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Keywords: biodegradation kinetics; CH4 concentration; methanotroph; microbial population structure; polyhydroxyalkanoate.

Corresponding Author: Dr. Raul Munoz, PhD

Corresponding Author's Institution: Valladolid University

First Author: Juan C López, PhD student

Order of Authors: Juan C López, PhD student; Guillermo Quijano, PhD; Rebeca Pérez, PhD; Raul Munoz, PhD



Prof. Berrin Tansel Civil and Environmental Engineering Department Florida International University, USA

Dear Editor,

Please find enclosed the revised version of the paper "Assesing the influence of CH₄ concentration during culture enrichment on the biodegradation kinetics and population structure" co-authored by Juan C. López, Guillermo Quijano, Rebeca Pérez and Raúl Muñoz. The manuscript is submitted for publication in Journal of Environmental Management considering that is the best-suited journal for the research area of the present work (subject classification code: 100, Biofiltration), according to the mutually agreement of the four authors. The manuscript contains 5512 words including the main text and references (figures and tables were excluded).

The present work assessed the influence of the concentration of the greenhouse gas CH₄ during enrichment on the CH₄ biodegradation kinetics, microbial population structure and ability to couple CH₄ abatement to polyhydroxyalkanoate (PHA) production. Methanotrophic consortia with high species evenness/richness, as well as high specific biodegradation rates and affinities for CH₄ were enriched in the stirred tank reactors regardless of the CH₄ concentration. Culture enrichment under sequential N limitations did not promote the accumulation of polyhydroxybutyrate (PHB) in the cultures, with the maximum PHB cell contents achieved under exposure to higher CH₄/biomass ratios. Type I methanotrophs were dominant in the cultures enriched at the three concentrations tested, which explains the high CH₄ biodegradation potencial of the cultures with lower PHB cell contents presented a higher polyhydroxyvalerate (PHV) content.

We are confident this paper will make a very significant contribution to this journal and will attract international attention.

We look forward to your evaluation. Best regards,

Juan C. López

Raúl Muñoz





Prof. Berrin Tansel Civil and Environmental Engineering Department Florida International University, USA

Ms. Ref. No. JEMA-D-14-01208 "Assessing the influence of CH₄ concentration during culture enrichment on the biodegradation kinetics and population structure" submitted for publication in Journal of Environmental Management.

Dear editor,

The authors would like to thank you for the attention given to our manuscript during this peerreview process. The manuscript has been carefully revised and modified in accordance to your requests and most reviewer's recommendations and comments. More specifically:

COMMENTS BY THE EDITOR

1. Due to space limitations in the printed journal, we are requesting that all authors reduce the length of their papers by at least 10% if possible. If your paper includes large tables or datasets, it is preferred that these be published as supplementary material in Science Direct rather than in print.

The length of the manuscript was reduced from 6721 to 6003 words in accordance to the Editor's request. Former Table 1 was moved to the Supplementary Material section. Former Table 2 was consequently renamed in the current version of the manuscript as Table 1.

2. When submitting your revised paper, we ask that you include the following items: Manuscript and Figure Source Files (mandatory), Highlights (mandatory), Graphical Abstract (optional).

A graphical abstract was included in the revised version of the manuscript as suggested by the Editor:



3. Highlights: Please place a period at the end of each sentence.

A period was placed at the end of each sentence in the Highlights section.

4. References should be prepared according to the author guidelines provided at the journal web site. Please note that journal names should be abbreviated according to the ISI format. Volume numbers should be removed as appropriate. Abbreviated words should have a period. There are some inconsistencies and inaccuracies in punctuation and abbreviations for journal names in the references section. The authors should carefully check the accuracy of the references and ensure that they are prepared according to the JEM style requirements before resubmitting.

The References section was carefully revised and modified according to the author guidelines of Journal of Environmental Management.

5. Fig. 1. Some print size is too small. Fonts and font size used in figures should be legible after 1/4th reduction.

Font sizes of Figure 1 were increased resulting in a legible version for the readers:



6. Tables should be prepared in 3-line format (if possible using 3 horizontal lines). Lines between the similar rows should be eliminated if they are not providing additional clarification or categorization.

The current Tables were prepared in 3-line format as recommended by the Editor.

REVIEWER 1

1. I am not sure whether all the references are actually referred to.

The match between the references cited in the text and in the References section was carefully revised and modified accordingly. In addition, the reference format was carefully checked and updated according to the JEM style requirements.

2. In the text a list of abbreviations would be helpful.

The authors agree with Reviewer 1 and included a list of abbreviations in the current version of the manuscript (current line 422):

Nomenc	clature	
STR	Stirred tank reactor	
VOC	Volatile organic compound	
PHB	Poly-3-hydroxybutyrate	
PHV	Poly-3-hydroxyvalerate	
TSS	Total suspended solids (g L^{-1})	
TOC	Total organic carbon (mg L^{-1})	
Н	Shannon-Wiener diversity index (dimensionless)	
K _S	Half-saturation constant (M)	
q _{max}	Maximum specific biodegradation rate (gCH ₄ g ⁻¹ _{biomass} h ⁻¹)	

3. Can you analyse in a paragraph whether the CH_4 levels you established would be typical for any type of wastewater (landfill leachate, water in sewers, ...). When would one go for decomposition of CH_4 , when for using it, e. g. to provide heat and/or electricity?

Please note that the CH₄ concentrations used in the three STRs (0.2, 2 and 20 g m⁻³) are in the range of those emissions found in wastewater treatment facilities (0-0.2 g m⁻³), mines and old landfills (up to 100 g m⁻³) (former lines 37-40 and 64-66).

