

Small-scale drinking water treatment unit of filtration and UV disinfection for remote area

Kassim Chabi, Jie Zeng, Lizheng Guo, Xi Li, Chengsong Ye and Xin Yu

ABSTRACT

People in remote areas are still drinking surface water that may contain certain pollutants including harmful microorganisms and chemical compounds directly without any pretreatment. In this study, we have designed and operated a pilot-scale drinking water treatment unit as part of our aim to find an economic and easily operable technology for providing drinking water to people in those areas. Our small-scale treatment unit contains filtration and disinfection (UV–C irradiation) stages to remove pollutants from source water. The water quality index was determined based on various parameters such as pH, temperature, dissolved oxygen, nitrate, nitrite, ammonium, phosphorus, dissolved organic carbon and bacteria. Water and media samples after DNA extraction were sequenced using Illumina MiSeq throughput sequencing for the determination of bacterial community composition. After the raw water treatment, the reduction of bacteria concentration ranged from 1 to 2 log₁₀. The average removal of the turbidity, ammonium, nitrite, phosphorus and dissolved organic carbon reached up to 95.33%, 85.71%, 100%, 28.57%, and 45%, respectively. In conclusion, multiple biological stages in our designed unit showed an improvement of the drinking water quality. The designed drinking treatment unit produces potable water meeting standards at a lower cost of operation and it can be used in remote areas.

Key words | drinking water treatment unit, filtration, remote area, small-scale, UV disinfection

HIGHLIGHTS

- The pilot-scale study can contribute to solving the problem of drinking water deficiency in remote areas.
- The pilot-scale unit provides potable water complying with international and national standards.
- The drinking water treatment unit is effective, low cost, and easy to operate.
- Biofiltration and UV have a great role in water purification.
- *Nitrospira* and *Nitrosomonas* species on GAC surface oxidize ammonia and nitrite to nitrate.

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(Romani & Anderson 2002). It is worth mentioning that safe drinking water is a fundamental human need; humans can survive for 50 days without food, but for water this cannot happen as it is an essential element in cellular metabolic activity (Saltmarsh 2001; Choose Health LA Moms 2015).

Filtration and disinfection are among the most important drinking water treatment methods. Filtration is the main process in drinking water treatment, in which the water passes through a filter to get rid of particulates and flocs from the water being primary treated (Bourke et al. 1995). Filtration is used to remove the suspended particulates including pathogens. Biological and physical processes have been used to filter water on a full scale and pilot-scale. The classical techniques were largely limited to sand-based water filtration. Slow sand filtration is largely adapted for household use, and it works mainly through biological activity that occurs on the surface of a sand bed. The slow sand filter is operated and maintained at a low cost compared with other filtration technologies used in water treatment. It is the most commonly used method for small areas to provide good quality and safe water (Pooi & Ng 2018). The upper layer of a slow sand filter (biological layer or in German *schmutzdecke*) can be effective in removing turbidity, microorganisms, pesticides, and ammonia. Slow sand filters are maintained by scraping the biological layer periodically. Rapid sand filtration focused on the physical treatment of water is often used to control the quality of water. Rapid sand filters can be found as single medium, dual-medium or multimedia. The flow rate of a slow and rapid sand filter varies from 0.1 to 0.3 m h⁻¹ and from 5 to 30 m h⁻¹, respectively (Page et al. 2006). Granular activated carbon (GAC) with the aid of sand is used in filtration processes. GAC has the property of removing the pollutants, particularly organic compounds, that may react with chlorine to produce trihalomethanes and other disinfection by-products. It is well reported that GAC is colonized by bacteria during drinking water treatment. This colonization is the result of several reasons. The first, the porous surface of GAC provides a protective environment for microorganisms from fluid shear forces. The second, functional groups on the carbon surface enhance the growth of microbes. The third, nutrients are sieved by the carbon surface and act as a food source for many microorganisms (Stewart et al. 1990; Oh et al. 2018).

Disinfection is highly recommended in order to prevent the wide spread of harmful bacteria and other pollutants after sand filtration. UV disinfection is one of the disinfectants that has attracted growing interest as an alternative technology for water disinfection. UV irradiation is known as an effective disinfectant due to its powerful germicidal ability. UV irradiation is able to kill or inactivate microorganisms by destroying nucleic acids and disrupting their DNA, leaving them unable to perform vital cellular functions or cause an infection. UV disinfection offers several advantages, including high efficiency in inactivating chlorine-resistant organisms (e.g., *Giardia* and *Cryptosporidium*), no chemical addition and reduction of disinfection by-product formation (Timmermann et al. 2015; Wang et al. 2017).

