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DOI
10.1016/j.watres.2019.03.053
Publication date
2019
Document Version
Final published version
Published in
Water Research

Citation (APA)
https://doi.org/10.1016/j.watres.2019.03.053

Important note
To cite this publication, please use the final published version (if applicable).
Please check the document version above.

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“Candidatus Accumulibacter delftensis”: A clade IC novel polyphosphate-accumulating organism without denitrifying activity on nitrate

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A R T I C L E   I N F O

Article history:
Received 6 August 2018
Received in revised form 18 March 2019
Accepted 26 March 2019
Available online 2 June 2019

Keywords:
Candidatus Accumulibacter
DPNA
PAO
Denitrification
Anoxic phosphate uptake
Genome-centric metagenomics

A B S T R A C T

Populations of “Candidatus Accumulibacter”, a known polyphosphate-accumulating organism, within clade IC have been proposed to perform anoxic P-uptake activity in enhanced biological phosphorus removal (EBPR) systems using nitrate as electron acceptor. However, no consensus has been reached on the ability of “Ca. Accumulibacter” members of clade IC to reduce nitrate to nitrite. Discrepancies relate to the diverse operational conditions which could trigger the expression of the Nap and/or Nar enzyme and/or to the accuracy in clade classification. This study aimed to assess whether and how certain operational conditions could lead to the enrichment and enhance the denitrification capacity of “Ca. Accumulibacter” within clade IC. To study the potential induction of the denitrifying enzyme, an EBPR culture was enriched under anaerobic–anoxic–oxygen (A2O) conditions that, based on fluorescence in situ hybridization and ppk gene sequencing, was composed of around 97% (on a biovolume basis) of affiliates of “Ca. Accumulibacter” clade IC. The influence of the medium composition, sludge retention time (SRT), polyphosphate content of the biomass (poly-P), nitrate dosing approach, and minimal aerobic SRT on potential nitrate reduction were studied. Despite the different studied conditions applied, only a negligible anoxic P-uptake rate was observed, equivalent to maximum 13% of the aerobic P-uptake rate. An increase in the anoxic SRT at the expenses of the aerobic SRT resulted in deterioration of P-removal with limited aerobic P-uptake and insufficient acetate uptake in the anaerobic phase. A near-complete genome (completeness = 100%, contamination = 0.187%) was extracted from the metagenome of the EBPR biomass for the here-proposed “Ca. Accumulibacter delftensis” clade IC. According to full-genome-based phylogenetic analysis, this lineage was distant from the canonical “Ca. Accumulibacter phosphatis”, with closest neighbor “Ca. Accumulibacter sp. UW-LDO-IC” within clade IC. This was cross-validated with taxonomic classification of the ppk1 gene sequences. The genome-centric metagenomic analysis highlighted the presence of genes for assimilatory nitrate reductase (nap) and periplasmic nitrate reductase (nap) but no gene for respiratory nitrate reductases (nap). This suggests that “Ca. Accumulibacter delftensis” clade IC was not capable to generate the required energy (ATP) from nitrate under strict anaerobic–anoxic conditions to support an anoxic EBPR metabolism. Definitely, this study stresses the incongruence in denitrification abilities of “Ca. Accumulibacter” clades and reflects the true intra-clade diversity, which requires a thorough investigation within this lineage.

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https://doi.org/10.1016/j.watres.2019.03.053
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1. Introduction

Enhanced biological phosphorus removal (EBPR) is a process applied worldwide to remove phosphorus in wastewater treatment plants (WWTP) (Henze et al., 2008). EBPR is carried out by microorganisms that are capable of storing phosphorus beyond their growth requirements as polyphosphate (poly-P), known as polyphosphate-accumulating organisms (PAOs) (Comeau et al., 1986). The PAO guild comprises multiple genera (Stolkmolm-Bjerggaard et al., 2017), with “Candidatus Accumulibacter” as well-described primary population. The relative abundance of “Ca. Accumulibacter” (hereafter referred to as PAO) has been correlated with good EBPR in WWTPs with different configurations worldwide (Kong et al., 2002; Zilles et al., 2002; Saunders et al., 2003; He et al., 2005; Wong et al., 2005). “Ca. Accumulibacter” performs different metabolic processes depending on the availability of terminal electron acceptors. Under anaerobic conditions (i.e., no electron acceptor available according to environmental engineering lexicon), this PAO stores carbon (e.g., acetate, propionate) as poly-β-hydroxyalkanoates (PHAs) at the expense of polyphosphate (poly-P) hydrolysis and glycogen degradation. Thereafter, when an electron acceptor is available such as dissolved oxygen under aerobic conditions, and nitrate and presumably nitrate under anoxic conditions, the organism consumes the stored PHA to replenish its poly-P and glycogen storage pools, for biomass synthesis and cellular maintenance (Comeau et al., 1986; Wentzel et al., 1986; Smolders et al., 1994a, 1994b; Kuba et al., 1996b).

Previous studies have suggested that members of the PAO guild have different affinities and potentials to use nitrate or nitrite as electron acceptors for anoxic P-uptake (Kerns-Jesperesen and Henze, 1993; Kuba et al., 1993, 1996a, 1997; Ahn et al., 2001a, 2001b). Kerns-Jesperesen and Henze (1993) have postulated the existence of two types of PAOs: one denitrifying-PAO type able to use nitrate and oxygen as electron acceptors (herein identified as or DPAO) and another PAO type capable of using only oxygen. Through the long-term operation of two sequencing batch reactors (SBRs) operated under anaerobic-anoxic (A2) and anaerobic-oxic conditions (A/O), Kuba et al. (1993) have observed that DPAO could exhibit an anoxic EBPR activity similar to that of PAO on oxygen.

Carvalho et al. (2007) observed that rod-shaped PAOs exhibited satisfactory anoxic P removal on nitrate while coccus-shaped PAO showed poor anoxic EBPR activity. Later on, based on fine-scale differences in the genetic sequences of the ppk1 gene, Peterson et al. (2008) identified the existence of two “Ca. Accumulibacter” clades I and II, with several subclades (IA-ID and IIA-IIG). Oligonucleotide probes and primers set were designed on this molecular basis for rapid detection by fluorescence in situ hybridization (FISH) and polymerase chain reaction (PCR). Based on these findings and correlations with process performances, Oehmen et al. (2010a, b) re-assessed the different PAO phenotypes observed by Carvalho et al. (2007), and suggested that clade I was responsible for the anoxic P-uptake activity observed in EBPR systems. In agreement, Flowers et al. (2009) observed that a culture enriched in clade I (ca. 70 ± 11% based on FISH bio-volume) was able to denitrify without requiring any acclimatization step, while a culture dominated by clade II (approx. 55 ± 7% clade II and 32 ± 0.5% clade I per bio-volume) could not. Nevertheless, after a 24-h acclimatization period to the presence of nitrate, both EBPR systems performed a simultaneous denitrification and P-uptake activity. The anoxic P-uptake activity observed in the latter clade II culture was associated to the presence of the clade I fraction in the system (Flowers et al., 2009).

Lanham et al. (2011) enriched a clade I culture (approx. 90% bio-volume) under anaerobic-anoxic-oxic (A2O) conditions. Their enrichment was capable to take-up about 12 mg PO4-P g1 VSS h1 using nitrate as electron acceptor. Contrary to the strict A2 operating conditions of Kuba et al. (1993), the authors reported that maintaining anoxic stage seemed to have been a key condition to secure the reactor stability and obtain a highly enriched clade I culture. On the other hand, through the execution of short-term studies, Saad et al. (2016) and Rubio-Rincón et al. (2017a) reported that clade I (further identified via ppk gene sequence analysis as populations of “Ca. Accumulibacter” clade IC) was unable to use nitrate as electron acceptor as efficient as oxygen, or nitrite. They suggested that when anoxic P-uptake takes place, the underlying members of clade IC may use the nitrate generated from the reduction of nitrate by side populations within the microbial community, possibly glycogen-accumulating organisms (GAOs) or ordinary heterotrophic organisms (OHOs). Nevertheless, both studies were based on the conduction of short-term (hours) batch activity tests with a culture of clade IC affiliaires enriched under A/O conditions. In contrast, recent studies performed by Camejo et al. (2016) have suggested that some populations of clade IC can efficiently use nitrate as electron acceptor for the oxidation of PHA and P-uptake.

