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Publication date:
2016

Citation for published version (APA):

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A GAO hiding among the PAO: The role of the Propionivibrio spp. in biological phosphorus removal

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BACKGROUND
Enhanced biological phosphorus removal (EBPR) is widely applied to remove phosphorus (P) from wastewater. The process relies on polyP accumulating organisms (PAOs) that are able to take up P in excess of what is needed for growth, whereby P can be removed from the wastewater by wasting the biomass. However, glycogen accumulating organisms (GAOs) may reduce the EBPR efficiency as they compete for substrates with PAOs, but do not store excessive amounts of polyP. The model PAO are the betaproteobacterial “Candidatus Accumulibacter spp.” (Accumulibacter). Here, we report the discovery of a GAO from the genus Propionivibrio, which is closely related to Accumulibacter.

IDENTIFICATION OF A NOVEL GAO
A 6L lab scale sequencing batch reactor configured for EBPR was operated for 3 months using volatile fatty acids (VFAs) as the carbon source. Biochemical transformations indicated a mixed PAO-GAO community.

STUDY PERSPECTIVES
The Propionivibrio spp. are abundant GAO in EBPR systems. Results from studies applying the PAOmix probes should be interpreted with care given they also target a GAO. Comparative expression studies of the Accumulibacter PAO, and the closely related Propionivibrio GAO, may be key to determining the genetic and regulatory mechanisms that give rise to the PAO phenotype.

GENOMIC ANALYSES
Metagenomics was applied to obtain representative genomes from the abundant Accumulibacter and Propionivibrio species. Annotation supported a typical GAO physiology for the Propionivibrio spp. where aerobically stored glycogen is predicted to provide the energy and reducing equivalents to support anaerobic uptake and storage of VFAs as PHAs (Fig. 2).

IN SITU ANALYSES
In situ staining revealed that both Accumulibacter spp. and Propionivibrio spp. stored VFAs as polyhydroxyalkanoates (PHAs) under anaerobic conditions while only the former cycled polyP (Fig. 3). This is consistent with the Accumulibacter and Propionivibrio behaving as PAO and GAO, respectively.

**Fig. 1**. Phylogeny (16S rRNA gene) and FISH analysis of the reactor biomass community.

**Fig. 2**. Metabolic model for the Propionivibrio GAO in EBPR systems.

**Fig. 3**. In situ staining of the biomass.