



Effect of different salinity adaptation on the performance and microbial community in a sequencing batch reactor



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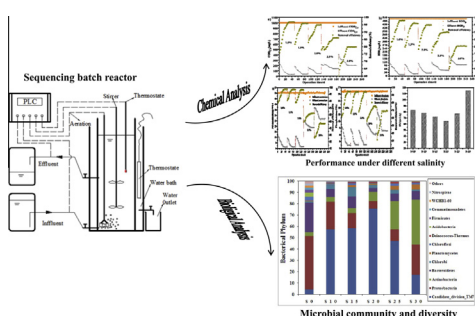
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HIGHLIGHTS

- Salinity greatly affected pollutants degradation and microbial communities in a SBR.
- The SBR could maintain good performance below 2.0 wt% salinity.
- The good performance was associated to abundance of TM7 at 2.0 wt% salinity.
- Actinobacteria was getting dominant at salinity higher than 2.5 wt%.

GRAPHICAL ABSTRACT



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ABSTRACT

The performance and microbial community profiles in a sequencing batch reactor (SBR) treating saline wastewater were studied over 300 days from 0 wt% to 3.0 wt% salinity. The experimental results indicated that the activated sludge had high sensitivity to salinity variations in terms of pollutants removal and sedimentation. At 2.0 wt% salinity, the system retained a good performance, and 95% removal rate of chemical oxygen demand (COD), biochemical oxygen demand (BOD), $\text{NH}_4\text{-N}$ and total phosphorus (TP) could be achieved. Operation before addition salinity revealed the optimal performance and the most microbial diversity indicated by 16S rRNA gene clone library. Sequence analyses illustrated that *Candidate_division_TM7* (TM7) was predominant at 2.0 wt% salinity; however, *Actinobacteria* was more abundant at 3.0 wt% salinity.

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1. Introduction

High salinity wastewaters include a large quantity of organic compounds and soluble inorganic salts, which are generally produced by the seafood processing industry and petroleum industry (Zhang et al., 2012, 2014). Salinity may directly or indirectly inhibit

cell division and enlargement and finally the growth, productivity and performance of the wastewater treatment plants (Bencherif et al., 2015). Therefore, the treatment of saline wastewater has drawn great attention from the society due to its important use in sewerage engineering and marine environmental protection (Jang et al., 2013; Wang et al., 2015). For decades, many significant studies have been reported on the saline wastewater treatment with activated sludge evolved into a mature area of biological engineering (Bassin et al., 2011; Pradhan et al., 2016; Ye et al., 2009). For example, Ye et al. (2009) have studied the effect of influent

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salinity and inhibition time on short-cut nitrogen removal from real domestic saline sewage, and detected the performance of nitrification in activated sludge in SBR. The impact of salinity build-up on the performance of membrane bioreactor such as the removal and fate of trace organic chemicals, nutrient removal, and biomass characteristics were discussed in many studies (Luo et al., 2015). Mannina et al. (2016) have reported the performance of nitrification, sludge viscosity and dewater ability in a membrane bioreactor pilot plant designed to treat synthetic shipboard slops. It can be seen from the above-mentioned results that most existing reports are focused on the study of pollutants degradation performance under different salinity. Although pioneer researches have made some progress, few studies have investigated the complete performance index of activated sludge including COD, BOD, Sludge Volume Index (SVI), nitrogen and phosphorus under different salinity shock.

In the decades, 16S rRNA-based techniques were used to investigate microbial communities (Yu et al., 2015). Guadie et al. (2014) used clone library analysis to reveal the effect of intermittent aeration cycle on microbial community in a fluidized bed reactor-membrane bioreactor combo system. However, compared with the study of pollutants degradation performance of activated sludge with salinity increasing in the system, the research on the variation of microbial community structure has attracted little attention. In the past decade, few studies have reported the effects of different salinities on microbial community. For example, the microbial adaptation to salt illustrated that the long-term effect of salt had more preponderance than the short-term effect (Moussa et al., 2006). The microbial community structure was studied with effects of salt in an aerobic granular sludge reactor (Bassin et al., 2011). However, to the best of authors' knowledge, there are not any related results which have made a detailed study on both the dynamics of microbial community composition and phylogenetic analysis under salinity increase.

