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EFFECTS OF HEAT TREATMENT ON MICROBIAL COMMUNITIES OF GRANULAR SLUDGE FOR BIOLOGICAL HYDROGEN PRODUCTION

--Manuscript Draft--

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Corresponding Author:	Sergio Casella University of Padova Legnaro, ITALY
Corresponding Author Secondary Information:	
Corresponding Author's Institution:	University of Padova
Corresponding Author's Secondary Institution:	
First Author:	Luca Alibardi, PhD
First Author Secondary Information:	
Order of Authors:	Luca Alibardi, PhD Lorenzo Favaro, PhD Maria Cristina Lavagnolo, PhD Marina Basaglia Sergio Casella
Order of Authors Secondary Information:	
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Abstract:	<p>Dark fermentation shares many features with anaerobic digestion with the exception that to maximize hydrogen production, methanogens and hydrogen consuming bacteria should be inhibited. Heat treatment is widely applied as inoculum pre-treatment due to its effectiveness in inhibiting methanogenic microflora but it may not exclusively select for hydrogen producing bacteria. This work evaluated the effects of heat treatment on microbial viability and structure of anaerobic granular sludge. Heat treatment was carried out on granular sludge at 100°C with four residence times (0.5, 1, 2 and 4 hours). Hydrogen production of treated sludges were studied from glucose by means of batch test at different pH values.</p> <p>Results indicated that each heat treatment strongly influenced the granular sludge resulting in microbial communities having different hydrogen productions. The highest hydrogen yields (2.14 mole of hydrogen per mole of glucose) were obtained at pH 5.5 using the sludge treated for 4 hour characterized by the lowest CFU concentration (2.3 x 10³ CFU/g sludge). This study demonstrated that heat treatment should be carefully defined according to the structure of the sludge microbial community allowing the selection of highly efficient hydrogen producing microbes.</p>

DIPARTIMENTO DI AGRONOMIA ANIMALI ALIMENTI
RISORSE NATURALI E AMBIENTE

DAFNAE

DEPARTMENT OF AGRONOMY FOOD NATURAL RESOURCES
ANIMALS AND ENVIRONMENT



UNIVERSITÀ
DEGLI STUDI
DI PADOVA

Viale dell'Università 16
35020 Legnaro (Padova)
tel +39 049 827 2922
fax +39 049 827 2929
sergio.casella@unipd.it

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EFFECTS OF HEAT TREATMENT ON MICROBIAL COMMUNITIES OF
GRANULAR SLUDGE FOR BIOLOGICAL HYDROGEN PRODUCTION.
by Alibardi A. et al.

Dear Editor,

Thank you very much for the suggestions related to our manuscript No. WST-WSTWS-EM111401.

We proceeded to modify the text according to the indications of the Reviewers. A file with the answers, point by point, to the comments/questions of the Reviewers is contextually submitted with the revised version of the manuscript.

Please, note that the amended text contains several sections in red typing in order to make the changes more evident.

Thank you in advance for your consideration

Best regards

Sergio Casella

1 **Reviewer #1:**

2
3 The aim of the work as stated and as was made to understand to the reader in the introduction was
4 to see whether heat treatment that aims in eliminating hydrogen consumers is selective enough to
5 support all the hydrogen producers. The authors hypothesized that in this selection process the non
6 spore forming hydrogen producers will also get inactivated and thus instead of higher hydrogen
7 production, it might actually decrease the hydrogen production. However based on the methodology
8 and the results that was presented in the manuscript, the authors have achieved higher hydrogen
9 production with heat treatment and they could not provide a proper justification by their initial
10 hypothesis failed. The 16S sequencing work that they have done was from only the cultivable
11 microflora that does not give a proper representation of the actual microbial diversity of the sludge.
12 This is a good piece with a good hypothesis. But the justification provided and the methodology
13 used was not proper. Thus in my understanding the manuscript is not ready for publication.
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17 Response: In this study, we demonstrated that heat treatment should be carefully defined
18 according to the structure of the sludge microbial community allowing the selection of highly
19 efficient hydrogen producing microbes. In other words, we wanted to define the most appropriate
20 heat treatment time to achieve the highest hydrogen yields obtainable by culturable bacteria. The
21 Reviewer states that “The authors hypothesized that in this selection process the non spore forming
22 hydrogen producers will also get inactivated and thus instead of higher hydrogen production, it
23 might actually decrease the hydrogen production.”. However, we must clarify that our aim was a
24 little different and the above hypothesis was only one among others. In this specific case, our initial
25 hypothesis was “to verify if” the non-spore forming hydrogen producers will get inactivated by heat
26 treatments, so affecting the final hydrogen production. Indeed, in the Introduction we reported that
27 “Although heat treatment aims to kill methanogens, it does not select exclusively for hydrogen
28 producing bacteria. Therefore, while spore-forming H₂-consuming bacteria can survive, non-spore
29 forming hydrogen-producers may be inactivated.” As a consequence, a sort of balance between
30 “non-spore forming H₂ consumers” and “non-spore forming H₂ producers” that have been affected
31 by the heat treatment is the crucial point making the real difference. The various time treatments
32 used were specifically applied to find the optimal treatment to make this balance as positive as
33 possible. The same concept can be applied also for the spore forming bacteria.
34 In the Results and Discussion, we have reported that, after a short heat treatment, non-spore forming
35 hydrogen-producers were inactivated. As a result, rather than increasing H₂ production, 1 h heat
36 treatment has actually negatively affected H₂ yield (Page 9, lines 284-300). However, as reported in
37 Table 3, longer heat treatments greatly enhanced hydrogen productions.

38 We agree with the reviewer about the fact that 16S sequencing work done in this study only on the
39 culturable microbes does not give a proper representation of the actual microbial diversity of the
40 sludge. However, since this work was focused on the heat-treatment of granular sludge to start the
41 development of microbial inoculants to be used for the conversion of organic wastes into hydrogen,
42 we wanted to select for culturable bacteria.

43 To better explain why in this work we limited our research to the culturable bacterial populations,
44 the following sentence has been added in the Introduction (Page 2, lines 90-92):

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53 *“This work evaluated the potential of heat treatment as enrichment strategy of granular sludge to
54 select H₂-producing microbial consortia with promising yields, even in view of the future
55 development of efficient microbial inoculants.”*

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58 Nevertheless, to better understand the microbiological and biochemical aspects of using the heat-
59 treated sludges to produce hydrogen, the study of the whole microbial community structure by
60 means of DNA-based techniques is in progress and will be the matter of a future manuscript.
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1 **Reviewer #2**

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3 Effects of heat treatment on microbial community of granular sludge for biological hydrogen
4 production

5 The present work is a well written and present interesting data about the application of "dark
6 fermentations" and production of alternative energy sources.

7 The used methods are adequate and the results well-presented and discussed.

8 I would like to recommend the present work to be accepted for publication in Water Science and
9 Technology after minor revisions.

10 I would like to recommend to the authors to check again entire manuscript for the style of the Water
11 Science and Technology.
12
13

14
15 Response: The manuscript has been entirely checked for the style of the Water Science and
16 Technology Journal.
17

18 However, I have some questions and remarks, which in my opinion will make the manuscript more
19 clear.
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21
22 1) Can you please explain better the statement from page 2, line 58-59. Why CO₂ from biogenic
23 sources not contributing to the greenhouse effect?
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25
26 Response: During the biological production of hydrogen by fermentation process, bacteria
27 produce a mixture of gas composed by hydrogen and carbon dioxide as by-product of the metabolic
28 process of degradation of organic substances. This carbon dioxide emission is considered carbon
29 neutral (thus not contributing to the green house effect) because it is derived from organic
30 substances produced by fixing atmospheric CO₂ from a photosynthetic process (biogenic), therefore
31 with a very short carbon cycle (some month, if the growth of a crop is considered).
32

33 On the contrary the production of hydrogen based on the utilization of fossil fuel (steam reforming
34 or thermal cracking of natural gas, coal gasification, electrolysis of water or other thermochemical
35 processes based on the utilization of energy from fossil fuels) is not carbon neutral due to the
36 emission into the atmosphere of carbon dioxide that was trapped millions of years ago as fossil
37 carbon.
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39 To better explain this concept, the sentence (Page 2, lines 58-60) has been reinforced as following:
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43 *"In this perspective, biological hydrogen production processes represent a sustainable opportunity.
44 In fact, hydrogen producing bio-processes involve CO₂ emissions, but from biogenic sources, thus
45 not contributing to the green house effect due to the brevity of the carbon cycle (Hellenbeck,
46 2009)".*
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49 2) Please, when you start sentences, avoid use of numbers or chemical formulas (see page 2, line
50 60, etc.).
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52 Response: the text has been amended accordingly throughout the text.
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55 3) On page 3, line 113, you can introduce the abbreviation for Nutrient Agar as "NA" and use later
56 in the manuscript.
57