In conventional drinking water treatment facilities, coagulation, flocculation, and sedimentation followed by filtration and disinfection are used to remove pollutants from source water (Pooi & Ng 2018). However, these water treatment plants are costly and difficult to operate in remote areas compared with portable small-scale drinking water treatment units. Accordingly, the primary goal of this study was to design a pilot-scale water treatment unit including filtration (biological and physical) and disinfection (UV) sections to treat and provide safe drinking water to people in remote areas. To evaluate the performance of the designed water treatment unit, physicochemical and microbiological parameters were monitored all through the treatment process. High-throughput 16S rRNA gene-based pyrosequencing analysis was performed for the identification of the bacterial community in the different treatment stages of the treatment unit.

MATERIALS AND METHODS

Design and operation of pilot-scale drinking water treatment unit

The pilot-scale system was composed of six treatment stages including UV disinfection as the last treatment stage. In the first stage of treatment, there were two different media: gravel (pore size: 12–16 mm, height: 0.1 m) and sand (pore size: 2–3 mm, height: 1 m). The second, third and fourth stages contained gravel (diameter: 5–10 mm; height = 0.1 m) at the

bottom, sand (diameter: 0.5–1.25 mm; height = 0.6 m) at the middle and biological activated carbon (BAC) (diameter: 1–2 mm; height = 0.6 m) at the top. The fifth stage was composed of gravel (diameter: 5–10 mm; height = 0.1 m) at the bottom and sand (diameter: 0.5–1.2 mm; height = 1 m) at the top. The final effluent of our pilot-scale unit was sterilized by high-pressure UV lamp (type C: 16 watts, wavelength = 254 nm, intensity = 5 mWcm⁻²) (Figure 1). The pilot-scale unit operated with a hydraulic retention time (HRT) of 0.03 day, which was determined by the equation $HRT = V/Q$, where V represents the volume of water in the column (m³) and Q is the influent flow-rate (m³ d⁻¹) (Zuo et al. 2008). The flow rate and hydraulic loading for the slow sand filter (first stage) were 0.12 m³ h⁻¹ and 1.32 m³ h⁻¹ m⁻², respectively. Each rapid sand filter (from second stage to fifth stage) operated with a flow rate and hydraulic loading rate of 0.04 m³ h⁻¹ and 5.09 m³ h⁻¹ m⁻², respectively (Figure 1). The backwash of the slow sand filter (the first stage) was done with 2.1 m³ h⁻¹ of tap water and 3.5 m³ h⁻¹ of dry air. The cleaning of the other columns (from the second to the fifth stages) was done every two days by forcing water upward (supernatant level = 30%).

Samples and sampling site

The raw water from the man-made stream (24° 36' 43.1964" N 118° 3' 29.6964" E) draining water from Jimei to Xinglinwan Reservoir in Xiamen City, China, was used to test the efficacy of our small-scale water treatment unit. The operation of the pilot-scale unit was continued from April to

September 2019. The water samples were collected from raw water and after each treatment step. The water samples were collected in sterilized Duran laboratory glass bottles (capacity = 1 L). For sterilization, the bottles were soaked in HCl aqueous solution (10% by volume) for 24 hours and rinsed with large amounts of ultra-pure water. The bottles were then reesterilized in an autoclave (time = 30 min, temperature = 121 °C) and dried in an oven (time = 60 min, temperature = 60 °C).

Physicochemical parameters

The pH and temperature of water samples were measured by a pH meter (Eutech Instruments PH 700). The turbidity was measured using a turbidimeter (Orion AQ4500; Thermo, USA). Dissolved oxygen was estimated by a multi-measuring instrument (WTW, Multi 3420, Germany).

Ammonium (NH₄⁺-N), nitrate (NO₃⁻-N), nitrite (NO₂⁻-N) and phosphate (PO₄³⁻-P) concentrations were determined by using a UV₂₅₄ spectrophotometer (Shimadzu, TU-1810 pc Japan). The persulfate wet oxidation technique (Shimadzu TOC-V WP, Japan) was used for determining dissolved organic carbon (DOC). The percentage removal efficiency of all physicochemical parameters in water samples was calculated based on the following equation: removal efficiency (%) = $\frac{C_0 - C}{C_0} \times 100$ (de la Luz-Pedro et al. 2019), where C_0 is the concentration of the parameter at the inlet and C is its concentration in the effluent.

