Enhanced anaerobic digestion of organic contaminants containing diverse microbial population by combined microbial electrolysis cell (MEC) and anaerobic reactor under Fe(III) reducing conditions

Jingxin Zhang, Yaobin Zhang *, Xie Quan, Shuo Chen, Shahzad Afzal

Key Laboratory of Industrial Ecology and Environmental Engineering, Ministry of Education, School of Environmental Science and Technology, Dalian University of Technology, Dalian 116024, China

HIGHLIGHTS

• Addition of Fe(OH)₃ to a MEC combined anaerobic reactor (R1) improved both of COD and color removal.
• Microbial Fe(III) reduction assisted anode oxidation of organics and anaerobic digestion.
• The increased activity and abundance of bacteria responsible for the high treatment performance.
• Pyrosequencing compared microbial communities among anode biofilm, R1 and reference reactor.
• Microbial communities in anode biofilm and the bottom sediment of R1 are more diverse.

ABSTRACT

Microbial electrolysis cell (MEC) devices are efficient for wastewater treatment, but its application was limited due to low anode oxidation rate. The objective of this study was to improve anode performance of a MEC combined anaerobic reactor (R1) for high concentration industrial wastewater treatment via dosing Fe(OH)₃. For the first 53 days without power, the addition of Fe(OH)₃ in R1 enhanced the degradation of reactive brilliant red X-3B dye and sucrose. Applying a voltage of 0.8 V in R1 resulted in a higher decolorization and COD removal through driving the redox reactions at electrodes under Fe(III)-reducing conditions. Real-time PCR and enzyme activity analysis showed that the abundance and azoreductase activity of bacteria were improved in R1. Pyrosequencing revealed that dominant populations in anode biofilm and R1 were more diverse and abundant than the common anaerobic reactor (R2), and there was a significant distinction among anode film, R1 and R2 in microbial community structure.

1. Introduction

Microbial electrolysis cell (MEC), developed from microbial fuel cell (MFC), is a bio-electrochemical system for biological hydrogen production via the biodegradation of organic matter using exoelectrogenic microbes on anode biofilm (Rozendal et al., 2006). Nevertheless, MEC has not been widely used in practice due to the limitations of high resistance, over potential and expensive cathode catalyst. Methanogenesis is unfavorable in a traditional MEC, because methanogens compete with exoelectrogenic bacteria for using organic acids and consume H₂ (Wrana et al., 2010). Although this problem can be solved by a two-chamber MEC, it is inevitable to increase the construction cost, ohmic resistance and pH gradients. Due to the limitation of anode oxidation rate, the MEC reactors are usually used to treat low concentration wastewater (Clauwaert and Verstraete, 2009).

When a pair of electrodes is inserted into an anaerobic reactor to form a MEC combined anaerobic digestion system, not only high concentration organics in wastewater can be degraded effectively via anaerobic fermentation, but also electrode reaction of MEC can be used for advanced treatment of residual contamination and decomposition of toxic contamination. Therefore, this single-chamber MEC-anaerobic reactor has a great potential to treat high-strength industrial wastewaters containing toxic or refractory substance. In our recent work, a pair of plate electrodes was packed into an upflow anaerobic sludge blanket (UASB) reactor for enhancement of azo dye wastewater treatment (Zhang et al., 2012a). Similar studies are also conducted by other researchers for anaerobic digestion of wastewater (Tarakovsky et al., 2011). In order to further enhance the performance of this coupling system for removing remained contaminants or treating refractory wastewaters, the anode oxidation rate should be accelerated.

* Corresponding author. Tel.: +86 411 8470 6460; fax: +86 411 8470 6263. E-mail address: zhangyb@dlut.edu.cn (Y. Zhang).

0960-8524/$ - see front matter © 2013 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biortech.2013.02.103
Recently, several reports about MEC/MFC on account of iron(III) reducing bacteria (IRB) was concerned (Ringeisen et al., 2006). It has been accepted that most of exoelectrogenic bacteria on anode biofilm belonged to IRB e.g., Geobacter that performs both electricity production and dissimilatory Fe(III) reduction (Bond and Lovley, 2003; Gralnick and Newman, 2007). The addition of Fe(III) oxides such as Fe(OH)_3 could enhance dissimilatory Fe(III) reduction through the enrichment of IRB (Stabnikov et al., 2004). Thus, it was speculated that anode oxidation rate of MEC was likely to be intensified via the addition of Fe(OH)_3 in the MEC combined anaerobic reactor, which may further accelerate the decomposition of volatile organic acids (VFAs) or toxic substances. Moreover, the enhanced electrodes reactions would create a favorable environment for improving the species diversity and the enrichment of specific species (Lu et al., 2012; Liu et al., 2010), which was likely to further enhance the biodegradability of complex substances.

