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## STUDIES ON EXCESS SLUDGE REDUCTION AND MICROBIAL COMMUNITY GROWING IN A NOVEL A+OSA REACTOR

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### Abstract

Excess biomass produced in the degradation processes of organic pollutants is creating environmental challenges for wastewater treatment plants. The A+OSA system, a modification of the anoxic / oxidic (A/O) process via insertion of a sludge holding tank into a sludge return line, has been demonstrated to be capable of achieving simultaneous nutrient removal and sludge reduction. Here we report the results of an investigation aimed at evaluating the impact of the sludge holding tank on the biomass growth, the microbial population and their metabolic characteristics. The results demonstrate that a 13%-27% sludge reduction can be attained. The sludge reduction can be attributed to the interaction of the sludge decay in the holding tank and the sludge growth in the main reaction units. Additionally, the sludge decay is the main reason for the excess sludge reduction, and the net growth of the sludge was the interaction of the compensative increase and lower sludge yield with equilibrium point near 5.56h. The carbon element analysis showed the carbon mineralization rate of the main reaction units was lower than it of the reference, and the ratios of carbon converted into gaseous of the sludge holding tank increased with the hydraulic retention time (HRT) increasing. Denaturing gradient gel electrophoresis (DGGE) analysis revealed that the insertion of the sludge holding tank had distinct effect on the microbial communities. Moreover, the bacterial communities found in samples from the A+OSA operated under different conditions were statistically similar amongst themselves. The most abundant phenotypes discovered in the A+OSA were those related to *β-proteobacteria*; followed by *Bacteroidetes*, which can adapt to the alternate oxidic/anoxic/anaerobic environment and of these microbes, the PAOs, anaerobic fermentative bacteria and slow growers were the contributors to the sludge reduction.

*Key words:* feasting/fasting, PCR-DGGE, sludge decay, excess sludge, microbial community

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