From a molecular and microbial perspective, early genome-centric metagenome analyses of populations of “Ca. Accumulibacter” clades IA and IC have not been able to detect the respiratory nitrate reductase gene (nar) required for nitrate respiration (Flowers et al., 2013; Skennerton et al., 2014), similar to clade IIA and IIF. Recently, Camejo et al. (2018) have identified one “Ca. Accumulibacter” population of clade IC harbouring a nar gene. The denitrification pathway of the aforementioned clades, only includes the presence of the periplasmic nitrate reductase gene (nap) and the required genes to denitrify from nitrite onwards (García Martín et al., 2006; Flowers et al., 2013; Skennerton et al., 2014). According to Moreno-Vivián et al. (1999) the main difference among these genes is the potential of their expressed enzyme (Nap, Nar) to generate energy as ATP. While both enzymes can reduce nitrate to nitrite only the Nar enzyme has been correlated with enough generation of energy as ATP to sustain bacterial growth and other microbial processes (Moreno-Vivián et al., 1999). As such and in view of the contradictory findings previously described, the gene expression mechanisms could be responsible for the different anoxic P-uptake activities of clade IC phylotypes in EBPR systems reported in literature, as first suggested by Skennerton et al. (2014).

It remains unclear which fraction of “Ca. Accumulibacter” clade IC species harbor the nap or nar genes, and, if these genes are present in their genome, which operational factors could induce their enzymatic expression. We aimed to assess the influence of different operating conditions on a clade IC enriched culture (Rubio-Rincón et al., 2017a). The main factors studied were: (i) a high P/COD ratio (0.06 g P g−1 COD); (ii) a long sludge detention time (SRT) of 15 d; (iii) a low P/COD ratio of 0.03 g P g−1 COD; (iv) a short aerobic SRT of 1.5 d; and, (v) pulse and continuous nitrate dosing modes. Combining mixed-culture stoichiometry and kinetics investigation with molecular biology and genome-centric metagenomics analysis of the here proposed “Ca. Accumulibacter delftensis” clade IC, this study contributes to assess conditions that may stimulate and enhance the use of nitrate and elucidate their potential role in EBPR systems. It further stresses the need to reappraise metabolic functionalities inside and across clades of the “Ca. Accumulibacter” lineage — and microbial lineages in general — beyond correlations observed between relative abundances of clades and biochemical conversions monitored.
2. Materials and methods

2.1. Reactor operation

A culture of a “Ca. Accumulibacter” clade IC population was enriched in a 3-L, double-jacket, stirred-tank reactor (Applikon, Delft, The Netherlands) with a working volume of 500 L. A volume of 500 mL of activated sludge from the EBPR WWTP Nieuwe Waterweg (Hoek van Holland, The Netherlands) was used as inoculum. Prior to the start of the study, the reactor was operated under anaerobic-anoxic (A/O) conditions for more than a year (experimental period A; Rubio-Rincón et al., 2017a). Thereafter, the operational conditions were changed to anaerobic-anoxic-oxic (A2O) (experimental period B; Table 1). Once the system was operated under A2O in a pseudo steady state (experimental period B), the medium composition was changed from the one used by Smolders et al. (1994a,b) to the one used by Kuba et al. (1993) (experimental period C) with low and high potassium concentration, respectively. In order to give the opportunity to the (assumed slow-growing) DPAOs to proliferate, the SRT was extended from 8 to 15 d in the experimental period D. Due to the potential role of GAOs in the denitrification activities observed in EBPR systems (Rubio-Rincón et al., 2017a), the feeding P/COD ratio was decreased from 0.06 to 0.03 g P g⁻¹ COD (experimental period E and F, respectively). In the experimental period G, to address if DPAOs could be r- or k-strategists, the nitrate dosing mode was changed from a pulse feeding carried out in 1 min to a longer feeding period of 30 min at a 1 mL/min flowrate (as studied by Kuba et al., 1993; Tu and Schuler, 2013), keeping the same nitrate concentration dosed (±10 mg NO₃⁻N L⁻¹). Finally, to wash the aerobic PAOs out and select for DPAOs, the length of the anaerobic phase was gradually decreased, and consequently the aerobic SRT was shortened from 2.2 days to 0.9 days (in experimental period G) and further to 0.4 days (in experimental period H), which is lower than the minimum aerobic SRT estimated by Brdjancovic et al. (1998) (of about 1.25 d) for A/O-enriched PAO.

The hydraulic retention time (HRT) was 12 h. The pH was controlled at 7.6 ± 0.1 with the addition of 0.4 mol L⁻¹ NaOH and 0.1 mol L⁻¹ HCl. Temperature was controlled at 20 ± 1 °C. In order to create and maintain the anaerobic conditions, dinitrogen gas was sparged at the bottom of the reactor during the first 30 min of the anaerobic phase and a water lock was installed at the off-gas outlet. Nitrate was fed either as pulse or continuously for 30 min (in accordance to the corresponding experimental period) from a bottle containing a 1 g NO₃⁻N L⁻¹ stock solution. The dissolved oxygen (DO) concentration was controlled at 20% of the saturation level by sparging on/off compressed air and dinitrogen gas. Both gases were controlled at 10 L h⁻¹. DO and pH levels were monitored continuously. Ortho-phosphate (PO₄⁻P), mixed liquor suspended solids (MLSS) and mixed liquor volatile suspended solids (MLVSS) concentrations were measured twice per week. When no significant changes in these parameters were observed for more than 3 SRTs, it was assumed that the system had reached pseudo steady-state conditions.

2.2. Nitrate-based DPAO batch activity tests

In order to assess if the biomass-specific organic load (food-to-microorganisms, F/M ratio), affecting the anaerobic PHA storage and therefore the intracellular carbon availability and its potential impact on the anoxic phosphorus uptake, two batch tests were carried out ex situ with half (batch 1D) and twice (batch 2D) the F/M ratio (37 and 148 mg COD g⁻¹ VSS, respectively) applied in the regular operation of the parent reactor. The medium composition was the same like in the operation of the parent reactor. Each batch test was performed with 200 mL of MLSS (collected and transferred during experimental period D, Table 1) in a double jacketed reactor operated at 20 °C with a 400 mL working volume. The cycle of the batch tests was composed of 1 h of anaerobic and 4 h of anoxic phases. In each batch test, nitrate was fed as a pulse reaching a concentration of around 45 mg NO₃⁻N L⁻¹. Dinitrogen gas was continuously sparged at the bottom of the reactor at 10 L h⁻¹ in order to maintain the anaerobic conditions. pH was kept at 7.6 ± 0.1 with the automatic addition of 0.4 mol L⁻¹ HCl and 0.4 mol L⁻¹ NaOH.

2.3. Cultivation medium

The cultivation medium were prepared in two separate bottles of 10 L (carbon and mineral solutions), and concentrated 10 times. The influent medium fed contained per liter: 400 mg COD (composed by acetate and propionate supplied in a 3:1 COD ratio), 4 mg Ca⁺⁺, 36 mg SO₄²⁻, 9 mg Mg²⁺, 1 mg yeast extract, 20 mg N-alllylthiourea (ATU) and 300 µL of trace element solution prepared according to Smolders et al. (1994a,b). In addition, the influent medium for (i) the experimental periods A and B contained per liter: 36 mg NH₄⁻N, 25 mg PO₄⁻P, 19 mg K⁺, and 18 mg Na⁺; (ii) for periods C, D and E the medium composition was change to increase the concentration of potassium as reported by Kuba et al. (1993) to: 83 mg NH₄⁻N, 25 mg PO₄⁻P, 50 mg K⁺ and 0 mg Na⁺; and, (iii) for F, G and H: 83 mg NH₄⁻N, 15 mg PO₄⁻P, 38 mg K⁺, and 0 mg Na⁺ per liter.

2.4. Chemical analyses

Ortho-phosphate (PO₄⁻P), nitrite (NO₂⁻N), MLSS, and MLVSS were analyzed according to APHA (2005). Nitrate (NO₃⁻N) was measured according to ISO 7890/1 (1986). Acetate and propionate were measured using a Varian 430-GC Gas...
Chromatograph (GC) equipped with a split injector (200 °C) and a WCOT Fused Silica column (105 °C) coupled to a FID detector (300 °C). Helium was used as carrier gas and 50 µL of butyric acid as internal standard.

