

Detection of Prokaryotic *amoA* Gene Diversity and Abundance in a Polyacrylamide Transportation System of an Oil Field

CAIYUN LI¹, JI-DONG GU², BO-ZHONG MU^{1*}

¹ State Key Laboratory of Bioreactor Engineering and Institute of Applied Chemistry, East China University of Science and Technology, Shanghai 200237, P.R. China (licaiyun@mail.ecust.edu.cn, *correspondence: bzm@ecust.edu.cn)

² School of Biological Sciences, The University of Hong Kong, Pokfulam Road, Hong Kong, P.R. China (jdgu@hku.hk)

Some ammonia-oxidizing bacteria related to nitrogen cycling have significant influence to ammonia removing in petroleum reservoirs. Although the presence of ammonia-oxidation bacteria (AOB) and ammonia-oxidation archaea (AOA) were detected in some sites, but the study about their existence in the oil reservoirs especially in the water injection pipeline are limited. This study investigated the functional diversity and abundance of AOB and AOA in 9 samples including solution and biofilm samples from a high-molecular-weight polyacrylamide transportation pipeline of an oil field by using phylogenetic analysis based on 16S rRNA and *amoA* genes. AOB was found from 3 samples and AOA was only found in one sample out of 9 samples together with different physicochemical properties. As some ammonia was transferred from the amide bond of polyacrylamide, the detection of AOB and AOA is beneficial to reveal the linkage between the nitrogen cycling and polyacrylamide biodegradation. Further investigation about the sample properties are in progress and ongoing work to reveal their correlation with the diversity and abundance of AOB and AOA to help identify the key microbes and unveil the potential nitrogen cycling pathways for this special environment.