In present study, Fe(OH)_3 was dosed into a MEC combined anaerobic reactor with the aim to enhance anode oxidation of complicated contaminants. To highlight the performance of this coupling reactor, high concentration azo dye wastewater was used as source of influent. To date, few reports focus on enhancing dye wastewater treatment by a MEC-an anaerobic reactor under the effect of microbial Fe(III) reduction.

2. Methods

2.1. Reactor construction and operation

A pair of carbon felt electrodes (70 mm width × 70 mm length) was inserted into an acrylic plastic up-flow anaerobic blanket reactor (UASB) (280 mm length × 100 mm width × 100 mm height) accompanied with the addition of Fe(OH)_3 powder (30 g, analytical reagent). The interior of the UASB reactor consisted of three regions from the bottom to the top i.e., sludge blanket layer, suspended sludge layer and settling section. The anode felt was located in the anaerobic sludge phase and placing the cathode in the surface of settling section to form a MEC combined UASB reactor (hereafter referred to as R1). The electrodes were supplied by a regulated DC power source through an electric wire. The working volume of the reactor was 2 L. The control reactor R2 was conducted in a common UASB reactor that was the same as R1 but without electrodes and Fe(OH)_3 dosing. Another control reactor R3 was an abiotic reactor that was also the same to R1 but without biological sludge and Fe(OH)_3 dosing.

After being seeded, these three reactors were operated in parallel under a continuous mode at 35 ± 1 °C with a hydraulic retention time (HRT) of 24 h. Synthetic wastewater containing azo dye reactive brilliant red X-3B (X-3B in abbreviation) was used in this study. Sucrose, NH_4Cl and KH_2PO_4 were added into the wastewater as the carbon, nitrogen, and phosphorus sources, respectively, to give a COD:N:P ratio of 200:5:1. The trace elements were added according to the following composition: 1 mL/L of a sodium phosphate buffer (20 mM, pH 7.0). The washed sludge was suspended in 40 ml sodium phosphate buffer and then sonicated at 20 kHz (at 4 °C for 30 min, Ultrasonic processor CPX 750, USA). The extracts was stored at 4 °C and used for enzyme activity determination next. The azoreductase activity of extracts was determined by monitoring the absorbance decrease at 539 nm in a 6 ml reaction mixture containing 5 ml cell extracts, 500 μl X-3B and 500 μl NADH in sodium phosphate buffer (20 mM, pH 7.0).

2.3. DNA extraction and high-throughput 16S rDNA gene pyrosequencing

After 97 days of operation, carbon felt was cut from anode and crushed using scissors. Anaerobic sludge was sampled from the bottom of the reactor. The samples were washed with phosphate-buffered saline (pH 7.4), after which the genomic DNA of the sample was extracted using an extraction kit (Biotek Corporation, Beijing, China) according to the manufacturer’s instructions. The quality of the extracted DNA was checked by determining its absorbance at 260 and 280 nm.

