

Evolution of microbial communities and nutrient removal performances in aerobic granular sludge sequencing batch reactor during change of substrate

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Aerobic granular sludge (AGS) is a promising alternative wastewater treatment to the conventional activated sludge system. As AGS has enhanced settling abilities and provides different redox conditions across the granules at the same time, the processes based on AGS allow substantial space, energy and chemical products savings. A few wastewater treatment plants (mainly hybrid or pilot plants) are already using AGS. Nevertheless the performances of lab-scale reactors fed with simple synthetic wastewater are usually different from those of plants treating real wastewater where nutrient removal performances are more versatile and granules have a fluffy structure. Moreover, if the microbial community structures from AGS reactor fed with simple synthetic substrate have been extensively studied, it is less the case of the biomass from AGS reactors fed with more complex substrates or real wastewater. In order to make a step toward the comprehension of AGS used to treat municipal wastewater, this experiment was designed to study the impact of polymeric organic compounds on nutrient removal performances and microbial communities. These properties were monitored on a lab scale AGS sequencing batch reactor during a progressive substrate transition from volatile fatty acids (VFAs), to a more complex substrate mixture containing VFAs, glucose and amino acids, and finally to a synthetic wastewater containing VFAs, starch and oligo-peptides. With the lowered VFA concentrations, phosphorus (P)-removal performances were impaired. At the same time, amino acids fermentation significantly increased the ammonium concentration, thus extending the time required for total nitrification. The composition of the artificial wastewater was further adapted in order to recover efficient P- and nitrogen (N)-removal. Molecular analyses will show how the changes in substrate composition have influenced the AGS bacterial community structure that has kept its high settling ability and the granule size distribution throughout the first substrate transition.