Bacteriological parameters

The collected samples were serially diluted individually in sterile physiological saline (0.9% w/v NaCl) according to the expected number of colonies, and 0.1 ml aliquots from the appropriate dilutions were spread on the surface of nutrient agar media to determine total bacterial counts. The inoculated plates were incubated at 37 °C for 48 hours before counting. The log₁₀ removal efficiency of total viable bacterial counts was calculated by using the following formula: removal efficiency (log₁₀) = $\log_{10} \left(\frac{C}{C_0} \right)$ (Tartanson et al. 2014), where C and C_0 are the total bacterial counts of the influent and effluent, respectively.

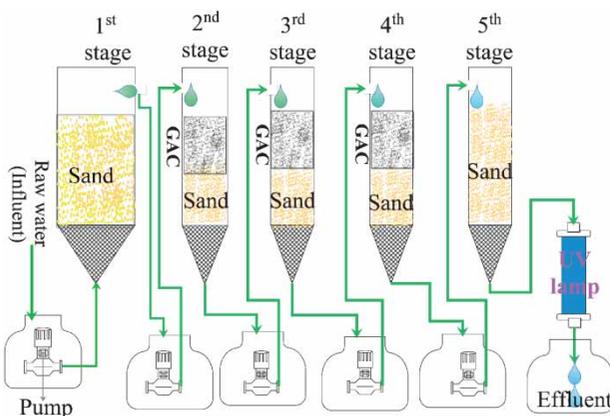


Figure 1 | Schematic diagram of the pilot-scale unit.

Determination of bacterial community composition

Water samples from the inlet and different treatment stages were filtered through 0.22 μm membrane filters. For filter media, 0.5 g from each sample was subjected to DNA extraction. The FastDNA™ spin kit for soil (MP Biomedicals, Santa Ana, CA, USA) was used to extract DNA of the microbial communities in the filter media and on the obtained membranes according to the instructions of the manufacturer. A Nano Drop Spectrophotometer (Thermo Scientific, USA) was utilized to measure the concentration and purity of the obtained DNAs. The extracted DNAs were sequenced using Illumina MiSeq throughput sequencing (Shanghai Majorbio Bio-pharm Technology Co., Ltd, China). The 16S primers (319F and 806R) were utilized to amplify the hypervariable V3–V4 region of the bacterial 16S rRNA genes. Our primers included Illumina sequencing adapter, pad, linker, and the reverse primer contained a 12-bp error-correcting barcode. The 300 bp reads were truncated at any site receiving an average quality score <20 over a 50 bp sliding window, discarding the truncated reads that were shorter than 50 bp. Reads containing N-bases were also removed. Data analysis was conducted by the I-Sanger Cloud Platform (<http://www.i-sanger.com/>) provided by Majorbio Bio-Pharm Technology Co., Ltd.

Statistical analyses

The paired *t*-test and one-way analysis of variance (ANOVA) was used to assess a change that occurred in the physicochemical parameters across stages of water treatment in our pilot-scale unit. The change was significant at $P < 0.05$. All analyses were created by Graph Pad Prism 7.00 version.

RESULTS

Water quality characteristics

The heterotrophic bacteria counts in raw water were comprised of a range from 10^3 to 4.5×10^3 CFU mL⁻¹. The small-scale drinking water unit was able to remove 2 log₁₀ of bacteria (Figure 2). In effect, after complete treatment in effluent, the bacterial concentration was comprised of

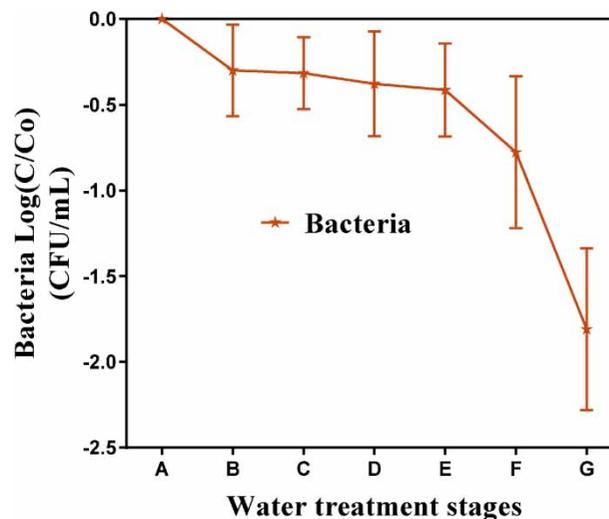


Figure 2 | Removal of bacteria in different stages of drinking water treatment.