58 Response: the text has been amended accordingly throughout the text.
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1 4) On page 3, line 115, please replace "were recorded" with "were determined". Word "recorded" is
2 used for the directly obtained numbers, when you calculate (like in case of CFU), the correct word
3 is "determined".
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5 Response: the text has been amended accordingly throughout the text.
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8 5) On page 3, line 117, please replace "picked" with "collected".
9

10 Response: the word "picked" has been changed with "collected" according to the reviewer's
11 suggestion.
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14 6) On page 3, line 128, please replace "checked" by "visualized"
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16 Response: the word " checked " has been changed with "visualized" according to the
17 reviewer's suggestion.
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21 7) On page 3, line 131, please, specify if the 96% is sufficient for the taxonomic identification.
22 Several authors use 98% as a breaking point for the identification purposes.
23

24 Response: For taxonomic identification, different similarity percentage values have been
25 used in literature: from 95 to 100% (see Mazzon et al. (2008) Presence of specific symbiotic
26 bacteria in flies of the subfamily Tephritinae (Diptera Tephritidae) and their phylogenetic
27 relationships: proposal of 'Candidatus Stammerula tephritidis'. Int. J. Syst. Evol. Microbiol., 58
28 (2008), pp. 1277–1287).
29

30 In this study, the similarity level considered for taxonomic attribution was always above 98% with
31 the exception of two cases in which the similarity were found to be 96%. For this reason, we have
32 reported in the Material and Methods that "A minimum sequence similarity level of 96% was
33 considered for taxonomic attribution". However, the sentence has been modified as following (Page
34 3, lines 134-135) in order to improve the clarity:
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38 *"A minimum sequence similarity level of 96% was considered for taxonomic attribution, although*
39 *the majority of the isolates showed a similarity level higher than 98%."*
40

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42 8) On page 3, lines 152-153. Last sentence needs to be rephrased.
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44 Response: The sentence has been adjusted as following to improve the clarity (Page 4, Lines
45 154-157):
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48 *"Biogas composition in terms of hydrogen, carbon dioxide and methane were measured by a gas*
49 *chromatograph (HP5890) equipped with thermal conductivity detector (TCD), HP- MOLSIV and*
50 *HP-PLOT U columns, nitrogen as carrier gas."*
51

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53 9) On page 4, line 173, please replace "triplicate experiments" with "3 repetitions".
54

55 Response: the word " triplicate experiments" has been changed with "3 repetitions" according to the
56 reviewer's suggestion.
57

10) On page 4, table 1. In my opinion will be better to present this table in logarithmic form.

Response: We have proposed Table 1 not in logarithmic form because, in our opinion, the reader can better appreciate the differences between the CFU values. As a consequence, we propose Table 1 to remain as it is.

11) On page 5, table 2. Please explain the values obtained for *Bacillus flexus* at 1h (3.8) and for *Brevibacterium brevis* at 1h (11.5). Why these bacteria are present after 1h treatment, but not after 0.5h? Is this related with an ecological interaction between species presented in this system? This is an interesting result and deserves a better discussion. Spelling of *Shinella* sp. is correct?

Response: The fact that *Bacillus flexus* and *Brevibacterium brevis* were not detected in the sludge heat-treated for 0.5 hour should not be considered surprising. The above bacterial species were not detected in both non-treated and 0.5 h heat-treated sludges because their population sizes were much lower than those detected at 10^{-6} dilution level (see Table 1), used for the plate counting method. Once the majority of the other bacterial species was killed by 1 h heat treatment, *Bacillus flexus* and *Brevibacterium brevis*, evidently able to tolerate the longer heat stress, can be easily detected at lower dilution levels (10^{-4} instead of 10^{-6}).

The spelling of the genus *Shinella* has been checked and it is correct.

Reviewer #3:

Review of manuscript number WST-WSTWS-EM111401, "Effects of heat treatment on microbial communities of granular sludge for biological hydrogen production".

The paper reports on the effect of the duration of heat treatment (100°C) on hydrogen production in batch culture and on the viability and microbial community structure. Different durations of treatments were used - 0.5, 1, 2, 3 and 4 hours. It was found that the best hydrogen production yield and the lowest diversity of the culture occurred when the granular sludge was treated for 4 hours. The paper makes a useful contribution with regard to the methodology needed to select for hydrogen formers. Before the paper is published I would recommend the following modifications:

1) In the abstract, it is important to mention that the best hydrogen yield was obtained when the sludge was heat treated for 4 hours. I believe it is erroneous to say , "the lowest amounts of microbes produced the highest hydrogen levels?". In the methods (page 3) the food to microorganism level was kept constant.

Response: We thank the reviewer for the suggestion about the abstract. Reviewer is right saying that the F/M ratio was kept constant for all the experiments. We would like to specify that the F/M ratio is based on the volatile solids of glucose and volatile solids of treated granular sludge. The heat treatment did not effect the Total Solids (TS) and Volatile Solids (VS) concentrations of the sludge as well as its chemical characterization. On the contrary, heat treatment strongly affected sludge microbial viability (see Table 1). Therefore, the sludges treated at different durations have the same value of VS (and therefore all experiments had the same F/M ratio) but different CFU concentrations. In other words, the same amount of VS brings to the batch different proportions of living microorganisms (those able to make hydrogen) and heat-killed bacteria. To clarify this aspect in the paper, the paragraph regarding the brief presentation of the results in the abstract has been changed as following:

1 “Results indicated that each heat treatment strongly influenced the granular sludge resulting in
2 microbial communities having different hydrogen productions. The highest hydrogen yields (2.14
3 mole of hydrogen per mole of glucose) were obtained at pH 5.5 using the sludge treated for 4 hour
4 characterized by the lowest CFU concentration (1.5×10^2 CFU/g sludge).”
5

6 Moreover, in the section “Batch test for hydrogen production” of Material and Methods, the
7 paragraph (Page 3, lines 148-150) has been modified as following:
8

9
10 “Food to microorganism ratio (F/M) was set at 1 gVS/gVS. Since heat treatment did not change the
11 TS and VS of the sludge, every reactor was inoculated with 10 grams of treated or non-treated
12 sludge.”
13

14
15 2) In Table 3, indicate whether the hydrogen produced is normalised to glucose consumed or added.
16 Also indicate the number of measurements that make up the average.
17

18
19 Response: The data about hydrogen production are normalised to added glucose. Each value
20 reported in Table 3 is the average of 3 replicates. The caption of Table 3 has been revised
21 accordingly as following:
22

23 “**Table 3.** Average cumulative hydrogen productions (\pm SD, n=3), hydrogen yields and
24 mathematical model results. Hydrogen productions are normalized to glucose added to batch tests.”
25

26
27 3) In Table 2, it is very surprising that no Clostridial species were found upon analysis. Could the
28 authors confirm if all the data has been presented.
29

30
31 Response: Table 2 shows all the results we obtained from non-treated and treated sludge
32 samples. We agree with the reviewer about the unexpected absence of *Clostridium* sp. strains in the
33 granular sludge. In the literature, it is reported that the microbial species involved in bio-hydrogen
34 production are mainly *Clostridium* sp. and, in lower extent, *Bacillus* sp. strains (Kapdan I.K. and
35 Kargi F. 2006. Bio-hydrogen production from waste materials. Enzyme Microb. Technol., 38, 569-
36 582.
37

38 However, in this study *Clostridium* sp. strains were not detectable in the anaerobically incubated
39 plates resulting from the non-treated granular sludge. Since Clostridia are anaerobic, gram positive
40 bacteria, able to resist to heat shocks by forming spores, the fact that after long heat-treatments, no
41 *Clostridium* strains have been detected from the granular sludge seems to confirm that the sludge
42 used in this study had no *Clostridium* species or alternatively the *Clostridium* sp. population size
43 was always under the detection limit of the plate counting method (see response to the second
44 reviewer). In future studies, DNA-based molecular techniques (i.e., DGGE-PCR) will be applied to
45 confirm both hypothesis and to further study the peculiar microbial structure of the granular sludge
46 used in this work.
47

48 Nevertheless, the microbial community of the non-treated sludge revealed to be quite similar to
49 those of other previously studied granular sludges at least at phylum level (Narihiro *et al.*, 2009).
50 This concept was already discussed at Page 4 (lines 201-204).
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54 4) Is it possible to include pH as a variable in equation 1?
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56 Response: We thank the reviewer for the question. It is not possible to include the pH in the
57 equation [1]. The equation reported in the article was used only to compare the cumulative
58 hydrogen productions from the different tests with a mathematical formula that represents the best
59 fitting of the experimental data.
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On the contrary, pH and heat treatment duration were evaluated in the two ways factorial ANOVA. The interaction between pH and thermal duration was found to be statistically significant (Page 8, line 274).