2.5. Characterization of microbial community compositions

In order to estimate the relative abundance of the microbial communities along the different experimental periods, FISH analyses were performed as described by Amann (1995). Since Pro-pionivibrio was not observed with 16S rRNA gene-based amplicon sequencing, and because the PAO 651 FISH probe suggested by Albertsen et al. (2016) has a coverage of 71% of the species from the genus “Ca. Accumulibacter”, the mix probe of PAO 651, PAO 462, and PAO 846 suggested by Crocetti et al. (2000) was used to target the “Ca. Accumulibacter” genus (with a 89% coverage). To differentiate among the different PAO clades, the probes Acc-1-444 (PAO I) and Acc-2-444 (PAO II) were used (Flowers et al., 2009). Glycan-accumulating organisms (GAOs) were identified with the GB probe according to Kong et al. (2002). Defuviococcus clades 1 and 2 were identified with TFO-D215, TFO-D618, DF988, and DF1020 probes (Wong et al., 2004; Meyer et al., 2006). Vectashield with DAPI was used to avoid the fading of staining and stain all living organisms (Nielsen et al., 2009). FISH quantification of each probe was performed by image analysis of 25 random pictures taken with an Olympus BX5i microscope and analyzed with the software Cell Dimensions 1.5. The standard error of the mean was calculated as the standard deviation divided by the square root of the number of pictures.

2.6. Analyses of bacterial community compositions by V4–V6 16S rRNA gene-based amplicon sequencing

Genomic DNA (gDNA) was extracted using the UltraClean Microbial DNA extraction kit supplied by MOBIO laboratories Inc. (CA, USA) according to the manufacturer’s protocol except that the bead-beating was substituted by a combination of 5 min heating at 65 °C and 5 min bead-beating to ensure maximum yields. To check for quality and quantity, the gDNA extracts were loaded onto a 1% agarose gel in 1x TAE running buffer. Analysis of the extracted gDNA showed a large high molecular weight fraction and well visible DNA yields in comparison to the Smart ladder (Eurogentech Nederland b.v.).

The extracted gDNA was subsequently used for a two-step PCR reaction targeting the 16S rRNA gene of most bacteria and archaea, using the primers 515F (5′-GTGYCAGCMGCCGCGGTAT-3′) and 926R (5′-CCGTCAATTCCTTTTRAGTTT-3′) following Wang and Qian (2009). The first amplification step was performed to enrich for 16S rRNA genes, via quantitative PCR (qPCR). The qPCR reaction comprised 2x iQ™ SYBR® Green Supermix (Bio-rad, CA, USA), 500 nmoi L-1 primers each, and 1–50 ng gDNA template added per well (final volume of 20 µL by adding MiQ water). The qPCR program went along a first denaturation at 95 °C for 5 min followed by 20 cycles of denaturation at 95 °C for 30 s, annealing at 50 °C for 40 s and elongation at 72 °C for 40 s, prior to final elongation at 72 °C for 7 min. During the second step, 45–4454 (Roche) and MID tags at the U515F primer, were added to the products of step one. This protocol was similar to the ones previously described, but only Taq PCR Master Mix (QiaGen Inc, CA, USA) was used. The program was run for 15 cycles, the template, product from step one was used as template DNA and diluted ten times. After the second amplification, 12 PCR products were pooled in equimolar ratio and purified over an agarose gel using a GeneJet Gel Extraction Kit (Thermo Fisher Scientific, The Netherlands). The resulting library was sent for 454 sequencing and run in 1/8 lane with titanium chemistry by Macrogen Inc. (Seoul, Korea).

After sequencing, the reads library was imported into the CLC genomics workbench v7.5.1 (CLC Bio, Aarhus, DK) and (quality, limit = 0.05 and max. two ambiguities allowed) trimmed to a minimum of 200 bp and average of 284 bp. After trimming, the datasets were de-multiplexed resulting in 12 samples with an average of 7800 reads per sample. A build-it SILVA 123.1 SSURef Nr99 taxonomic database was used for BLASTn analysis on the reads under default conditions. To identify chimeric sequences we used the online tool DECIPHER (Wright et al., 2012). A very small portion of reads had a non-significant match and were discarded. The chimera check was done, but eventually not implemented as they were in minor amounts present and of non-significant importance to the final results. Sequences were only included if the E-value was sufficient low (<e-50). The top result was imported into an excel spreadsheet and used to determine taxonomic affiliation and species abundance.

2.7. Molecular analysis of “Ca. Accumulibacter” clades by PCR amplification and sequencing of the ppk1 functional gene

A direct PCR was performed to identify the “Ca. Accumulibacter” clade enriched in the biosystem based on the polyphosphate kinase (ppk1) functional gene as described by McMahon et al. (2007). The PCR amplicons were produced using ACCppk1-254F (5′-TCAC CACC GACG GCAA GAC-3′) and ACCppk1-1376R (5′-TCCA CTAC ATCT TGCC-3′) primers, and (Sanger) sequenced by BaseClear, Leiden, the Netherlands. Both strands were quality checked and found non-ambiguous. Subsequently both were aligned to yield a high quality, near complete, ppk1 gene. The phylogenetic tree was constructed using the neighbor joining method implemented in the CLC genomics workbench package, as described by Saad et al. (2016). In total 332 amino-acid positions were used for calculations.

2.8. Genome-centric metagenomic analysis of the “Ca. Accumulibacter” and blinking lineages present in the reactor

Two biological samples collected during the anaerobic-aerobic and anaerobic-anoxic-aerobic operations were selected for metagenome sequencing analysis. Wet-lab treatments of aliquots of the EBPR biomass were performed to suppress their background contribution of accompanying populations to the metagenomes and to eventually isolate the “Ca. Accumulibacter” genome bin by differential coverage. Synthetic shifts in relative abundances of microbial populations were achieved by contacting the biomass to different substrate, temperature, and dissolved oxygen conditions in shake flasks.

genDNA was extracted from these samples using the Fast DNA Spin Kit for Soils (MP Biomedicals, USA) by 4 series of 40 s of bead beating. The bacterial community compositions were characterized beforehand by V1–V3 16S rRNA gene-based amplicon sequencing analysis (primer pair 8F/518R) according to the MiDAS field guide of activated sludge (McIlroy et al., 2015). The gDNA extracts were purified and prepared for sequencing of the metagenomes using the Nextera XT DNA Sample Preparation Kit (Illumina, USA) according to manufacturer’s instructions. All purifications steps were performed using the Agencourt AMPure XP clean-up system (Beckman Coulter, USA). The dual-multiplexed pools of tagmented and indexed DNA fragments were sequenced on a MiSeq benchtop sequencer (Illumina, USA) at a sequencing depth of 1 Gbp per sample with paired-end reads of 300 × 300 bp. Quality controls were performed using DNA Analysis D1000 ScreenTape assays on a 2200 TapeStation instrument (AgilentTechnologies, USA). gDNA concentrations were accurately measured using Quant–IT dsDNA Assay Kits (ThermoFischer
Scientific, USA) on an Infinite M1000 PRO plate reader (Tecan, Switzerland).

The metagenomics sequencing raw datasets were processed using the CLC Genomics Workbench (Qiagen Bioinformatics, Denmark). The resulting de novo assembly and coverage files of the metagenomes of the EBPR sludge and background community treatment were loaded into mmgenome (Karst et al., 2016) in R for dual coverage binning of the near-complete genome of the “Ca. Accumulibacter” and flanking lineages present in the bioreactor following the method initially developed by Albertsen et al. (2013).

The single-lineage genome assemblies were uploaded into a KBase narrative (Arkin et al., 2016) for phylogenetic classification and functional gene annotation using the RAST toolkit (Brettin et al., 2005), ARB Silva, RNAmmer, tRNAscan-SE, and QUAST. The obtained assembly of the near-complete genome of the “Ca. Accumulibacter” population selected in the system was taxonomically classified at high resolution against the 28 draft genome assemblies available for this lineage in on-line databases such as NIH GenBank (Benson et al., 2005), NCBI RefSeq (O'Leary et al., 2016), and JGI IMG (Chen et al., 2017), and imported manually in KBase. Reference genome assemblies that were deprived of gene and protein annotations of coding sequences were annotated in KBase prior to phylogenetic tree reconstruction.