In addition, how the characteristics of microbial community structure changes with the increasing salt concentrations is an important question that should be taken into consideration, especially the variations in diversity and abundance. In this paper, a

lab-scale SBR was operated to investigate the long term performance of the activated sludge system (COD, BOD, SVI, nitrogen and phosphorus) on treating wastewater and the variations of microbial community structure under the conditions of increasing salinity step by step from 0 wt% to 3.0 wt%. By 16S rRNA gene based methods, the microbial succession was illustrated, and the predominant microbes in the SBR at different operating salinity were also demonstrated.

2. Methods

2.1. Reactor operation

A lab-scale experimental setup of a SBR with volume of 10 L (Fig. 1) was operated for about 300 days. The activated sludge system was controlled by PLC automatic control system, and the aeration was supported by an air pump. The environmental temperature of the SBR was kept at $27 \pm 1^\circ\text{C}$ using a water bath, and the pH value was kept at 7.0–7.5 then agitated at 210 rpm. Four cycles per day was operated with the SBR: (1) aeration for 4 h, (2) blending for 1 h, (3) sedimentation for 0.5 h, (4) effluent discharge for 0.25 h, and (5) nutrients feeding for 0.25 h, respectively. In SBR system, the water temperature, pH value, sludge concentration, sludge sedimentation ratio, and concentrations of COD_{Cr} , BOD_5 , $\text{NH}_4\text{-N}$ and TP in the influent and effluent were measured.

2.2. Synthetic wastewater

Wastewater was synthesized with distilled water. The sucrose was used as the carbon source. NH_4Cl and KH_2PO_4 were added as nutrients according to the ratio of C:N:P = 100:5:1. $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ 4000 mg/L, $\text{EDTA} \cdot \text{Na}_2$ 4000 mg/L, $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ 80 mg/L, $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ 300 mg/L, $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ 100 mg/L, H_3BO_4 1200 mg/L and ZnCl_2 1000 mg/L were added for 10 L synthetic waste water. NaHCO_3 was provided to adjust the pH value at 7.3 ± 0.2 in the SBR. The main parameters of the reactor were shown in Table 1.

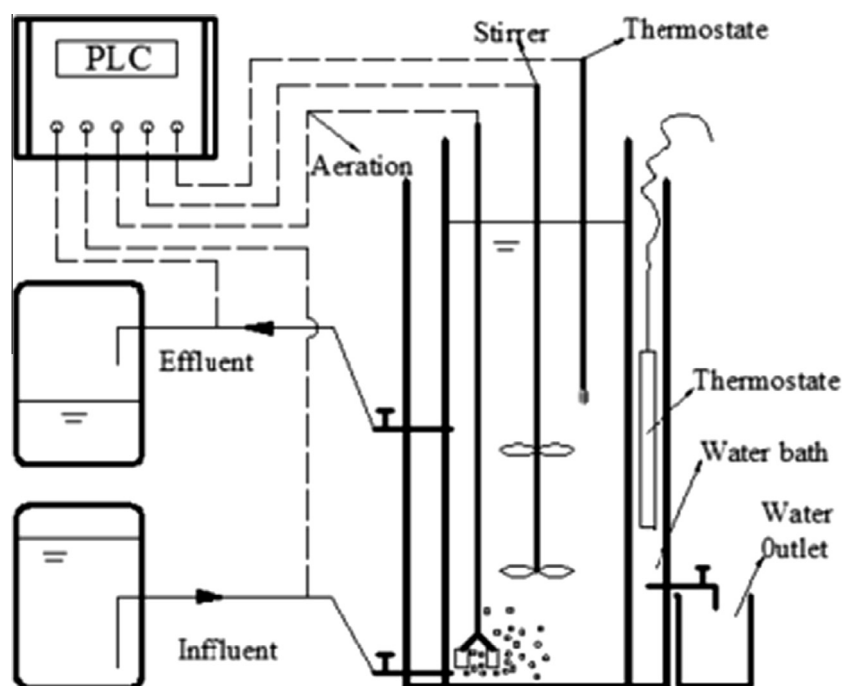


Fig. 1. Scheme of the sequencing batch reactor.

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