5) A comparison of the best results in this study and results from other studies in the literature should be made.

Response: We thank the reviewer for the comment. In the original version of the paper, the references Fang et al., (2002) and Kapdan and Kargi, (2006) were used in the text to compare the data obtained in this study with other results reported in the scientific literature.

In the current version of the manuscript, Table 4 has been added according to the reviewer's suggestion and the following sentence has been inserted in the Results and Discussion section (Page 8, lines 275-277).

“The yield of 2.14 moles of hydrogen per mole of glucose obtained at pH 5.5 with the 4 hour treated sludge seems to be promising if compared to those previously reported from glucose (Table 4).”

Table 4. Comparison of hydrogen yields from different studies. All the data regard batch experiments using glucose as substrate and mixed culture as inoculum.

Reference	Inoculum	Inoculum pre-treatment	Fermentation temperature	Fermentation pH	Hydrogen yields (mol H ₂ /mol glucose)
This study	UASB granular sludge	heat treatment (100°C, 4 h)	35°C	5.5	2.14
This study	UASB granular sludge	heat treatment (100°C, 2 h)	35°C	5.5	1.82
Davila-Vazquez <i>et al.</i> (2008)	UASB granular sludge	heat treatment (100°C, 40 min)	37°C	7.5	1.46
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	35°C	5.5	1.00
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	41°C	5.5	1.67
Morimoto <i>et al.</i> (2004)	sludge compost	aerobic conditions (60°C, 3 days)	60°C	3.97*	2.1
Morimoto <i>et al.</i> (2004)	anaerobic pond sludge	-	50°C	4.02*	1.6
Morimoto <i>et al.</i> (2004)	compost	-	60°C	-	1.5
Logan <i>et al.</i> (2002)	soil used for tomato plants	heat treatment (104°C, 2 h)	26°C	6	0.92
Fang and Liu (2002)	anaerobic sludge from a CSTR reactor	-	36°C	5.5	2.1

* final pH

1 The following references have been added :
2

3 Morimoto M., Atsuko M., Atif A.A.Y., Ngan M.A., Fakhru'l-Razi A., Iyuke S.E., Bakir A.M.
4 (2004). Biological production of hydrogen from glucose by natural anaerobic microflora. *Int. J.*
5 *Hydrogen Energy*, 29, 709-713.
6

7 Mu Y., Zheng X.J., Yu H.Q., Zhu R.F. (2006). Biological hydrogen production by anaerobic sludge
8 at various temperatures. *Int. J. Hydrogen Energy*, 31, 780-785.
9

10 Logan B.E., Oh S.E., Kim I.S., Van Ginkel S. (2002). Biological hydrogen production measured in
11 batch anaerobic respirometers. *Environ. Sci. Technol.*, 36, 2530-2535.
12

13 Fang H.H.P., Liu H. (2002). Effect of pH on hydrogen production from glucose by a mixed culture.
14 *Bioresour. Technol.*, 82, 87-93.
15

16 Davila-Vazquez G., Alatraste-Mondragon F., de Leon-Rodriguez A., Razo-Flores E. (2008).
17 Fermentative hydrogen production in batch experiments using lactose, cheese whey and glucose:
18 influence of initial substrate concentration and pH. *Int. J. Hydrogen Energy*, 33, 4989-4997.
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24 6) Data on glucose consumption and fermentation metabolites should be provided. A COD balance
25 should also be done.
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27
28 **Response:** Residual glucose concentration of Hydrogen Production Medium (HPM) was
29 measured after 8 days of incubation using the peroxidase-glucose oxidase method from the D-
30 Glucose assay kit (Boehringer Mannheim). In all batch tests, glucose was not detectable (< 80
31 mg/l).
32

33 The manuscript has been revised according to the reviewer's suggestions. In the section of "Batch
34 test for hydrogen production" of Material and Methods, the following sentence has been added
35 (Page 4, lines 158-159):
36

37
38 *"After 8 days of incubation, residual glucose in the HPM medium was measured using the*
39 *peroxidase-glucose oxidase method from the D-Glucose assay kit (Boehringer Mannheim)."*
40

41 Moreover, in the Results and Discussion (Page 6, lines 243-244), the following sentence has been
42 inserted:
43

44
45 *"After 8 days of incubation, glucose was completely depleted in all the batch tests"*
46
47

48 Data about metabolites and COD balance were not reported because this paper aimed at the
49 definition of a proper granular sludge heat treatment to obtain the highest hydrogen yields from the
50 resulting microbial populations.

51 Results showed that heat treatment has reduced the size of microbial population of treated sludges,
52 selecting the bacteria having the best hydrogen production performances at the pH of 5.5.

53 These strains (both as pure cultures and microbial consortium) will be evaluated in further studies to
54 analyse their fermentative performances from glucose and other substrates. We believe that data
55 about metabolites represent a more interesting information if they are related to a specific
56 population, as different microbial populations can perform differently depending by the operational
57 conditions.
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59 We agree with the reviewer on the fact that the COD balance is a powerful tool to evaluate the
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performances of fermentation process. We also believe that a COD balance is an essential tool whether complete modelling (biomass growth yields, hydrolysis and uptake rates, products and by-products formation) of biological processes is done using data from experimental tests. Therefore, in the present work, we decided to evaluate only cumulative hydrogen productions using the same equation (Equation [1]) to compare the different results. Moreover, no data about the biomass growth yields and consumption rates have been reported because the inoculum utilized for the batch test was not only composed of living (active) biomass due to the effect of heat treatment. In fact, as already answered to question n°1, the heat treated sludges had the same VS but not the same amount of viable organisms.

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1 **Title: EFFECTS OF HEAT TREATMENT ON MICROBIAL COMMUNITIES OF**
2 **GRANULAR SLUDGE FOR BIOLOGICAL HYDROGEN PRODUCTION**

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5 **Authors:** Luca Alibardi¹, Lorenzo Favaro², Maria Cristina Lavagnolo¹, Marina Basaglia², Sergio
6 Casella^{2*}

7
8
9 **Affiliation:** ¹ Department of Civil, Environmental and Architectural Engineering, University of Padova,
10 Lungargine Rovetta 8, 35127 Padova, Italy.
11 luca.alibardi@unipd.it, mariacristina.lavagnolo@unipd.it
² Department of Agronomy Food Natural Resources Animals and Environment (DAFNAE),
12 University of Padova, Agripolis, Viale dell'Università 16, 35020 Legnaro (PD), Italy
13 lorenzo.favaro@unipd.it, marina.basaglia@unipd.it, sergio.casella@unipd.it
14
15

16
17 * Corresponding author:
18 **Prof. Sergio Casella**
19 e-mail: sergio.casella@unipd.it
20 telephone: +39 049-8272922
21 fax: +39 049-8272929
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23

24 **Abstract**

25
26 Dark fermentation shares many features with anaerobic digestion with the exception that to
27 maximize hydrogen production, methanogens and hydrogen consuming bacteria should be
28 inhibited. Heat treatment is widely applied as inoculum pre-treatment due to its effectiveness in
29 inhibiting methanogenic microflora but it may not exclusively select for hydrogen producing
30 bacteria. This work evaluated the effects of heat treatment on microbial viability and structure of
31 anaerobic granular sludge. Heat treatment was carried out on granular sludge at 100°C with four
32 residence times (0.5, 1, 2 and 4 hours). Hydrogen production of treated sludges were studied from
33 glucose by means of batch test at different pH values.

34 **Results indicated that each heat treatment strongly influenced the granular sludge resulting in**
35 **microbial communities having different hydrogen productions. The highest hydrogen yields (2.14**
36 **mole of hydrogen per mole of glucose) were obtained at pH 5.5 using the sludge treated for 4 hour**
37 **characterized by the lowest CFU concentration (2.3 x 10³ CFU/g sludge). This study demonstrated**
38 **that heat treatment should be carefully defined according to the structure of the sludge microbial**
39 **community allowing the selection of highly efficient hydrogen producing microbes.**

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41 **Keywords:** bio-hydrogen; dark fermentation; granular sludge; heat treatment; microbial
42 communities.
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52 **Introduction**

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54 Increasing attention is currently being focused on hydrogen, in an attempt to reduce the
55 consumption of fossil fuels and their impact on climate changes. Hydrogen may be considered a
56 truly clean energy source only if the emission of greenhouse gasses is avoided, even during the
57 production phase. In this perspective, biological hydrogen production processes represent a
58 sustainable opportunity. In fact, hydrogen producing bio-processes involve CO₂ emissions, but from
59 biogenic sources, thus not contributing to the green house effect **due to the brevity of the carbon**
60 **cycle** (Hellenbeck, 2009).

