the world. The removal of organic compounds in waters can usually be enhanced by chemical oxidation, membrane filtration and biological filtration. Following sand filtration, biological activated carbon (BAC) filtration has been widely applied to remove biodegradable organic compounds, thus controlling the microbial regrowth and disinfection byproducts (DBPs) formation in drinking water distribution systems (DWDS). The indigenous microbial population attached to the porous surface of granular activated carbon (GAC) is responsible for this biological process. A stable, thin and active biofilm is ideal for BAC filtration [1]. It has been commonly accepted that knowledge of the microbial communities in BAC filters can increase our understanding of the biological processes [2,3]. Many techniques have been used to assess either microbial biomass density or its activity in BAC filters, such as oxygen consumption, heterotrophic plate counts, total direct cell counts, scanning electron microscopy, phospholipids, uptake of labeled substrates and reduction of tetrazolium salts [5]. However, these conventional microbiological methods cannot provide accurate information on the bacterial populations in the BAC filters. Moreover, BAC filtration performance might not be related to biomass amounts [6,7].

Culture-dependent methods have provided some useful information on bacterial population in BAC filters [8–10]. However, most of the microorganisms in the environment are refractory to cultivation and the deviation from the original environmental parameters may inaccurately reflect the original structure of microbial community [11]. Phospholipid fatty acid (PLFA) analysis has been widely used to depict microbial community dynamics in drinking water biofilters [4,12–14]. Moreover, based on 16S ribosomal RNA (rRNA) sequences, denaturing gradient gel electrophoresis (DGGE) and terminal restriction fragment length polymorphism (TRFLP) fingerprinting have been commonly used for the rapid analysis of microbial diversity and dynamics in BAC filters [6,15–18]. However, neither of PLFA, TRFLP and DGGE analysis could provide direct phylogenetic information on microbial communities. Up to date, only few studies using 16S rRNA gene clone library analysis have been carried out to characterize the bacterial populations or ammonia-oxidizing bacteria (AOB) communities in BAC filters [19–21]. Therefore, the links of the biological processes occurring in the BAC filters with the microbial communities remain poorly understood.

The vertical differences of biomass concentration in the drinking water biofilters have been well-documented. Biomass density

* Corresponding author. Tel.: +86 10 62751923; fax: +86 10 62751923.
E-mail address: xiesg@pku.edu.cn (S. Xie).

1359-5113/$ – see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.procbio.2012.12.016

usually decreases with increasing filter depth (and corresponding contact time) as the result of gradual consumption of substrates [3,8,12,20,22]. Due to variation of substrates in influents, biomass density in drinking water biofilters may also change with service time. Unfortunately, very few studies have reported the change of biomass density in drinking water biofilters with service time [3,8].

The properties and concentrations of the available carbon source can affect microbial community structure in water and biofilm [23–26]. However, little information is available on the vertical heterogeneity of microbial community structures in drinking water biofilters. Moreover, the change of microbial community in biofilters with service time remains largely unknown. In the current study, pilot-scale BAC filters used for drinking water treatment were constructed to evaluate the performance in the reduction of organic matter. The changes of biomass and bacterial populations with contact time and service time were characterized using PLFA and 16S rRNA gene clone library analyses, respectively. This work could provide new insights into the evolution of bacterial communities and their ecological function in the drinking water biofilter.

2. Materials and methods

2.1. Experimental setup

Fig. 1 shows the schematic diagram of the pilot-scale downflow BAC filtration system. Both columns were Plexigas cylinders and with height and inner diameter of 1.9 m and 40 cm, respectively. The BAC filtration columns were provided with sampling ports for water and GAC. The BAC filtration system received the influent at the hydraulic loading of 8 m/h. The influent of the system was lake water pretreated with pre-ozonation, rapid mixing, flocculation, sedimentation, sand filtration and post-ozonation. Before the beginning of experiments, the filters had been under continuous operation for six months in order to enable biofilm formation. During this study, the pH values and oxygen concentrations of the influent ranged between 7.5 and 8.3, and 6.5 and 7.5 mg O_2/L, respectively.

2.2. Analytical methods

The water samples and GAC samples were collected on day 0 and day 160. For physicochemical analysis, dissolved oxygen (DO) and pH were determined as previously described [2]. Dissolved organic carbon (DOC) was measured using a Shimadzu 5000A TOC analyzer. Assimilable organic carbon (AOC) bioassay was conducted according to the standard method [27]. The biomass attached to the GAC was quantified by a phospholipids assay [8].