The genome-centric phylogenetic tree was computed in KBase from reference alignments based on 49 highly conserved clusters of orthologous groups of proteins and using the FastTree2 approximate maximum likelihood method. The FastANI algorithm was used to discriminate between unique genomes (<95%, new population) or to highlight overlapping genomes (>99%) by fast computation of pairwise average nucleotide identity (FastANI) values. The genome-based phylogenetic tree was cross-validated with the pkp1-gene-based taxonomic classification across the “Ca. Accumulibacter” lineage: the pkp1 gene sequence was retrieved from the genome assembly and matched against sequences of pkp1 gene PCR amplicons obtained from the EBPR biomass. Based on the uniqueness of the near-complete genomes obtained, we here proposed the provisional novel species names “Ca. Accumulibacter delftensis sp. nov.”, “Ca. Nocardioides delftensis sp. nov.”, and “Ca. Thermomonas delftensis sp. nov.”. Since no isolate and pure culture is available for these organisms, the provisional names were proposed according to recommendations of Murray and Stackebrandt and principles of the International Code of Nomenclature of Prokaryotes. A digital protologue table was developed for the description of the provisional taxa, following identical procedure adopted lately by Andersen et al. The genome assemblies and annotations are deposited in KBase, and will be made publicly available in GenBank/European Nucleotide Archive (in progress). Output milestones of the genome-centric metagenomics analysis are available in Supporting Information.

2.9. Stoichiometric and kinetic parameters of interest

The ratio of phosphorus released to VFA uptake (P/VFA) under anaerobic conditions was calculated based on the observed net phosphorus released at the end of the anaerobic period per VFA consumed. The phosphorus content in the biomass was calculated based on a mass balance performed using data from the pseudo steady-state conditions, as described by Kuba et al. (1993). The anaerobic metabolic activity of the sludge was characterized using the following anaerobic biomass-specific rates of interest:

i) \( q_{\text{P,VFA}}^{\text{MAX}} \) Maximum observed anaerobic phosphorus release rate, in mg PO₄-P g⁻¹ VSS h⁻¹.

ii) \( m_{\text{PO₄,AN}} \) Anaerobic endogenous phosphorus release rate observed once VFA were taken up, in mg PO₄-P g⁻¹ VSS h⁻¹.

iii) \( q_{\text{P,VFA}} \) Anaerobic phosphorus release rate due to VFA uptake, calculated according to:

\[
q_{\text{P,VFA}} = q_{\text{P,VFA}}^{\text{MAX}} - m_{\text{PO₄,AN}}
\]

iv) \( q_{\text{P,VFA}}^{\text{MAX}} \) Maximum observed anaerobic VFA uptake rate observed, in mg COD g⁻¹ VSS h⁻¹.

Oxygen uptake rate (OUR) profiles were determined based on DO consumption over time. In order to measure the DO consumption, during the anoxic stages the EBPR sludge was recirculated from the parent reactor through a separate 10 mL biological oxygen monitor (BOM) unit for 2–3 min. Once the DO measurements were stable, the sludge recirculation was stopped and the DO concentration profiles were recorded. The DO concentrations were kept above a set point of 2 mg O₂ L⁻¹ by periodically re-starting the sludge recirculation. This procedure was repeated along the anoxic phases. The BOM unit was equipped with a WTW OXi 340i DO probe (Germany). The anoxic and aerobic biomass-specific rates of interest were:

i) \( q_{\text{NO₃,Ax}} \) Nitrate uptake rate, in mg NO₃-N g⁻¹ VSS h⁻¹.

ii) \( q_{\text{P,Ax}} \) Anoxic phosphorus uptake rate, in mg PO₄-P g⁻¹ VSS h⁻¹.

iii) \( q_{\text{P,Or}} \) Aerobic phosphorus uptake rate, in mg PO₄-P g⁻¹ VSS h⁻¹.

All rates were calculated by linear regression based on the observed profiles as described in Smolders et al. (1995).

3. Results

3.1. Operation of the reactor under anaerobic-oxic (A/O) conditions

The EBPR reactor was operated for more than a year under A/O conditions showing a pseudo steady-state performance (Fig. 1A). All VFAs were anaerobically consumed during the first 15 min of reaction at a maximum biomass specific rate of 269 mg COD g⁻¹ VSS h⁻¹ (\( q_{\text{VFA}}^{\text{MAX}} \)), with a phosphorus release of 199 mg PO₄-P g⁻¹ VSS h⁻¹ (\( q_{\text{PO₄,AN}}^{\text{MAX}} \)). Once all VFA were taken up, a residual P-release rate of 2.5 mg PO₄-P g⁻¹ VSS h⁻¹ (\( m_{\text{PO₄,AN}} \)) was observed and assumed to correspond to the anaerobic endogenous P-release (i.e., for cellular maintenance). Under the presence of oxygen, phosphorus was taken up at a rate of 58 mg PO₄-P g⁻¹ VSS h⁻¹ (\( q_{\text{PO₄,Or}} \)). The observed ratio of phosphorus taken up per total oxygen consumed was 1.63 mg P mg⁻¹ O₂ (equivalent to 0.42 mol P mol⁻¹ e⁻ transferred during respiration).

3.2. Long-term operation under anaerobic-anoxic-oxic (A₂O) conditions

As observed in Fig. 1 B-G, in the anaerobic stage of the A₂O system, all VFAs were taken up and phosphorus was released at a maximum anaerobic rate (\( q_{\text{PO₄,AN}}^{\text{MAX}} \)) of between 164 and 254 mg COD g⁻¹ VSS h⁻¹. The P/VFA ratios were rather stable in the experimental periods B, C, and E (12.0 ± 0.8 mg PO₄-P g⁻¹ VSS h⁻¹) than in D, F, and G (1.9 ± 0.7 mg PO₄-P g⁻¹ VSS h⁻¹). The P/VFA ratios were rather stable in the experimental periods B, C, D, and E (0.66 ± 0.06 mg PO₄-P g⁻¹ COD), and higher than in F and G (0.50 ± 0.06 mg PO₄-P g⁻¹ COD). Under anoxic conditions, accumulation of nitrite was never
detected, in none of the experiments (Fig. 1B–G). A slightly higher denitrification activity of 3.9 mg NO₃⁻N·g⁻¹·VSS·h⁻¹ was observed in the first experimental period (B) after switching to the A₂O conditions. In the rest of the experimental periods, the denitrification rates did not increase considerably and remained around 2.2 ± 0.5 mg NO₃⁻N·g⁻¹·VSS·h⁻¹. Table 2 shows the A₂O rates and stoichiometry parameters calculated in each experimental period. Compared to the aerobic P-uptake rates (of up to 79 mg PO₄⁻P·g⁻¹·VSS·h⁻¹), a relatively low anoxic P-uptake rate (qPO₄,A) was observed in periods B, C, and F (5.0 ± 0.3 mg PO₄⁻P·g⁻¹·VSS·h⁻¹), which even decreased to 3.7 mg PO₄⁻P·g⁻¹·VSS·h⁻¹ in period G, and became negligible in period D. As much, the relative anoxic phosphorus uptake rates reached 13% of the aerobic phosphorus uptake rates (Table 2). In all cases, phosphorus was fully removed during the oxic phase (Fig. 1).

3.3. Minimal aerobic SRT

In the experimental phase H, as an attempt to favor the growth of a DPAO capable of using nitrate over strict aerobic PAOs, the oxic SRT was reduced below the minimum required for aerobic PAOs to grow as described by Brdjanovic et al. (1998). After two days of operation with an oxic SRT of approximately 0.4 d, the VFAs started to leak into the anoxic phase (74 mg COD·L⁻¹ at day 2 of operation). Likewise, the anaerobic phosphorus release decreased from 117 mg PO₄⁻P·L⁻¹ to 32 mg PO₄⁻P·L⁻¹ on the 3rd day of operation. The nitrate dose was increased daily to prevent nitrate limitation, while avoiding to exceed a concentration of more than 3 mg NO₃⁻N·L⁻¹ in the oxic phase, which may leak into the anaerobic stage. Despite these measures, no DPAO activity was observed and no phosphorus was removed in neither the anoxic nor the oxic phases. Thus, up to 27 mg PO₄⁻P·L⁻¹ were observed at the end of the oxic phase (day 2 of operation).