61 Hydrogen is biologically produced by means of two microbial processes: photosynthesis and
62 anaerobic fermentation. **Hydrogen** production by fermentative bacteria, not light dependent, is
63 known as “dark fermentation” and takes place during the fermentative phase of anaerobic digestion.
64 Dark fermentation represents not only an energy production process but also a first stage of
65 stabilization for organic substrates since it degrades complex organic matter to readily
66 biodegradable compounds (volatile fatty acids and alcohols) suitable for methane production by
67 anaerobic digestion (Kapdan and Kargi, 2006).

68 During anaerobic digestion, hydrogen is formed as an intermediate product with H₂ producers and
69 H₂ consumers microbes working together to finally produce methane. In order to maximize
70 hydrogen production via dark fermentation, methanogens and hydrogen consuming bacteria should
71 be inhibited. Moreover, optimal process conditions, as type and pre-treatment of inoculum, pH,
72 temperature and substrate characteristics, should be defined in order to promote the metabolic
73 pathways resulting in hydrogen production (Liu and Fang, 2002).

74 Anaerobic sludges collected from full scale digesters are frequently reported to be used as inoculum
75 for hydrogen production and their pre-treatments are essential for the inhibition of methanogenic
76 microbial species. Several methods have been proposed to achieve this aim, including heat
77 treatment, acidification, basification, freezing or dehydration (Van Ginkel and Sung, 2001; **Ting et**
78 **al., 2004**; Kawagoshi *et al.*, 2005; **Tommasi et al., 2008**).

79 Heat treatment is widely applied due to its effectiveness on methanogenic inhibition. Different
80 temperatures and residence times should be defined according to the structure of the microbial
81 community in the sludge (Alibardi *et al.*, 2009). Temperature values reported in literature range
82 from 50° to 105° C while residence times are described to be efficient from 30 to 300 minutes (Lay
83 *et al.*, 1999; Kapdan and Kargi, 2006).

84 Although heat treatment aims to kill methanogens, it does not select exclusively for hydrogen
85 producing bacteria. Therefore, while spore-forming H₂-consuming bacteria can survive, non-spore
86 forming hydrogen-producers may be inactivated. Rather than increasing H₂ production, heat
87 treatment may actually negatively affect H₂ yield (Kraemer and Bagley, 2007).

88 There is little information about the effects on microbial viability and hydrogen productivity of the
89 inoculum due to increasing heat treatment durations and particularly on the use of temperature to
90 enrich granular sludge of efficient H₂-producing bacteria. **This work evaluated the potential of heat**
91 **treatment as enrichment strategy of granular sludge to select H₂-producing microbial consortia with**
92 **promising yields, even in view of the future development of efficient microbial inoculants.** The
93 effects of heat treatment were evaluated on the microbial viability and community structure of
94 granular sludge. The hydrogen production performances of treated sludges were studied by means
95 of batch test at different pH values. Hydrogen productions were assessed also using a mathematical
96 model applied to cumulative hydrogen productions.

97
98 **Materials and methods**

99
100 **Sludge pre-treatment**

101 Granular sludge used as inoculum for batch test was collected from a full scale Upflow Anaerobic
102 Sludge Blanket (UASB) anaerobic digester treating wastewater of a brewery factory located in

103 Padova, Italy. Total solids (TS) and volatile solids (VS) of granular sludge were 16% and 76%,
104 respectively. Total organic carbon (TOC), total kjeldahl nitrogen (TKN) and total phosphorus
105 were 30%, 3.8%, 0.1% referred to TS, respectively. TS, VS, TKN and total phosphorus were
106 analysed according to standard methods (APHA, 1999). Organic carbon was quantified using a
107 Total Carbon Analyzer (TOC-V CSN, Shimadzu).

108 Heat treatment was carried out on granular sludge in a rotary water bath incubator at a fixed
109 temperature of 100°C with four increasing residence times (0.5, 1, 2 and 4 hours). After each
110 treatment, samples of sludge were used as inoculum of batch test for hydrogen production.

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112

113 **Microbiological analyses**

114 To study the effects of heat treatment on the microbial viability of inoculum, samples of heat treated
115 and non-treated sludges were dispersed into an aqueous suspension by vortexing in sterile 0.9%
116 NaCl solution for 5 minutes. The suspensions were serially diluted, plated on Nutrient Agar (NA)
117 medium (pH 7.0, Sigma) and incubated at 37°C under aerobic and anaerobic conditions for 5 days
118 after which CFU (Colony Forming Units) were **determined**. Anaerobic conditions were obtained in
119 anaerobic jars (OXOID) flushed with N₂ gas. Experiments were conducted in triplicate.

120 From each sampling, about 60 colonies were randomly **collected** from plates, purified by streaking
121 twice and stored as stock cultures in 20% (v/v) glycerol at -80° C for their genetic identification as
122 described below.

123

124 **Genetic identification of microbial strains**

125 Bacterial strains, aerobically and anaerobically isolated as reported before, were genetically
126 identified by 16S rDNA sequencing. Genomic DNA was extracted as follows: a small colony of
127 each strain, grown for 24 h on NA plates, were picked up with a sterile toothpick and resuspended
128 in 50 µL of lysis solution (0.05 M NaOH, 0.25 % SDS). The suspension was heated at 94 °C (15
129 min) and then centrifuged (10,000 x g, 15 min).

130 Prokaryotic small rDNA subunits were amplified using bacterial universal primers 1389r and 63F
131 as described in Hongoh *et al.* (2003). Amplification products were **visualized** by agarose gel
132 electrophoresis and then subjected to sequencing. Species identification was done after BLASTN
133 alignment (NCBI, 2011) of the obtained sequences with those present in the GenBank public
134 database. A minimum sequence similarity level of 96% was considered for taxonomic attribution,
135 **although the majority of the isolates showed a similarity level higher than 98%.**

136

137 **Batch test for hydrogen production**

138 Batch reactors, 0.5 litre Pyrex vessels, were filled with 250 ml of hydrogen production medium
139 (HPM) contained glucose (5 g/l) and yeast extract (3 g/l) (Oh *et al.*, 2003). The pH of HPM was
140 buffered at 5.5 and 7.0 using MES (2-N-Morpholino-EthaneSulfonic acid, Sigma). Phosphate buffer
141 was used to adjust the pH at 8.5. Different pH values of the medium were used to evaluate the
142 hydrogen production performances at optimal environmental conditions for hydrogen producing
143 microbes (acid pH values: 4.5-6.0) as well as for methanogenic bacteria (neutral to basic pH
144 values:7.0-8.0) (Cooney *et al.*, 2007).

145 After pH adjustment, HPM medium and the vessels were sterilized by autoclave (121° C, 20
146 minutes) in order to evaluate the performances of the bacteria introduced exclusively with the
147 sludge that was aseptically transferred into the reactors as inoculum.

148 Food to microorganism ratio (F/M) was set at 1 gVS/gVS. **Since heat treatment did not change the**
149 **TS and VS of the sludge**, every reactor was inoculated with 10 grams of treated or non-treated
150 sludge.

151 After inoculation, the reactors were hermetically closed using a silicon plug. Once flushed with N₂
152 gas for 3 minutes, the vessels were incubated without stirring in a thermostatic chamber at 35° ±
153 2°C.

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154 The amount of biogas produced was recorded daily, using the water displacement method. Biogas
155 composition in terms of hydrogen, carbon dioxide and methane were measured by a gas
156 chromatograph (HP5890) equipped with thermal conductivity detector (TCD), HP- MOLSIV and
157 HP-PLOT U columns, nitrogen as carrier gas.

158 After 8 days of incubation, residual glucose in the HPM medium was measured using the
159 peroxidase-glucose oxidase method from the d-Glucose assay kit (Boehringer Mannheim). All
160 experiments were carried out in triplicate for each treated sludge and pH value. The obtained results
161 were averaged.