3–60 CFU mL⁻¹. The water quality parameters of the source and treated water during the operating time are summarized in Table 1. The variation of physicochemical parameters obtained from the analysis of water samples of different treatment stages is shown in Figure 3. The range of pH in water was between 6.75 and 7.99, while the temperature varied from 22.9 to 29.8 °C. Generally, the measurements of DO in water samples varied between 4.5 and 7.67 mg L⁻¹. The dissolved oxygen (DO) measured from treated water (the final effluent from our pilot-scale unit) and raw water corresponded to 7.41 and 5.55 mg L⁻¹ as averages, respectively. For the DOC, the average concentrations were 2.62 mg L⁻¹ in final treated water and 4.76 mg L⁻¹ in source water (Table 1). The treatment stages containing BAC were an important process for DOC removal (efficiency ~15% per column containing BAC). The DOC removal process is illustrated in Figure 3(e). The removal of turbidity, ammonium, nitrite and phosphorus across treatment stages is illustrated in Figure 3.

The removal efficiency of turbidity was >95% of source water turbidity. The turbidity of effluent samples was below 0.5 NTU. Sand filtration and BAC filtration subsequently removed 85.71% of the ammonium (Table 1). The nitrite in the raw water samples was between 0.07 and 0.15 mg L⁻¹, while it was 0.0 mg L⁻¹ in the final effluent. Our treatment unit showed a significant removal of nitrite ($P < 0.05$) with a removal percentage reaching 100%. However, nitrate concentration increased from 0.18–0.41 mg L⁻¹ in raw water to 0.42–0.84 mg L⁻¹ in the final effluent during

Table 1 | The relative values of water quality characteristics compared with WHO standards

Parameters		Influent	Effluent	Removal efficiency (%)	WHO Standards (World Health Organization 2018)
DO (mg L ⁻¹)	Range	4.5–6.08	7.07–7.67	—	—
	Average	5.55	7.41		
Temperature (°C)	Range	22.9–28.9	22.9–29.8	—	15–35
	Average	26.19	27.23		
pH	Range	6.75–7.49	7.09–7.99	—	6.5–8.5
	Average	7.27	7.57		
Turbidity (NTU)	Range	2.44–10.05	0.26–0.44	95.33	<0.5
	Average	7.5	0.35		
DOC (mg L ⁻¹)	Range	3.28–6.08	2.31–2.73	44.94	2–4
	Average	4.76	2.62		
NH ₄ ⁺ -N (mgL ⁻¹)	Range	0.3–1.69	0.02–0.28		—
	Average	0.91	0.13	85.71	
NO ₂ ⁻ -N (mgL ⁻¹)	Range	0.07–0.15	0.00–0.00	100	3
	Average	0.11	0.00		
NO ₃ ⁻ -N (mgL ⁻¹)	Range	0.18–0.41	0.42–0.84	—	50
	Average	0.27	0.71		
PO ₄ ³⁻ -P (mg L ⁻¹)	Range	0.21–0.23	0.11–0.18	28.57	—
	Average	0.21	0.15		

— Not set.

the treatment processes because of a higher relative abundance of some species affiliated to phylum Nitrospirae (a type of bacteria) which can oxidize ammonia and nitrite to nitrate (Figure 4). Phosphorus (PO₄³⁻-P) in the raw water samples and the final effluents exhibited concentrations of 0.21–0.23 mg L⁻¹ and 0.11–0.18 mg L⁻¹, respectively (Figure 3(f)). More strikingly, the obtained concentrations of nitrite, nitrate and phosphorus matched the requirements of the international drinking water standards (Table 1).