3.4. Assessment of the effects of the F/M ratio on the anoxic phosphorus uptake activity

In the batch activity test 1D (conducted ex situ with half of the F/M ratio applied to the parent reactor), the acetate uptake rate (qPO₄,VA) and the maximum phosphorus release rate (qPO₄,AN) were 75.2 mg COD·g⁻¹·VSS·h⁻¹ and 72.2 mg PO₄⁻P·g⁻¹·VSS·h⁻¹, respectively. These rates were considerably slower than the ones.
Table 2

<table>
<thead>
<tr>
<th>Exp. Period</th>
<th>qMAX</th>
<th>qMAX</th>
<th>qPO4</th>
<th>qPO4</th>
<th>qNOx</th>
<th>P/NOx</th>
<th>P/O2</th>
<th>VSS/TSS</th>
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<tbody>
<tr>
<td></td>
<td>mgCOD/gVSS.h</td>
<td>mgPO4-P/gVSS.h</td>
<td>mgPO4-P/gVSS.h</td>
<td>mgPO4-P/gVSS.h</td>
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<tr>
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<td>N.A</td>
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<tr>
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<tr>
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<tr>
<td>D</td>
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<td>130</td>
<td>3.8</td>
<td>0.2</td>
<td>50</td>
<td>2.5</td>
<td>0.01</td>
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<tr>
<td>E</td>
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<td>12.0</td>
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<td>79</td>
<td>2.0</td>
<td>0.13</td>
<td>0.50</td>
</tr>
<tr>
<td>F</td>
<td>210</td>
<td>164</td>
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<td>5.4</td>
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<td>N.C.</td>
</tr>
<tr>
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<td>0.3</td>
<td>3.7</td>
<td>79</td>
<td>1.8</td>
<td>0.22</td>
<td>0.43</td>
</tr>
</tbody>
</table>

- A) half F/M (37 mg COD g⁻¹ VSS) and B) twice high F/M (148 mg COD g⁻¹ VSS) ratio applied in the parent reactor.

3.5. Identification of predominant bacterial populations along the experimental periods

FISH analyses were performed to identify the predominant microorganisms present in the systems and potentially involved in EBPR over the different experimental periods. Fig. 3 shows a representative image of the microbial composition at the start and end of this research (experimental periods A and G, respectively). The relative abundance of PAOs related to the genus “Ca. Accumulibacter” (PAOmix probe set) compared to all organisms (stained with DAPI) decreased from 98%, 95%, 76%–52% along the experimental periods A, B, D and G, respectively. Despite these differences, the fraction of the “Ca. Accumulibacter” clade I (Acc-1-444 probe) within PAOs did not change along the experiments (97 ± 4%; Fig. 3). Across experimental periods, GAOs were never abundant: the genera “Ca. Competibacter” and Defluviicoccus composed less than 5% of the total microbial populations, according to both FISH (Fig. 3) and V3–V4 16S rRNA gene amplicon sequencing (Table 3).

The amplicon sequencing profiles displayed a decrease in the relative abundance of the genus “Ca. Accumulibacter” from 53% to 33% from experimental periods A to G, respectively (Table 3).

Fig. 4 shows a representative image of the microbial composition at the start and end of the experiments.

3.6. Near-complete genomes of “Ca. Accumulibacter delftensis” clade IC and two flanking populations were retrieved from the metagenome of the EBPR biomass and enabled genome-centric analysis

Three near-complete genomes were retrieved by differential coverage binning (Fig. 5A) for sub-lineages of the main gammaproteobacterial-betaproteobacteriales genus “Ca. Accumulibacter” (genomic size of 5.3 Mbp, completeness of 100%, contamination of 0.2%, GC content of 62.2%) and of the two accompanying actinobacterial genus Nocardoides (4.7 Mbp, 99.2%, 0.7%, 68.6%) and gammaproteobacterial genus Thermomonas (2.9 Mbp, 99.5%, 0.4%, 68.4%) (Table 5) from the metagenome of the EBPR biomass exposed to A/O and subsequently A/O conditions. Note that the class of Betaproteobacteria has recently been reclassified as order Betaproteobacterales in the class of Gammmaproteobacterales. Detailed features of the genome bins are provided in Fig. S1 and Table S1 of the Supplementary Information. The genome assemblies were submitted to GenBank/European Nucleotide Archive (in progress).

Phylogenetic classification of the high-quality genome assemblies against reference genomes of these lineages available in online databases allowed to delineate key populations involved in the biosystem, from alignments based on 49 highly conserved
clusters of orthologous groups of proteins. A new population of the here-proposed “Ca. Accumulibacter delftensis sp. nov.” clade IC was identified by fine-scale differentiation out of the about 30 (draft) genomes of “Ca. Accumulibacter” publicly available. The recently characterized “Ca. Accumulibacter sp. UW-LDO-IC” was the closest neighbor but formed a different phylotype inside clade IC (Fig. 5B). Computation of pairwise average nucleotide identity (ANI) scores stated the uniqueness of the candidate species “Ca. Accumulibacter delftensis” (pairwise ANI < 95%). The two main accompanying populations of the here-proposed “Ca. Nocardioides delftensis sp. nov.” and “Ca. Thermomonas delftensis sp. nov.” affiliated with closest neighbors of Nocardioides jensenii and Thermomonas fusca, respectively, but also formed new candidate species according to pairwise ANI scores (<95%). Extraction of the full-length 16S rRNA genes (Table S4) from the three genomic datasets and mapping against NCBI and ARB Silva databases provided additional verification. The digital protologue Table 5 provides the main characteristics of the near-complete genomes of these proposed, yet not-isolated, new candidate species. The ANI analysis further highlighted that several genome assemblies that have been previously deposited in databases under different reference numbers for the “Ca. Accumulibacter” lineage are overlapping (pairwise ANI > 99%). This has notably arisen from re-use of deposited sequencing data- sets in bioinformatics studies. The pangenome of ANI-filtered unique single-lineage genomes of “Ca. Accumulibacter” populations displayed diverse non-core genetic features in the assemblies (Fig. S2).

3.7. Matching of genome-based and ppk1-based phylogenetic characterizations

The phylogenetic output of the high-resolution analysis conducted on the near-complete genome of “Ca. Accumulibacter delftensis” clade IC was cross-validated to the sequencing of ppk1-gene based PCR amplicons. The sequence of the ppk1 gene retrieved from the genome assembly of “Ca. Accumulibacter delftensis” clade IC (Table S5) displayed a perfect match to the sequence of the ppk1 gene amplified from the DPAO biomass. In the functional-gene-
based phylogenetic tree, its ppk1 nucleotide composition was closely related to reference sequences of clade IC. It formed a separate population than “Ca. Accumulibacter sp. UW-LDO-IC” after comparison with the ppk1 sequence retrieved from the deposited assembly of the latter lineage. Thereafter, the genome-based and ppk1-based classification approaches matched, resulting in phylogenetic trees of analogous structures and robust molecular differentiation of the lineages.


The underlying coding sequences of the 3 retrieved near-complete genomes of “Ca. Accumulibacter delftensis”, “Ca. Nocardioides delftensis”, and “Ca. Thermomonas delftensis” were annotated and assigned to 30 functional gene categories (Table S2), including the nitrogen metabolism (Table 4 and Table S3). Functional gene annotations of the genome assemblies highlighted a putative complementary interaction between these populations along the nitrogen cycle (Table 4, and Table S3 in Supplementary Information). The “Ca. Accumulibacter delftensis” genome assembly comprised genes coding for nitrate/nitrite transporter, assimilatory nitrate reductase (nis gene), periplasmic nitrate reductase precursor, and periplasmic nitrate reductases (nap), but no genes coding for respiratory nitrate reductases (nar). It further harbored a whole set of nitrite (nir), nitric oxide (nor), and nitrous oxide (nos) reductases. The “Ca. Nocardioides delftensis” genome assembly contained assimilatory nitrate reductase, nitrate/nitrite transporter, nitrite reductase [NAD(P)H] large subunit, and respiratory nitrate reductases, but no further denitrification genes. Interestingly, the “Ca. Thermomonas delftensis” genome assembly mainly harbored respiratory nitrate reductases (alpha, beta, delta, and gamma chains), and some denitrification gene homologues (nir, nor).