The diversity of microbial communities was deeply investigated by 454 GS-FLX pyrosequencing technology. A set of bacterial primers 8F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 533R (5′- TTACCGCGGTGTGCTGCA-3′) was used to amplify the hypervariable V1–V3 region of bacterial 16S rRNA gene (Lu et al., 2012). In order to sort multiple samples during pyrosequencing, 10-base barcodes were incorporated between 454 adapter and the forward primer. After being purified and quantified, the PCR products of V1–V3 region of 16S rRNA gene was determined by pyrosequencing using the Roche 454 FLX Titanium sequencer (Roche 454 Life Sciences, Branford, CT, USA) according to the methodology described by Margulies et al. (2005). To obtain the effective sequencing data, raw pyrosequencing results was processed as follows: (1) check the completeness of the barcodes and the adapter; (2) remove sequences containing ambiguities (“Ns”); (3) remove sequences shorter than 200 bps. (4) remove low-quality sequence i.e., a sequencing quality value lower than 20. Subsequently, effective sequences were clustered into operation taxonomic unit (OTUs) by a 3% or 5% level using the MOTHUR program. Rarefaction curves, Shannon diversity index, species richness estimator of COD was determined according to the standard methods (APHA, 2005). The concentration of Fe(II) ions was determined using an UV spectrophotometer (China) at an absorbance of 510 nm. The pH was recorded using a pH analyzer (Sartorius PB-20, Germany). MLSS and MLVSS were determined based on the weighing method after being dried at 103–105 °C and burnt to ash at 550 °C. The solid and liquid phases were separated by centrifugation (8000 r/min). Azo dye color was measured spectrophotometrically at the wavelength of maximum absorbance, 539 nm (Techcomp, UV-2301, Shanghai, China). The abundance of bacteria was quantified by real-time PCR. The primer sets Eu27F (5′-AGA GTTGTAGCTCCTGGCAG-3′) and 1490R (5′-GTACTACCTGTAGC- ACTT3′) was used to target all bacteria (Harms et al., 2003). The detailed steps of real-time PCR for the quantification of bacteria was conducted according to the methods described by Harms et al. (2003). The activity of azoreductase was determined. Briefly, 25 ml of mixture taken from anaerobic reactor was centrifuged at 12,000×g for 20 min and washed thrice with sodium phosphate buffer (20 mM, pH 7.0). The washed sludge was suspended in 40 ml sodium phosphate buffer and then sonicated at 20 kHz (at 4 °C for 30 min, Ultrasonic processor CPX 750, USA). The extracts was stored at 4 °C and used for enzyme activity determination next. The azoreductase activity of extracts was determined by monitoring the absorbance decrease at 539 nm in a 6 ml reaction mixture containing 5 ml cell extracts, 500 μl X-3B and 500 μl NADH in sodium phosphate buffer (20 mM, pH 7.0).
Chao1 and Beta diversity index were conducted by MOTHUR to identify the species diversity for each sample. The OTUs defined by a 3% distance level were classified using the RDP-II classifier at a 50% confidence threshold. Venn diagram was used to analyze shared OTUs among the three samples from anode, R1 and R2. Principal component analysis (PCA) was completed using MOTHUR with the aim to distinguish the dominant species that has made a great contribution to the difference among the three samples.

3. Results and discussion

3.1. COD removal and decolorization under Fe(III)-reducing conditions at different dye concentrations

To evaluate the role of microbial Fe(III) reduction, initially the MEC combined UASB reactor was operated as a MFC combined UASB reactor for dye wastewater treatment which is in line with the running mode of MEC described by Liu et al. (2010). For the first 53 days, reactor R1 and its control reactors (R2 and R3) were operated in parallel, and the electrodes of R1 were connected in a closed loop without the addition of powder. Fig. 1 showed the treatment performance for both COD removal and decolorization with the increasing dye concentration from 100 to 900 mg/L.

When the dye concentration was maintained at 100 mg/L, the color removal in reactor R1 and R2 ranged from 89.5% to 91.6% and the COD removal was maintained between 76.5% and 80.8%. As the influent dye concentration increased gradually to 900 mg/L, the color removal decreased to 75.8% in R1 while it was only 45.9% in R2 and 1.5% in R3. At this time, the COD removal (82.3%) in R1 was still significantly higher than that in R2 (69.3%). As the COD removal of R3 was lower than 1%, its contribution to COD removal could be ignored. The addition of Fe(OH)₃ in R1 presented a positive effect for the degradation of organics that was similar to the report of Coates et al. (2005) who found that Fe(III) supplementation can enhance the effect of microbial Fe(III) reduction, improving the degradation of organisms and methane production.

At the beginning of the experiment, the current between the electrodes of R1 could not be detected. The main reason was attributed to the deficiency of exoelectrogenic bacteria on anode biofilm. It is known that microorganisms on the anode can serve as biological catalyst to lower anodic overpotential and facilitate electrons to the cathode, at which the azo dye is reduced (Mu et al., 2009). After enrichment period (53 days), stable electricity was generated by the MFC of R1, eventually reaching 23.2 mW/m² (168 mV; 0.678 mA) on day 53. The power generation was mainly attributed to the anode oxidation of VFAs (Logan and Regan, 2006), indicating the successful enrichment of exoelectrogenic bacteria on anode biofilm. Even so, when the closed loop was opened (from 53 to 55 day), the treatment performance of R1 has no significant change. It indicated that the performance of MFC in R1 is relatively poor for COD and color removal due to the low electrical efficiency that limited the system efficiency when exposed to high concentration wastewater.