162 **Mathematical model of cumulative hydrogen production**

163 Cumulative hydrogen productions from experimental tests were analysed using a mathematical
164 model in order to compare the results. Hydrogen productions have been modelled using the
165 following equation:

$$166 \quad P(t) = P_{tot} \frac{t}{K_t + t} \quad [1]$$

167
168
169 Where:

170 $P(t)$: cumulative hydrogen production at time t (Nml/g);

171 P_{tot} : maximum cumulative hydrogen production (Nml/g);

172 K_t : time at which the cumulative hydrogen production is half of the maximum (h);

173 t : time of fermentation from the beginning of the test (h).

174
175 Average values of cumulative hydrogen production from each experimental condition were used to
176 obtain the values of the parameters P_{tot} and K_t . These parameters were estimated by minimizing
177 the sum square of errors between experimental data and results from the model. The estimations
178 were carried out by using the ‘Solver’ function in Calc of OpenOffice.

179 **Statistical analysis.**

180 The results presented in this study are the average of a minimum of three repetitions. The bars in
181 Figure 1 represent standard deviation. Statistical analysis of cumulative hydrogen productions was
182 performed by two ways factorial ANOVA (ANalysis Of Variance) using Duncan test *post hoc*
183 means differentiation. Heat treatment duration and pH medium were the factors considered in
184 ANOVA.

185 **Results and discussion**

186 **Effects of heat treatment on microbial viability and community structure of granular sludge**

187 The non-treated sludge and the treated sludge (boiled at 100°C for 0.5, 1, 2 and 4 hours) were
188 characterized for their microbial viability and results are reported in Table 1. All tested sludges,
189 heat treated and non-treated, showed a higher number of microbial colonies when plates were
190 anaerobically incubated. This evidence could be explained considering that the used granular sludge
191 was collected from an industrial scale UASB anaerobic digester where most of microbial species
192 had adapted to grow at very low oxygen concentration in the environment.

193 The non-treated granular sludge presented 1.3×10^7 CFU/g and 5.5×10^6 CFU/g after anaerobic and
194 aerobic incubation of plates, respectively. As shown in Table 1, heat treatment strongly affected the
195 sludge microbial viability. When determined in anaerobic condition, the viability of the granular
196 sludge dropped from 1.3×10^7 CFU/g of the non-treated sludge to the 1.0×10^5 CFU/g of the sludge
197 boiled only for 0.5 hours.

198 Heat treatment of granular sludge strongly influenced also its microbial community structure
199 (Table 2). The bacterial community structure of the non-treated sludge was quite similar to those
200 reported for twelve granular sludges collected from different types of full-scale UASB reactors

204 (Narihiro *et al.*, 2009). Bacterial 16S rDNA sequencing of microbial strains isolated from the non-
 205 treated sludge revealed that the most dominant phylum was *Proteobacteria* with about 59% of the
 206 identified isolates. The main species was *Sphingopyxis granuli* (12%), recently isolated from a
 207 brewery wastewater-treating UASB reactor (Kim *et al.*, 2005). The remaining bacterial isolates
 208 belong to the *Firmicutes* phylum and were mainly affiliated to the *Bacillaceae* family.
 209

210 Table 1. Effect of the thermal treatments on granular sludge microbial viability.

Duration of heat treatment (100°C) on granular sludge	CFU/g sludge	
	Aerobic incubation	Anaerobic incubation
No heat treatment	$5.5 \pm 0.5 \times 10^6$	$1.3 \pm 0.2 \times 10^7$
0.5 hour	$3.5 \pm 0.4 \times 10^4$	$1.0 \pm 0.1 \times 10^5$
1 hour	$1.6 \pm 0.1 \times 10^4$	$4.5 \pm 0.5 \times 10^4$
2 hours	$6.5 \pm 0.1 \times 10^2$	$3.3 \pm 0.2 \times 10^3$
4 hours	$1.5 \pm 0.3 \times 10^2$	$2.3 \pm 0.6 \times 10^3$

211
 212
 213 Table 2. 16S rDNA sequencing of bacterial strains aerobically and anaerobically isolated from non-
 214 treated and 0.5, 1, 2, 4 hours treated granular sludge.
 215

Phylum	Closest species in GenBank	Number of isolates identified in granular sludge samples				
		non-treated	0.5 h	1 h	2 h	4 h
Firmicutes	<i>Bacillus</i> sp.	5.9 ^a	25.0	26.9	45.5	12.5
	<i>Bacillus badius</i>	5.9	25.0	23.1	-	-
	<i>Bacillus beijingensis</i>	-	9.4	7.7	-	-
	<i>Bacillus farraginis</i>	-	3.1	7.7	9.1	37.5
	<i>Bacillus flexus</i>	-	-	3.8	-	-
	<i>Bacillus licheniformis</i>	2.9	3.1	7.7	-	-
	<i>Bacillus megaterium</i>	2.9	-	-	-	-
	<i>Brevibacillus</i> sp.	-	6.3	-	9.1	12.5
	<i>Brevibacillus brevis</i>	-	-	11.5	-	-
	<i>Brevibacillus parabrevis</i>	2.9	-	-	-	12.5
	<i>Paenibacillus</i> sp.	2.9	6.3	3.8	18.2	25.0
	<i>Paenibacillus cookii</i>	-	-	3.8	9.1	-
	<i>Planomicrobium</i> sp.	-	3.1	-	-	-
	<i>Sporosarcina</i> sp.	2.9	6.3	3.8	9.1	-
	<i>Staphylococcus saprophyticus</i>	8.8	-	-	-	-
	<i>Staphylococcus</i> sp.	5.9	-	-	-	-
Proteobacteria	<i>Alcaligenes</i> sp.	8.8	-	-	-	-
	<i>Alishewanella</i> sp.	8.8	-	-	-	-
	<i>Enterobacter</i> sp.	8.8	6.3	-	-	-
	<i>Enterobacter cloacae</i>	-	3.1	-	-	-
	<i>Pseudomonas</i> sp.	8.8	-	-	-	-
	<i>Shinella</i> sp.	8.8	-	-	-	-
	<i>Sphingopyxis granuli</i>	11.8	-	-	-	-
	Uncultured beta proteobacterium	2.9	-	-	-	-

216 ^a Frequency of isolates assigned with a genus or species in percentage of the total number of
 217 isolates analyzed for each sample of sludge.
 218

218 Once boiled for only 0.5 hour, the sludge exhibited a considerable reduction of the microbial
 219 diversity: *Firmicutes* became the predominant phylum, accounting for the 90% of the microbial
 220 strains. The remaining isolates, belonging to *Enterobacter* sp. and *E. cloacae*, were affiliated with
 221 *Proteobacteria* phylum. Therefore, the sludge was mainly enriched with spore-forming microbes,
 222 capable of withstand the thermal stress. However, few isolates of non-spore forming bacteria
 223 (*Planomicrobium* sp. and *Enterobacter* sp.) were detected. This finding may be explained
 224 considering that the complex structure of the granules in the sludge could have allowed them to
 225 tolerate the short thermal stress. Longer heat treatments, indeed, exclusively selected for spore-
 226 forming bacteria affiliated with *Firmicutes* phylum (Table 2). After 1 hour, the most abundant
 227 known species were *Bacillus badius* (23%) and *Brevibacillus brevis* (11%); however a significant
 228 amount of unknown *Bacillus* sp. was also present (27%). As a result, in the 1 hour heat treated
 229 sludge, the predominant genus was found to be *Bacillus* sp.. This genus represents strict or
 230 facultative aerobes having diverse metabolic activities potentially useful in the treatment of
 231 wastewater and in the production of hydrogen from several organic wastes (Kalia and Purohit,
 232 2008).

233 Increasing the heat treatment times resulted in the reduction of both size and microbial structure of
 234 granular sludge (Table 1 and 2). The main genera of the 2 hours heat-treated sludge were *Bacillus*
 235 sp. and *Paenibacillus* sp. while, after 4 hours boiling time, the majority of the isolates belonged to
 236 *B. farraginis* and *Paenibacillus* sp..

