



Review

# A review: Driving factors and regulation strategies of microbial community structure and dynamics in wastewater treatment systems



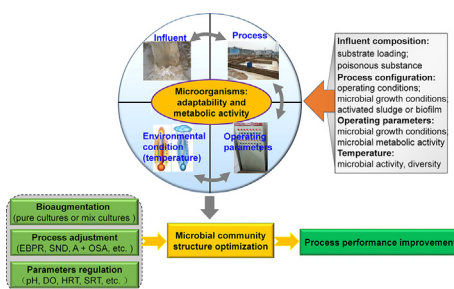
Yangwu Chen <sup>a, b, c</sup>, Shuhuan Lan <sup>a, b</sup>, Longhui Wang <sup>a, b</sup>, Shiyang Dong <sup>a, b, c</sup>, Houzhen Zhou <sup>a, b</sup>, Zhouliang Tan <sup>a, b, \*</sup>, Xudong Li <sup>a, b</sup>

<sup>a</sup> Key Laboratory of Environmental and Applied Microbiology, Chengdu Institute of Biology, Chinese Academy of Sciences, 610041, Chengdu, PR China  
<sup>b</sup> Environmental Microbiology Key Laboratory of Sichuan Province, Chengdu Institute of Biology, Chinese Academy of Sciences, 610041, Chengdu, PR China  
<sup>c</sup> University of Chinese Academy of Sciences, 100049, Beijing, PR China

HIGHLIGHTS

- Different driving factors for microbial community structure variation are reviewed.
- The mechanisms of microbial community structure and dynamics are discussed.
- Some regulation strategies for microbial community structure are summarized.

GRAPHICAL ABSTRACT



ARTICLE INFO

**Article history:**  
 Received 14 October 2016  
 Received in revised form 24 January 2017  
 Accepted 25 January 2017  
 Available online 27 January 2017

Handling Editor: A Adalberto Noyola

**Keywords:**  
 Microbial structure and dynamics  
 Influent composition  
 Process configuration  
 Operating parameters  
 Temperature  
 Microbial community structure regulation

ABSTRACT

The performance and stabilization of biological wastewater treatment systems <sup>1</sup>are closely related to the microbial community structure and dynamics. In this paper, the effects and mechanisms of influent composition, process configuration, operating parameters (dissolved oxygen [DO], pH, hydraulic retention time [HRT] and sludge retention time [SRT]) and environmental condition (temperature) to the change of microbial community structure and process performance (nitrification, denitrification, biological phosphorus removal, organics mineralization and utilization, etc.) are critically reviewed. Furthermore, some strategies for microbial community structure regulation, mainly bioaugmentation, process adjustment and operating parameters optimization, applied in the current wastewater treatment systems are also discussed. Although the recent studies have strengthened our understanding on the relationship between microbial community structure and wastewater treatment process performance, how to fully tap the microbial information, optimize the microbial community structure and maintain the process performance in wastewater treatment systems are still full of challenges.

© 2017 Elsevier Ltd. All rights reserved.

Contents

1. Introduction ..... 174  
 2. Driving factors for microbial community structure variation in WWTP(s) ..... 174

\* Corresponding author. Key Laboratory of Environmental and Applied Microbiology, Chengdu Institute of Biology, Chinese Academy of Sciences, 610041, Chengdu, PR China.

E-mail address: [tanzhl@cib.ac.cn](mailto:tanzhl@cib.ac.cn) (Z. Tan).

2.1. Influent composition .....	174
2.2. Process configuration .....	175
2.3. Operating parameters .....	175
2.3.1. DO concentration .....	175
2.3.2. pH variation .....	176
2.3.3. HRT and SRT .....	176
2.4. Temperature .....	176
3. Strategies for microbial community structure regulation .....	177
3.1. Bioaugmentation .....	177
3.2. Wastewater treatment process adjustment and development .....	178
3.3. Operational parameters optimization and regulation .....	179
4. Conclusions .....	179
Acknowledgements .....	180
References .....	180

