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Construction of lactic acid overproducing *Clostridium thermocellum* through enhancement of lactate dehydrogenase expression

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Abstract: Rapid expansion of global market of lactic acid (LA) has prompted research towards cheaper and more eco-friendly strategies for its production. Nowadays, LA is produced mainly through fermentation of simple sugars or starchy biomass (e.g. corn) and its price is relatively high. Lignocellulose could be an advantageous alternative feedstock for LA production owing to its high abundance and low cost. However, the most effective natural producers of LA cannot directly ferment lignocellulose. So far, metabolic engineering aimed at developing microorganisms combining efficient LA production and cellulose hydrolysis has been generally based on introducing designer cellulase systems in natural LA producers. In the present study, the approach consisted in improving LA production in the natural cellulolytic bacterium *Clostridium thermocellum* DSM1313. The expression of the native lactate dehydrogenase was enhanced by functional replacement of its original promoter with stronger ones resulting in a 10-fold increase in specific activity, which resulted in a 2-fold increase of LA yield. It is known that eliminating allosteric regulation can also increase lactic acid production in *C. thermocellum*, however we were unable to insert strong promoters upstream of the de-regulated *ldh* gene. A strategy combining these regulations and inactivation of parasitic pathways appears essential for developing a homolactic *C. thermocellum*.

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Cover letter

Dear Editor,

please find enclosed the manuscript entitled "Construction of lactic acid overproducing *Clostridium thermocellum* through enhancement of lactate dehydrogenase expression". Lactic acid has several applications including the production of biodegradable plastics, namely polylactide and its copolymers. However, a significant reduction of the cost of lactic acid production is necessary to make polylactide cost competitive with oil-derived plastics. Development of microbial strains that combine efficient metabolization of lignocellulose and biosynthesis of lactic acid by metabolic engineering can enable development of cheap single-step fermentation processes. So far, most studies have attempted to confer cellulolytic ability to native lactic acid producers. In the present study, we improved lactic acid production in one of the best cellulose degraders isolated so far, namely *Clostridium thermocellum*. By functional replacement of the original promoter of lactate dehydrogenase with stronger ones we could double lactic acid yield. As far as we know, this is the first example of improvement of lactic acid production in a native cellulolytic microorganism by targeted metabolic engineering. Apart from successful results presented here, the present investigation provided information of complex relationship between fermentative pathways in *C. thermocellum* and hints for further enhancement of lactic acid production in this strain.

We hope that the present study will be worth of interest for publication in Enzyme and Microbial Technology. Waiting for your answer we thank you very much in advance for your attention.

Yours Sincerely,

Roberto Mazzoli



Università degli Studi di Torino
**DIPARTIMENTO di SCIENZE DELLA VITA E
BIOLOGIA DEI SISTEMI**



Torino, May, 28th 2020

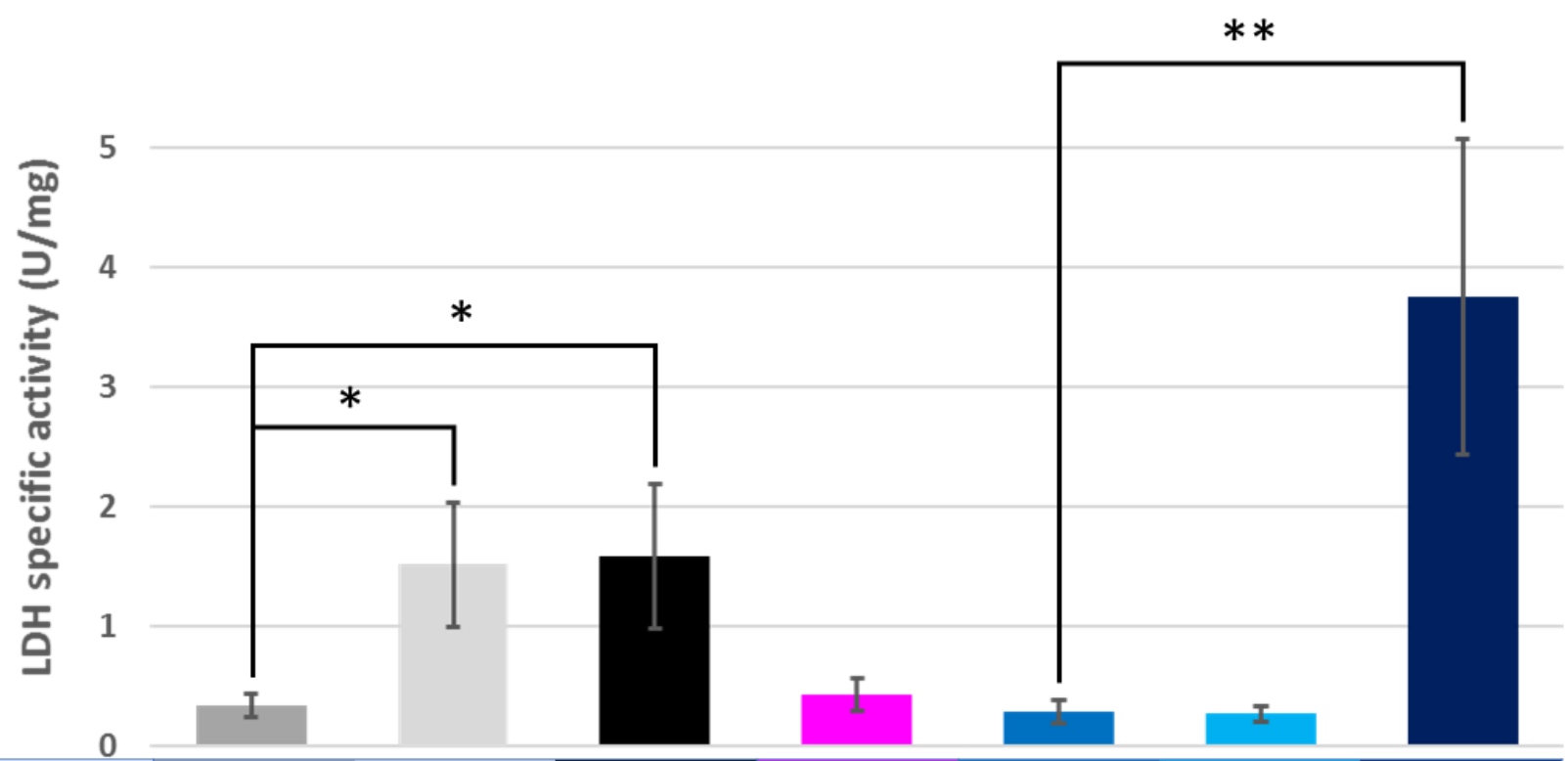
Author agreement

By the present letter, I do certify that all the authors have seen and approved the final version of the manuscript entitled “Construction of lactic acid overproducing *Clostridium thermocellum* through enhancement of lactate dehydrogenase expression” that has being submitted at Enzyme and Microbial Technology. I warrant that the article is the authors' original work, hasn't received prior publication and isn't under consideration for publication elsewhere.

Sincerely yours,

Roberto Mazzoli

A handwritten signature in blue ink, appearing to read "Roberto Mazzoli", written over the printed name.