Metagenomic analyses of bacterial community during water treatment processes

The operating taxonomic units (OUTs) at different taxonomic levels indicated the abundance of 29 phyla, 62 classes, 160 orders, 238 families, 375 genera, and 563 species from 13 samples collected during treatments in the small-pilot scale unit. The phyla detected in our pilot-scale samples were Proteobacteria, Cyanobacteria, Bacteroidetes, Actinobacteria, Nitrospirae, Patescibacteria, Planctomycetes, Chloroflexi, Acidobacteria, others, Dependientiae, Verrucomicrobia, Firmicutes, Deinococcus-Thermus and Armatimonadetes. The most predominant phyla in the source water were

Actinobacteria (34%), Proteobacteria (32%), and Bacteroidetes (30%). On the other hand, it was found that the most frequent phylum in the first treatment stage was Proteobacteria (32%). It was noticed that Proteobacteria (30%) and Actinobacteria (35%) were the most dominant in the second treatment stage. In the third and fourth drinking water treatment stages, Proteobacteria (30% and 31%, respectively) and Cyanobacteria (37% and 32%, respectively) were the most frequent phyla. In the fifth treatment stage, only Proteobacteria (42%) was the most dominant phylum. In the disinfection stage (last stage) the members of the Proteobacteria (89%) were the most dominant species. In the media (sand and BAC) of different stages of treatment, we found that the most frequent phylum was Proteobacteria (23% and 43%, respectively) (Figure 4).

DISCUSSION

Water quality characteristics

In the present study, we designed and construct a pilot-scale drinking water treatment unit in order to provide drinking