On the other hand, the authors agree with the rationale presented by Reviewer 1 regarding the fact that a CH_4 concentration limit for energy production purposes should be established. A threshold value of 400 g m⁻³ was included in current lines 47-50:

"Moreover, the gradual application of the EU landfill Directive 1999/31 will result in emissions with lower CH_4 concentrations, which will significantly restrict the implementation of CH_4 abatement technologies based on energy recovery (applied at CH_4 concentrations higher than ~400 g m⁻³)."

4. What is the realistic perspective for PHB and/or PHV recovery?

The recovery of polyhydroxyalkanoates such as PHB or PHV includes downstream processes (pretreatment, extraction and purification) which account for up to 50% of the overall production costs. A deeper analysis on the economics of PHA production from CH_4 emissions is clearly out of the scope of this work, which was more related to the acquisition of fundamental knowledge. The economics of PHB/PHV recovery should evaluate the feasibility of different downstream processes such as extraction with solvents or enzymes. Please note that no additional discussion was added in the revised version of the paper addressing this issue, since the Editor asked for reducing the length of the manuscript, and this topic was not essential to understand the main outcomes of the study.

5. Rotation speed of stirrer at 250 rpm: is this speed not a bit high? Can you explain?

Please note that the magnetic stirring provided in our setup did not cause a detrimental shear stress in the bacterial communities as the magnetic stir bar was placed at the bottom of the bioreactors (see current Figure 1). Since CH_4 is a poorly water soluble pollutant, this agitation rate was set to improve the gas/liquid mass transfer of CH_4 .

6. The conclusions are very brief. Could you include:

- Whether biodegradation changes depending on the variables under study
- What the adaptation of population actually means for capability to biodegrade
- What the relation of your findings to environmental management is: regarding climate change, regarding implications for wastewater treatment, etc.
- Any conclusions, how PHB, PHV production could increased: like simultaneous extraction of products via membranes, etc.
- Any practical or economic potential in applying your findings?

The authors agree with Reviewer 1 and the Conclusions section was modified accordingly in order to include information about the important topics mentioned above (current lines 400-413):

"The analysis of the pair-wise similarity indexes clearly showed that CH₄ concentration during culture enrichment determined the structure of the microbial populations, which exhibited rapid dynamics and high species evenness and richness. In addition, kinetic assays revealed high specific

biodegradation capacities and affinities for CH₄, correlated to the dominance of type I/II methanotrophs rather than to CH₄ concentration. On the other hand, the use of sequential N limitations under continuous CH₄-laden air flow did not promote a high PHB accumulation in the cultures likely due to the low abundance of type II methanotrophs. Interestingly, the communities with lower PHB contents exhibited higher PHV contents. These findings brought new insights on the development of specific inocula not only to reduce the start-up period of bioreactors devoted to CH₄ abatement, but also to co-produce high-added value products. Although further experiments on optimizing the conditions for PHB/PHV production are still necessary, the industrial use of these high-added value products will certainly promote the application of biological processes for GHG emissions abatement.

We hope that these modifications will comply with the requests of the editor and the reviewer. Please do not hesitate to contact us at your convenience if you need further information.

Juan Carlos López

Raúl Muñoz



Highlights

- ✓ The enriched methanotrophic communities exhibited high species evenness and richness.
- \checkmark CH₄ concentration significantly influenced the microbial population structure.
- ✓ Dominance of type I methanotrophs regardless of the CH₄ concentration.
- $\checkmark~$ The enriched methanotrophs exhibited high q_{max} and low K_S values.
- ✓ Maximum PHB cell contents were achieved by increasing CH₄/biomass ratio.

1	Assessing the influence of CH ₄ concentration during culture
2	enrichment on the biodegradation kinetics and population structure
3	
4	Juan C. López, Guillermo Quijano, Rebeca Pérez, Raúl Muñoz *
5	
6	Department of Chemical Engineering and Environmental Technology, University of
7	Valladolid, Dr. Mergelina, s/n. 47011, Valladolid, Spain, Tel. +34 983186424, Fax:
8	983423013
9	<i>y</i> 03123013.
10	*Corresponding author: mutora@ig.uva.es
11	Corresponding aution. <u>matora e quava es</u>
12	Abstract
13	Methanotrophic communities were enriched in three stirred tank reactors continuously
14	supplied with CH ₄ -laden air at 20, 2 and 0.2 gCH ₄ m ⁻³ in order to evaluate the influence
15	of CH_4 concentration on the biodegradation kinetics, population structure and potential
16	polyhydroxyalkanoate production under sequential nitrogen limitations. The population
17	structure of the enriched cultures, dominated by type I methanotrophs, was influenced
18	by CH ₄ concentration. No significant correlation between CH ₄ concentration and the
19	maximum specific degradation rate (q_{max}) or the half-saturation constant (K_s) was
20	recorded, microorganisms enriched at 2 gCH ₄ m ⁻³ presenting the highest q_{max} and those
21	enriched at 20 and 0.2 gCH ₄ m ⁻³ exhibiting the lowest K _s . Maximum
22	polyhydroxybutyrate contents of 1.0% and 12.6% (w/w) were achieved at 20 and 2 g
23	CH ₄ m ⁻³ , respectively. Polyhydroxyvalerate was also detected at PHV:PHB ratios of up
24	to 12:1 and 4:1 in the communities enriched at 20 and 0.2 gCH ₄ m ⁻³ , respectively.
25	

Keywords: biodegradation kinetics, CH₄ concentration, methanotroph, microbial
population structure, polyhydroxyalkanoate.