3.2. Decolorization and COD removal under Fe(III)-reducing conditions in an electric field

After a period of operation, we presumed that a variety of microbes especially exoelectrogenic bacteria on the electrodes were...
decolorization and 7.1% COD removal per kilowatt. It means that
conditions
3.3. Characteristics of anaerobic sludge under Fe(III)-reducing
Fig. 2A, from day 55 to day 97, the decolorization efficiency of R1
extra energy consump
tion in R1 was 0.0036 W (voltage
enriched. In order to further enhance the treatment performance of
COD removal and decolorization, a voltage of 0.8 V was applied be-
tween the electrodes in R1 on day 55, which formed a MEC–UASB
combined system for dye wastewater treatment. As shown in
Fig. 2A, from day 55 to day 97, the decolorization efficiency of R1
increased rapidly from 75.8% to 93.7% which is 35.8% higher than
the cumulative efficiency of R2 and R3. Similarly, the COD removal
in R1 also increased by 7.1% due to the positive effect of electric
field (Fig. 2B). As the COD removal in R3 was lower than 1%, so
the contribution of single electrodes to COD removal could be ig-
nored. Therefore, the increased COD removal was mainly attrib-
uted to the biocatalytic effect which is in line with the report of
Lalaurette et al. (2009) who claimed that effective COD removal
could be available by anode oxidation of organics during MEC pro-
cess. The enhanced anode oxidation of organics could generate
more electrons that can be transferred to cathode for the degrada-
tion of azo dye.
When exposed to high concentration dye wastewater, the high
performance of R1 was mainly attributed to the synergistic effect
between anaerobic digestion and MEC process under Fe(III)-reduc-
ning conditions. At the bottom of R1, the organic compounds were
firstly degraded to various organic acids by fermentative and homo
acetogenic bacteria which can be further mineralized by methano-
genic and exoelectrogenic bacteria. At the end of the operation, the
extra energy consumption in R1 was 0.0036 W (voltage \( U = 0.8 \) V,
current \( I = 4.5 \) mA), which accounted for the increase of 17.9%
decolorization and 7.1% COD removal per kilowatt. It means that
1 kW - h of power consumption could degrade 3.73 kg of azo dye
X-3B and 1.64 kg of COD.

Table 1
Azoreductase activity and copy numbers of 16S rRNA gene of bacteria in R1 and R2
on day 97.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Azoreductase activity (µg X-3B mg protein⁻¹ h⁻¹)</th>
<th>16S rRNA gene copies/ng-DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sludge of R1</td>
<td>14.9 ± 0.42</td>
<td>1.741 ± 0.34</td>
</tr>
<tr>
<td>Sludge of R2</td>
<td>10.1 ± 0.57</td>
<td>1.027 ± 0.47</td>
</tr>
</tbody>
</table>

Table 2
Biodiversity estimation of 16S rRNA gene libraries from the pyrosequencing analysis.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Effective reads</th>
<th>Observed OTUs</th>
<th>Estimated OTUs by chao1</th>
<th>Shannon</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>6953</td>
<td>816</td>
<td>1454</td>
<td>7.78</td>
</tr>
<tr>
<td>R2</td>
<td>9960</td>
<td>632</td>
<td>1113</td>
<td>6.915</td>
</tr>
<tr>
<td>Anode</td>
<td>8363</td>
<td>641</td>
<td>1163</td>
<td>5.933</td>
</tr>
</tbody>
</table>

