

Article

Minimization of n₂o Emission through Intermittent Aeration in a Sequencing Batch Reactor (Sbr): Main Behavior and Mechanism

Tang Liu ¹, Shufeng Liu ^{1,*}, Shishi He ², Zhichao Tian ² and Maosheng Zheng ²

Supplementary Materials

Procedures of qPCR amplification

The qPCR amplification was performed in a 20- μ L reaction mixture, which consisted of 2.0- μ L template DNA, 10- μ L SYBR Premix Ex Taq and 0.5- μ L forward and reverse primers for each sample [1]. The PCR procedure contained 15-min enzyme activation and initial denaturation at 95 °C, followed by 40 cycles of 30-s denaturing at 95 °C, 30-s annealing at 58 °C and 45-s extension at 72 °C. The specificity of PCR products was confirmed by dissociation curve, then visualized using 1.2% agarose gel electrophoresis. Standard curves were generated using standard plasmids containing corresponding genes and parallelly performed with DNA. The target gene copies in the unit volume template were calculated through the standard curve.

Table 1. Primer sets of qPCR amplification used in this study.

Target Gene	Primer Name	Primer Sequence (5'-3')	Amplified Length	References
Comammox- <i>amoA</i>	<i>comamoA</i> AF	AGGNGAYTGGGAYT TCTGG	436	[1]
	<i>comamoA</i> 3SR	CCGVACATACATRA AGCCCAT		
AOB- <i>amoA</i>	<i>amoA</i> 1F	GGGGTTTCTACTGGT GGT	491	[2]
	<i>amoA</i> 2R	CCCCTCKGSAAAGC CTTCTTC		
AOA- <i>amoA</i>	<i>archamoA</i> 19F	ATGGTCTGGYTWAG ACG	629	[3]
	<i>archamoA</i> 616R	GCCATCCABCKRTA NGTCCA		

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