1. Introduction

Methane (CH₄) contributes to approximately 20% of the worldwide greenhouse gas (GHG) emissions, with an atmospheric concentration increase of 150% from the pre-industrial era to 2011 (EPA, 2013; IPCC, 2013). CH₄ presents a global warming potential 25 times higher than that of CO₂ (excluding additional harmful effects of water vapour production from CH₄ breakdown) and is mainly emitted from organic waste treatment activities such as landfilling, composting and wastewater treatment (122 million the CO₂-eq in the EU-15), coal mining (6 million the CO₂-eq in the EU-15) and livestock farming (120 million tn CO₂-eq in the EU-15) (EEA, 2013). CH₄ concentration in anthropogenic emissions greatly varies from 0 - 0.2 gCH₄ m⁻³ in compost piles or livestock farms up to 20 - 100 gCH₄ m⁻³ in old landfills (Nikiema et al., 2007).

Based on the urgent need to limit the increase in the global average temperature to a maximum of 2°C above pre-industrial levels, the EU committed itself under the upgraded Kyoto Protocol to reduce its GHG emissions by 20% in 2020 (compared to 1990) (EEA, 2013; IPCC, 2013). In this context, apart from the actions oriented to reduce CO₂ emissions from fossil fuel combustion, additional measurements such as an active CH₄ abatement must be considered in order to achieve these target emission cuts. Moreover, the gradual application of the EU landfill Directive 1999/31 will result in emissions with lower CH₄ concentrations, which will significantly restrict the implementation of CH₄ abatement technologies based on energy recovery (applied at CH₄ concentrations higher than ~400 g m⁻³). Therefore, there is an urgent need to

develop cost-efficient and sustainable technologies for the active abatement of CH_4 diluted emissions. Biotechnologies could become, if properly tailored, a platform technology for the abatement of diluted CH_4 emissions based on their proven robustness and cost-effectiveness for the treatment of malodours or industrial VOC emissions (Estrada et al., 2012b; López et al., 2013).

However, despite the fact that methanotroph-based technologies such as biofiltration or biotrickling filtration have been implemented over the past 40 years for the active abatement of CH₄, the performance of such conventional biotechnologies is still limited by the low CH₄ mass transfer rates from the gas phase to the microorganisms and by the insufficient knowledge on the microbiology underlying CH₄ oxidation (López et al., 2013; Yoon et al., 2009). In this regard, microorganisms with high specific oxidation rates (q_{max}) and a high affinity for CH₄ (low half-saturation constant, K_S) are desirable to guarantee an efficient biocatalytic activity during the treatment of diluted CH₄ emissions and to reduce the start-up period of bioreactors. However, CH₄ biodegradation kinetic studies under non-mass transfer limiting conditions are scarce, especially at the trace level CH₄ concentrations (~mg m⁻³) often encountered under real case applications (Estrada et al., 2012a; López et al., 2013). On the other hand, the economic sustainability of biological CH₄ oxidation processes, often compromised by the high gas residence time required to overcome mass transfer limitations, can be positively impacted by the co-production of high-added value products such as biopolymers (i.e. poly-3-hydroxybutyrate, PHB) (Zúñiga et al., 2011). Unfortunately, the potential of methanotrophic communities to accumulate polyhydroxyalkanoates during the continuous biodegradation of CH₄ at trace level concentrations has been poorly explored.

This study evaluated the influence of CH_4 concentration during methanotrophic community enrichment on biodegradation kinetic parameters and population structure. Moreover, the influence of CH_4 concentration and the CH_4 /biomass ratio on the ability to accumulate PHB under nitrogen limiting scenarios was also assessed.

80 2. Materials and methods

81 2.1. Chemicals and mineral salt medium

Methane was purchased from Abelló Linde S.A. (Barcelona, Spain) with a purity of at least 99.5%. Poly-3-hydroxybutyrate, chloroform (> 99.5%), phosphotungstic acid solution 10% (w/v), uranyl acetate dihydrate ($\geq 98\%$), propylene oxide (> 99%) and benzoic acid (> 99.5%) were obtained from Sigma-Aldrich[®] (Sigma-Aldrich, St. Louis, MO, USA). Osmium tetroxide was obtained from EMS with a purity of at least 99.95% (Hatfield, USA). Lead nitrate and sodium citrate were purchased from Merck (Darmstadt, Germany). The Spurr resin kit TK4 4221D-1 was obtained from TAAB Laboratories Equipment Ltd. (Aldermaston, England). Paraformaldehyde and ethanol (96%) were purchased from AppliChem (Darmstadt, Germany). The rest of reagents and chemicals were purchased from Panreac® (Barcelona, Spain) with a purity of at least 99%.

The mineral salt medium (MSM) used for microbial enrichment and the in-vitro kinetic assays was composed of (in g L⁻¹): Na₂HPO₄·12H₂O 6.15, KH₂PO₄ 1.52, MgSO₄·7H₂O 0.2, CaCl₂·2H₂O 0.0503, NaNO₃ 1.32 and 10 mL L⁻¹ of SL4 trace element solution (containing per liter: EDTA 0.5 g, FeSO₄·7H₂O 0.2 g, ZnSO₄·7H₂O 0.01 g, MnCl₂·4H₂O 0.003 g, H₃BO₃ 0.03 g, CoCl₂ 0.011 g, CuCl₂·2H₂O 0.443 g, NiCl₂·6H₂O 0.002 g, Na₂MoO₄·2H₂O 0.003 g).