Strain	LL345	LL1624	LL1640	LL1111	LL1147	LL1625	LL1626
Parent strain	LL345			LL1111	LL1147		
<i>ldh</i> promoter	WT	P _{Thl}	P ₂₆₃₈	WT	WT	P _{Thl}	P ₂₆₃₈
Y _{LA} (mol/mol cellobiose)	0.4 (0.0)	0.8 (0.1)	0.8 (0.1)	2.5 (0.5)	0.2 (0.0)	0.0 (0.0)	0.4 (0.0)

Highlights

- Strong (P_{Th1} , P_{2638}) promoters were inserted upstream of *C. thermocellum ldh* gene
- Functional replacement of *ldh* promoter induced up to 13-fold overexpression of LDH
- Increase of LDH activity doubled lactate yield in engineered *C. thermocellum*
- LDH upregulation induced additional metabolic (ethanol, formate) rearrangements

Abstract

Rapid expansion of global market of lactic acid (LA) has prompted research towards cheaper and more eco-friendly strategies for its production. Nowadays, LA is produced mainly through fermentation of simple sugars or starchy biomass (e.g. corn) and its price is relatively high. Lignocellulose could be an advantageous alternative feedstock for LA production owing to its high abundance and low cost. However, the most effective natural producers of LA cannot directly ferment lignocellulose. So far, metabolic engineering aimed at developing microorganisms combining efficient LA production and cellulose hydrolysis has been generally based on introducing designer cellulase systems in natural LA producers. In the present study, the approach consisted in improving LA production in the natural cellulolytic bacterium *Clostridium thermocellum* DSM1313. The expression of the native lactate dehydrogenase was enhanced by functional replacement of its original promoter with stronger ones resulting in a 10-fold increase in specific activity, which resulted in a 2-fold increase of LA yield. It is known that eliminating allosteric regulation can also increase lactic acid production in *C. thermocellum*, however we were unable to insert strong promoters upstream of the de-regulated *ldh* gene. A strategy combining these regulations and inactivation of parasitic pathways appears essential for developing a homolactic *C. thermocellum*.

Construction of lactic acid overproducing *Clostridium thermocellum* through enhancement of lactate dehydrogenase expression

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Abstract

Rapid expansion of global market of lactic acid (LA) has prompted research towards cheaper and more eco-friendly strategies for its production. Nowadays, LA is produced mainly through fermentation of simple sugars or starchy biomass (e.g. corn) and its price is relatively high. Lignocellulose could be an advantageous alternative feedstock for LA production owing to its high abundance and low cost. However, the most effective natural producers of LA cannot directly ferment lignocellulose. So far, metabolic engineering aimed at developing microorganisms combining efficient LA production and cellulose hydrolysis has been generally based on introducing designer cellulase systems in natural LA producers. In the present study, the approach consisted in improving LA production in the natural cellulolytic bacterium *Clostridium thermocellum* DSM1313. The expression of the native lactate dehydrogenase was enhanced by functional replacement of its original promoter with stronger ones resulting in a 10-fold increase in specific activity, which resulted in a 2-fold increase of LA yield. It is known that eliminating allosteric regulation can also increase lactic acid production in *C. thermocellum*, however we were unable to insert strong promoters upstream of the de-regulated *ldh* gene. A strategy combining these regulations and inactivation of parasitic pathways appears essential for developing a homolactic *C. thermocellum*.

Key words: metabolic engineering, anaerobic bacteria, ethanol, transcriptional promoter, lignocellulose

1 **Introduction**

2 Lactic acid (LA) is among the most requested chemicals worldwide because of its broad range of
3 industrial applications [1]. The latter include the use as food preservative and flavor enhancer,
4 emulsifier and moisturizer in the cosmetic industry, precursor of pharmaceuticals and biodegradable
5 solvents, and building block for the synthesis of plastic polymers, i.e., polylactide (PLA) and its co-
6 polymers [2]. PLAs are biodegradable and biocompatible plastics whose application encompasses
7 several sectors including biomedicine (e.g. surgical thread, orthopedic implants, drug delivery),
8 packaging of food and goods, manufacturing of agriculture mulch films and disposable tableware
9 [2,3]. The potential of PLA to replace fossil-fuel-derived polymers as a general-purpose plastic has
10 been among the main forces driving the current global market expansion of LA. The growth of
11 global LA demand is currently estimated at 16.2% per year [2].

12 LA can be produced by either chemical synthesis from acetaldehyde or by microbial fermentation.
13 However, most (about 90%) LA production plants worldwide are based on fermentation of starchy
14 biomass (mainly corn) [2,4]. Biotechnological production of LA has many advantages over
15 chemical synthesis such as lower energy consumption and environmental concerns and higher
16 purity [2]. In particular, fermentative production can lead to optically pure L- or D-LA, while a
17 racemic mixture of the two LA enantiomers is obtained by chemical synthesis [5]. It is worth
18 remembering that a precise mixture of D- and L-LA is required for production of PLA with desired
19 physical-chemical characteristics [5]. Yet, for economic reasons, industrial production of PLA is
20 considered a relatively immature technology [4]. PLA is still too expensive to compete with fossil-
21 derived plastics and this is mainly due to the cost of LA. The current cost of LA is relatively high
22 (\$1.30-4.0/kg) and suffers from significant variations of the price of starch or sugar feedstocks used
23 for the fermentation process [6]. In fact, the cost of the feedstock is among the most relevant
24 parameters determining the fermentation cost. This concern has stimulated research towards
25 utilization of alternative feedstocks such as milk whey, food waste, glycerol, or microalgae [1,2,4].

26 In particular, significant attention has been dedicated to lignocellulosic biomass owing to its high
27 abundance and low cost. Lignocellulose includes most waste biomass such as agricultural/land by-
28 products (cereal straw, sugar cane bagasse, forest residues), municipal solid wastes and industrial
29 wastes (e.g. paper mill sludge) [7]. However, the most efficient natural producers of LA, i.e. lactic
30 acid bacteria (LAB), bacteria belonging to the *Bacillus* genus and fungi belonging to the *Rhizopus*
31 genus, cannot ferment lignocellulosic material without prior biomass saccharification [8,9].
32 Biomass pre-treatment and, in particular, exogenous cellulase supplementation are highly expensive
33 and significantly increase the cost of the entire process thus making it not-viable from an economic
34 standpoint [10,11]. Development of consolidated bioprocessing (CBP), that is one-pot fermentation,
35 of lignocellulose is therefore highly desirable, as a mean to significantly lower the cost of
36 lignocellulose fermentation to LA and make PLA cost-competitive with oil-derived plastics.
37 Recently, an example of CBP based on an artificial consortium consisting of a cellulolytic fungus
38 (i.e. *Trichoderma reesei*) and a LAB (i.e. *Lactobacillus pentosus*) has been reported (Shahab et al.,
39 2018). However, industrial exploitation of this approach requires improved robustness, stability and
40 reproducibility of co-cultures [12]. Metabolic engineering has been used to develop recombinant
41 strains that combine high LA production and efficient biomass fermentation. Most studies have
42 been aimed at introducing cellulolytic characteristics (e.g. by expression of heterologous cellulases)
43 in natural LA producers, such as LAB [8]. In the present study, we used a different approach, i.e.
44 we attempted to improve LA production in a native cellulolytic microorganism, namely *Clostridium*
45 *thermocellum*. Metabolic engineering strategies addressed to native cellulolytic microorganisms
46 have generally been focused on increasing biofuel, namely ethanol and butanol, production [13,14].
47 However, these studies have also indicated suitable metabolic targets for improving LA production
48 [9].

