A GAO hiding among the PAO

The role of the Propionivibrio spp. in biological phosphorus removal

McIlroy, Simon Jon; Albertsen, Mads; Stokholm-Bjerregaard, Mikkel; Karst, Søren Michael; Nielsen, Per Halkjær

Creative Commons License
Unspecified

Publication date:
2016

Link to publication from Aalborg University

Citation for published version (APA):

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

? Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
? You may not further distribute the material or use it for any profit-making activity or commercial gain
? You may freely distribute the URL identifying the publication in the public portal

Take down policy
If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.
A GAO hiding among the PAO: The role of the Propionivibrio spp. in biological phosphorus removal

Simon J. Mclroy1,2, Mads Albertsen1,2, Mikkel Stokholm-Bjerregaard1,2, Søren M. Karst1 and Per Halkjær Nielsen1
1Center for Microbial Communities, Department of Chemistry and Bioscience, Aalborg University, Aalborg, Denmark
2Krüger A/S, Aalborg, Denmark
*These authors contributed equally to this work

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.

Phylogenetic (Fig. 1B) and FISH (Fig. 1A) analyses revealed that the reactor was dominated by two populations representing related genera - Accumulibacter and Propionivibrio. The PAOmix probes designed to target the Accumulibacter target both populations Fig. 1. A novel probe was designed to target the Propionivibrio (Prop207). The PAO651 probe alone is recommended to target the Accumulibacter.

Surveys of full scale EBPR systems reveal a high abundance of the Propionivibrio – sometimes in higher abundance than the Accumulibacter PAO.

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.