100 2.2. Inoculum and cultivation conditions

Fresh aerobic activated sludge from Valladolid wastewater treatment plant (Valladolid, Spain), soil from the cover of an abandoned landfill (Almazán, Spain) and sludge from an aerobic lagoon stabilizing the effluents from a full-scale anaerobic digester treating swine manure (Almazán, Spain) were used as inoculum for the enrichment of methanotrophs. Aliquots of the 3 microbial sources were equally mixed (on a volume basis), diluted in MSM in a 1:18 ratio and then incubated at 25°C and 150 rpm for 1 h in a rotary shaker.

109 2.3. Experimental set-up and operation mode

Three 500 mL jacketed stirred tank reactors (STRs) (Afora S.A., Spain) initially containing 380 mL of MSM were inoculated with 20 mL of the mixed inoculum above described. The cultivation broth was maintained at 25°C and magnetically agitated at 250 rpm with a stir bar placed at the bottom of each STR. Inert polyurethane polymers (0.92 g) were introduced in each reactor in order to prevent the formation of biofilm onto the reactor walls, thus avoiding the underestimation of biomass concentration. CH₄ was continuously supplied via aeration (400 mL min⁻¹) at 20 g m⁻³, 2 g m⁻³ and 0.2 g m⁻³ into reactors 1 (R1), 2 (R2) and 3 (R3), respectively, using 10 µm porous stainless steel diffusers located at the bottom of the reactors. The concentrations of CH₄ were regulated via mass flow controllers (AalborgTM, USA) by mixing an air stream with either pure methane or serial dilutions of CH₄-laden air streams (Fig. 1). The pH of the enrichment broths was maintained at 7.2 ± 0.2 by periodic addition of HCl (0.2 M). Distilled water was added every two days to compensate for water losses by evaporation. Double concentrated MSM without nitrogen was also added to compensate for sampling losses and to provide enough nutrients for microbial growth. The enrichment of potential

PHB-accumulating methanotrophs was performed by operating the reactors under 8 sequential periods of N limitation (48 - 72 h per period) within the entire 310-days experimentation period. N-NO₃⁻ concentration was restored at 248.8 ± 65.3, 48.1 ± 22.9, 17.2 ± 6.9 mg L⁻¹ in R1, R2 and R3, respectively, after each limitation period. At the end of the 8th N limitation cycle, the influence of the CH₄/biomass ratio on microbial PHB accumulation under N limiting conditions was assessed for a period of 18 days by diluting the biomass concentration in R1 and R2 to the levels of R3.

<Figure 1>

Liquid samples (3 mL) were periodically drawn from the reactors to determine the concentration of biomass via culture absorbance measurements (OD₆₅₀), dissolved total organic carbon (TOC) and total nitrogen (TN). Additionally, 15 mL liquid samples were drawn on days 95 - 100 (week 14) and 130 - 135 (week 19) to determine the CH₄ biodegradation kinetic parameters and periodically monitor the total suspended solid concentration (TSS). Liquid samples of 3 mL were also drawn to quantify the bacterial PHB content and to confirm PHB accumulation by transmission electron microscopy at the end of each 3 days nitrogen limitation period. Liquid samples were also taken on days 28 (week 4), 95 (week 14) and 130 (week 19) to determine the dynamics of microbial population structure by denaturing gradient gel electrophoresis (DGGE). CH₄ and CO₂ gas concentrations were monitored by GC-TCD at the inlet and outlet of the reactors.

- - 146 2.4. Kinetics of CH₄ biodegradation

The maximum specific CH₄ biodegradation rate q_{max} (gCH₄ g⁻¹_{biomass} h⁻¹) and the Monod half-saturation constant K_s (g m⁻³) under non-limiting N conditions were determined for R1, R2 and R3 cultures on days 95 – 100 (week 14) and 130 – 135 (week 19) in order to

record the dynamics of CH₄ biodegradation kinetics. These assays were conducted in 120-mL glass bottles containing 20 mL of MSM and inoculated with fresh biomass at an initial concentration of 51.7 \pm 14.7 g_{biomass} m⁻³, which ensured that the kinetic parameters were obtained under non-limiting mass transfer conditions (according to preliminary tests). The bottles were closed with butyl septa, sealed with aluminum caps and supplied with CH₄ at initial headspace concentrations of 91.5 \pm 3.9 g m⁻³, 17.9 \pm 0.8 g m⁻³ and 4.7 \pm 0.4 g m⁻³ (corresponding to initial methane aqueous concentrations of 3.1 ± 0.1 g m⁻³, 0.61 ± 0.1 g m⁻³ and 0.16 ± 0.1 g m⁻³, respectively). The bottles were incubated at 25°C and 150 rpm for 25 h. The concentrations of CH₄ and CO₂ in the headspace of the bottles were periodically measured by GC-TCD. The Lineweaver-Burk correlation (Equation 1) was used to determine the biodegradation kinetic parameters from the initial CH₄ biodegradation rates (Walkiewicz et al., 2012):

163
$$1/q = K_S/q_{max} \times 1/[CH_4] + 1/q_{max}$$
 (1)

where q represents the initial CH_4 biodegradation rate (g CH_4 m⁻³_{liq} h⁻¹) and [CH_4] the methane concentration in the aqueous phase (g m⁻³_{liq}) estimated using the dimensionless Henry's law constant at 25°C and 1 atm (29.4).

