

Nutpornnapat Sinthusith 2014: Identification and Quantification of Bacteria and Archaea Responsible for Ammonia Oxidation in Different Activated Sludge System. Master of Engineering (Environmental Engineering), Major Field: Environmental Engineering, Department of Environmental Engineering. Thesis Advisor: Associate Professor Pongsak Noophan, Ph.D. 49 pages.

Eutrophication is a serious problem in water bodies, which intensifies the significance of nitrogen removal in a cost-effective manner. Nitrification, the primary reaction of biological nitrogen removal, is the first choice in the standpoint of cost-effectiveness and broader applicability. Ammonia oxidation, the first step of nitrification, has been mediated by ammonia-oxidizing bacteria (AOB). However, recent studies have revealed some archaea, also known as ammonia oxidizing archaea (AOA) are capable of oxidizing ammonia under oligotrophic conditions. Such surprising discovery allows researchers to investigate their physiological and phylogenetical traits. This means that AOA are potentially important players in WWTPs to oxidize ammonium. Nonetheless, the information of AOA is still lacking. The aims of this research were to compare the abundance and sequences of bacteria and archaeal ammonia monooxygenase (*amoA*) genes in different wastewater treatment plants, which located in Thailand, Japan and United States of America (USA) and to survey significant parameters which could affect the abundance of *amoA* gene, responsible for ammonia oxidation to hydroxylamine which is known as the first oxidation step of biological nitrogen removal. Activated sludge samples were taken from three full-scale wastewater treatment plants. These samples were mainly analyzed by using molecular technique: quantitative real-time PCR (qPCR) and PCR-DGGE. The qPCR and PCR-DGGE were used to find the comparative abundance and identify sequences of AOB and AOA. The results from this study were found that the abundance and identify of AOB and AOA were elucidate in three different activated sludge systems. The number of AOA *amoA* genes was in every sample from Phuket, Thailand. The number of AOB *amoA* genes was the same number amount both Japan and USA. The main reason, AOA were found in Phuket wastewater treatment plant because there were high temperature, long retention time and low dissolved oxygen.

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Thesis Advisor's signature