49 *Clostridium thermocellum* DSM1313 is a thermophilic cellulolytic bacterium among the best
50 cellulose degraders and the most promising candidates for application in CBP of plant biomass to

51 biofuels and other high-value chemicals. A significant amount of information on the central
52 metabolism and, more in general, on the biology of *C. thermocellum* is currently available [15–17].
53 Furthermore, reliable methods for transformation, inducible gene expression and markerless gene
54 deletion have been developed for this strain [18,19]. Wild type *C. thermocellum* produces a mixture
55 of organic acids (including acetic acid, formic acid and LA), ethanol, H₂ and CO₂. The main carbon
56 catabolites are ethanol and acetate, while LA yield is very low (i.e. 0.01 mol/mol hexose equivalent)
57 [20]. Improvement of the production of a chemical in a microorganism can be obtained through
58 increased expression of enzyme(s) directly involved in its biosynthesis, and/or disruption of
59 competing pathways [21]. Recently, dramatic increase in LA yield in *C. thermocellum* was obtained
60 by deleting the autologous *adhE* gene, that encodes the main bifunctional alcohol/aldehyde
61 dehydrogenase [20]. This modification almost abolished ethanol production in the engineered strain
62 (i.e. strain LL1111) and significantly re-directed *C. thermocellum* carbon flux towards production
63 of LA. Actually, LA is the main end-catabolite of LL1111 which is the *C. thermocellum* strain with
64 the highest LA yield (40% of the maximum theoretical yield) obtained so far [20]. It is worth noting
65 that LL1111 also features a spontaneously occurred mutation of its *ldh* gene resulting in a LDH
66 whose activity is independent from allosteric activation by fructose 1,6 bisphosphate (F1,6BP) [20].
67 The strategy used in the present study aimed at enhancing the expression of native LDH by
68 functionally replacing the original transcriptional promoter of the unique *ldh* gene (Clo1313_1160)
69 [22] with stronger ones. Such modification has been performed on the “wild type” *C. thermocellum*
70 (LL345) and on strains LL1147 [23] and LL1111 [20] that were recently engineered. Strain LL1147
71 is repressed in H₂ production because of functional inactivation of all four hydrogenases. Most
72 attempts were successful and led to significant improvement (4.5-13 fold) of LDH activity and LA
73 yield in the engineered strains.

74

75 **Materials and Methods**

76 ***Bacterial strains and culture conditions***

77 All reagents used in this study were of molecular grade, and obtained either from Sigma Aldrich or
78 Fisher Scientific, unless otherwise stated. *C. thermocellum* DSM1313 was obtained from the DSMZ
79 culture collection. It was grown in either chemically defined MTC-5 medium at initial pH of 7.4
80 [24] or in rich CTFUD medium at initial pH of 7.0 [18] supplemented with 5 g/l cellobiose as the
81 main carbon source. Cultures were incubated at 55°C under anaerobic conditions either in conical
82 tubes in anaerobic chambers (Coy Laboratory Products, Grass Lakes, MI, USA) or in 125 ml
83 (containing 50 ml of medium) butyl stoppered vials.

84 For measurement of growth parameters, strains were grown in a 96-well plate on in 200 µl of MTC-
85 5 medium and absorbance at 600 nm was determined every 3 min for 72 h in a Powerwave XS plate
86 reader as previously described [25]. For measurement of fermentation products, strains were grown
87 in CTFUD medium. Samples were harvested immediately after inoculation of the medium, and
88 after 72 h of growth. Data for fermentation products and growth rate are averages from biological
89 triplicate experiments.

90

91 ***Analytical techniques***

92 Cellobiose, glucose, acetate, citrate, formate, ethanol, lactate, malate, pyruvate and succinate were
93 measured by HPLC using an Aminex HPX-87H column (BioRad, CA, USA) equipped with both
94 refractive index and UV detector as previously reported [26].

95

96 ***Gene modification***

97 Gene modification was performed in the genetically tractable Δhpt strain of *C. thermocellum*
98 DSM1313 (referred as LL345) [22], and two strains derived from LL345 with additional deletion

99 of: i) *hydG* and *ech* genes (i.e. strain LL1147), encoding HydG, involved in maturation of the three
100 [Fe-Fe] hydrogenases, and the [Ni-Fe] hydrogenase, respectively [23]; ii) *adhE* (i.e. strain LL1111)
101 encoding the main aldehyde/alcohol dehydrogenase [20].

102 Gene modification consisted in insertion of the thiolase (*thlA*) promoter (P_{Thl}) of *Clostridium*
103 *acetobutylicum* [27] or the promoter of Clo1313_2638 (P_{2638}) of *C. thermocellum* DSM1313 [28]
104 upstream (position 1,381,634 of *C. thermocellum* chromosome) of *ldh* gene (Clo1313_1160) of *C.*
105 *thermocellum*. The inserted P_{Thl} sequence corresponded to nucleotide 2450 to 2612 of the shuttle
106 vector pSOS95 (GenBank accession number: AY187686.1), while P_{2638} included nucleotide
107 3,106,958 to 3,106,750 of *C. thermocellum* chromosome. Two gBlocks (Integrated DNA
108 Technologies), one containing the 500 bp fragment upstream (5' flank) of *ldh* gene and the other
109 consisting of 500 bp upstream (5' flank) of *ldh* gene, the promoter of choice and the first 500 bp of
110 *ldh* gene (3' flank), were designed (Supplementary Table S1). The gBlocks were cloned into the
111 pDGO145 plasmid (GenBank accession number: KY852359) in the EcoRV and PvuII sites by
112 Gibson assembly so as to obtain the plasmids for promoter integration into *C. thermocellum*
113 chromosome [18]. The plasmids were transformed in T7 express chemiocompetent *E. coli* cells to
114 ensure proper methylation [29]. Methylated plasmids were transformed into *C. thermocellum* by
115 electroporation as described previously [18]. Integration of P_{Thl} and P_{2638} in the suited genome locus
116 was obtained for *C. thermocellum* strain LL345 (thus resulting in strains LL1624 and LL1640,
117 respectively) and LL1147 (thus resulting in strains LL1625 and LL1626, respectively) but not in
118 strain LL1111. Genetic modifications were confirmed by whole-genome resequencing by the
119 Department of Energy Joint Genome Institute. Raw genome resequencing data are available from
120 the NCBI Sequence Read Archive (SRA; <http://www.ncbi.nlm.nih.gov/Traces/sra>). Data were
121 analyzed with the CLC Genomic Workbench version 11.0.1, (Qiagen Inc., Hilden, Germany), as
122 previously described [26]. Strains used in this study are listed in Table 1.

123

124 ***Enzyme assays***

125 Cells were grown in CTFUD medium to an optical density at 600 nm (OD_{600nm}) of 0.6 and
126 harvested by centrifugation (7,000 x g, 10 min, 4°C). Harvested cells were washed twice in
127 anaerobic conditions with cold 100 mM Tris-HCl pH 7 (12,000 x g, 5 min) and stored at -80°C.
128 Protein extracts were prepared by incubating cells with lysozyme as previously described [20].
129 Protein content was measured by Bio-Rad protein dye reagent with bovine serum albumin (Thermo
130 Scientific) as the standard. Lactate dehydrogenase (LDH) activity assays were performed as
131 previously described [20]. Briefly, assays were performed at 55°C in a Coy anaerobic chamber with
132 an 85% N₂, 10% CO₂, and 5% H₂ atmosphere maintained under anoxic conditions using a
133 palladium catalyst. NADH consumption was monitored by measuring absorbance at 340 nm using
134 an extinction coefficient of 6,220 M⁻¹ cm⁻¹. The reaction conditions for lactate dehydrogenase
135 (LDH) activity were 200 mM Tris-HCl (pH 7.3), 0.22 mM NADH, 10 mM sodium pyruvate, and 1
136 mM fructose 1,6-bisphosphate (F1,6BP). The reaction was started by addition of sodium pyruvate.