169 2.5. Molecular biology analysis

To evaluate the richness and composition of the microbial community, biomass samples from the inoculum (A) and from R1, R2 and R3 were collected on week 4 (B, C and D, respectively), 14 (E, F and G, respectively) and 19 (H, I and J, respectively) and stored immediately at -20°C. The procedures of the DNA extraction, PCR amplification, 174 DGGE analysis, sequencing and DNA sequence analysis can be found in the175 Supplementary Data Annex.

177 2.6. Electron microscopy analysis

Liquid samples of 1 mL drawn from the STRs at the end of the 3rd limitation period were centrifuged at 4000 rpm and 4°C for 5 min. Subsequent biomass fixation, dehydration and embedding were carried out according to Bozzola (2007). The samples were finally cutted and contrasted according to Wendlandt et al. (2001). A TEM JEOL JEM-1011 electron microscope (Teknolab, Indonesia) with an ES1000W Erlangshen CCD camera (Gatan, Germany) was used for the analysis.

185 2.7. Measurement of PHB

The quantitative determination of the cellular PHB content was carried out according to
Zúñiga et al. (2011) using chloroform as extraction solvent.

189 2.8. Analytical procedures

CH₄ and CO₂ gas concentrations were determined in a Bruker 430 GC-TCD (Palo Alto, USA) equipped with a CP-Molsieve 5A (15 m \times 0.53 µm \times 15 µm) and a CP-PoraBOND Q (25 m \times 0.53 μ m \times 10 μ m) columns. The oven, injector and detector temperatures were maintained at 45°C, 150°C and 200°C, respectively. Helium was used as the carrier gas at 13.7 mL min⁻¹. Samples for the determination of TOC/TN concentrations were filtered through 0.22 µm glass fiber filters (Merck Millipore, USA) prior to analysis in a TOC-VCSH analyzer (Shimadzu, Japan) coupled with a chemiluminescense detection TN module (TNM-1) (Shimadzu, Japan). Culture

absorbance measurements at 650 nm were performed using a Shimadzu UV-2550 UV/Vis spectrophotometer (Shimadzu, Japan). The determination of TSS concentration was performed according to standard methods (APHA, 2005). Temperature and pH were on-line monitored using a multiparametric analyser C-3020 (Consort, Belgium). PHB concentration was quantified in an Agilent 6890N GC-MS equipped with a DB-WAX column (30 m \times 0.250 mm \times 0.25 µm) (J&W Scientific[®], CA, USA). The injector temperature was set at 250°C. The oven temperature was initially maintained at 40°C for 5 min, increased at 10°C min⁻¹ up to 200°C, then at 5°C min⁻¹ up to 240°C and finally maintained at 240°C for 2 min.

3. Results and discussion

3.1. Methane biodegradation performance during culture enrichment

CH₄ biodegradation in the three enrichment STRs was indirectly assessed by CO₂ production and biomass growth rather than by CH₄ consumption based on the higher reliability of CO₂ measurements and the low CH₄ removal rates achieved. Since the reactors were not designed to maximize CH₄ abatement, the removal rates obtained were lower than the average error of the GC-FID method. In this context, a rapid CH₄ oxidation was recorded at the highest CH₄ concentration in R1 from the second day of operation, with an increase in CO₂ production up to 104 g m⁻³ h⁻¹ concomitant with a rise in biomass concentration up to 4 g L^{-1} (Fig. 2a, b). However, CH₄ mineralization progressively decreased to average values of 60 gCO₂ m⁻³ h⁻¹ from day 40 to 60 and fluctuated at 42.3 \pm 17 g m⁻³ h⁻¹ from day 60 onwards. Biomass concentration stabilized at 4 g L^{-1} from days 33 to 45 and at 6 g L^{-1} from days 75 to 125 likely due to the accumulation of both metabolites and cell lysis products in the cultivation broth. The complete renewal of MSM in R1 (prior biomass centrifugation) by days 45 and 125

restored TOC concentrations at $110 - 120 \text{ mgC L}^{-1}$ and supported further biomass growth (Fig. 2c). The CO₂ production rates in R2 and R3 underwent less variations than those recorded in R1, with average values of 7.9 and 3.7 g m⁻³ h⁻¹, respectively (Fig 2a). These lower CO₂ production rates were attributed to the lower CH₄ concentration gradients and therefore mass transfer rates at 2 and 0.2 g m⁻³, compared to R1. Biomass growth in R2 and R3 was also significantly lower than that recorded in R1 as a result of the lower CH₄ loading rates (10 and 100 times lower, respectively). Maximum biomass concentrations of 2.1 and 0.7 g L^{-1} were achieved, respectively, in R2 and R3 by days 113 and 180, to finally decrease to 1.2 and 0.2 g L⁻¹, respectively. Likewise, TOC concentrations in both reactors remained constant at $\sim 40 \text{ mg L}^{-1}$, which suggests that the accumulation of metabolites or cell lysis products in R2 and R3 was not significant during the experimentation period (Fig. 2c). The CO₂ production rates recorded in R1 and R2 were similar to those reported by Rocha-Rios et al. (2010, 2009) in STRs at CH₄ loading rates of approximately 65 and 210 g m⁻³ h⁻¹ (10 and 80 g CO₂ m⁻³ h⁻¹, respectively).