4. Discussion

4.1. Effect of different operating conditions on anoxic phosphorus uptake activity

The anoxic phosphorus uptake rates observed in the experimental periods conducted under different operating conditions were considerably lower than the oxic P-uptake rates (Table 2). The anoxic P-uptake rate reached at most 13% of the oxic P-uptake rate. Thus, even though there could be some denitrification associated with an anoxic P uptake, this seems not be significant when compared with the oxic P uptake. This is in agreement with the study of Lanham et al. (2011) who observed a faster oxic than anoxic P-uptake rate in an A2O reactor. Alternatively, Kuba et al. (1993) and Lee and Yun (2014) reported that nitrate could be used as electron acceptor as efficient as oxygen by PAO for P-uptake. However, Kuba et al. (1993) and Lee and Yun (2014) have applied an A2 configuration in contrast to this study where an A2O configuration was used. This suggests that the oxic phase in each cycle may have hampered the selection for a PAO and/or a microbial population which could enhance the use nitrate as efficient oxygen for P-uptake. The aim of this study was to evaluate whether various operational conditions could enhance the denitrification capacities of a “Ca. Accumulibacter” clade I culture. Operational changes were applied for a relatively short time, allowing for the enzymatic induction but minimizing any shifts in the microbial community composition.
Fig. 5. Extraction and phylogenetic analysis of the near-complete genome of “Ca. Accumulibacter delftensis” clade IC out of the metagenome of the EBPR biomass. (A) Differential coverage plot used to extract the single-lineage genomes of “Ca. Accumulibacter delftensis” (blue scaffolds), “Ca. Nocardioides delftensis” (orange scaffolds), and “Ca. Thermomonas delftensis” (pink scaffolds) populations via the mmgenome workflow. Genome scaffolds are displayed by circles scaled by nucleotide length (bp) and colored after taxonomic classification of essential genes at phylum level. Two sequencing datasets were used here to generate the differential coverage, namely from the biomass sample directly collected from the denitrifying EBPR reactor stage (scaffold coverage 1, C166) and the wet-lab treatment of the biomass used to generate a synthetic shift in predominant populations (scaffold coverage 1, C168). Each set of isolated and colored scaffolds represent a genome. (B) Phylogenetic analysis of the near-complete genome of “Ca. Accumulibacter delftensis” clade IC highlighted in yellow against all single-lineage genomes of “Ca. Accumulibacter” populations recovered from the 28 assemblies available in on-line public databases such as NIH GenBank (GCA accession numbers), NCBI RefSeq (GCF accession numbers), and JGI MGM (Ga accession numbers). The “Ca. Accumulibacter” lineage is composed of two primary clades I (subgroups A-E) and II (subgroups A-I) (see Fig. 4). “Ca. Accumulibacter delftensis” clade IC was classified within “Ca. Accumulibacter” clade IC together with the UW-LDO-IC population characterized by Camejo et al. (2018) but remains a different phylotype, underlying the difference in denitrification patterns. The two other single-lineage near-complete genomes of “Ca. Nocardioides delftensis” and “Ca. Thermomonas delftensis” recovered from the metagenome of the EBPR biomass are also displayed on this tree (highlighted in yellow); the phylogenetic identification of these near-complete genomes is available in Fig. S2 of the supplementary information. The phylogenetic tree was computed in KBase from reference alignments based on 49 highly conserved clusters of orthologous groups of proteins and using the FastTree2 approximate maximum likelihood method. Scale bar: number of nucleotide substitutions per site. The pairwise average nucleotide identity (ANI) scores discriminates between unique genomes (ANI > 99%) and overlapping genomes (ANI < 95%). Several assemblies present in on-line databases under different registry numbers code for identical sub-lineages. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)
As the anoxic growth yield can be up to 70% of the aerobic growth yield (Kuba et al., 1993), the SRT was extended from 8 to 15 d in the experimental period D as suggested by Ahn et al. (2002). However, this exerted an adverse effect by decreasing the anoxic activity from 3.9 to 2.5 mg NO\textsubscript{3}\textsuperscript{-}/C \textsubscript{0} VSS h\textsuperscript{-}1 (experimental phase B, and D, respectively). In contrast to the studies of Kuba et al. (1993) and Ahn et al. (2002), a clear anoxic P-uptake was never observed. It may be concluded that either the denitrification activity observed in this study was not carried out by the “Ca. Accumulibacter” population selected in this system, or the culture was not capable to restore its poly-P storage pools under the applied conditions. Further activity tests with the biomass of experimental period D showed that under a low F/M ratio, phosphate was surprisingly released under anoxic conditions at a rate of 2.7 mg PO\textsubscript{4}\textsubscript{-}/C \textsubscript{0} VSS h\textsuperscript{-1}. Despite that nitrate was present in the activity test (Fig. 2A), the release of phosphate strongly suggests that the “Ca. Accumulibacter” affiliate of clade IC obtained in this enrichment culture could not use nitrate as electron acceptor to generate enough energy from its putative reduction. Thus, as suggested by Rubio-Rincón et al. (2017a) and Ribera-Guardia et al. (2016), this PAO may prefer to use nitrite (generated by side populations, among them possibly GA0s, via the reduction of nitrate to nitrite) as electron acceptor for the anaerobic oxidation of poly-P. The nitrite produced by side populations would be lower according to a decrease in the organic load per biomass (F/M), resulting in energy limitation by the oxidation of PHA by PAOs and a subsequent anoxic P-release as observed in Fig. 2A.

To further assess if a side population was responsible for the denitrification observed in the system, the P/COD ratio in the influent was decreased with the aim to increase the GA0 fraction from experimental period F onwards. The population of “Ca. Accumulibacter” clade IC remained the main PAO detected (approx. 97 ± 4%) but decreased from 98% to 52% from experimental periods A to G (Fig. 3), similar to the study of Carvalho et al. (2007). However, GA0s did not proliferate as expected (up to 1% in the experimental period G; Fig. 3). Likely, the relatively high pH of 7.6 limited the proliferation of GA0s (Smolders et al., 1995). At the same time, after the switch from A/O to A\textsubscript{2}O conditions, an increase in the fraction of potentially denitrifying Thermomonas and Chryseobacterium genera was observed (13% and 8%, respectively, in experimental period G; Table 3). Despite that Thermomonas and Chryseobacterium are capable to reduce both nitrate and nitrite (Mergaert et al., 2003; Kundu et al., 2014), the biomass-specific denitrification activity did not increase together with their enrichment (2.1 and 1.8 mg NO\textsubscript{3}\textsuperscript{-}/C \textsubscript{0} VSS h\textsuperscript{-1} in experimental periods F and G, respectively). The non-PAO-based denitrification activity measured in the system remained uncertain.

Additional analyses of mRNA-based functional gene expression or protein translation within the nitrogen cycle either via reverse transcription and qPCR or higher-throughput molecular analyses like metatranscriptomics and metaproteomics, respectively, would have helped to identify the biochemical pathways activated together with the bacterial populations involved. The role of the side populations within the microbial community (e.g., Thermomonas, Flavobacterium, Chryseobacterium, Terrimonas, Nocardioides) remains also unclear. Under the operating conditions applied here, they did not significantly contribute to the denitrification activity. This suggests that other factors or microorganisms interact and can (e.g., GA0s were suggested by Rubio-Rincón et al. (2017a)) enhance the anoxic P-uptake activity over nitrite in EBPR cultures. Kuba et al. (1993) enriched a DPAO culture under A\textsubscript{2}O conditions, dosing nitrate continuously during the anoxic stage. This dosing mode could benefit k-strategist DPAOs. Therefore, in period G, nitrate was dosed continuously during the anoxic phase as described earlier. Certain increase in the anoxic P-uptake per electron available was observed from 0.13 to 0.24 mol P mol\textsuperscript{-1} e\textsuperscript{-} (between periods F and G, respectively). The anoxic range from 0.13 to 0.24 mol P mol\textsuperscript{-1} e\textsuperscript{-} ratio observed along this study was comparable to the one of 0.19 mol P mol\textsuperscript{-1} e\textsuperscript{-} reported by Kuba et al. (1993). However, the anoxic P-uptake rate was slower than the reported by Kuba et al. (1993) (up to 5.4 mg PO\textsubscript{4}\textsuperscript{-}/P g \textsuperscript{-1} VSS h\textsuperscript{-1} compared to 30–46 mg PO\textsubscript{4}\textsuperscript{-}/P g \textsuperscript{-1} VSS h\textsuperscript{-1}, respectively). This indicated that the dosing mode did not play a role to enhance the anoxic phosphorus uptake activity of the sludge.

