The META-ASM model: a novel approach for modelling EBPR systems

Jorge Santos[1], Leiv Rieger[2], Ana B. Lanham[3] and Adrian Oehmen[1]

[1] UCIBIO, REQUIMTE, Departamento de Química, Faculdade de Ciências e Tecnologia, Universidade NOVA de Lisboa, Campus de Caparica, 2829-516 Caparica, Portugal (jmm.santos@campus.fct.unl.pt; a.oehmen@fct.unl.pt);
[2] inCTRL Solutions Inc., ON, Canada (rieger@inCTRL.ca);
[3] Water Innovation and Research Centre, University of Bath, U.K. (a.lanham@bath.ac.uk)

Abstract
This study demonstrates that META-ASM, a new integrated metabolic activated sludge model, provides an overall platform to describe the activity of the key organisms and processes relevant to Enhanced Biological Phosphorus Removal (EBPR) systems with robust default parameters. This model overcomes various shortcomings of existing EBPR models and has been tested against full-scale data. The META-ASM model is a useful tool to predict and mitigate EBPR upsets, optimise EBPR performance and to design new process configurations.

Keywords
Enhanced biological phosphorous removal (EBPR), metabolic modelling, microbial competition

INTRODUCTION

Enhanced biological phosphorous removal (EBPR) is a cost-effective and environmentally sustainable option for P removal and recovery. However, these systems are highly affected by conditions that lead to EBPR failure and the current models have not been able to predict and control process upsets (Menniti et al., 2016). In recent years, several studies have improved the understanding of the mechanisms behind microbial population dynamics as a function of operational conditions and suggested modifications to the currently available models. Examples of these developments include the description of various types of EBPR organisms (e.g. *Accumulibacter* type I and type II) and their competition with other bacterial populations (such as glycogen accumulating organisms, GAOs) (Oehmen et al., 2010), substrate preferences by the different organisms (Carvalheira et al., 2014a; Lopez-Vazquez et al., 2009), internal storage pool limitations (Carvalheira et al., 2014b; Lanham et al., 2014), denitrifying capabilities (Skennerton et al., 2015) and the effect of low dissolved oxygen concentrations on EBPR performance (Carvalheira et al., 2014c). Despite this available knowledge, such modifications have never been previously integrated into an overall activated sludge model to predict EBPR performance as a function of these conditions.

This work presents an integrated metabolic activated sludge model (referred to as META-ASM hereafter). The approach followed to develop this model was to: 1) combine two model approaches, the heterotrophic, hydrolytic and autotrophic processes from published activated sludge models (ASMs) and the EBPR processes from metabolic models (Lanham et al., 2014; Lopez-Vazquez et al., 2009; Oehmen et al., 2010); 2) identify their limitations; 3) gather information from targeted experiments and available literature to overcome these limitations; 4) reformulate and develop a new structure for the biokinetic model; 5) calibrate with different laboratory and pilot data sets and 6) validate through long-term simulation of full-scale systems.

MODEL DESCRIPTION

The META-ASM model was implemented in SIMBA# (ifak, Germany) and describes the simultaneous removal of COD, N and P. The activity of the following six microbial groups are described: the ordinary heterotrophic organisms (X_{OHO}), the ammonia oxidizing organisms (X_{AOO}), the nitrite oxidizing organisms (X_{NOO}), *Accumulibacter* PAOs (X_{PAO}), *Competibacter* GAOs (X_{CPO}) and *Defluviicoccus vanus* GAOs (X_{DFO}).

MODEL CALIBRATION AND VALIDATION

The kinetic parameters of the PAO-GAO metabolic model were the only parameters calibrated and validated in this study (Table 1) through the simulation of the experimental results obtained from: 1) lab-scale enriched PAO-GAO cultures described in Carvalheira et al. (2014a) and Carvalheira et al. (2014c) fed with different ratios of acetate to propionate and operated under different dissolved oxygen concentrations, respectively and 2) batch tests inoculated with full-scale sludge of 4 water resource recovery facilities (WRRFs) from Portugal and Denmark described in Lanham et al. (2014). Figure 1 shows that META-ASM is a robust and reliable model since the model was able to describe different case-studies using as default parameters the mean values determined for the kinetic rates during the calibration process. This validation highlights the utility of the META-ASM model to describe EBPR systems with a unique set of kinetic parameters, minimising or even eliminating the need for laborious calibration procedures. The kinetic rates for GAOs will be shown in the full paper. Long-term simulations of full-scale systems are ongoing and will also be demonstrated, under the scope of EU's H2020 project, SMART-PLANT.

TAKE HOME-MESSAGE

The META-ASM model summarises the current state-of-knowledge of EBPR systems. It has the capability of predicting EBPR upsets caused frequently by PAO-GAO competition, high environmental temperatures, high COD/P and acetate/propionate ratios in the influent, high dissolved oxygen concentrations and low organic loading or starvation conditions commonly observed in WRRFs. The default parameters of META-ASM are robust, as demonstrated by applying the model in different case-studies, reducing the need for model calibration. The META-ASM has been applied successfully to different EBPR process configurations including new process configurations (e.g. denitrifying PAO systems, side stream EBPR systems and P recovery), optimisation of energetic costs (e.g. low aeration systems) and the development of more efficient and robust control solutions.