<Figure 2>

3.2. Structure of the enriched communities

The Shannon-Wiener diversity index (*H*) ranges typically from 1.5 to 3.5 and accounts for both the number (richness) and the eveness of the species (evaluating and comparing the intensity of the bands), thus allowing to obtain semi-quantitative results from the DGGE analysis (McDonald, 2003). In our particular case, the complex inoculum exhibited the lowest species evenness and richness among the samples analyzed as demonstrated by its low *H* of 2.6. Despite the increase in microbial diversity of the communities at week 4 in R1, R2 and R3 (*H* of 2.9, 3.2 and 3.1, respectively), culture

aging mediated a lower biodiversity at week 14 as confirmed by the decrease in Hvalues to 2.4, 3.1 and 2.8 in R1, R2 and R3, respectively. Further culture aging resulted in the stabilization in microbial diversity by week 19 in R2 and R3 at H of 2.7, and at H of 2.9 in R1. It is noteworthy that these H values were achieved using CH_4 as the sole C and energy source and were not significantly influenced by CH₄ concentration. In contrast, Estrada et al. (2012a) observed that high toluene concentrations supported lower biodiversity indexes, which was attributed to the high toxicity of the model VOC used in the study.

<Figure 3>

The analysis of the pair-wise similarity indexes revealed a low correspondence between the inoculum and the cultures in the three STRs, even by week 4 (Fig. 4a). Hence, similarity coefficients of 8%, 18% and 34% were recorded between the seed and the cultures R1, R2 and R3 by week 4, respectively (Fig. 4b). These results confirmed the rapid dynamics of the methanotrophic communities in the STRs and agreed well with the differences observed among the Shannon-Wiener diversity indexes. The highest similarities in the phylogenetic composition of the communities were obtained between the communities on weeks 14 and 19 (88% in R1, 80% in R2 and 75% in R3) (Fig. 4a, b). These empirical findings confirmed the stabilization of the methanotrophic populations from week 14 onward regardless of the CH₄ concentration evaluated. Moreover, the comparison of communities in the STRs by week 19 revealed that cultures enriched at CH₄ concentrations differing in one order of magnitude were more similar (similarities of 51% between R1 and R2, and 66% between R2 and R3) than those enriched at CH₄ concentrations differing in two orders of magnitude (32% between R1 and R3) (Fig. 4b). Thus, these results confirmed the significant influence of

CH₄ concentration during culture enrichment on the structure of the microbial populations.

<Figure 4>

Three different phyla were retrieved according to the RDP classifier tool among the 18 bands sequenced from the DGGE gel (Fig. 3): Proteobacteria (15 bands), Firmicutes (1 band) and Actinobacteria (1 band), while the sequence of the last band remained unclassified. The closest matches for each bacterial sequence from the NCBI database are provided in the Supplementary Data Annex (Table 1) with indication of the similarity percentages and sources of origin. In addition, the presence and relative abundance of each band within the samples analyzed are also shown in the Supplementary Data Annex (Table 1). Most bands were affiliated to the phylum Proteobacteria and more specifically to Alphaproteobacteria, Betaproteobacteria and Gammaproteobacteria classes. Despite CH₄-oxidizing bacteria belonging to type I methanotrophs (Methylosarcina, Methylomicrobium, Methylosoma and Methylobacter genera) were detected in the three STRs along the entire enrichment, type I methanotrophs were more abundant in R1 and R2 (samples B, C, E, F, H and I) and their abundance gradually deteriorated over time. Type II methanotrophs (Methylocystis genus) were also present in the three STRs and gradually increased their abundance in R2 and, in a lesser extent, in R3 (samples F, G, I and J). The fact that type II methanotrophs exhibited a lower abundance than type I methanotrophs in the STRs can be attributed to the enrichment of cultures at high Cu^{2+} concentrations. In this context, preliminary quantitative-PCR results revealed the higher expression of particulate methane monooxygenases (pMMO) compared to the type II-specific soluble methane monooxygenases (sMMO), which also supported the predominance of type I methanotrophs along the entire enrichment in the STRs (data not shown). Most

methanotrophic genera here described were previously identified in CH₄ abatement bioreactors (Gebert et al., 2008; Veillette et al., 2011), which confirmed their ability to degrade CH₄. Thus, the methylotrophic *Methylobacillus* and *Hyphomicrobium* genera have been detected in sewers and biofilters treating CH₄, respectively (Chistoserdova et al., 2007; Kim et al., 2013). In our particular study, the Hyphomicrobium genus (DGGE band 15) was significantly present in almost all samples analyzed, while bacteria from the Methylobacillus genus (DGGE band 12) were only found in R1 by week 19 (sample H). Despite members of the Dokdonella, Rhodanobacter, Turicibacter and Rhodococcus genera (DGGE fragments 10, 11, 16 and 17, respectively) were also detected by week 4 in the three STRs, these microorganisms gradually disappeared likely due to their incapability to assimilate CH₄, CH₄-derived metabolites or cell lysis products. Bacteria from the Rhodanobacter genus were previously detected in a CH₄ abatement bioreactor, but their role in this particular microbial community was not clearly identified (Veillette et al., 2011).