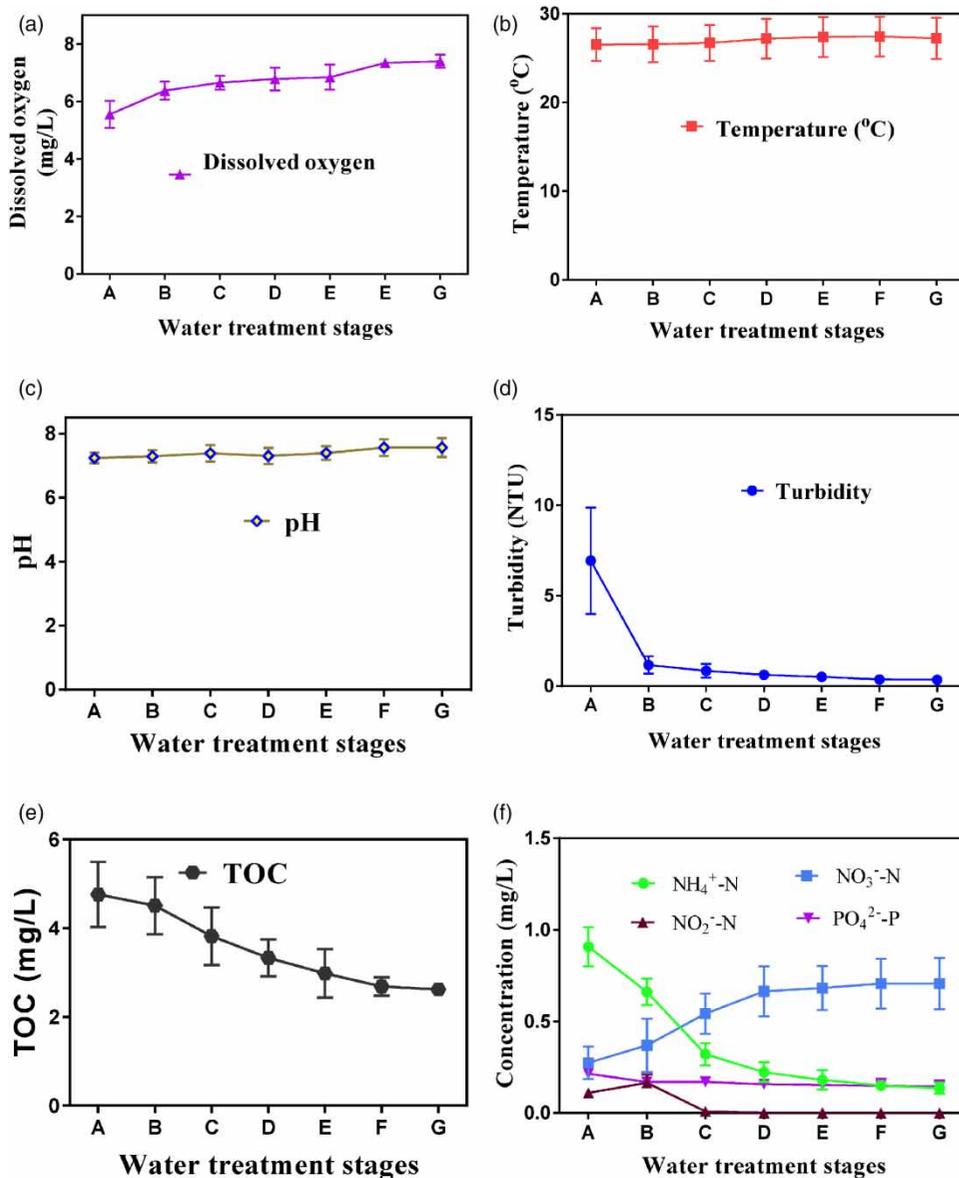


Figure 3 | The improvement of physicochemical parameters during different treatment stages. A – influent, B – 1st stage, C – 2nd stage, D – 3rd stage, E – 4th stage, F – 5th stage, G – effluent. Each point represents the mean values + standard deviation (SD).

water with good quality at low-cost operation. According to the obtained results of the physicochemical and microbiological parameters of the final treated water, this unit is useful for treating water in remote areas. Dissolved oxygen is one of the most important indicators of water quality. It is essential for the survival of organisms in the aquatic environment. The increase of dissolved oxygen during the treatment (Figure 3(a)) could be attributed to the improvement of water quality during the treatment together with the photosynthesis carried

out by algae, which attached on the gravel surface (i.e. the media at the bottom of each column in our unit) or on the inner walls of the columns (i.e. stages of water treatment) in the presence of sunlight. During photosynthesis, the algae were able to fix CO_2 in the presence of sunlight and water to produce carbohydrates and O_2 . Our results were in line with the results of the previous study (Zeng *et al.* 2018).

The pH is also an important parameter in the determination of water quality. It is limited between 6.5 and 8.5 in

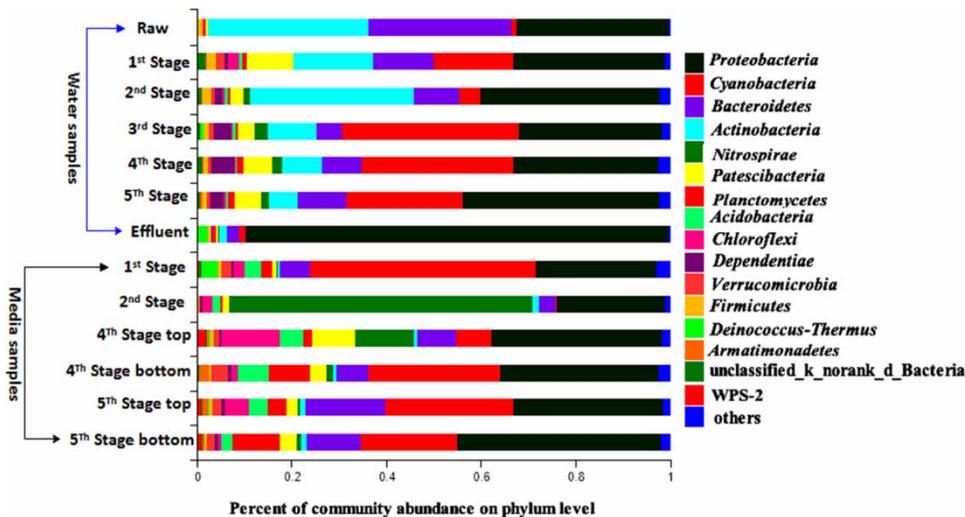


Figure 4 | Barplot analysis for bacterial community in media and water of the treatment unit.

drinking water. In the current study, the pH of the drinking water ranged from 7.09 to 7.99. It was noted when the pH slightly increased, the concentration of the chemical compounds (DOC, $\text{NH}_4^+\text{-N}$, $\text{NO}_2^-\text{-N}$ and $\text{PO}_4^{3-}\text{-P}$) decreased (Figure 3(c) and 3(f)). This slight variation influenced the quality of the water, and this was a possible benefit to sand and BAC used during the filtration. Moreover, the improvement in DO as well as pH values with progress in the drinking water treatment (Figure 3), might be due to rapid sand and biological filtration stages in our treatment unit.