3.4. Pyrosequencing analysis of bacterial communities

3.4.1. Sequence results and biodiversity of bacteria phylotypes
At the end of the operation, sludge samples taken from R1, R2
and the surface of anode were used for pyrosequencing analysis. After pyrosequencing, a total amount of 6953 (R1), 9960 (R2) and
8363 (anode) effective sequence tags were obtained through pri-
mer and barcodes matching with raw reads and a series of filtering
process. As shown in Fig. 3, the observed number of operational
taxonomic units (OTUs) at a 3% distance were 816, (R1), 632 (R2)
and 641 (anode), respectively. From Table 2, as a metric for species
richness, the estimated total number of OTUs by analyser of Chaol
were 1454 (R1), 1113 (R2) and 1163 (anode), respectively. The
Shannon diversity index was usually applied to present the species
diversity in a sample. Among the three samples, R1 showed the
highest diversity (Shannon: 7.78) than that in R2 (Shannon: 5.933) and anode (Shannon: 6.915), indicating that the microbial
community in R1 and anode biofilm was more rich under Fe(III)-
reducing conditions as compared to that in R2. It was accepted that
high biodiversity can enhance ecological stability (Wrighton et al.,
2010) which usually has high ability to resist toxic or refractory
substance and result in high reactor performance in terms of COD
removals and hydrogen production (Liu et al., 2010; Lu et al., 2012).
Thus, high microbial diversity in the anode biofilm and R1 might have a significant contribution to maintain high treat-
ment performance including detoxification and mineralization even exposed to high concentration dyes (Fig. 2). As compared, rela-
tive low microbial diversity in R2 caused low COD and color
removal.

3.4.2. Bacterial community comparisons
Beta diversity index was used to investigate the difference of spe-
cies diversity among these three samples. The closer the beta diver-
sity index approached to 1, there will be more difference in the
species diversity among the observed samples. As shown in Table,
S2, the species diversity between R3 and anode presented the highest
difference with a high beta diversity index of 0.801, suggesting that
the effect of electricity can significantly change the microbial struc-
ture on anode under Fe(III)-reducing conditions. The difference of microbial community among these three samples was also clarified by the principal component analysis (PCA). From Fig. 4, it can be seen that the microbial community structure among these three samples was different and diverse with a sufficient distance between each other. Five microbe groups i.e., Clostridiaceae_1, Anaerolineaceae, Campylobacteraceae, Propionibacteriaceae, Armatimonadetes_family_incertae_sedis, made a great contribution to the difference among these three samples. Different community structure and PCA meant different functions in reactor R1 and R2 that was in accordance with the high performance of R1.

The total OTUs in the three samples was 2089, in which only 121 OTUs was shared by them, accounting for 5.8% of total OTUs (Fig. 5). The major bacterial community in the shared OTUs were Chlorobi (22.41%), Firmicutes (12.62%) and Proteobacteria (15.36%). The shared OTUs between R1 and anode was 252, which was significantly higher than that of 173 between R2 and anode. This result indicated that the enrichment of partial bacterial

![Fig. 4. Principal component analysis (PCA) of bacterial communities in the anode biofilm, R1 and R2.](image1)

![Fig. 5. Venn diagram of bacterial communities with shared and unique OTUs among the anode biofilm, R1 and R2. The taxonomic affiliations of the shared OTUs was based on the phylum level. The number in the enclosed area showed the amount of OTUs.](image2)
community on the anode should be attributed to the inoculum of R1. However, additional 389 OTUs in anode can not be shared with R1, which was attributed to the addition of electric field.

3.4.3. Bacterial taxonomy analyses

In order to clarify the difference of species diversity among the three samples from R1, R2 and anode in depth, the relative bacterial community abundance was investigated at four levels of phyla, class and genera (Fig. 6). On the phyla level, Bacteroidetes, Chloroflexi, Proteobacteria and Firmicutes were dominated in these three samples. Few sequences belonged to the Phyla of Actinobacteria, Armamonadetes, Spirochaetes and Synergistetes. In spite of this, there were still 33.1% (R1), 20.7% (R2) and 20.8% (anode) of total reads were not identified at the phylum level, indicating that some novel bacteria can not be found until now. However, the relative abundance of dominant species at the phylum level was diverse among R1, R2

Fig. 6. Taxonomic classification of the dominant phylogenetic groups from anode biofilm, R1 and R2 at the (A) phylum, (B) class and (C) genus levels. Relative abundance is defined as the number of sequences affiliated with that taxon divided by the total number of sequences per sample (%). The relative abundance of phyla, classes and genus less than 1% of total composition in the three libraries were defined as “others”.

