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Impact of dissolved oxygen on the microbial community structure of an intermittent biological aerated filter (IBAF) and the removal efficiency of gasification wastewater

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ABSTRACT

A novel IBAF system (altered conventional biological aerated filter (BAF) for intermittent aeration) was used to treat BDD anodes electrochemical oxidation gasification wastewater effluent, after which 454 pyrosequencing was applied to investigate the bacterial community of IBAF and demonstrate the relationship between dissolved oxygen (DO) and the bacterial community. The results showed that the concentration of COD, NH_4^+-N and NO_3^--N reached 55.08, 7.64 and 7.76 mg/L, respectively, in IBAF effluent because of changes in the DO concentration at 30 days after system start-up. The bacterial community results revealed that the 40 cm sample had the highest bacterial diversity. The bacterial species were approximate in total samples at phylum and family level, but the relative abundance was significantly different because of change in DO concentration. In addition, sample distance analysis indicated that the similarity of different samples was related to the DO concentration at different heights.

1. Introduction

The biological aerated filter, is a form of the biological contact oxidation technology that is widely applied for the treatment of actual wastewater, including domestic sewage (Zhang et al., 2014; Zhang et al., 2013), landfill leachate (Wang et al., 2012; Wu et al., 2011b) and industrial wastewater (Shen et al., 2009; Zhuang et al., 2014) because of its high treatment efficiency and low economic cost (Bao et al., 2016; Zhang et al., 2017a). A great deal of research shows that the COD of wastewater is degraded and that ammonia nitrogen could also be removed by conventional BAF (Feng et al., 2017; Feng et al., 2012; Wu et al., 2011a). However, the conventional BAF is limited because the continuous aeration, leading to the nitrate nitrogen is difficult to be efficiency removed (Wang et al., 2015c). In a previous study, bio-pretreatment coking wastewater was treated using BDD anodes combined with BAF (Wang et al., 2015b). The results of that study indicated COD and NH_4^+-N were effectively removed by BDD anodes oxidation, but the concentration of NO_3^--N remained the same. After treatment of BDD anodes effluent using BAF, the concentration of NO_3^--N and NH_4^+-N reached 13.34 mg/L and 0.62 mg/L, respectively, which met the USEPA ammonia Discharge Monthly Report limit for NH_4^+-N of < 10 mg/L, but the concentration of NO_3^--N remained at a high level (Suchetana et al., 2017). The quality characteristics of Lurgi gasification wastewater are similar to those of cooking wastewater, and BAF is usually utilized to further remove residual organic materials and nitrogen after advanced oxidation technology (Ji et al., 2016; Xu et al., 2015). Therefore, the aeration strategy was altered-intermittent aeration to improve the removal efficiency of NO_3^--N based on previous research.

The aeration strategy of IBAF contributed to alternate form anaerobic-aerobiotic conditions inside the biofilm, which provided a more suitable environment for the denitrification reaction and effectively eliminated nitrogen. Antonio et al. investigated the influence of aeration conditions on the removal of nitrogen by partially aerated biological filter (Albuquerque et al., 2012). In this paper, partial aeration led to the concentration of dissolved oxygen differing in the BAF. Specifically, in the upper section of the BAF, the dissolved oxygen remained higher, resulting in the effective removal of COD and ammonia nitrogen. Conversely, denitrification was observed at low dissolved oxygen concentrations in the bottom of the BAF. Lim et al. investigated the impact of intermittent aeration on organic and nitrogen removal in a membrane bioreactor and found that the organic compounds were completely degraded under intermittent aeration conditions, while extending the non-aeration time benefited nitrogen removal (Lim et al., 2007). Therefore, intermittent aeration was used to control the DO concentration at different heights of the IBAF which resulted in

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denitrification reaction occurring under anoxic condition.

The microbial communities of the biological membrane play important roles in water treatment, and their diversity and structures have a direct influence on practical application (Tian et al., 2017). Currently, the concentration of dissolved oxygen can have a decisive influence on the distribution and relative abundance of the bacterial community. It has been reported that the distinction of dissolved oxygen between different activated sludges from different wastewater treatment plants had a decisive influence on bacterial community structure (Ibarbalz et al., 2013). Moreover, a modified A^2/O has been proposed for treatment of industrial wastewater, and the bacterial community structure during different process periods was investigated (Zhang et al., 2017b). The results showed that dissolved oxygen plays an important role in the distribution of the bacterial community. Therefore, changes in the concentration of DO led to different bacterial communities at different heights of the IBAF. However, these studies only focused on the removal performance and optimum conditions, while the influence of the bacterial community was largely neglected. In addition, the denitrification efficiency in the IBAF was found to be closely related to the bacterial community structure. As a result, the formation of denitrifying bacteria due to intermittent aeration may be beneficial to the process of denitrification in the IBAF.

Therefore, in this study, an intermittent biological aerated filter was used to remove organic materials and nitrogen of gasification wastewater after BDD electrochemical oxidation under intermittent aeration conditions. Additionally, 454 high throughput sequencing was applied to investigate the relationship between the microbial community of the IBAF and dissolved oxygen.

2. Materials and methods

2.1. Influent and analytical methods

The influent of the IBAF was obtained from the BDD electrochemical oxidation gasification wastewater and the parameters of the main pollutants of the influent were as follows: 154–165 mg/L of COD, 0.35–0.37 of BOD_5/COD ratio, 16.49–16.58 mg/L of NH_4^+-N, 31.29–31.60 mg/L of NO_3^--N, 7.2–7.9 mg/L of phenol, 4.5–5.3 mg/L of quinoline and 2.3–2.7 mg/L of indole.