237 **Effects of heat treatment on hydrogen production of granular sludge**

238 The average cumulative hydrogen productions obtained from tested experimental conditions are
 239 reported in Table 3. Equation [1] resulted the best fitting mathematical model of the experimental
 240 data of cumulative hydrogen productions. The parameters P_{tot} and Kt obtained from the
 241 Equation [1] are reported in Table 3. Cumulative hydrogen productions at different pH values of the
 242 heat-treated granular sludges are represented in Figure 1. **After 8 days of incubation, glucose was
 243 completely depleted in all the batch tests.**

244 **Table 3. Average cumulative hydrogen productions (\pm SD, n=3), hydrogen yields and mathematical
 245 model results. Hydrogen productions are normalized to glucose added to batch tests.**

Test conditions		Average experimental results		Mathematical model results	
Duration of heat treatment (h)	pH	Cumulative hydrogen production per gram of glucose (Nml/g)	Hydrogen production per mole of glucose (mol H ₂ /mol)	Cumulative hydrogen production P_{tot} (Nml/g)	Kt value (h)
4	5.5	265 \pm 10 ^f	2.14	272	4.3
	7.0	180 \pm 5 ^{de}	1.44	184	3.1
	8.5	58 \pm 14 ^a	0.47	59	3.0
2	5.5	226 \pm 27 ^{ef}	1.82	244	12.0
	7.0	183 \pm 17 ^{de}	1.47	194	8.6
	8.5	57 \pm 16 ^a	0.47	59	7.4
1	5.5	161 \pm 21 ^d	1.30	168	6.0
	7.0	110 \pm 32 ^{bc}	0.88	115	6.5
	8.5	51 \pm 20 ^a	0.41	52	4.8
0.5	5.5	171 \pm 5 ^d	1.38	175	2.9
	7.0	150 \pm 5 ^{cd}	1.21	156	5.8
	8.5	102 \pm 5 ^b	0.82	104	3.9

249 Means with different superscript letters are significantly different ($p \leq 0.01$).

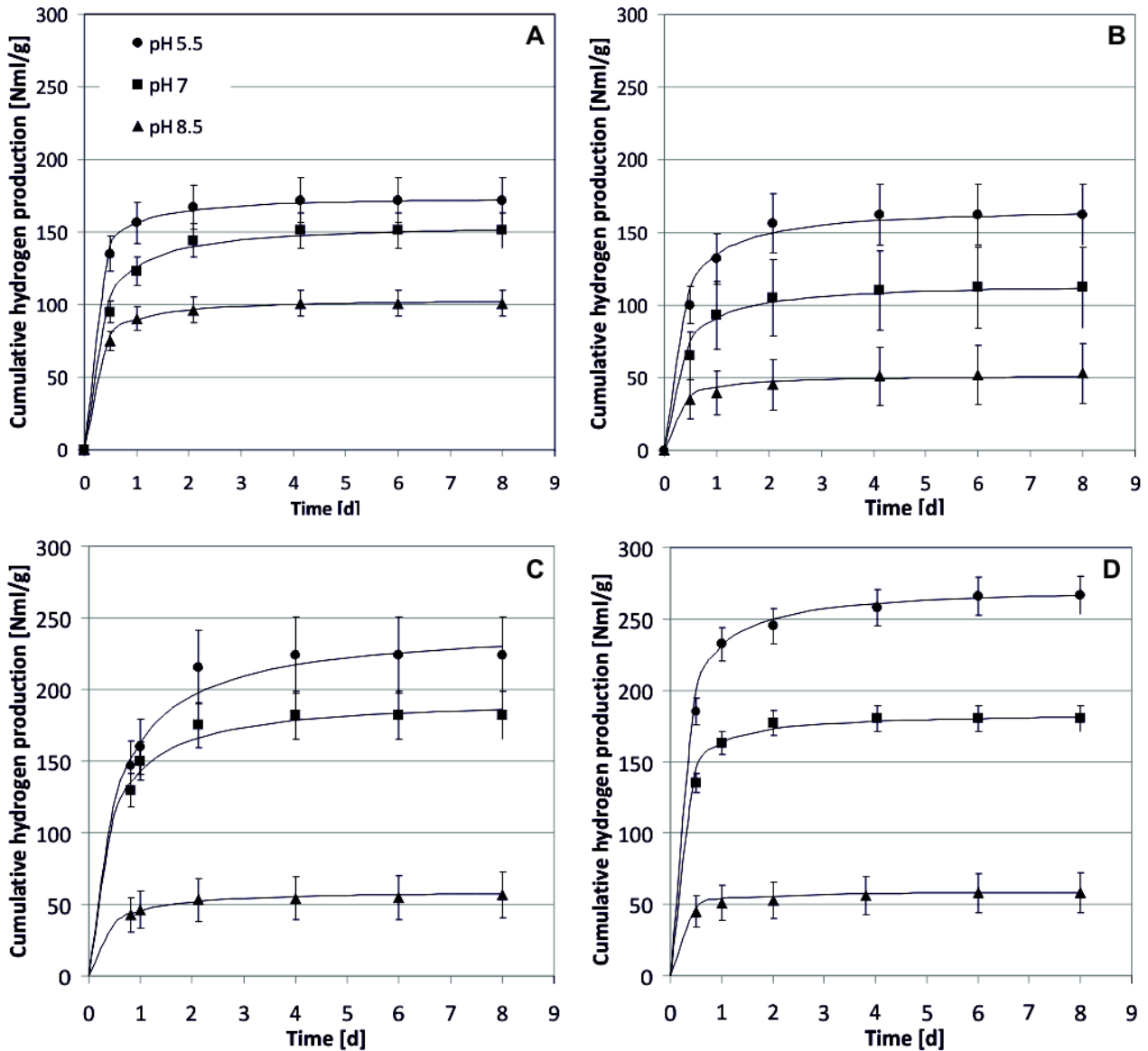


Figure 1. Cumulative hydrogen productions from average experimental data (symbols) and from the mathematical model (continuous line) at the three pH levels of the sludge heat-treated for 0.5 hour (A), 1 hour (B), 2 hours (C) and 4 hours (D). Error bars represent the standard deviation of experimental data.

During all hydrogen production batch tests no methane was detected, even at pH values favourable for methane producing microbes (7.0 and 8.5). On the contrary, when non-treated sludge was used as inoculum during batch tests, the system under study produced only methane and not hydrogen at all pH values (data not shown). Thermal pre-treatments were therefore efficient in the inhibition of the methanogenic bacteria.

It is evident from Figure 1 that pH had a clear effects on hydrogen production potentials. The higher the initial pH, the lower the total hydrogen production was ($p \leq 0.01$). In the tested conditions, the highest hydrogen levels were obtained with pH 5.5. This is in accordance with earlier works where this pH value was reported as optimal for hydrogen production (Lay *et al.*, 1999; Van Ginkel and Sung, 2001; Kapdan and Kargi, 2006).

As shown in Table 3, the heat treatment resulted in a marked effect on hydrogen production performances ($p \leq 0.01$). Increasing the treatment duration resulted in increasing hydrogen production levels. The tests inoculated with sludge treated for 0.5 and 1 h boiling time (Figure 1 A,B) converted glucose into H_2 at lower levels than those with the 2 and 4 hour treated

270 sludge (Figure 1 C,D). This indicates that inoculum thermal conditioning efficiently selected in the
 271 sludge the microbial species mainly involved in the hydrogen production: under the most
 272 favourable pH conditions, the higher levels of H₂ production were obtained with longer duration of
 273 sludge treatment. This finding is confirmed by ANOVA analysis showing that the interaction
 274 between pH and thermal duration was statistically significant ($p \leq 0.01$).

275 Highest hydrogen production was achieved using 4 hour heat-treated sludge. The yield of 2.14
 276 moles of hydrogen per mole of glucose obtained at pH 5.5 with the 4 hour treated sludge seems to
 277 be promising if compared to those previously reported from glucose (Table 4).
 278

279 **Table 4. Comparison of hydrogen yields from different studies. All the data regard batch**
 280 **experiments using glucose as substrate and mixed culture as inoculum.**
 281

Reference	Inoculum	Inoculum pre-treatment	Fermentation temperature	Fermentation pH	Hydrogen yields (mol H ₂ /mol glucose)
This study	UASB granular sludge	heat treatment (100°C, 4 h)	35°C	5.5	2.14
This study	UASB granular sludge	heat treatment (100°C, 2 h)	35°C	5.5	1.82
Davila-Vazquez <i>et al.</i> (2008)	UASB granular sludge	heat treatment (100°C, 40 min)	37°C	7.5	1.46
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	35°C	5.5	1.00
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	41°C	5.5	1.67
Morimoto <i>et al.</i> (2004)	sludge compost	aerobic conditions (60°C, 3 days)	60°C	3.97*	2.1
Morimoto <i>et al.</i> (2004)	anaerobic pond sludge	-	50°C	4.02*	1.6
Morimoto <i>et al.</i> (2004)	compost	-	60°C	-	1.5
Logan <i>et al.</i> (2002)	soil used for tomato plants	heat treatment (104°C, 2 h)	26°C	6	0.92
Fang and Liu (2002)	anaerobic sludge from a CSTR reactor	-	36°C	5.5	2.1

* final pH

284 Analysing the data reported in Table 3, the hydrogen productions at pH 7.0 and 8.5 obtained
 285 with 0.5 hour heat treatment were statistically higher ($p \leq 0.01$) than those achieved with 1 hour heat-
 286 treated sludge. On the contrary, at pH 5.5, the productions were similar. This observation could
 287 suggest that different species of hydrogen consuming and/or non hydrogen forming bacteria could
 288 be still present and may have negatively affected the net amount of produced H₂. Moreover, non
 289 spore-forming hydrogen producers, able to survive after 0.5 h of heat treatment, may be killed once
 290 exposed to longer treatment. In this case, rather than increasing H₂ production, heat treatment have
 291 actually reduced H₂ yield at the considered pH values. This is in accordance with Kraemer and
 292 Bagley (2007), reporting contradictory results on beneficial or negative effects of heat treatment
 293 compared to non-heat-treated systems and other inoculum conditioning methods (Zhu and Bèland,
 294 2006).