3.3. Determination of kinetic parameters

The highest q_{max} obtained from the Lineweaver-Burk linearization (4.8 \times 10 $^{-4}$ \pm 8.1 \times 10^{-5} gCH₄ g_{biomass}⁻¹ h⁻¹) was recorded at week 14 in the communities enriched in R2, which was attributed to the high biodiversity encountered both for type I and II methanotrophic bacteria. No significant differences were observed between the communities of R1 and R3 in terms of q_{max} at week 14, with values of $2.7 \times 10^{-4} \pm 5.6 \times$ 10^{-5} and $1.6 \times 10^{-4} \pm 1.8 \times 10^{-5}$ gCH₄ g_{biomass}⁻¹ h⁻¹, respectively (Fig. 5a). The q_{max} values determined at week 14 in the three microbial communities were higher than those previously reported in the literature, which typically ranged from 4.2×10^{-5} to 1.3×10^{-4} gCH₄ g_{biomass}⁻¹ h⁻¹ (Bender and Conrad, 1992; Gebert et al., 2003). These findings can be

explained by the fact that biomass concentration was optimized in the biodegradation assays in order to avoid CH₄ mass transfer limiting conditions, resulting in more realistic kinetic parameters. On the contrary, most kinetic studies reported for methanotrophs were carried out at high biomass concentration, which did not ensure the absence of mass transport limitations and, therefore, the validity of the kinetic parameters obtained. At week 19, the communities of R1 and R2 exhibited lower q_{max} compared to week 14 $(1.1 \times 10^{-4} \pm 3.1 \times 10^{-5} \text{ and } 1.9 \times 10^{-4} \pm 5.4 \times 10^{-5} \text{ gCH}_4 \text{ g}_{\text{biomass}}^{-1}$ h^{-1} , respectively), while q_{max} in the community of R3 remained similar. These findings suggested that culture aging negatively affected the specific CH₄ biodegradation rate of the microbial communities exposed to the two highest CH₄ concentrations likely due to the presence of a higher inert biomass fraction.

<Figure 5>

On the other hand, no significant differences in the K_s of the microbial communities enriched in the three STRs were recorded at week 14, exhibiting values of $1.2 \times 10^{-5} \pm$ 1.7×10^{-6} M (Fig. 5b). K_s values at week 19 significantly decreased in the communities enriched in R1 and R3 ($5.2 \times 10^{-6} \pm 1.4 \times 10^{-6}$ M and $4.8 \times 10^{-6} \pm 5.3 \times 10^{-7}$ M, respectively) and remained constant in R2 ($1.6 \times 10^{-5} \pm 8 \times 10^{-7}$ M). The results here obtained indicated that long-term culture exposure to CH₄ would promote the enrichment of high affinity (low K_s) microorganisms, although no significant influence of CH₄ concentration on K_S was observed. This empirical finding was in agreement with the fact that type I (which exhibit the highest affinities for CH₄) rather than type II methanotrophs were dominant in both R1 and R3. Whalen et al. (1990) reported K_S values for type I methanotroph-like cultures isolated from landfill cover soils as low as 2.5×10^{-6} M under gas CH₄ concentrations of 1 – 1.7 g m⁻³, which are comparable to those recorded at week 19 in R1 and R3. In contrast, K_S values of $6.8\times10^{-5}-4.7\times10^{-4}$

M are typically reported in literature for type II methanotrophs (Delhoménie et al., 2009;
Hornibrook et al., 2009).

3.4. PHB accumulation

PHB was present as refractive inclusions or granules inside the methanotrophic cells, which were identified in the enriched cultures by their intracytoplasmatic membranes (Fig. 6). The transmission electron micrographs confirmed the microbiological feasibility of coupling CH₄ abatement with the production of an added value product such as PHB, which could significantly contribute to improve the economic viability of the process. Polyhydroxyalkanoate accumulation in methanotrophs can be induced under excess of C source and limitation in the availability of nutrients such as N, P or Mg (Asenjo and Suck, 1986), N limitation being the best scenario for PHB accumulation according to Wendlandt et al. (2001). Hence, the enrichment of methane-oxidizing bacteria capable of accumulating PHB was performed by operating the reactors under 8 sequential periods of N limitation. To the best of our knowledge, this is the first systematic study assessing the influence of different CH₄ concentrations and CH₄/biomass ratios on PHB accumulation by methanotrophic consortia.

<Figure 6>

PHB cell contents of 0.3 - 0.5% (*w/w*), 2.9 - 9.7% (*w/w*) and 0.1 - 0.8% (*w/w*) were recorded following the N limitation periods in R1, R2 and R3, respectively (Table 1). Despite sequential N limitations were expected to induce an increasing PHB accumulation, the biopolymer content was low and neither correlated with CH₄ concentration nor with the time course of the enrichment. Similar results were obtained by Pieja et al. (2012) in batch reactors subjected to sequential N limitations, although 371 sequential CH₄ and N limitations indeed promoted PHB accumulation up to 24% (w/w). 372 These results, compared to our particular study, were likely due to the use of the PHB-373 producer *Methylocystis parvus OBBP* and the use of C and N feast-famine strategies. 374 Methanotroph cultivation at higher CH₄/biomass ratios following the 8th N limitation 375 episode initially resulted in the highest PHB cell contents in both R1 and R2 (1% and 376 12.6%, respectively), likely due to the higher bioavailability of the C source.

<Table l>

The differences in the PHB cell content of the communities enriched in the reactors at the different CH₄ concentrations can be explained by the different structure of these methanotrophic communities revealed by DGGE analysis (Fig. 3; Supplementary Data Annex). The key role of the type of methanotrophs on the ability to accumulate PHB was recently highlighted by Pieja et al. (2011), who suggested that only type II methanotrophs exhibited the ability to accumulate PHB under N limiting conditions. In our particular case, the highest abundance of type II methanotrophs (Methylocystis genus) was found in R2, which also corresponded to the community with the highest PHB contents.

