

Improved Biological Phosphorus Removal Induced by Oxidic/Extended-Idle Process Using Glycerol and Acetate at Equal Fraction

Jianwei Zhao ^{a,b}, Dongbo Wang ^{a,b*}, Xiaoming Li ^{a,b}, Guangming Zeng^{a,b}, Qi Yang ^{a,b*}

^a College of Environmental Science and Engineering, Hunan University, Changsha 410082, China

^b Key Laboratory of Environmental Biology and Pollution Control, Hunan University, Ministry of Education, Changsha 410082, China

The first author: Jianwei Zhao E-mail: zhaojianwei1213@yahoo.com

Corresponding author

Tel: +86 731 88823967; fax: +86 731 88822829;

E-mail: w.dongbo@yahoo.com (D. WANG), yangqi@hnu.edu.cn (Q. YANG).

Journal: RSC Advance

The Number of Pages: 4

The Number of Figures: 1

The Number of Tables: 1

* Corresponding author at: College of Environmental Science and Engineering, Hunan University, Changsha 410082, China. Tel.: +86 731 88823967; fax: +86 731 88822829.

E-mail addresses: w.dongbo@yahoo.com (D. Wang), yangqi@hnu.edu.cn (Q. YANG).

Materials and Methods

Table S1. Oligonucleotide probes used in this study

| Probe | Sequence5'-3' | Specificity | Reference |
|------------|------------------------------------|---|------------------------|
| PAO462 | CCG TCA TCT ACW CAG GGT ATT AAC | Most <i>Accumulibacter</i> | Crocetti et al. (2000) |
| PAO651 | CCC TCT GCC AAA CTC CAG | Most <i>Accumulibacter</i> | Crocetti et al. (2000) |
| PAO846 | GTT AGC TAC GGC ACT AAA AGG | Most <i>Accumulibacter</i> | Crocetti et al. (2000) |
| EUB338-I | GCT GCC TCC CGT AGG AGT | Most bacteria | Amann et al. (1995) |
| EUB338-II | GCA GCC ACC CGT AGG TGT | <i>Planctomycetales</i> | Daims et al. (1999) |
| EUB338-III | GCT GCC ACC CGT AGG TGT | <i>Verrucomicrobiales</i> | Daims et al. (1999) |
| GAOQ431 | TCC CCG CCT AAA GGG CTT | Some <i>Competibacter</i> | Crocetti et al. (2002) |
| GAOQ989 | TTC CCC GGA TGT CAA GGC | Some <i>Competibacter</i> | Crocetti et al. (2002) |
| GB_G2 | TTCCCCAGATGTCAAGGC | Some <i>Competibacter</i> | Kong et al. (2002) |
| TFO-DF218 | GAA GCC TTT GCC CCT CAG | ' <i>Defluviicoccus</i> '-related organisms | Wong et al. (2004) |
| TFO-DF618 | GCC TCA CTT GTC TAA CCG | ' <i>Defluviicoccus</i> '-related organisms | Wong et al. (2004) |
| DF988 | GAT ACG ACG CCC ATG TCA AGG G | ' <i>Defluviicoccus</i> '-related organisms | Meyer et al. (2006) |
| DF1020 | CCG GCC GAA CCG ACT CCC | ' <i>Defluviicoccus</i> '-related organisms | Meyer et al. (2006) |