137

138 **Results**

139 ***Functional replacement of ldh promoter in C. thermocellum***

140 Plasmids for inserting the promoter (P_{Thl}) of thiolase gene (*thlA*) from *C. acetobutylicum* or of the
141 promoter (P₂₆₃₈) of Clo1313_2638 of *C. thermocellum* DSM1313 upstream of the *ldh* gene
142 (Clo1313_1160) of *C. thermocellum* DSM1313 were constructed and transformed in *C.*
143 *thermocellum* strains LL345, LL1111 and LL1147. Both promoters are known for being strong and
144 constitutive [27,28]. LL345 was obtained by disruption of the *hpt* gene in *C. thermocellum*
145 DSM1313, but can be considered as the wild-type strain from a metabolic standpoint, since the *hpt*
146 gene was deleted to allow for 8AZH counter-selection, and it does not affect the fermentation
147 phenotype [22]. LL1111 and LL1147 have been obtained from LL345 respectively by: i) deletion of

148 the gene encoding the main bifunctional alcohol/aldehyde dehydrogenase AdhE (Lo et al., 2015); ii)
149 disruption of *hydG*, encoding maturase of the three [FeFe] hydrogenases, and *ech*, encoding the
150 [NiFe] hydrogenase, resulting in a *C. thermocellum* strain that lacks hydrogenase activity (Biswas et
151 al., 2015). In the present study, functional replacement of *ldh* promoter with P_{Thl} has been obtained
152 in the *C. thermocellum* strains LL345 (wt) and LL1147 (hydrogenase knockout), resulting in strains
153 LL1624 and LL1625, respectively. Insertion of P₂₆₃₈ in strains LL345 and LL1147 resulted in
154 strains LL1640 and LL1626, respectively. Attempts to introduce P_{Thl} or P₂₆₃₈ upstream of the *ldh*
155 gene in strain LL1111 (*adhE* deletion) were unsuccessful. Genome re-sequencing of all the
156 engineered strains confirmed successful modification of the *ldh* locus in strains LL1624, LL1625,
157 LL1626 and LL1640.

158

159 ***LDH activity of engineered strains***

160 LDH activity in parent and engineered strains was measured (Figure 1). Furthermore, LDH assays
161 were performed on strain LL1111 (*adhE* deletion) since it is the *C. thermocellum* strain with the
162 highest LA production yield (40% of the maximum theoretical yield) obtained so far (Lo et al.,
163 2015). In three out of the four strains engineered in this study (i.e. LL1624, LL1626 and LL1640),
164 specific LDH activity was significantly improved with respect to their parent strains by a factor
165 ranging from 4.5 to 13-fold (Figure 1). This confirms that the promoters chosen were stronger than
166 the original *ldh* promoter. With respect to their parent strain, namely LL345, strains LL1624 and
167 LL1640 showed about 4.5-fold increased LDH specific activity, which suggests that P_{Thl} and P₂₆₃₈
168 have similar strength. However, these promoters did not have the same effect in the LL1147
169 (hydrogenase deletion) background. The highest LDH specific activity was measured in LL1626,
170 that is LL1147 with P₂₆₃₈, with an increase of more than 13-fold with respect to the parent strain
171 LL1147. Unexpectedly, no enhancement of LDH activity was detected in LL1625 carrying the P_{Thl}
172 in LL1147 genetic background (Figure 1).

173

174 ***Growth and fermentation profiles of engineered strains***

175 Overexpression of LDH had little effect on growth of recombinant *C. thermocellum* strains obtained
176 in the present study (Table 2). Most frequently, a slight (ranging from 26 to 29%) reduction in the
177 specific growth rate was observed, i.e. in strains LL1624 and LL1626, with respect to parent strains.
178 An even weaker reduction (8-9 %) of final biomass was shown by strains LL1626 and LL1640
179 (with respect to parent strain LL1147 (hydrogenase deletion) and LL345 (wt)). Although functional
180 replacement of the *ldh* promoter did not increase LDH activity, strain LL1625 showed a
181 significantly lower growth rate (17%) and slightly increased final biomass with respect to LL1147.

182 Determination of substrate and fermentation product concentrations was performed immediately
183 after inoculation, and then 72 hours later, after growth had stopped (Table 2). Cellobiose
184 consumption was largely unchanged by the introduction of different promoters driving the *ldh* gene.
185 In several cases, however, overexpression of *ldh* resulted in less glucose production (strains
186 LL1624, LL1625, and LL1626).

187 Apart from sugar consumption, also the profile of fermentation end-products of the engineered
188 strains was affected. In strains where higher LDH activity was measured, also LA yield was
189 improved although to a lower extent. In the wild type strain background (LL345), overexpression of
190 LDH approximately doubled the LA yield (strains LL1624 and LL1640), consistent with enzyme
191 assay data. In the hydrogenase deletion background (LL1147), overexpression of LDH had a
192 variable effect on LA yield. The P_{Thl} promoter decreased LA yield (LL1625), while the P₂₆₃₈
193 promoter increased (about 2-fold) LA yield (LL1626). Maximum LA yield obtained in this study
194 (i.e. 0.8 mol/mol cellobiose, strain LL1640) is still dramatically lower than that of LL1111, i.e. the
195 *C. thermocellum* strain with the highest LA yield obtained so far (Lo et al., 2015). Apart from
196 disruption of *adhE* gene, in strain LL1111 a spontaneous mutation of the *ldh* gene appeared,

197 resulting in a mutant LDH having high catalytic activity even without its allosteric activator,
198 namely F1,6BP [20].

199 Overexpression of LDH induces other re-arrangements of the metabolic network of *C.*
200 *thermocellum*, and the overall fermentation profile of the engineered strains is significantly different
201 from that of the parent strains. Most frequently, improved LA yield is accompanied by increased
202 ethanol yield (strains LL1624 and LL1626) and/or reduction of formate yield (strains LL1640 and
203 LL1626) (Table 2). Interestingly, catabolite profiles of LL1624 and LL1640 differ from each other,
204 although they show similar LDH activity and LA yield and both derive from LL345. LL1624 shows
205 a significant reduction of acetate yield and an increase of ethanol and malate production. In
206 LL1640, only formate yield resulted as significantly decreased with respect to LL345. Metabolite
207 profiles of strains derived from LL1147 were more similar between each other. Both LL1625 and
208 LL1626 showed decreased production of formate and malate and remarkable (more than 2-fold)
209 increase in ethanol yield. It is worth noting that LL1626 has the highest LDH specific activity
210 measured in this study and its LA yield is about 2-fold higher than that of LL1647, but LL1625 has
211 LDH levels similar to the parent strains.

212

213 **Genome sequencing of engineered strains**

214 After strain construction, correct insertion of the promoter upstream of *ldh*, as well as the absence of
215 point mutations in or upstream of the *ldh* gene was verified by whole genome resequencing.
216 However, there were several unexpected results from the enzyme assay and fermentation data, so
217 we looked to see if these results could be explained by any of the secondary mutations we observed.
218 The LDH enzyme activity in strain LL1625 was no different from that of its parent strain, LL1147,
219 despite the presence of the P_{Thl} promoter. We identified seven mutations that were present LL1625,
220 but not in its parent strain (LL1147) (Figure 2). Of these mutations, the one starting at position
221 279492 (coordinates based on Genbank sequence NC_017304.1) should be ignored because it is

222 present in both strains LL1625 and LL1626. Of the remaining six mutations, we do not have any
223 direct evidence to favor one over another. There are two which deserve additional scrutiny. There is
224 a point mutation in the Clo1313_1324 gene. This gene is thought to encode *rpoD*, which is the
225 sigma factor associated with basal expression (i.e. "housekeeping" genes), and could affect
226 transcription from the P_{Thi} promoter. There is also a mutation in the Clo1313_1122 start codon that
227 changed it from an ATG to a GTG. This type of mutation is typically associated with reduced
228 transcription. This is interesting because in LL1147, the parent strain of LL1625, this position was
229 mutated from GTG to ATG, so in strain LL1625, the mutation reverted back to the wild type.