## 1. Introduction

Microbial community diversity reflects the richness of species in a specific ecological system. In biological wastewater treatment system, microbial diversity not only influences the treatment performance (Wang et al., 2013a,b,c) but also the stability of the system (Mielczarek et al., 2013). Previous studies have shown that the system will be more stable when the microbial diversity is high (Rowan et al., 2003; Ma et al., 2013). It is well known that the microbial community is affected by various factors (Sun et al., 2014). Among the eight wastewater treatment plants (WWTPs) surveyed by Wang et al. (2010), Ammonia Oxidizing Bacteria (AOB) in municipal WWTPs showed a higher diversity than industrial or mixed WWTPs, indicating that the influent composition has great impact on the microbial community structure. In addition, different process constitution also leads to different microbial community structure, even when the influent is identical. For instance, the Huairou Wastewater Treatment Plant (Beijing, China) had two sets of process operating at the same time, a Membrane Bioreactor (MBR) and an Oxidation Ditch (OD). 454-pyrosequencing analysis showed that the most predominant phylum in sample OD was *Bacteroidetes*, while it was *Proteobacteria* in sample MBR (Hu et al., 2012). Furthermore, operational parameters can also affect the microbial community structure greatly. Limpiyakorn et al. (2005) pointed out that sludge retention time (SRT) primarily influences the abundance of AOB, while dissolved oxygen (DO) mainly affects the ammonia oxidation activity.

Therefore, understanding the impacts and mechanisms of various factors on microbial community is of great significance for the regulation of microbial community structure and improving process performance. This review describes the major factors that affect the microbial community structure; discusses how these factors drive the performance and microbial structure changes; summarizes the methods and strategies to optimize and regulate microbial community structure based on these driving forces, and prospects the potential developmental direction for microbial community structure optimization and process performance improvement.

## 2. Driving factors for microbial community structure variation in WWTP(s)

According to Zhou et al. (2010), influent composition, operational parameters, and environmental conditions influenced the microbial community structure in WWTP(s). In this paper, the driving effects and mechanisms of the influences on microbial community structure and dynamics were mainly analyzed from the

following four aspects: influent composition, process or reactor configuration, operating parameters and environmental condition (temperature).

### 2.1. Influent composition

The microbial community structure in wastewater treatment systems is closely related to the substrate concentration and the content of inhibiting components existed in influent (Guo et al., 2009; Fernandes et al., 2013; Li et al., 2015) (Fig. 1).

Influent substrate loading affecting microbial community structure is mainly due to the difference of substrate affinity, metabolic activity and resistance for various microorganisms (Pan et al., 2013). Due to the high affinity to ammonia and reducing nitrogen of ammonia-oxidizing archaea (AOA), these microorganisms predominated in many environment conditions with the ammonia concentration lower than that needed for in situ ammonia utilization by AOB (Kasuga et al., 2010). Also, the community structure of AOB was seriously influenced by substrate loading (Rodriguez-Caballero et al., 2012). Previous studies reported that the ammonia nitrogen ( $\text{NH}_4^+\text{-N}$ ) half-saturation coefficient was lower for *Nitrosospira* sp. than for *Nitrosomonas europaea*, thus *Nitrosomonas* always predominant in high  $\text{NH}_4^+\text{-N}$  concentration conditions and might facilitate nitrification (Terada et al., 2013; Gonzalez-Martinez et al., 2016). In terms of nitrite oxidizing bacteria (NOB), *Nitrospira* has a high substrate affinities and low growth rate for nitrite, and usually outcompete *Nitrobacter* under substrate-limiting conditions (Terada et al., 2013).

Three different Upflow Anaerobic Sludge Blanket (UASB) systems were applied in synthetic dairy wastewater treatment. As the organic loading was increased from 20 to 30 g COD/L/d, hydrogen production bacteria, *Clostridium tyrobutyricum*, *Citrobacter freundii* and *Enterobacter aerogenes*-like bacteria, were selectively enriched (Carrillo-Reyes et al., 2014). Two UASB were employed for methanol wastewater treatment, starch was added in one of the reactors. As the organic loading gradually increased from 30 kg COD/m<sup>3</sup>/d to 120 kg COD/m<sup>3</sup>/d, *Methanosaeta* occurred in the reactor with the addition of starch. This might happen due to the production of acetic acid in the process of starch degradation, which promoted the proliferation of *Methanosaeta* (Kobayashi et al., 2011).

Obviously, microbial community structure would be changed when the components of influent varied (Hall et al., 2010). Kovacic et al. (2010) investigated the changes of microbial community structure in response to influent disturbance in a UASB system. The results showed that the main microbes in the simulated brewery wastewater (SBWW) treatment plant were methanogenic archaea (*Methanobacterium* and *Methanosaeta*), green non-sulfur bacteria

Download English Version:

<https://daneshyari.com/en/article/5747346>

Download Persian Version:

<https://daneshyari.com/article/5747346>

[Daneshyari.com](https://daneshyari.com)