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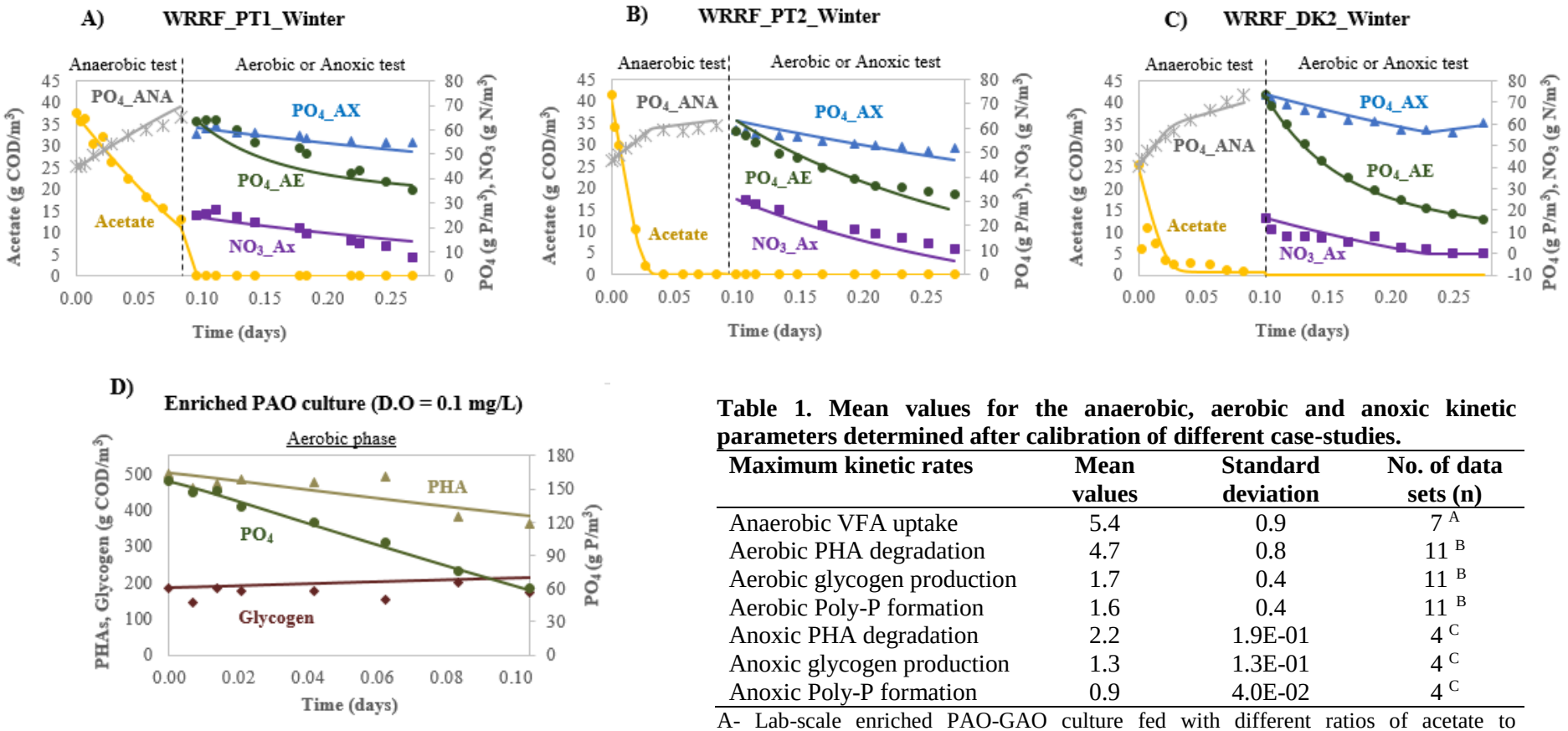

Figure 1. META-ASM model validation in different case-studies described in Lanham et al. (2014) (A, B, C) and in Carvalheira et al. (2014c) (D). A) WRRF from Beirolas, Portugal; B) WRRF from Setúbal, Portugal; C) WRRF from Aalborg East (Denmark) and D) lab-scale enriched PAO culture operated under low dissolved oxygen (D.O) concentrations (0.1 mg O_2/L). In these simulations the mean values defined in Table 1 were used as default parameters. Experimental results (symbols) and model descriptions (solid lines). ANA-anaerobic, AX- anoxic and AE-aerobic.

Table 1. Mean values for the anaerobic, aerobic and anoxic kinetic parameters determined after calibration of different case-studies.

Maximum kinetic rates	Mean values	Standard deviation	No. of data sets (n)
Anaerobic VFA uptake	5.4	0.9	7 [A]
Aerobic PHA degradation	4.7	0.8	11 [B]
Aerobic glycogen production	1.7	0.4	11 [B]
Aerobic Poly-P formation	1.6	0.4	11 [B]
Anoxic PHA degradation	2.2	1.9E-01	4 [C]
Anoxic glycogen production	1.3	1.3E-01	4 [C]
Anoxic Poly-P formation	0.9	4.0E-02	4 [C]

A- Lab-scale enriched PAO-GAO culture fed with different ratios of acetate to propionate (n=3) (Carvalheira et al., 2014a) and batch tests inoculated with full-scale sludge (n=4) (Lanham et al., 2014);
B- Lab-scale enriched PAO-GAO culture operated under different dissolved oxygen concentration, from 7.8 to 0.1 mg O_2/L (n=7) (Carvalheira et al., 2014c) and batch tests inoculated with full-scale sludge (n=4) (Lanham et al., 2014);
C- Batch tests inoculated with full-scale sludge (n=4) (Lanham et al., 2014).