230 Another unexplained phenotype is the increased ethanol production and decreased acetate
231 production of strain LL1624 relative to either its parent (LL345) or sibling (LL640) strains.
232 Although there are 17 potential mutations that are unique to strain LL1624, none of them are
233 obviously associated with ethanol production, acetate production, or redox balance.

234

235 **Discussion**

236 Production of LA through a 2nd generation biorefinery approach has attracted significant interest
237 because of the economic advantages that using lignocellulose as the fermentation feedstock could
238 bring on LA price [1,2]. The present study aimed at improving LA production in the native
239 cellulolytic bacterium *C. thermocellum* by enhancing the expression of its LDH. The final purpose
240 of this investigation is developing a strain able to catalyze direct fermentation of lignocellulose to
241 LA. Development of such CBP could significantly reduce the current cost of LA. Most previous
242 metabolic engineering strategies aimed at direct fermentation of lignocellulose to LA have
243 attempted to introduce (hemi)cellulolytic characteristics in natural producers of LA [30,31]. The
244 approach used in the present study focused on improving the expression of the native LDH of the
245 cellulolytic bacterium *C. thermocellum* DSM1313 by functionally replacing its native promoter

246 with stronger ones. To this aim, two strong and constitutive promoters, i.e. the one of thiolase (P_{Thl})
247 from *C. acetobutylicum* [27] and that of Clo1313_2638 (P_{2638}) from *C. thermocellum* DSM1313
248 [28], were used. In three out of the four strains engineered in this study (i.e. LL1624, LL1626 and
249 LL1640), functional replacement of the *ldh* promoter led to significant improvement of specific
250 LDH activity with respect to parent strains by a factor ranging from 4.5 to 13-fold (Figure 1). These
251 strains show the highest specific LDH activities reported in *C. thermocellum*, so far, that is about 4-
252 9 fold higher than that measured in strain LL1111 (i.e. the *C. thermocellum* strain with the highest
253 LA yield reported so far). It is worth remembering that, in many microorganisms, LDH expression
254 is under the control of the global redox-responsive transcription factor Rex [32]. Generally, Rex
255 acts as a gene transcription repressor in response to low intracellular [NAD(P)H]/[NAD(P)+] ratio.
256 Although this has not been confirmed in *C. thermocellum* yet, *ldh* promoter engineering obtained in
257 this study may have altered this regulation. Recently, a similar approach was used to improve the
258 expression of the *ldh* gene from *Caldicellulosyruaptor bescii* [33]. In this case the original promoter
259 was replaced with the xylose-inducible promoter P_{xi} but improvement of the specific LDH activity
260 with respect to the wild type strain (about 3 fold) was lower than that obtained in the present study.
261 However, the effect of *ldh* promoter replacement on LA production was milder since no more than
262 2-fold increase of LA yield with respect to parent strains was observed. Maximum LA yield
263 obtained in this study (i.e. 0.8 mol/mol cellobiose, strain LL1640) is still dramatically lower than
264 that of strain LL1111 (Lo et al., 2015). Apart from disruption of *adhE* gene, in strain LL1111 a
265 spontaneous mutation of the *ldh* gene appeared, resulting in a mutant LDH having high catalytic
266 activity even without its allosteric activator, namely F1,6BP [20]. LA yield of strain LL1626
267 (derived from the hydrogenase-deficient strain LL1147) was even lower despite this strain shows
268 the highest LDH specific activity (Figure 1). This observation is most probably related to the
269 different metabolic background of this strain. Strain LL1147 also shows dramatic reduction of LA
270 accumulation [23]. The exact cause of this metabolic phenotype was not determined but it was

271 speculated that disruption of hydrogenases could have altered intracellular levels of possible
272 allosteric regulators of LDH [23]. Apart from the abovementioned F1,6BP, the LDH enzymes may
273 also be activated by ATP and inhibited by pyrophosphate, e.g. in *Caldicellulosiruptor*
274 *saccharolyticus* [34]. Nicotinamide cofactors are other typical regulators of LDH activity such as in
275 *Caldicellulosiruptor saccharolyticus*, where NAD^+ is a competitive inhibitor [34], or in
276 *Thermoanaerobacter ethanolicus* where, curiously, LDH is inhibited by NADPH [35]. It is likely
277 that hydrogenase-deleted *C. thermocellum* features accumulation of reduced ferredoxin via PFOR
278 which could cause accumulation of other reduced electron carriers such as NADPH possibly
279 leading to inhibition of LDH [23].

280 The moderate increase of LA yield obtained by the present study was not completely unexpected.
281 Overexpression of an enzyme, although it can significantly divert the metabolism towards the
282 product of interest, as in this case, generally, is not sufficient for driving all the carbon flux towards
283 the pathway of interest. More in detail, previous studies have demonstrated that lactate production
284 in *C. thermocellum* is affected at multiple levels, i.e. by allosteric regulation and deletion of
285 competing pathways [20]. The present study has identified a third factor: transcriptional regulation,
286 since introducing stronger promoters upstream of the *ldh* gene increases both LDH enzyme activity
287 and LA production. All these factors contribute to sophisticated regulation of LA production in *C.*
288 *thermocellum*. A previous study has shown that the deletion of *adhE* likely have the largest impact
289 on lactate production [20]. Allosteric control and transcriptional control appear to have similar
290 strength based on similar LA yields of strains LL1624 or LL1640 compared to strain LL1160
291 carrying only the S161R mutation in LDH [20].

292 Actually, current information on *C. thermocellum* metabolism still have important gaps as regards
293 LA production. It is known that K_m for pyruvate *C. thermocellum* LDH is highly affected by
294 F1,6BP concentration [36], but regulation by further allosteric effectors (ATP, pyrophosphate,
295 nicotinamide cofactors) has been hypothesized [23]. The affinity of the other *C. thermocellum*

296 enzymes that directly compete for the same substrates, that is pyruvate and/or NADH, is currently
297 not known. Alternative reactions for dissimilation of pyruvate in *C. thermocellum* are catalyzed by
298 pyruvate ferredoxin oxidoreductase (PFOR) (E.C. 1.2.7.1) and by pyruvate formate lyase (PFL)
299 (E.C. 2.3.1.54). *C. thermocellum* genome harbors five genes or gene clusters annotated as encoding
300 PFOR [37]. Some evidence indicates that *pfor1* (Clo1313_0020-0023) and *pfor4* (Clo1313_1353-
301 1356) are the primary PFOR of *C. thermocellum* [37–39]. Actually, deletion of each of these gene
302 clusters causes about 80% reduction of PFOR activity in this strain [37]. However, the K_m for
303 pyruvate of these enzymes has not been determined. *C. thermocellum* PFL is encoded by *pflB* gene
304 (Clo1313_1717) but its K_m for pyruvate has not been measured.