278 J. Zhang et al. / Bioresource Technology 136 (2013) 273–280
and anode. The relative abundance of Firmicutes on the biofilm of anode (16.4%) was significantly higher than that in R1 (6.5%) and R2 (10.4%). It indicated that the selective enrichment of Firmicutes on the surface of anode might be attributed to its potential ability of electron transfer, which has been confirmed by Wrighton et al. (2008) who found that the Firmicutes own the functions of current generation in MFC. The relatively abundance of Proteobacteria on the surface of anode (16.6%) accounted for less portion as compared with that of 40.4% in R2 in spite of some known exoelectrogens (e.g., Geobacter and Shewanella) which were mainly belonged to the Proteobacteria. The Bacteroidetes was highest in the relative abundance in R1 (24.9%), followed by anode (11.4%) and R2 (15%), which mainly contained several fermentative bacteria that were induced in the anaerobic environment of the anode (Grabowski et al., 2005). Chloroflexi, as a common filamentous bacteria, was usually found in anaerobic reactor which was also enriched in anode (26.8%). It was reported that Chloroflexi species are specialized in polysaccharide and protein degradation (Nielsen et al., 2010).

The phylogenetic classification of samples from R1, R2 and anode at class level was investigated. As shown in Fig. 6B, a total amount of 11 bacterial classes were identified as the main composition in the three samples. The bacterial classes Bacteroidia, Actinobacteria and Betaproteobacteria were similar with each other among the three samples. The relatively abundance of Anaerolineae, Clostridia, Lentisphaeria and Alphaproteobacteria in the biofilm of anode was significantly higher than that in R1 and R2. Meantime, the Deltaproteobacteria also presented a higher abundance in R1 and anode as compared with that in R2. Both of Alphaproteobacteria and Deltaproteobacteria belonged to the phyla proteobacteria that has been identified as a major source of exoelectrogens such as Geobacter (Logan, 2009). Class Anaerolineae and Lentisphaeria as dominant bacteria have also been found in the anode biofilm of MFC (Zhang et al., 2012b). Some isolates from Class Anaerolineae can grow more efficiently in association with hydrogenotrophic methanogens as terminal biological electron acceptors (Yamada et al., 2006). The relative abundance of Class Sphingobacteria showed the highest level in R1. Both of Sphingobacteria and Clostridia belonged to fermentative bacteria with acetic and propionic acid as its major acidification products.

In order to deeply compare the microbial communities of the three samples from R1, R2 and anode, the effective reads were assigned on the genus level as shown in Fig. 6C. The relatively abundance of genus Pleuromorphomonas, Victivallis, Leptolinea, Clostridium_sensu_strict, Anaeroarculus, Longilinea, Paludibacter and Desulfovibrio in the biofilm of anode was higher than that in R2. Both of genus Longilinea and Leptolinea are the filamentous strict anaerobes fermenting carboxylates, which belonged to Class Anaerolineae and were usually isolated from thermophilic or mesophilic sludge (Yamada et al., 2006). Paludibacter, Victivallis and Clostridium_sensu_strict belonged to fermentative bacteria, which can ferment complex organics to the products of acetic, butyric, lactic acids and CO₂/H₂. Anaeroarculus has also been detected in another anode chamber of S-MFC using glucose as its substrate. It is reported that some species of sulfate reducing bacteria belonging to Desulfovibrio simultaneously own the ability of decolorization (Yoo et al., 2001) and current production in MFC (Ieropoulou et al., 2005). Both of genus Ideonella and Bacteroides were enriched in R1 with the highest relative abundance. Some Bacteroides sp. is known to be able to produce H₂ by fermentation and produce electricity in MFC (Kim et al., 2006). Ideonella is capable of growth by reductive dechlorination.

4. Conclusions

A novel approach for effective treatment of high concentration industrial wastewater was developed via dosing Fe(OH)₃ in a MEC combined anaerobic reactor (R1). As compared with the reference reactors (R2 and R3), the integrated system had higher performance for both of COD removal and decolorization. A more diverse and rich microbial community with high bioactivity in the anode biofilm and bottom sediment of R1 enabled the integrated reactor to resist recalcitrant and toxic pollutants effectively. In this way, the strategy of MEC assisted anaerobic digestion under Fe(III) reduction process has the potential to treat high concentration industrial wastewater.

Acknowledgements

The authors acknowledge the financial support from the National Basic Research Program of China (21177015), New Century Excellent Talent Program of the Ministry of Education of China (NCET-10-028) and the program for Liaoning representative office of China Environmental Protection Foundation.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.biortech.2013.02.103.

References

Nielsen, P.H., Mielczarek, A.T., Krågelund, C., Nielsen, J.L., Saunders, A.M., Kong, Y., et al., 2010. A conceptual ecosystem model of microbial communities in...