The results showed that the removal of turbidity after complete treatment was 95.33% in the final effluent. Additionally, the obtained values were compatible with the international drinking water standard requirements (World Health Organization 2018). Such good performance in removing the source water turbidity could be due to the biological and physical filters. DOC, $\text{NH}_4^+\text{-N}$, $\text{NO}_2^-\text{-N}$ and $\text{PO}_4^{3-}\text{-P}$ concentrations were decreased significantly in the effluent and the obtained results were within recommended ranges for drinking water (United States Environmental Protection Agency 2018; Zhang et al. 2019). The reduction of such chemicals was mainly due to our biological treatment (BAC filters) (Pipe-Martin 2008; Rattier et al. 2012; Mingo 2015; dos Santos & Daniel 2019). Similar results have been found in previous studies (Yapsakli et al. 2010; Feng et al. 2013). Normally, granular activated carbon (GAC) filter characterized by high surface area (1 g of GAC equivalent

to 930 m² of surface area) allows the adsorption of a large quantity of contaminant molecules. In adsorption, organic molecules contained in the water are attracted and bound to the surface of the pores of the activated carbon. During this phenomenon, water passes through the highly porous structure of the activated carbon. Because of van der Waals forces, BAC may exhibit a strong attraction for organic compounds and other non-polar contaminants (Patil et al. 2016). The adsorption becomes very weak for GAC in >2–3 months usage after all adsorption sites in the GAC are occupied. In fact, by that time, the GAC has been transformed into BAC. Then the bacteria in the biofilm attached to the activated carbon granular surface can degrade the organic pollutants. In addition, *Nitrospira* and *Nitrosomonas* that have colonized the BAC can oxidize ammonia into nitrite and nitrate (Daims et al. 2015). The mechanism by which $\text{NH}_4^+\text{-N}$ is removed can simply be explained based on previous findings (Suzuki et al. 1974; Koch et al. 2019). In the present study, the high-throughput 16S rRNA gene-based pyrosequencing analysis showed the colonization of such species in BAC (Figure 4). Moreover, it was noticed that with the decreasing of the $\text{NH}_4^+\text{-N}$ concentration, the concentration of $\text{NO}_3^-\text{-N}$ and $\text{NO}_2^-\text{-N}$ increased, while $\text{NO}_2^-\text{-N}$ was eliminated completely by using BAC. However, GAC is not able to remove some of the chemicals in water such as nitrate (Minnesota Department of Health 2013). Despite that, the concentration of nitrate was still below the standard requirements.

Bacterial community in different drinking water treatment stages

The study of the bacterial community has shown the presence of several types of bacterial species. These different species of bacteria that were present in the community used nutrients to survive. Normally, microbes use carbon, nitrogen and phosphorus to grow in biofilms (Yu *et al.* 2012; Chaves Simões & Simões 2013). In addition, the fluidization pretreatment can generate more nitrogen-enriched compounds (Yu *et al.* 2012) and this may explain the dominance of species belonging to the phylum Nitrospirae in media and water of the BAC stage. Our results indicated that the bacterial community structure changed during water treatment, with greater richness of bacterial types detected in different treatment stages. This observation is common because similar results were found from other studies (El-Chakhtoura *et al.* 2015) specifically during experiments with bench-scale and pilot-scale biologically active carbon reactors for water treatment (Li *et al.* 2010). These changes of structure observed in bacterial communities could be due to the amount of nutrients and the environmental factors (temperature and pressure). The dominance of Nitrospirae in the second treatment stage might be attributed to the higher concentration of ammonia and nitrite in this stage. Taxonomic analysis revealed that most of the OUTs in all the samples were associated with the phyla Proteobacteria (25–89%), Cyanobacteria (20–48%) and Bacteroidetes (3.5–17%) (Figure 4). We observed that the most predominant species were assigned to phylum Proteobacteria. Other previous studies reported the predominance of Proteobacteria in drinking water biofilters or finished drinking water as well (Sun *et al.* 2014; El-Chakhtoura *et al.* 2015). The bacterial community structure in drinking water distribution systems associated with a different primary source of water (surface and ground) were dissimilar, suggesting that their respective source water and/or water quality parameters shaped by the treatment processes may contribute to the differences in community structure observed (Gomez-Alvarez *et al.* 2015). Such differences in the bacterial communities in raw water versus treated drinking water in our study were observed as well. For example, the relative abundance of Bacteroidetes and Actinobacteria decreased in the obtained drinking water compared with the raw

water. Such results might explain the ability of UV irradiation to disinfect chlorine-resistant bacteria (e.g. Bacteroidetes). These findings are in line with a previous study (Ao *et al.* 2020).