305 Overexpression of LDH induces other, sometimes unexpected, re-arrangements of the metabolic
306 network and the overall fermentation profile of *C. thermocellum*. In two (strains LL1624 and
307 LL1626) out of three strains with increased LA yield, also ethanol yield was enhanced and/or
308 formate yield was diminished (strains LL1640 and LL1626) (Table 2). Additionally, strain LL1624
309 shows a significant reduction of acetate yield. It is worth remembering that acetate, formate and
310 ethanol biosynthesis compete with LA production. Inhibition of formate and acetate in LA
311 overproducing strains was therefore expected. However, improvement of ethanol yield in strains
312 LL1624 and LL1626 was surprising since ethanol production competes with LA synthesis for both
313 carbon intermediates and electrons. However, a number of observations made by previous and
314 present study may explain the beneficial effect of improvement of LDH activity on fermentation
315 efficiency and, in particular, ethanol production in *C. thermocellum*. Most probably enhancement of
316 LDH activity affects the redox balance of the cells and, in particular, lowers the NADH/NAD⁺ ratio,
317 which should be particularly high in strain LL1147, since it lacks hydrogenases. High
318 NADH/NAD⁺ ratios have been shown to inhibit the GAPDH reaction [40,41] and reduce the
319 glycolytic flux in *C. thermocellum* [42]. Improvement of LDH activity should benefit glycolytic
320 flux because it consumes both NADH and pyruvate (as demonstrated by the fact that strain LL1626

321 does not show any pyruvate accumulation while its parent strain LL1147 does, Table 2). Regarding
322 improvement of ethanol yield in strains LL1624 and LL1626, it is worth reminding that, recently,
323 the activity of one of the main PFOR of *C. thermocellum* (i.e. PFOR1) was shown to be inhibited by
324 NADH accumulation [43]. Furthermore, thermodynamic analysis indicated that while pyruvate
325 dissimilation through LDH or PFL reactions is favorable even in presence of high concentrations of
326 lactate or formate, respectively, the PFOR reaction becomes less favorable in highly reduced
327 conditions [44]. So, it can be speculated that improved LDH activity helps removing possible
328 inhibition of PFOR deriving from excess of reduced co-factors, and eventually this may lead to
329 improved conversion of acetyl-CoA to ethanol.

330 Future perspectives to improve pyruvate flux towards LA in *C. thermocellum* should aim at
331 improving LDH affinity for pyruvate by either: i) re-introducing the S161R mutation of *C.*
332 *thermocellum* LDH as found in strain LL1111 (*adhE* deletion) or; replacing *C. thermocellum*
333 original LDH with heterologous thermophilic LDH with higher affinity for pyruvate. As regards the
334 first strategy, i.e. introducing a strong promoter upstream of the mutant *ldh* from LL1111, attempts
335 to create this strain failed so far. Future attempts to create such a strain would benefit from
336 improved genetic tools, such as tightly repressed inducible promoters. A possible candidate for the
337 second strategy is LDH from *Thermus caldophilus* which shows a K_m for pyruvate which is 10-fold
338 lower than that of *C. thermocellum* LDH [45].

339

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347

348 **Conflict of interest**

349 L.R.L. is a founder of the Enchi Corporation, which has a financial interest in *Clostridium*
350 *thermocellum*. R.M and D.G.O declare no conflict of interest.

351

352 **Author contributions**

353 R.M., D.G.O. and L.R.L. conceived the experimental design. R.M. performed the experiments.
354 D.G.O. analyzed re-sequencing results and contributed to metabolite analysis. All the Authors
355 contributed to discussing the results and writing the manuscript.

356

357 **Compliance with Ethical Standards**

358 This article does not contain any studies with human participants or animals performed by any of
359 the authors.

360

361 **References**

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- 516

517

518 Table 1. *C. thermocellum* strains used in this study.

Strain	Description	SRA accession ¹	Reference
LL345	DSM 1313 Δhpt	SRX872655	[22]
LL1111	LL345 $\Delta adhE$ <i>ldh</i> (S161R)	SRX744221	[20]
LL1147	LL345 $\Delta hydG$ Δech	SRX2141488	[23]
LL1624	LL345 P _{Thl} - <i>ldh</i>	SRX5676996	This study
LL1625	LL1147 P _{Thl} - <i>ldh</i>	SRX5678334	This study
LL1626	LL1147 P ₂₆₃₈ - <i>ldh</i>	SRX5678333	This study
LL1640	LL345 P ₂₆₃₈ - <i>ldh</i>	SRX6875981	This study

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521 ¹ Sequence Read Archive <https://www.ncbi.nlm.nih.gov/sra>

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523

524 Table 2. Growth and fermentation profiles of the *C. thermocellum* strains. The data are the mean of three biological replicates \pm standard deviation.

525 Light red and light green indicate values which are significantly ($p < 0.05$) lower and higher than data observed in the parent strain, respectively.

526 n.d., not detected.

527

Strain	Name	LL345	LL1624	LL1640	LL1111	LL1147	LL1625	LL1626
	Parent strain	LL345			LL1111	LL1147		
	<i>ldh</i> promoter	WT	P _{Thl}	P ₂₆₃₈	WT	WT	P _{Thl}	P ₂₆₃₈
Fermentation profile	growth rate (h ⁻¹)	0.5 \pm 0.0	0.3 \pm 0.0	0.4 \pm 0.0	0.3 \pm 0.1	0.4 \pm 0.0	0.4 \pm 0.0	0.3 \pm 0.0
	final OD _{600nm}	1.6 \pm 0.0	1.4 \pm 0.0	1.4 \pm 0.0	1.3 \pm 0.0	1.3 \pm 0.0	1.4 \pm 0.0	1.2 \pm 0.0
	Initial cellobiose (mM)	27.6 \pm 0.4	27.0 \pm 0.3	27.4 \pm 0.5	27.0 \pm 0.4	26.9 \pm 0.3	26.7 \pm 0.3	27.1 \pm 0.1
	Consumed cellobiose (mM)	21.1 \pm 0.4	21.4 \pm 0.1	21.6 \pm 0.5	17.8 \pm 0.5	18.9 \pm 0.3	19.6 \pm 0.4	19.8 \pm 0.2
	residual cellobiose (mM)	6.5 \pm 0.3	5.6 \pm 0.2	5.8 \pm 0.2	9.2 \pm 0.8	8.0 \pm 0.1	7.1 \pm 0.4	7.2 \pm 0.3
	glucose (mM)	15.8 \pm 1.1	14.6 \pm 0.1	17.6 \pm 0.6	18.3 \pm 1.5	14.3 \pm 0.6	10.3 \pm 0.7	9.0 \pm 0.5
	Residual hexose equivalent %	52.1 \pm 1.2	47.7 \pm 0.2	53.3 \pm 2.1	67.8 \pm 5.0	56.5 \pm 1.4	45.9 \pm 2.1	43.3 \pm 1.6
	acetate (mM)	15.4 \pm 1.5	9.1 \pm 0.4	16.9 \pm 2.4	8.6 \pm 0.9	4.3 \pm 0.4	4.1 \pm 0.2	4.3 \pm 0.0