The COD, NO_3^--N and NH_4^+-N in effluent of IBAF were analyzed daily after filtering water samples through a 0.45 μm membrane filter. The chemical oxygen demand (COD) was measured by the fast digestion-spectrophotometric method (Wang et al., 2015a). The nitrate nitrogen (NO_3^--N) was monitored using an ion chromatograph (ICS-1100, Thermo Fisher, USA) equipped with an IonPac AS23 column (250 mm × 4 mm, Dionex) (Ma et al., 2018). The anionic eluent was a mixture of sodium carbonate (30 mmol) and sodium bicarbonate (4 mmol) and its volume was 1 L (1.0 mL/min flow rate, 30 °C column temperature and 55 mA SRS current). Ammonia nitrogen (NH_4^+-N) was detected by Nessler's reagent spectrophotometry (Han et al., 2013). Dissolved oxygen (DO) was measured using a DO meter (HQd 30, HACH, USA).

2.2. Experimental set-up

The laboratory scale device for the experiment is shown in Fig. 1. The experimental set-up consisted of three parts, a water tank, filter and control system. The water tank had two portions, an influent water tank and a backflush tank. The influent was the effluent water of BDD electrochemical oxidation gasification wastewater. The backflush was used to remove the supernumerary biofilm during the operation process. The IBAF reactor was made of cylindrical-organic glass with a height of 1.85 m and a diameter of 10 cm and packed with volcanics with a particle size of 3.5 mm and an effective packed height of 0.8 m. Four sample connections were installed in the outboard of the reactor, and the interval was 0.3 m. The control system included two sections, a temperature controller and an aeration controller. The temperature controller was used to maintain the water temperature at 33 °C, while the aeration controller was used to control the start-stop cycles of the air pump.

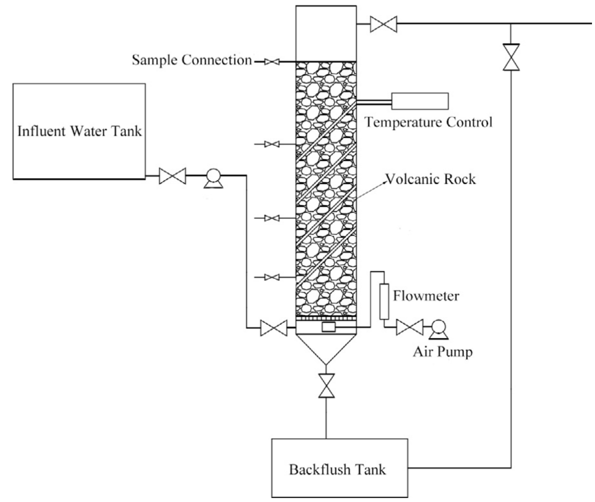

Fig. 1. Drawing of experimental device.

The operating conditions were determined before continuous operation of IBAF. The main operating parameters were as follows: 120 min of hydraulic retention time (HRT), 1:3 of aeration/non-aeration time ratio, 30 min of aeration and non-aeration period, 32 L/h of water-flow rate, 10 mL/min of gas-flow rate and 33 °C of water temperature.

2.3. DNA extraction, PCR amplification and pyrosequencing

A total of eight biofilm samples were collected from different heights from bottom to top at an interval of 10 cm. Biofilm samples were subjected to DNA extraction using an E.Z.N.A. Soil DNA Kit, according to the manufacturer's instructions (Li et al., 2014). The concentration of the DNA was measured using a Qubit 2.0 (Life, USA) to ensure that sufficient quantities of high-quality genomic DNA had been extracted. The V3-V4 hypervariable regions of the microbial 16S rRNA were amplified with the universal primers 341F (CCTACGGGNGGCWGCAG) and 805R (GACTACHVGGGTATCTA ATCC) (Zhang et al., 2017d). The PCR mixtures consisted of 5 μL of 10-fold PCR buffer, 0.5 μL of 10 mM dNTP, 10 ng of gDNA, and 1 μL of 50 μM of each primer, diluted to 50 μL with MilliQ H_2O. The initial PCR program was as follows: 1 cycle of denaturing at 95 °C for 3 min, first 5 cycles of denaturing at 95 °C for 30 s, annealing at 45 °C for 30 s, elongation at 72 °C for 30 s, then 20 cycles of denaturing at 95 °C for 30 s, annealing at 55 °C for 30 s, elongation at 72 °C for 30 s and a final extension at 72 °C for 5 min. Next, PCR products were checked using electrophoresis in 1% (w/v) agarose gels in TBE buffer (Tris, boric acid, EDTA) stained with ethidium bromide (EB) and visualized under UV light. A Qubit fluorimeter (Invitrogen, USA) was then used to measure the DNA concentration, after which all samples were mixed in equal volumes to investigate the bacterial diversity using the Illumina MiSeq system (Illumina MiSeq, USA) according to standard methods (Chen et al., 2017).

2.4. Statistical and bioinformatics analysis

Prior to bioinformatics analysis, the raw reads were meticulously processed as follows: (1) The two short Illumina readings were assembled by PEAR (v0.9.6) software according to the overlap, which could then be analyzed by standard methods; (2) Sequences containing ambiguous bases and any longer than 480 base pairs (bps) were dislodged and those with a maximum homopolymer length of 6 bps were