As an attempt to favor the growth of DPAOs over strict aerobic PAOs, the operational conditions were gradually modified from anaerobic-anoxic-oxic to anaerobic-anoxic (experimental periods G and H). However, once the aerobic SRT was reduced below the minimal required, acetate started to leak into the anoxic phase (after just 2 days of operation). Despite that nitrate was not limiting, likely PHAs were not completely oxidized during the anoxic and oxic phases. Thus, PAOs could not take up sufficient phosphorus or produce enough glycogen for anaerobic VFA uptake. This is in agreement with Lanham et al. (2011) who concluded that anoxic phase was essential to maintain a good removal of phosphorus, where most of the phosphorus uptake occurred. Therefore, it is suggested that the culture of “Ca. Accumulibacter delftensis” clade IC enriched in this study cannot solely rely on the use of nitrate for energy generation for metabolic processes (e.g., via PHA oxidation).

Recently, in contrast with these findings and those of Saad et al. (2016), where no significant anoxic phosphorus uptake was observed, Camejo et al. (2016) reported the anoxic P-uptake activity on nitrate (11 ± 1.7 mg PO\textsubscript{4}\textsuperscript{-}/P g \textsuperscript{-1} VSS h\textsuperscript{-1}) of a “Ca. Accumulibacter” clade IC culture. However, functional diversity in sub-lineages can happen, making that the pkp analysis cannot be used to anticipate denitrification capabilities. Hence, as discussed in the following sections, the correlates of differences in pppk1-based taxonomic classification and denitrification activities monitored in EBPR systems is no longer valid. The sole detection of microbial clades is not sufficient to explain biochemical conversions.

The genome-centric metagenomics analysis of the near-complete genomes of the “Ca. Accumulibacter delftensis” clade IC and “Ca. Thermomonas delftensis” lineages of the EBPR biomass subjected to A/O and A\textsubscript{2}O conditions interestingly highlighted a putative interaction potential between the two populations from nitrate reduction to nitrite by Thermomonas (harbors genes coding for respiratory nitrate reductases, nar but genes for nitrite reduction were not found in the assembly) prior to respiration of nitrite by “Ca. Accumulibacter” along with P-removal. The “Ca. Nocardioides delftensis” lineage harbored functional genes for both nitrate and nitrite respiration. The involvement of this population that can display filamentous phenotypes is supposed to primarily occur under disturbed conditions like those where VFA leak into the anoxic stage. These functional potentials underlie hypothetical interactions between “Ca. Accumulibacter” and these accompanying populations in the nitrogen cycle within the ecosystem of lab-scale denitrifying EBPR biomass. However, the previously proposed reduction mechanism from nitrate to nitrite performed by Thermomonas and/or Nocardioides might be conducted by other organisms in full-scale wastewater treatment plants. Further research and analytical methods are needed to elucidate microbial interactions between “Ca. Accumulibacter” and other genera (e.g., “Ca. Competibacter”, Thermomonas, Nocardioides, “Ca. Microthrix”) on the nitrogen cycle.

4.2. Possible metabolic pathway for nitrate reduction observed in this study

Only a marginal nitrate consumption of up to 3.9 mg NO\textsubscript{3}\textsuperscript{-}/N g \textsuperscript{-1}
VSS $h^{-1}$ was observed in the enriched “Ca. Accumulibacter” IC culture (experimental period B). Alternatively to the role of side-populations, the consumption of nitrate can be associated to growth (nitrate assimilation; Nas), generation of metabolic energy (nitrate respiration; Nar) and/or dissipation of the excess of reducing power (nitrate dissimilation; Nap) (Moreno-Vivian et al., 1999). According to previous studies (Skennerton et al., 2014) different clades of “Ca. Accumulibacter” contain either the nitrate respiration gene (nar; clade IIC) or the periplasmatic nitrate dissimilation gene (nap; clades IC, IA, IIA, IIF). Only the nap gene has been previously identified in the metagenomes of enriched EBPR cultures composed of the clades IA and IC (Flowers et al., 2013; Table 4).

### Functional signatures of the nitrogen cycle detected in single-lineage near-complete genomes (27 / 170 entries)$^a$

<table>
<thead>
<tr>
<th>Functional category</th>
<th>Entries</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nitrogen fixation</td>
<td>2 / 43 entries</td>
</tr>
<tr>
<td>Ammonia assimilation</td>
<td>12 / 24 entries</td>
</tr>
<tr>
<td>Nitric oxide reductase</td>
<td>10 / 11 entries</td>
</tr>
<tr>
<td>Denitrification</td>
<td>11 / 21 entries</td>
</tr>
<tr>
<td>Nitrate and nitrite ammonification</td>
<td>15 / 37 entries</td>
</tr>
</tbody>
</table>

$^a$ Number of entries reported across functional categories of the nitrogen metabolism. 57 different genes detected over a maximum possible total of 170

$^b$ Total of instances (sum of gene copies) detected per functional category

$^c$ Number of instances (gene copies) detected for each functional gene entry (line)

$^d$ Number of single entries detected among the total number of single entries per functional category.
From the nitrogen cycle perspective, the two most characterized clades IC and IC harbored \( \text{n} \) and \( \text{nap} \) genes but not the \( \text{nar} \) gene (Table 4), which could explain the low anoxic P-uptake activity measured in the bioreactor. Camejo et al. (2016) have suggested that an enriched clade IC population of \( \text{Ca. Accumulibacter sp. UW-LDO-IC} \) harbored \( \text{napA} \) and \( \text{napB} \) genes but not the \( \text{napC} \) gene, which seems to be an important precursor of the subunit NapA (Moreno-Vivián et al., 1999) was not detected in the genome assembly of \( \text{Ca. Accumulibacter delftensis} \) (Table S3 in Supporting Information). This is notable since \( \text{napA} \) that is responsible for the reduction of nitrate to nitrite can likely not be responsible for the reduction of nitrate to nitrite can likely not be promoted in absence of \( \text{napD} \). As described by Moreno-Vivián et al. (1999), the Nap enzyme is not involved in the anaerobic respiration as the enzyme is independent of the energy conserving cyctochrome \( b \) complex. Instead, the electron required for the reduction of nitrate can be obtained via NADH, which passes through proton translocating NADH dehydrogenases (Bedzyk et al., 1999). Interestingly, the subunit \( \text{napD} \) which seems to be an important precursor of the subunit NapA (Moreno-Vivián et al., 1999) was not detected in the genome assembly of \( \text{Ca. Accumulibacter delftensis} \) (Table S3 in Supporting Information). This is notable since \( \text{napA} \) that is responsible for the reduction of nitrate to nitrite can likely not be promoted in absence of \( \text{napD} \). Thus, based on such genetic impo}
absence of nar gene in the genome assembly underlines that this functionality cannot be achieved by the selected “Ca. Accumulibacter delftensis” clade IC.