ethanol (mM)	7.6 ± 2.1	14.7 ± 0.2	5.8 ± 2.9	n.d.	8.5 ± 1.7	27.0 ± 1.8	29.7 ± 0.8
formate (mM)	5.2 ± 0.2	4.6 ± 0.9	1.3 ± 0.2	0.1 ± 0.0	15.9 ± 0.0	14.2 ± 0.3	12.0 ± 0.3
lactate (mM)	4.8 ± 0.2	11.1 ± 1.6	10.8 ± 0.4	21.5 ± 1.1	1.9 ± 0.2	0.6 ± 0.0	5.4 ± 0.6
malate (mM)	1.6 ± 0.2	2.3 ± 0.2	3.1 ± 0.6	2.3 ± 0.3	1.0 ± 0.1	0.9 ± 0.0	0.5 ± 0.0
pyruvate (mM)	0.1 ± 0.2	n.d.	n.d.	n.d.	1.8 ± 0.1	0.1 ± 0.1	0.0 ± 0.0
succinate (mM)	-0.2 ± 0.0	-0.3 ± 0.0	-0.3 ± 0.0	-0.3 ± 0.1	0.0 ± 0.0	0.0 ± 0.1	-0.2 ± 0.0
Y _{acetate} (mol/mol cellobiose consumed)	1.2 ± 0.1	0.6 ± 0.0	1.3 ± 0.3	1.0 ± 0.2	0.4 ± 0.0	0.3 ± 0.0	0.3 ± 0.0
Y _{ethanol} (mol/mol cellobiose consumed)	0.6 ± 0.2	1.0 ± 0.0	0.4 ± 0.2	n.d.	0.7 ± 0.1	1.9 ± 0.1	1.9 ± 0.0
Y _{formate} (mol/mol cellobiose consumed)	0.4 ± 0.0	0.3 ± 0.1	0.1 ± 0.0	0.0 ± 0.0	1.4 ± 0.1	1.0 ± 0.0	0.8 ± 0.0
Y _{lactate} (mol/mol cellobiose consumed)	0.4 ± 0.0	0.8 ± 0.1	0.8 ± 0.1	2.5 ± 0.5	0.2 ± 0.0	0.0 ± 0.0	0.4 ± 0.0
Y _{malate} (mol/mol cellobiose consumed)	0.1 ± 0.0	0.2 ± 0.0	0.2 ± 0.1	0.3 ± 0.1	0.1 ± 0.0	0.1 ± 0.0	0.0 ± 0.0
Y _{pyruvate} (mol/mol cellobiose consumed)	0.0 ± 0.0	0	n.d.	n.d.	0.2 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Y _{succinate} (mol/mol cellobiose consumed)	-0.0 ± 0.0	-0.0 ± 0.0	-0.0 ± 0.0	-0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0

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530

531 **Figure legends**

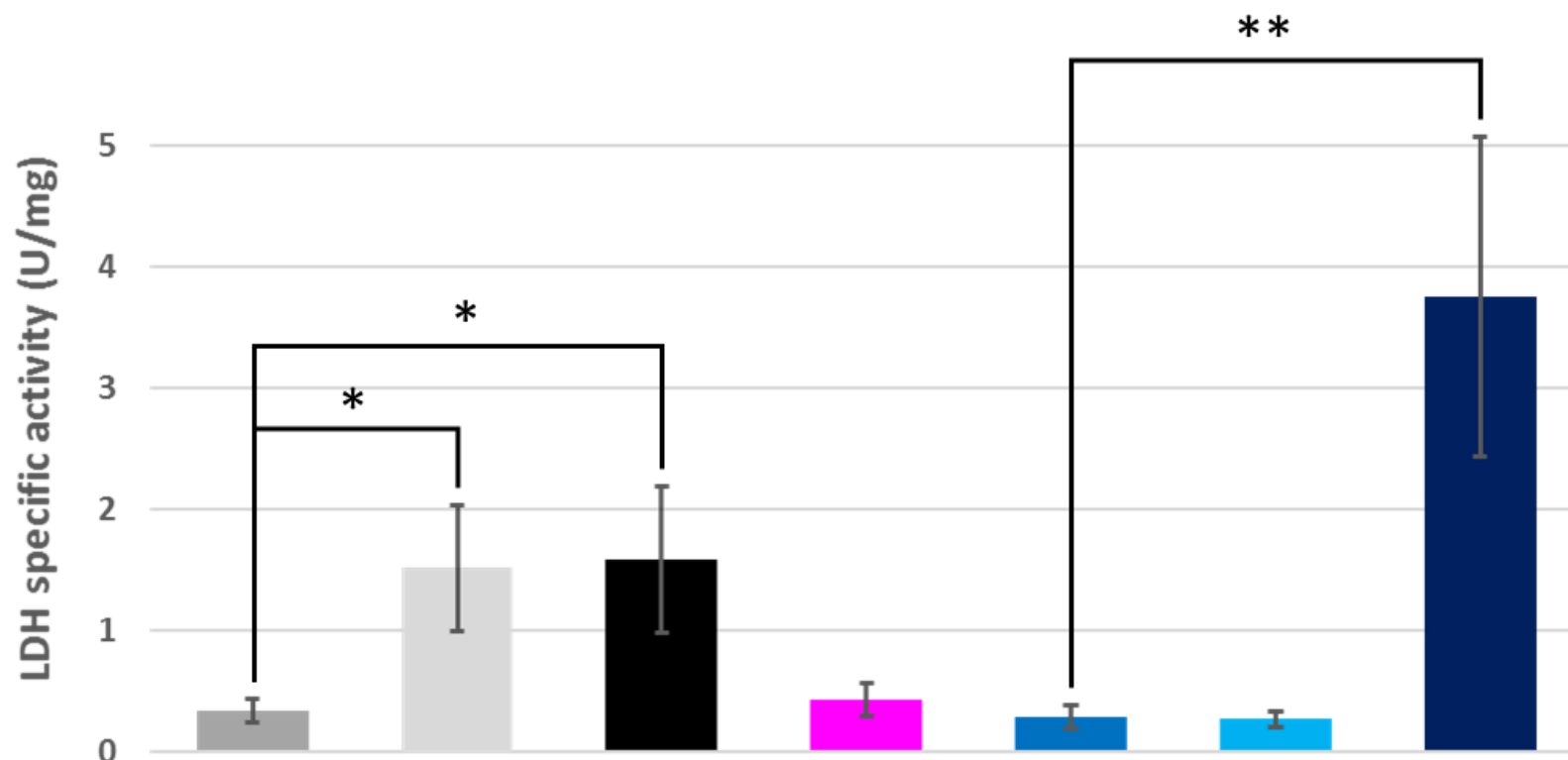
532 Figure 1. Lactate dehydrogenase (LDH) specific activity measured in the acellular crude extracts of
533 *C. thermocellum* strains and LA yields (Y_{LA}) determined in the same strains. The data are the mean
534 of three biological replicates \pm standard deviation (for Y_{LA} , standard deviation is in parentheses).
535 The * and ** labels indicate values that are significantly different ($p < 0.05$) from those observed in
536 the corresponding parent strain. *, $p = 0.007$; ** $p = 0.0003$

537

538 Figure 2. Mutations found through genome sequencing of the *C. thermocellum* strains engineered in
539 this study

540

Figure 1



Strain	LL345	LL1624	LL1640	LL1111	LL1147	LL1625	LL1626
Parent strain	LL345			LL1111	LL1147		
<i>ldh</i> promoter	WT	P _{Thl}	P ₂₆₃₈	WT	WT	P _{Thl}	P ₂₆₃₈
Y_{LA} (mol/mol cellobiose)	0.4 (0.0)	0.8 (0.1)	0.8 (0.1)	2.5 (0.5)	0.2 (0.0)	0.0 (0.0)	0.4 (0.0)