295 These observations seem to be confirmed considering the results of the bacterial 16S rDNA
296 sequencing (Table 2). The *Enterobacter* sp. and *E. cloacae* isolates, present in the 0.5 hour heat-
297 treated sludge, may have enhanced hydrogen productions at level higher than those detected in the
298 1 hour treated sludge having only species affiliated with *Firmicutes* phylum. The *Enterobacter*
299 genus, indeed, has been largely studied for H₂ production from glucose, sucrose and other substrates
300 (Kalia and Purohit, 2008).

301 Half of the maximum cumulative hydrogen production (P_{tot}) was obtained within the first 12 hours
302 as indicated by the Kt values (Table 3). No clear correlation was observed between the Kt values
303 and the heat pre-treatment duration. Low Kt values were measured both for long (4 hours) and for
304 short (0.5 hour) pre-treatments while higher Kt values were observed for tests at two hours of heat
305 pre-treatment even though the cumulative hydrogen productions were not the lowest. These
306 findings may be explained considering that each boiling duration have selectively enriched the
307 sludge with mixed microbial consortia (Table 2) having different hydrogen production potentials.
308 As a consequence, the most interesting hydrogen kinetics seem to be those obtained by the 4 hour
309 treated sludge having both the lowest Kt values and the highest cumulative hydrogen production
310 (P_{tot}).

311 The effects of heat-treatment on microbial community of sludge can be highlighted comparing the
312 data reported in Table 1 and Table 3. In fact after heat-treatment, the size of the microbial
313 population clearly decreased and the survived bacteria performed variable hydrogen yields at
314 different pH. This finding suggests that the treatments themselves produced an evident selection
315 within the entire microbial population.

316 Although the microbiological analyses reported that the 4 hour treatment strongly affected the
317 sludge microbial viability (Table 1), the lowest concentration of bacteria (2.33×10^3 CFU/g of
318 sludge in anaerobic conditions, corresponding to about 10^2 CFU per ml of suspension) exhibited the
319 best hydrogen yield at pH 5.5 (Table 3). These results could suggest that the 4 hour boiling
320 treatment resulted in the selection of the dominant microbial consortia of proficient hydrogen
321 producing microbes. Therefore, the isolates able to survive after the longest heat treatment duration,
322 mainly *B. farraginis* and *Paenibacillus* sp. (Table 2), may have the most promising hydrogen
323 yields.

324 325 **Conclusions**

326 This study showed that the 4 hour treatment seems to be efficient for the selection of microbial
327 populations exhibiting the best hydrogen performances. However, in order to maximize the
328 hydrogen production yields, the optimal combination of heat treatment duration and pH value
329 should be defined. As the highest hydrogen productions were obtained using the lowest microbial
330 concentrations, it is presumable that microbial strains capable of surviving after 4 hour boiling time
331 are very interesting as hydrogen producing bacteria. These isolates, belonging to the *Bacillaceae*
332 family, will be studied as selected inoculants with outstanding ability to produce hydrogen from
333 organic wastes and wastewater for industrial scale purposes.

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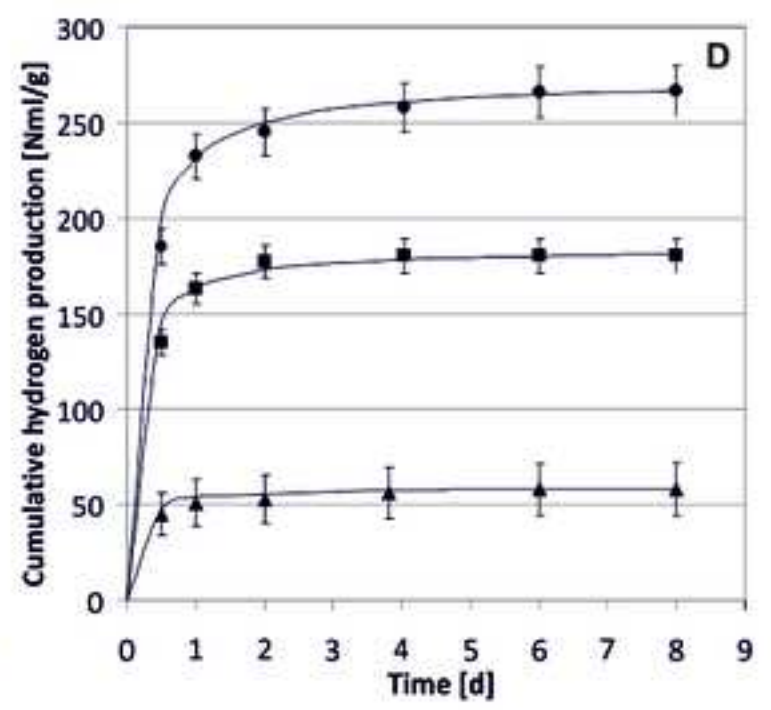
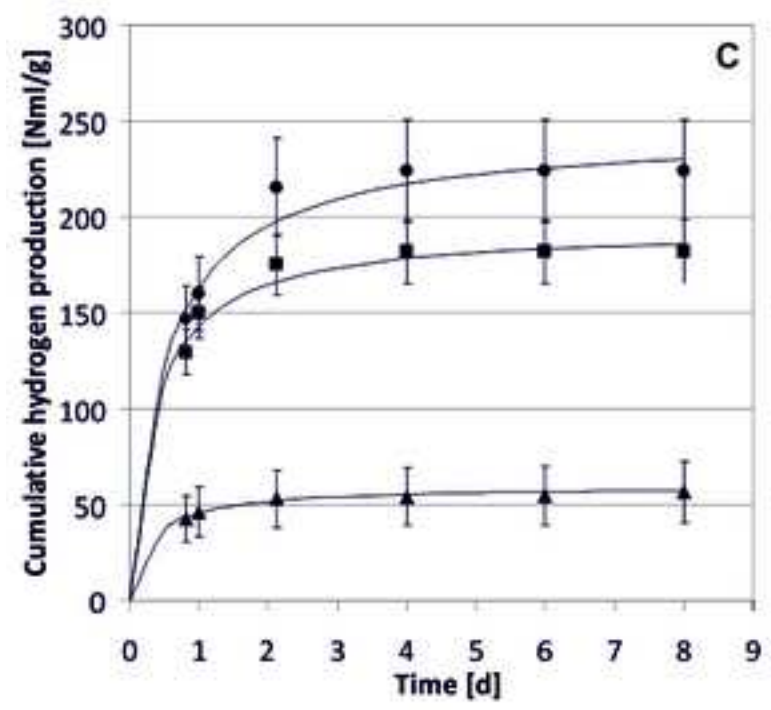
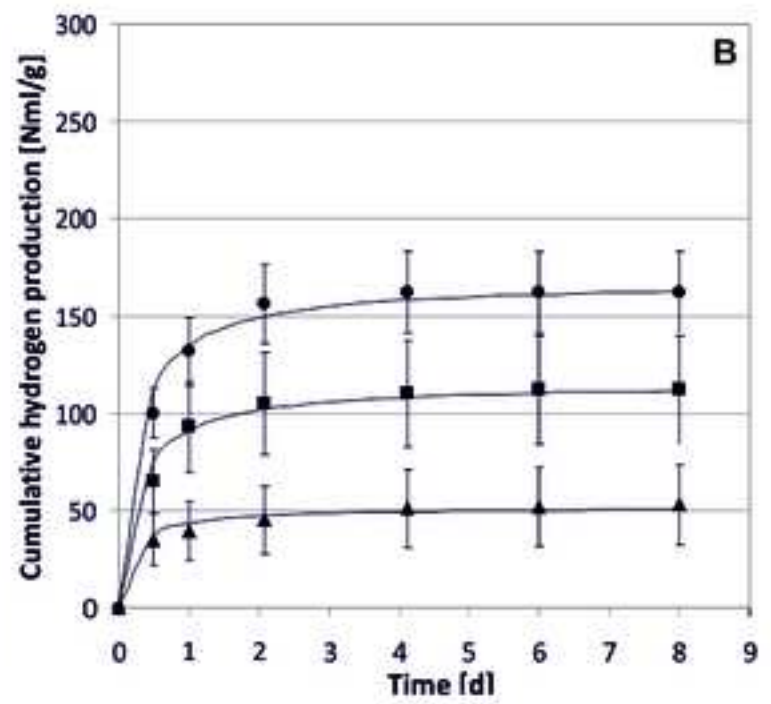
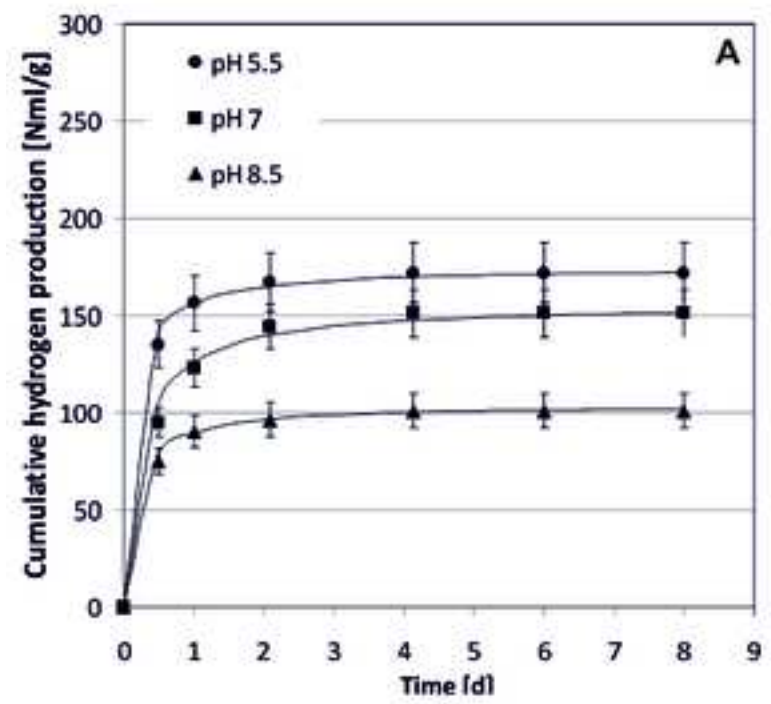
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Figure
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1
2 Table 1. Effect of the thermal treatments on granular sludge microbial viability.

