

Spatial distribution of microbial consortia on an anaerobic granular sludge from full-scale and lab-scale UASB reactor treating PTA wastewater

김지영¹, 이민우², 박종문^{3,4,†}

¹한국생명공학연구원; ²계명대학교 화학공학과;

³포항공과대학교 첨단원자력공학부;

⁴포항공과대학교 화학공학과/환경공학부

(jmpark@postech.ac.kr[†])

In this study, we were investigated difference insight into the microbial composition and structure of granule samples obtained from full-scale (F1) and sequential two stage lab-scale (R1 and R2) UASB reactors. In addition, as results of microbial community analysis, we were designed a specific oligonucleotide probe of five bacteria species and of three archaeal species. And then, we were investigated by the fluorescence in situ hybridization (FISH) technique combined with confocal laser scanning microscopy (CLSM) to visualize the locations of above mentioned microorganisms of particular interest in full-scale (F1) and sequential two stage lab-scale (R1 and R2) UASB reactors. As a results, syntrophus sp. was the most abundant type of bacteria in the all of granules. These granules contained mainly Proteobacteria. In archaeal communities, acetoclastic methanogens are more abundant than hydrogenotrophic methanogens. Quantification using fluorescence in situ hybridization showed that Methanosaeta was predominant (83 to 95% of the total active archaea) in all reactor granules.