Performance of the pilot-scale drinking water treatment unit

HRT is an important parameter to control the performance of water treatment. HRT has a great influence on the hydraulic conditions and the contact time (Pan *et al.* 2004). Our treatment unit of 0.03 day HRT was able to remove the pollutants efficiently (e.g. 85.71% removal of ammonium). However, Suprihatin *et al.* (2017) used a biofilter with higher HRT (0.08 day) to remove 82% of ammonium in a water supply, while Zuo *et al.* (2008) combined electrocoagulation and electroflotation with 0.02 day of HRT to remove 78.25% of fluoride from drinking water. In other words, our treatment unit performed well at the given HRT. Our pilot-scale unit showed an improvement in the removal of turbidity, which decreased from 7.5 NTU (average value) in raw water to 0.35 NTU (average value) in the final effluent, with a removal efficiency of about 95% (Table 1). Turbidity provides a medium for microbial growth and hinders disinfection (United States Environmental Protection Agency 2009). Our results showed that the combination of biological and physical treatments has good performance in removing the turbidity and other pollutants, compared with the results of other previous studies (Kim & Lee 2011; Trinh & Kang 2011; Abu Hasan *et al.* 2019). During the operation of our system, we noticed that each column (sand + BAC) removed around 15% of the DOC. So, to improve the DOC removal, we installed two extra columns of the same specifications. Also, the removal of ammonia was improved gradually by using the series of columns (treatment steps). After setting up the series of three identical columns, our results match the results of the previous studies (Kim & Lee 2011; Lundqvist *et al.* 2019), and comply with the international standard requirements (Table 1). Here, our pilot-scale system showed a significant removal efficiency for $\text{NH}_4^+\text{-N}$ (>85%) with average value (0.13 mgL^{-1}) lower than the drinking standard requirements. Our results were comparable with those obtained from different technologies such as a fluidized

biofilm process combined chemical coagulation and ultrafiltration system (Jin et al. 2009) and a manganese co-oxide filter film (MeOx) (Tian et al. 2019). The removal of bacteria through our pilot-scale treatment was about $2 \log_{10}$. This achievement was due to the removal of turbidity and by using UV-C (dose 20 mWs cm^{-2}). The WHO reported that for the removal of $4 \log_{10}$, the required UV doses should be $0.65\text{--}230 \text{ mJcm}^{-2}$ (World Health Organization 2017). The number of cultivable bacteria in the produced drinking water from our pilot-scale unit was low, and these results were in compliance with drinking water standard requirements (Bartram et al. 2003). In this study, UV-C disinfection has been used instead of ozone and other chemicals because those disinfectants can generate unbiodegradable and harmful by-products in the environment (e.g., trihalomethane compounds, haloacetic acids, organochlorine, and bromate) (Environmental Protection Agency 2011). The UV lamp is easy to install and simple to operate. Furthermore, UV disinfection has largely been applied for the disinfection of bacteria and protozoan parasites, as well as viruses at high UV dosage rate (Bhoskar & Ingle 2014). Also, UV light is lethal to bacteria that oxidize ammonia (Lájer 2012). So, *Nitrospira* and *Nitrosomonas* belonging to Nitrospirae disappeared in the final effluent (Figure 4). UV directly affects the nucleic acids (DNA, RNA) of microorganisms, which are responsible for their replication or multiplication, rendering them non-viable and non-infectious (United States Environmental Protection Agency 1999; Timmermann et al. 2015). Based on our observation, UV-C was effective at removing the most uncultivable bacteria (e.g., *Bacteroidia* and *Dongia*), which did not appear in the final treated water after exposure to UV-C.

CONCLUSION

This pilot study proved the effective performance of biofiltration, physical filtration and UV disinfection for removing pollutants from source water. The biofiltration process showed high removal of turbidity, nitrite and ammonium as well as DOC. The results of physicochemical and microbiological parameters match the requirements of international standards. Multiple biological stages in our designed unit showed an improvement of the drinking

water quality. BAC played an important role in the removal of organic pollutants and turbidity. *Nitrospira* and *Nitrosomonas*, which mainly occupy the surface layer of the BAC media in our system, played an important role in removing $\text{NH}_4^+\text{-N}$ through the microbial nitrification process. UV irradiation is recommended for drinking water disinfection because of its powerful germicidal ability and reduction of disinfectant by-product formation. Our study provides a design for a drinking water treatment system that can be used in remote areas at lower operating cost as well as producing potable water meeting international and national criteria.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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