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Microbial population dynamics within aerobic granular sludge exposed to a mixture of pharmaceuticals

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Aerobic granular sludge (AGS) technology is one of the most promising biotechnologies in wastewater treatment for which the number of full-scale facilities has been growing worldwide. AGS is a special case of biofilm composed of self-immobilized cells. Compared to conventional activated sludge, AGS holds a strong and compact microbial structure, excellent sedimentation properties and tolerance to chemical toxicity.

Pharmaceutical compounds are emerging environmental contaminants that have received growing attention over the last two decades. Their occurrence in various environmental matrices, such as domestic and hospital wastewater treatment plants (WWTP) effluents and surface waters has been largely reported. Although present at low levels, these micro-pollutants are bioaccumulative, pseudo-persistent and can affect the composition and activity of microbial communities or cause toxic effects on different organisms. To date, due to AGS technological novelty, there is a lack of information regarding the effect of pharmaceuticals on its microbial community and biological processes.

This study assessed the effects of a cocktail of pharmaceuticals from three different pharmacological classes commonly found in wastewaters, on the bacterial community of laboratory-scale AGS bioreactor. The bioreactor was operated for 86 days and from day 29 to 57 was continuously feed with an aqueous stream containing a cocktail of pharmaceuticals. The microbial structure of AGS bacterial community along bioreactor operation was examined through the combination of two culture-independent methods: Polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) and high-throughput pyrosequencing combined with the bioinformatics analysis. DGGE fingerprint revealed significant structural differences along bioreactor operation, which were probably related with the exposure to the pharmaceuticals. Pyrosequencing results showed significantly different taxonomic profiles in the AGS communities. At phylum level, the Bacteroidetes, Proteobacteria and Actinobacteria predominate within the sludge microbial community but the proportions of each phyla was significantly different among samples from different days.

These two molecular combined techniques offer versatility toward identifying the microbial population at a higher level of detail, significantly expanding the knowledge on the microbial biodiversity and population dynamics in AGS.

Keywords: Aerobic granular sludge; pharmaceuticals; PCR-DGGE; pyrosequencing.

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