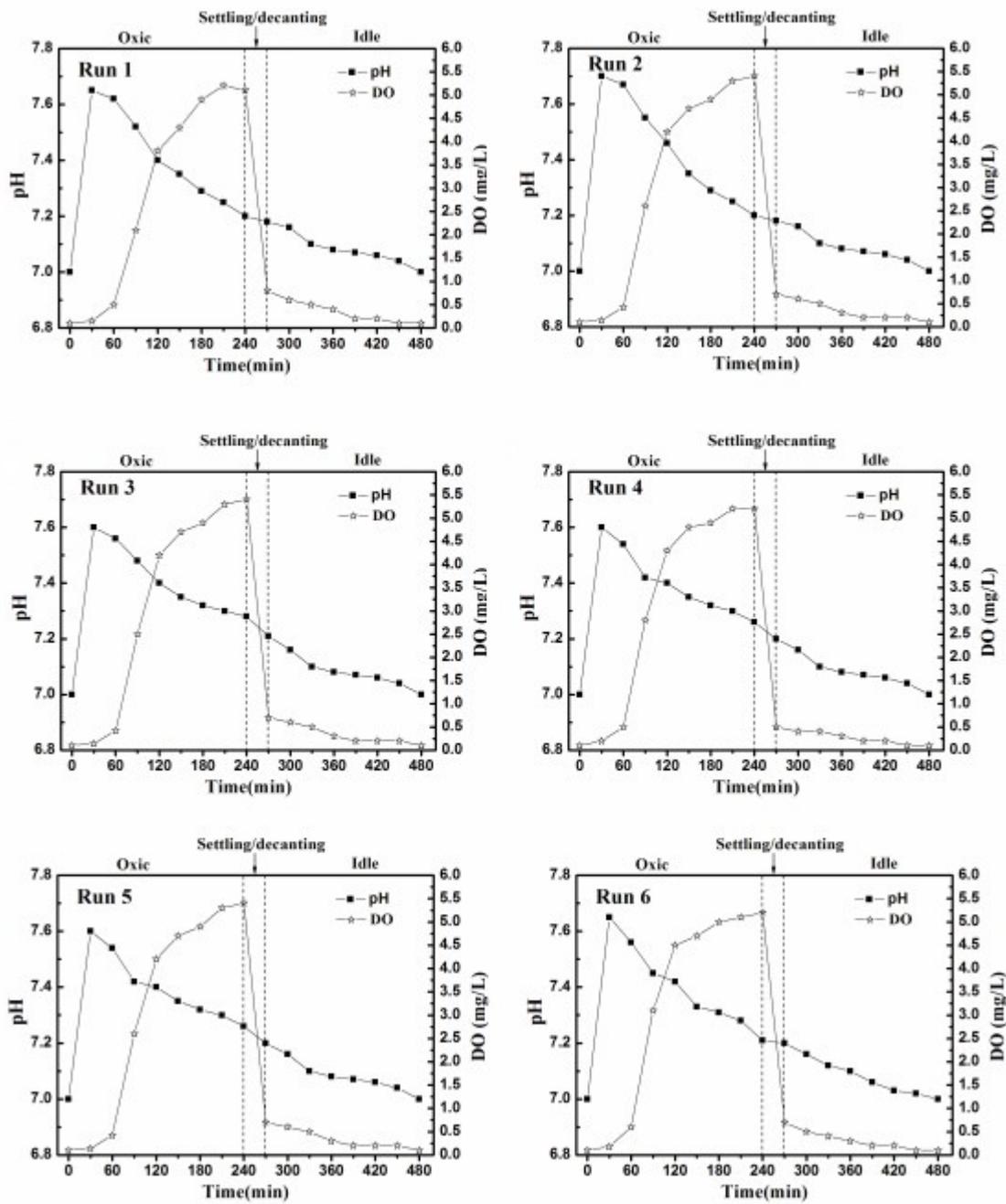


Figure S1. Profiles of pH and DO variations during a typical cycle of each Run in the O/EI reactor.

Supplementary Reference

- Amann, R., Ludwig, W., Schleifer, K.H., 1995. Phylogenetic identification and in situ detection of individual microbial cells without cultivation. *Microbiol. Rev.* 59 (1): 143-169.
- Crocetti, G.R., Hugenholtz, P., Bond, P.L., Schuler, A., Keller, J., Jenkins, D., Blackall, L.L., 2000. Identification of polyphosphate-accumulating organisms and design of 16S rRNA-directed probes for their detection and quantitation. *Appl. Environ. Microbiol.* 66 (3): 1175-1182.
- Crocetti, G.R., Banfield, J.F., Keller, J., Bond, P.L., Blackall, L.L., 2002. Glycogen-accumulating organisms in laboratory-scale and full-scale wastewater treatment processes. *Microbiol.* 148 (Pt 11): 3353-3364.
- Daims, H., Bruhl, A., Amann, R., Schleifer, K.H., Wagner, M., 1999. The domain-specific probe EUB338 is insufficient for the detection of all bacteria: development and evaluation of a more comprehensive probe set. *Syst. Appl. Microbiol.* 22 (3): 434-444.
- Kong, Y.H., Say, Ong, S.L., Ng, W.J., Liu, W.T., 2002. Diversity and distribution of a deeply branched novel proteobacterial group found in anaerobic-aerobic activated sludge processes. *Environ. Microbiol.* 4 (11): 753-757.
- Meyer, R.L., Saunders, A.M., Blackall, L.L., 2006. Putative glycogen-accumulating organisms belonging to the *Alphaproteobacteria* identified through rRNA-based stable isotope probing. *Microbiol.* 152 (Pt 2): 419-429.
- Wong, M.T., Tan, F.M., Ng, W.J., Liu, W.T., 2004. Identification and occurrence of tetrad-forming *Alphaproteobacteria* in anaerobic-aerobic activated sludge processes. *Microbiol.* 150 (Pt 11): 3741-3748.