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BOOK OF ABSTRACTS



11. Environmental Microbiology and Biotechnology

P59. Bacterial diversity shifts in AGS reactor treating food industry wastewater

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Aerobic granular sludge (AGS) is a promising technology for treating industrial wastewater, possessing higher biomass retention and tolerance to toxic substrates than conventional activated sludge systems. AGS presents a diverse microbial community responsible for the simultaneous removal of carbon and nutrients. These communities are protected by extracellular polymeric substances (EPS) that allow for the compact structure of the granules. As a result, bacteria present in the aerobic granules are more resistant to variable wastewater composition, as commonly produced in food industry. The main objective of this work is to study the microbial community dynamics of an AGS reactor treating wastewater from a fish canning plant. The reactor was monitored during 220 days, divided into eight operational phases. COD, NH_4^+ and PO_4^{3-} removal were assessed and biomass samples were collected throughout time for microbiome profiling.

The reactor presented good COD, PO_4^{3-} and NH_4^+ removal during phases I, II and III, but decreased performance during phase IV, when a higher organic load was applied. The removal processes recovered after phase IV until the end of operation. *Proteobacteria* were dominant in the inoculum (relative abundance of 64.8%) and dominated almost all reactor phases. *Bacteroidetes* were second dominant in the inoculum (17.5%) as well in most reactor phases, being present with higher relative abundance (55.5%) than *Proteobacteria* (38.4%) during phase IV. Within *Proteobacteria*, *Gammaproteobacteria* were initially more abundant but *Betaproteobacteria* predominated after phase

IV. For *Bacteroidetes*, the community dynamics has also changed from phase IV onwards, with *Flavobacteriia* losing its high relative abundance to *Saprospira* and *Cytophagia*. Several bacterial genera were detected throughout reactor operation, such as *Phenylobacterium* and *Flavobacterium*, while other were detected with higher abundance before (*Methylocaldum* and *Plasticicumulans*) or after phase IV (*Thauera* and *Paracoccus*). The relationship between bacterial community shifts and process performance was assessed. This study increases our knowledge on AGS technology application in real wastewater treatment.