In this study, the samples from the sampling points A–D on day 0 were referred to Samples A0, B0, C0, and D0, respectively. Similarly, the samples from the sampling points A–D on day 160 were referred to Samples A160, B160, C160, and D160, respectively. DNA from each GAC sample was subjected to clone library analysis as previously described [2,28,29]. Briefly, bacterial 16S rRNA genes were amplified using primers 27F and 1492R. The PCR products were cloned into pMD19-T vector (Takara Corp, Japan). The clones containing correct size were sequenced. The Ribosomal Database Project (MSU Center for Microbial Ecology) analysis tool "classifier" was utilized to classify the taxonomic identity of each bacterial sequence at confidence level of 80% [30]. The sequences obtained in this study were submitted to GenBank under accession numbers JQ398498–JQ398598, JQ937027–JQ937081, JQ926629–JQ926675, JX181665–JX181753, and JX402513–JX402602.

3. Results and discussion

3.1. Removal of DOC and AOC

Gradual removal of DOC with contact time was observed in the pilot-scale BAC filtration system (Fig. 2A). The BAC filtration system could effectively reduce DOC, with the calculated removal rates of 34.3% and 31.2% at days 0 and 160, respectively. AOC was also gradually reduced with contact time (Fig. 2B). The average AOC removal rates by the BAC filtration system were 60.6% and 51.2% at days 0 and 160, respectively.

The effective removal of DOC and AOC by biofiltration systems has been well-documented [17,31–33]. Ozonation followed by BAC

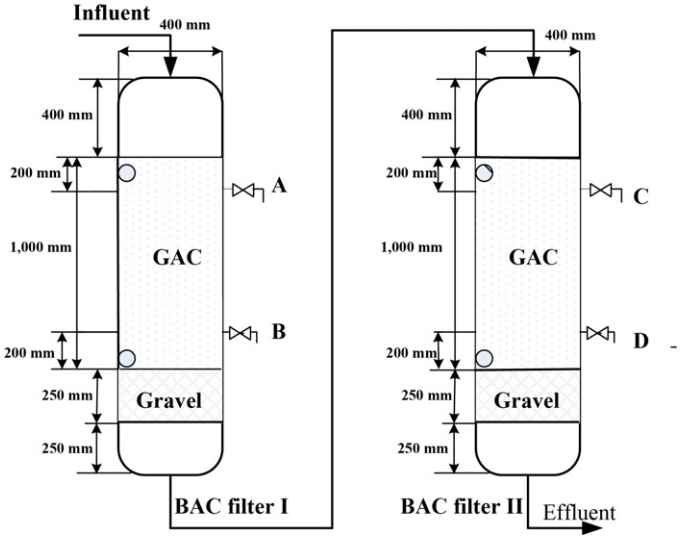

Fig. 1. Schematic of the pilot-scale BAC filtration system.

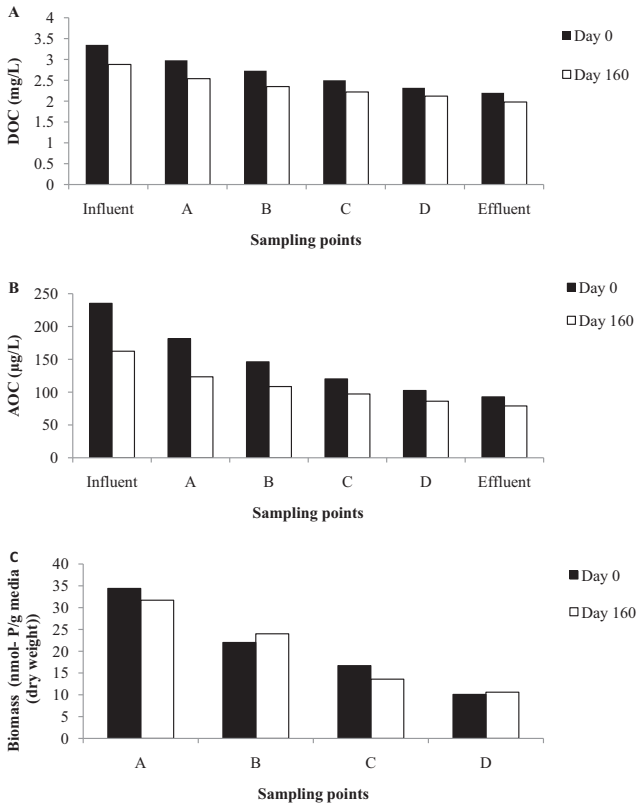

Fig. 2. (A) DOC, (B) AOC, and (C) biomass changes in the BAC filtration system.