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Duration of heat treatment (100°C) on granular sludge	CFU/gram sludge	
	Aerobic incubation	Anaerobic incubation
No heat treatment	$5.5 \pm 0.5 \times 10^6$	$1.3 \pm 0.2 \times 10^7$
0.5 hour	$3.5 \pm 0.4 \times 10^4$	$1.0 \pm 0.1 \times 10^5$
1 hour	$1.6 \pm 0.1 \times 10^4$	$4.5 \pm 0.5 \times 10^4$
2 hours	$6.5 \pm 0.1 \times 10^2$	$3.3 \pm 0.2 \times 10^3$
4 hours	$1.5 \pm 0.3 \times 10^2$	$2.3 \pm 0.6 \times 10^3$

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Table 2. 16S rDNA sequencing of bacterial strains aerobically and anaerobically isolated from non-treated and 0.5, 1, 2, 4 hours treated granular sludge.

Phylum	Closest species in GenBank	Number of isolates identified in granular sludge samples				
		non-treated	0.5 h	1 h	2 h	4 h
Firmicutes	<i>Bacillus</i> sp.	5.9 ^a	25.0	26.9	45.5	12.5
	<i>Bacillus badius</i>	5.9	25.0	23.1	-	-
	<i>Bacillus beijingensis</i>	-	9.4	7.7	-	-
	<i>Bacillus farraginis</i>	-	3.1	7.7	9.1	37.5
	<i>Bacillus flexus</i>	-	-	3.8	-	-
	<i>Bacillus licheniformis</i>	2.9	3.1	7.7	-	-
	<i>Bacillus megaterium</i>	2.9	-	-	-	-
	<i>Brevibacillus</i> sp.	-	6.3	-	9.1	12.5
	<i>Brevibacillus brevis</i>	-	-	11.5	-	-
	<i>Brevibacillus parabrevis</i>	2.9	-	-	-	12.5
	<i>Paenibacillus</i> sp.	2.9	6.3	3.8	18.2	25.0
	<i>Paenibacillus cookii</i>	-	-	3.8	9.1	-
	<i>Planomicrobium</i> sp.	-	3.1	-	-	-
	<i>Sporosarcina</i> sp.	2.9	6.3	3.8	9.1	-
	<i>Staphylococcus saprophyticus</i>	8.8	-	-	-	-
	<i>Staphylococcus</i> sp.	5.9	-	-	-	-
Proteobacteria	<i>Alcaligenes</i> sp.	8.8	-	-	-	-
	<i>Alishewanella</i> sp.	8.8	-	-	-	-
	<i>Enterobacter</i> sp.	8.8	6.3	-	-	-
	<i>Enterobacter cloacae</i>	-	3.1	-	-	-
	<i>Pseudomonas</i> sp.	8.8	-	-	-	-
	<i>Shinella</i> sp.	8.8	-	-	-	-
	<i>Sphingopyxis granuli</i>	11.8	-	-	-	-
	Uncultured beta proteobacterium	2.9	-	-	-	-

^a Frequency of isolates assigned with a genus or species in percentage of the total number of isolates analyzed for each sample of sludge.

Table 3. Average cumulative hydrogen productions (\pm SD, n=3), hydrogen yields and mathematical model results. Hydrogen productions are normalized to glucose added to batch tests.

Test conditions		Average experimental results		Mathematical model results	
Duration of heat treatment (h)	pH	Cumulative hydrogen production per gram of glucose (Nml/g)	Hydrogen production per mole of glucose (mol H ₂ /mol)	Cumulative hydrogen production <i>P_{tot}</i> (Nml/g)	<i>K_t</i> value (h)
4	5.5	265 \pm 10 ^f	2.14	272	4.3
	7.0	180 \pm 5 ^{de}	1.44	184	3.1
	8.5	58 \pm 14 ^a	0.47	59	3.0
2	5.5	226 \pm 27 ^{ef}	1.82	244	12.0
	7.0	183 \pm 17 ^{de}	1.47	194	8.6
	8.5	57 \pm 16 ^a	0.47	59	7.4
1	5.5	161 \pm 21 ^d	1.30	168	6.0
	7.0	110 \pm 32 ^{bc}	0.88	115	6.5
	8.5	51 \pm 20 ^a	0.41	52	4.8
0.5	5.5	171 \pm 5 ^d	1.38	175	2.9
	7.0	150 \pm 5 ^{cd}	1.21	156	5.8
	8.5	102 \pm 5 ^b	0.82	104	3.9

Means with different superscript letters are significantly different ($p \leq 0.01$).

Table 4. Comparison of hydrogen yields from different studies. All the data regard batch experiments using glucose as substrate and mixed culture as inoculum.

Reference	Inoculum	Inoculum pre-treatment	Fermentation temperature	Fermentation pH	Hydrogen yields (mol H ₂ /mol glucose)
This study	UASB granular sludge	heat treatment (100°C, 4 h)	35°C	5.5	2.14
This study	UASB granular sludge	heat treatment (100°C, 2 h)	35°C	5.5	1.82
Davila-Vazquez <i>et al.</i> (2008)	UASB granular sludge	heat treatment (100°C, 40 min)	37°C	7.5	1.46
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	35°C	5.5	1.00
Mu <i>et al.</i> (2006)	waste activated sludge	anaerobic storage for 6 month and heat treatment (85°C, 1h)	41°C	5.5	1.67
Morimoto <i>et al.</i> (2004)	sludge compost	aerobic conditions (60°C, 3 days)	60°C	3.97*	2.1
Morimoto <i>et al.</i> (2004)	anaerobic pond sludge	-	50°C	4.02*	1.6
Morimoto <i>et al.</i> (2004)	compost	-	60°C	-	1.5
Logan <i>et al.</i> (2002)	soil used for tomato plants	heat treatment (104°C, 2 h)	26°C	6	0.92
Fang and Liu (2002)	anaerobic sludge from a CSTR reactor	-	36°C	5.5	2.1

* final pH