GC-MS analyses revealed also the accumulation of poly-3-hydroxyvalerate (PHV) in the cultures enriched (Table 1). The highest PHV:PHB ratios were found in R1 (up to 12:1) and R3 (up to 4:1), which corresponded to the communities with the lowest PHB contents. The low PHB cell contents detected in both reactors could be attributed to the preferential microbial accumulation of PHV. In this regard, Zúñiga et al. (2013) reported maximum PHV:PHB ratios of 7:11 in a STR fed with CH₄ and citrate as carbon sources and highlighted that the co-production of polyhydroxyalkanoates such as PHV together with PHB can improve the mechanical properties and biodegradability of the composite biopolymers. In our particular study, the different PHV:PHB ratios obtained could be attributed to the use of consortia and CH_4 instead of pure cultures and CH_4 /cosubstrates, as reported by Zúñiga et al. (2013).

399 4. Conclusions

The analysis of the pair-wise similarity indexes clearly showed that CH₄ concentration during culture enrichment determined the structure of the microbial populations, which exhibited rapid dynamics and high species evenness and richness. In addition, kinetic assays revealed high specific biodegradation capacities and affinities for CH₄, correlated to the dominance of type I/II methanotrophs rather than to CH₄ concentration. On the other hand, the use of sequential N limitations under continuous CH_4 -laden air flow did not promote a high PHB accumulation in the cultures likely due to the low abundance of type II methanotrophs. Interestingly, the communities with lower PHB contents exhibited higher PHV contents. These findings brought new insights on the development of specific inocula not only to reduce the start-up period of bioreactors devoted to CH₄ abatement, but also to co-produce high-added value products. Although further experiments on optimizing the conditions for PHB/PHV production are still necessary, the industrial use of these high-added value products will certainly promote the application of biological processes for GHG emissions abatement.

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Valladolid) in the transmission electronic microscopy analyses are also gratefully

422	Nomenclature
423	STR Stirred tank reactor
424	VOC Volatile organic compound
425	PHB Poly-3-hydroxybutyrate
426	PHV Poly-3-hydroxyvalerate
427	TSS Total suspended solids (g L^{-1})
428	TOC Total organic carbon (mg L ⁻¹)
429	H Shannon-Wiener diversity index (dimensionless)
430	K _s Half-saturation constant (M)
431	q_{max} Maximum specific biodegradation rate (gCH ₄ g ⁻¹ _{biomass} h ⁻¹)
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Figure Captions

Figure 1. Schematic representation of the experimental set-up. 1 CH₄ gas cylinder, 2 air compressor, 3 jacketed 500-mL glass reactors, 4 mass flow controllers, 5 needle valve, 6 T-connections, 7 pH data acquisition system, 8 PC data logger, 9 rotameters, 10 inlet sampling points, 11 outlet sampling points.

Figure 2. Time course of CO_2 production rate (a), biomass concentration (b) and TOC concentration (c) during methanotroph enrichment in R1 (\blacktriangle), R2 (\blacklozenge) and R3 (\Box).

Figure 3. DGGE profiles of the bacterial communities present in: A Inoculum, B R1 on week 4, C R2 on week 4, D R3 on week 4, E R1 on week 14, F R2 on week 14, G R3 on week 14, H R1 on week 19, I R2 on week 19, J R3 on week 19. The name of the samples and their Shannon-Weiner diversity indexes are shown in the upper part of the gel.

Figure 4. Bacterial similarity dendrogram (UPGMA clustering) (a) and matrix (b) with error resampling (500 resampling experiments) for: A Inoculum, B R1 on week 4, C R2 on week 4, D R3 on week 4, E R1 on week 14, F R2 on week 14, G R3 on week 14, H R1 on week 19, I R2 on week 19, J R3 on week 19. The names of the samples in the dendogram are shown in the lower part of the figure.

Figure 5. Influence of CH₄ concentration during enrichment on the CH₄ biodegradation kinetic parameters q_{max} (**a**) and K_S (**b**) at week 14 (black bar) and 19 (scratched bar).

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Figure 6. Transmission electron micrographs of methanotrophic cells containing PHB enriched in R1 (a), R2 (b) and R3 (c) (60 000 \times , 120 000 \times and 100 000 \times magnification, respectively).

Figure 1.







Figure 4.



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	R1		R2		R3	
Cycle	%PHB [♭]	PHV:PHB	%PHB	PHV:PHB	%PHB	PHV:PHE
1	nd	nd	nd	nd	0.8 ± 0.0	3:1
2	nd	nd	3.2 ± 0.2	1:2	0.8 ± 0.0	2:1
3	nd	nd	3.1 ± 0.1	1:2	0.6 ± 0.0	2:1
4	nd	nd	9.7 ± 0.2	1:4	0.5 ± 0.1	3:1
5	nd	nd	7.5 ± 0.0	1:4	0.4 ± 0.0	4:1
6	0.3 ± 0.1	11:1	2.9 ± 0.1	1:2	0.5 ± 0.0	3:1
7	0.5 ± 0.1	10:1	4.3 ± 0.1	1:2	0.1 ± 0.0	3:1
8	0.3 ± 0.0	12:1	5.5 ± 0.2	1:3	0.5 ± 0.0	2:1
8 (3 days)	1.0 ± 0.1	3:1	12.6 ± 0.9	1:6	0.5 ± 0.0	3:1
8 (6 days)	0.6 ± 0.0	7:1	6.2 ± 0.1	1:7	0.4 ± 0.0	3:1
3 (10 days)	0.7 ± 0.0	6:1	6.4 ± 0.1	1:5	0.5 ± 0.0	4:1
3 (18 days)	0.6 ± 0.0	6:1	5.5 ± 0.3	1:5	1 ± 0.0	1:1

^and: not determined

^b%PHB = (gPHB/gTSS) \times 100

Appendix A. Supplementary Data Click here to download e-component: Appendix A. Supplementary Data.docx