Regarding the current molecular techniques applied, based on fine-scale genetic analyses of the ppk1 gene, it is possible to differentiate among the “Ca. Accumulibacter” lineages (McMahon et al., 2007). Despite the general correlative assumptions that these clades seem to have the same encoding for denitriﬁcation, they exhibit different anoxic P-uptake capabilities on nitrate (e.g., anoxic activities of clades IC and IIA) (García Martín et al., 2006; Flowers et al., 2008, 2013; Oehmen et al., 2010b, 2010c; Skennerton et al., 2014; Camejo et al., 2016, 2018; Ribera-Guardia et al., 2016; and this study). In view of these observations, the traditionally accepted engineering classiﬁcation of the denitriﬁying populations of “Ca. Accumulibacter” grouped based on the ppk gene as either clade I (“with full denitriﬁcation capacity from nitrate onwards”) or clade II (“from nitrite onwards”) as modeled by Oehmen et al. (2010c) does not seem to be valid and supported as a stand-alone approach. Further studies should include detection and expression of the key denitriﬁing genes (e.g., nar) or proteins (e.g., Nar), in addition to the clade differentiation using the ppk marker gene. It should be thoroughly investigated how different operating conditions (e.g., pH or the selection of DPAOs, the activation of their genetic signatures, and their catabolic regulation depending on terminal electron acceptors available. The inﬂuence of environmental and operational conditions on the gene regulation (Skennerton et al., 2014) and their interaction with the different metabolic pathways and energy consumption deserve special attention.

Definitely, microbial ecology have suggested that many functional traits are not necessarily conserved between lineages (Martiny et al., 2015). Ancestral genome reconstructions have shown that denitriﬁcation genes are part of the ﬂexible genome, and that numerous other important genes of EBPR metabolisms have been acquired by horizontal transfer (Oyserman et al., 2016). Hence, the incongruency between studies on denitriﬁcation traits of “Ca. Accumulibacter” clades does reﬂect the true intra-clade diversity, which requires thorough investigation within the “Ca. Accumulibacter” lineage. This statement can be broadened over the complexity of clades of heterotrophic denitriﬁers, whose genetic pools may result from a rather random acquisition process. Certainly, the concepts and justiﬁcation of clades need strong reappraisal across microbial tree of life (Parks et al., 2017) toward a more accurate representation of actual metabolisms, together with consideration of horizontal transfer of catabolic genes in activated sludge microorganisms.

4.3. Possible sources of carbon for denitriﬁcation by side populations

If ultimately the selected DPAOs are not able to denitriﬁy from nitrate at relevant and applicable rates, it remains possible that the denitriﬁcation observed in EBPR systems is carried out partially (from nitrate to nitrite) by other microbial populations. However, such potential heterotrophic denitriﬁers should be provided with electron donors. This adds up to the former questions regarding the factors (e.g., organic substrate availability and substrate storage under anaerobic conditions) and underlying the presence of a diversity of potential denitriﬁers in the bacterial community of EBPR processes (Weissbrodt et al., 2014). Previous research on EBPR have reported the leakage of certain residual concentrations of (non-VFA) organic compounds as a function of the HRT (Ichihashi et al., 2006). The residual organic compounds present in the anoxic stage could be potentially used by ordinary heterotrophic organisms (OHOs) as carbon source for denitriﬁcation purposes. Kuba et al. (1993) have observed around 5 mg TOC L⁻¹ leaking into an anoxic phase, which have led to up to 3.8 mg NO₃⁻N L⁻¹ reduction (if nitrate was reduced to nitrite). Moreover, nitrate (from anoxic zones) can also intrude into anaerobic stages (via internal recirculation ﬂowrates or due to the residual concentrations of these components observed in the end of the alternating aerobic or anaerobic phases), independently of the experimental periods. Thus, OHOs could grow in the system on the VFAs fed and nitrate available contributing to the direct denitriﬁcation from nitrate to nitrite and even in the subsequent anoxic phase triggered by the endogenous processes. In some cases, the presence of nitrate in anaerobic stages have nevertheless been reported to favor the growth of DPAOs in EBPR systems (Ahn et al., 2001b).

Another possibility is the potential presence of other microorganisms capable to store VFAs under anaerobic conditions and then to oxidize them using nitrate. Tu and Schuler (2013) proposed that under carbon limiting conditions PAOs would outcompete other PHA-accumulating organisms such as GAOs. This could be the case in the activity test 1 D performed here with half the organic loading per biomass (Fig. 2A), where a denitriﬁcation rate of 0.8 mg NO₃⁻N g⁻¹ VSS h⁻¹ was observed together with an anoxic P-release rate of 2.7 mg PO₄-P g⁻¹ VSS h⁻¹. On the contrary, in the activity test 2D conducted with double the organic loading per biomass, a denitriﬁcation rate of 1.95 mg NO₃⁻N g⁻¹ VSS h⁻¹ with an anoxic phosphorus uptake rate of 0.7 mg PO₄-P g⁻¹ VSS h⁻¹ were observed. Thus, it is suggested that the anoxic P-uptake observed in this study was carried out over the nitrite generated by other PHA-accumulating organisms that might have beneﬁted from the relatively higher availability of electron donors.

Ekama and Wentzel (1999) pointed out that alternating anoxic-oxidic conditions stimulated the presence of filamentous bacteria. The appearance of filamentous bacteria has also been reported in the studies of Kern-Jespersen and Henze (1993) and comprised up to 10% of the biomass in the studies of Lanham et al. (2011). Early studies of Kuba et al. (1993) also reported considerable amounts of sludge washed out through the efﬂuent due to settling problems, suggesting the presence of filamentous bacteria. These filamentous bacteria (as the frequently observed Thiothrix (type 021N) or and “Ca. Microthrix” in wastewater treatment plants) can reduce nitrate into nitrite (Williams and Unz, 1985; Nielsen et al., 2000; Hesselsoe et al., 2005; McIlroy et al., 2013) and have also been identiﬁed as one of the most abundant side populations present in EBPR lab-systems (Garcia-Martin et al., 2006). Interestingly, recently some of these (e.g., Thiothrix) have been reported to also contribute to EBPR (Rubio-Ríncon et al., 2017b). Further characterization of the metabolisms of the side populations is needed to elucidate their potential involvement in the anoxic P-uptake activities of EBPR cultures.

5. Conclusions

The “Ca. Accumulibacter delftensis” clade IC culture enriched and genetically characterized in this study did not exhibit a considerable anoxic P-uptake on nitrate: it was as high as 13% of the phosphorus uptake observed under aerobic conditions. A decrease in the organic load fed per biomass resulted in the anoxic release of phosphorus, indicating that this speciﬁc population of the clade IC was unable to use nitrate as electron acceptor. Eventually, the system collapsed when the aerobic SRT decreased below the minum required, reinforcing the idea that our clade IC cannot rely solely on the use of nitrate as terminal electron acceptor. The putative complementary interaction potential between side populations of the genera Thermomonas and Nocardioiides (nitrate respiration) and the “Ca. Accumulibacter” population (nitrite respiration) was highlighted from single-lineage genome
assemblies extracted from the biomass subjected to A/O and A2O conditions. We further showed that genome-based and ppk1 gene-based phylogenies were congruent for the classification of known populations within the “Ca. Accumulibacter” lineage, with genome-centric metagenomics approach providing definite advantage to capture functional potential of the phylotypes. Next research should target functional expression and ecophysiological analyses to validate actual biochemical pathways involved by targeted populations, together with microbial interactions in denitrifying EBPR systems. We here stressed that correlating denitrifying activities to “Ca. Accumulibacter” clade differentiation by ppk gene is not valid. Deep reconsideration of the true intra-clade diversity in functional traits, that results from evolutionary and horizontal gene transfer processes, is paramount.

6. Nucleotide sequence accession numbers

The ppk1 gene sequences obtained in this study were deposited in the GenBank database under accession numbers MK044800-MK044801-MH899086. The 16S-rRNA gene amplicon libraries have been deposited as a SRA archive under project PRJNA495757. The genome assemblies are deposited on KBase, and are submitted to GenBank/ENA (in progress). The sequences of the full-length 16S rRNA gene and of the ppk1 retrieved from the genomes are submitted to GenBank/ENA (in progress).

Acknowledgements

The authors acknowledge Jane Ildal and Søren Karst for excellent wet-lab hints provided to David Weissbrodt at Aalborg University on the preparation and sequencing of the metagenome libraries. Special thanks to Jack van de Vossenberg and Leonor Guedes da Silva for the discussions and input. The authors would like to acknowledge the lab staff from IHE-Delft, and the TU Delft which continuously helped our research.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jwires.2019.03.053.

7. Declaration of interests

☐ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References