Figure 2

Start Region ¹	Description	Type	Annotation name	Annotation description	Read fraction ²			
					LL1624	LL1640	LL1625	LL1626
4279	A --> -	Deletion	130 bp upstream of Clo1313_0005	cce:Ccel_0005 hypothetical protein	0,0	1,0	0,0	0,0
200106	A --> -, Ile127fs	Deletion	Clo1313_0185	phosphoribosyltransferase	0,0	1,0	0,0	0,0
279492	G --> -	Deletion	no CDS match		0,0	0,0	1,0	1,0
477437	C --> T, Leu38Phe	SNV	Clo1313_0422	ATP phosphoribosyltransferase catalytic region	1,0	0,0	0,0	0,0
494751	A --> -, Ile79fs	Deletion	Clo1313_0439	Sulfate transporter/antisigma-factor antagonist STAS	0,0	1,0	0,0	0,0
523339	A --> -, Lys28fs	Deletion	Clo1313_0478	type III restriction protein res subunit	0,0	0,0	0,0	0,0
618489	G --> A	SNV	288 bp upstream of Clo1313_0559	act:ACLA_088240 heat shock Hsp30-like protein, putative	1,0	0,0	0,0	0,0
677241	T --> C	SNV	no CDS match		0,4	0,0	0,0	0,0
677241	T --> T	SNV	no CDS match		0,6	0,0	0,0	0,0
724743	A --> G, Ile71Thr	SNV	Clo1313_0638	histone family protein DNA-binding protein	1,0	0,0	0,0	0,0
754780	ATTTAGTA --> -	Deletion	93 bp upstream of Clo1313_0663	dae:Dtox_2165 hypothetical protein	0,0	0,0	0,0	1,0
1058282	A --> -, Lys43fs	Deletion	Clo1313_0908	phosphoribosyltransferase	1,0	0,0	0,0	0,0
1193090	G --> T, Trp221Cys	SNV	Clo1313_1020	leucyl-tRNA synthetase	1,0	0,0	0,0	0,0
1198434	C --> T	SNV	Clo1313_1021	PKD domain containing protein	0,4	0,0	0,0	0,0
1198434	C --> C	SNV	Clo1313_1021	PKD domain containing protein	0,6	0,0	0,0	0,0
1232526	G --> T, Glu114*	SNV	Clo1313_1035	tRNA/rRNA methyltransferase (SpoU)	1,0	0,0	0,0	0,0
1271372	IS120	Insertion	no CDS match		0,0	1,0	0,0	0,0
1341055	A --> G	SNV	97 bp upstream of Clo1313_1122	metal-dependent phosphohydrolase HD sub domain	0,0	0,0	1,0	0,0
1370265	G --> A	SNV	45 bp upstream of Clo1313_1152	VanW family protein	1,0	0,0	0,0	0,0
1381635	P ₂₆₃₈	Insertion	ldh	Lactate/malate dehydrogenase	0,0	1,0	0,0	1,0
1381635	P _{Thl}	Insertion	ldh	Lactate/malate dehydrogenase	1,0	0,0	1,0	0,0
1438373	IScTh10	Insertion	89 bp upstream of Clo1313_1211	aspartate/glutamate/uridylate kinase	0,0	0,0	0,0	0,0
1570061	C --> A, Ala230Asp	SNV	Clo1313_1324	sigma-70 region 3 domain protein	0,0	0,0	1,0	0,0
1719993	T --> C, Val125Ala	SNV	Clo1313_1467	aminotransferase class I and II	0,0	0,0	1,0	0,0

1932207	IS120	Insertion	no CDS match		0,0	1,0	0,0	0,0
2314895	C --> T, Met85Ile	SNV	Clo1313_1970	Rhomboid family protein	1,0	0,0	0,0	0,0
2343123	- --> TATA	Insertion	14 bp upstream of Clo1313_1989	VTC domain	0,0	0,0	0,0	0,9
2624673	A --> T	SNV	no CDS match		1,0	0,0	0,0	0,0
2941043	C --> C	SNV	no CDS match		0,6	0,0	0,0	0,0
2941043	C --> T	SNV	no CDS match		0,4	0,0	0,0	0,0
2964040	G --> G	SNV	no CDS match		0,5	0,6	0,0	0,0
2988982	G --> A, Ala104Val	SNV	Clo1313_2549	peptidase S41	1,0	0,0	0,0	0,0
3001017	ISCth10	Insertion	Clo1313_2560	Carbamoyl-phosphate synthase L chain ATP-binding	0,0	0,0	1,0	0,0
3132643	C --> T	SNV	Clo1313_2666	rca:Rcas_1719 hypothetical protein	1,0	1,0	0,0	0,0
3151076	A --> C	SNV	132 bp upstream of Clo1313_2686	transposase IS200-family protein	0,0	0,0	0,0	0,5
3151076	A --> A	SNV	132 bp upstream of Clo1313_2686	transposase IS200-family protein	0,0	0,0	0,0	0,5
3301521	G --> T, Phe253Leu	SNV	Clo1313_2809	cpy:Cphy_2889 hypothetical protein	0,0	0,0	1,0	0,0
3359106	C --> T, Gly358Glu	SNV	Clo1313_2858	Carbohydrate binding family 6	0,0	1,0	0,0	0,0

¹ Start region is based on the coordinates from the *C. thermocellum* genome, Genbank accession number NC_017304.1

² Read fraction indicates the fraction of reads which support the presence of a given mutation. Read fractions > 0.95 indicate a mutation was called with high confidence. Lower read fraction values can result from a variety of causes, including duplicated genome regions, low read counts, and sequencing instrument noise.

Supplementary online material for

Construction of lactic acid overproducing *Clostridium thermocellum* through enhancement of lactate dehydrogenase expression

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Supplementary Table S1. Sequence of the gBlocks used to construct plasmids for functional replacement of the *ldh* promoter with the promoter of the thiolase (*thlA*) (P_{Thl}, gBlock XD904) of *Clostridium acetobutylicum* or the promoter of Clo1313_2638 (P₂₆₃₈, gBlock XD902) of *C. thermocellum* DSM1313. Underlined sequences correspond to the sequence of the promoters.

gBlock name (length)	Purpose	Sequence (5'-3')
XD901 (549 bp)	5' flank	TAGGCGTATCACGAGGCGATCTTTTTCCCCAAAACCTCCGCAACAGTCTCCTTTGTAAGGTCATCCTGCGTGGGGCCGAGTCCTCCGGTCATAATAAC AAGGTCGCACCTTTCCAAAGCTGCAAGAAGACATTTTTTCAGCCGAACGGAATTGTCCCCACCACACTGTGATAATACACATTCACACCAATGTCAT TGAGCCTTTTGATATATACTGGGCATTGGTATTTGCTATCTGCCCATTAAGCTCGGTTCCAACCGCTAATATCTCCGCATTCATATTGAAAGACC CCTTAAATTTAACTTTTTGTAACCTATTATATCAATTAGTGTTATAAAAATAAAAGGGAAAAAGAATTTAAATCAAAGGTTTCAAGAGCAGCCGTATC ACCCGTAAAAGTTTCAGCCGATTCAACCTTTTTACACATAAAAACCTTTCAAAAATTGATGACTTACAATTATCAAGTAGGATATAATATTACTAATGCTA AACAGTTATTGATAAAGGAGGAAGGAATATCGTGGGAATAGGCATGGA
XD902 (1249 bp)	insertion of promoter P ₂₆₃₈	TACCTGGCCAGTAGTTCAGCTTTTTCCCCAAAACCTCCGCAACAGTCTCCTTTGTAAGGTCATCCTGCGTGGGGCCGAGTCCTCCGGTCATAATAAC AAGGTCGCACCTTTCCAAAGCTGCAAGAAGACATTTTTTCAGCCGAACGGAATTGTCCCCACCACACTGTGATAATACACATTCACACCAATGTCAT TGAGCCTTTTGATATATACTGGGCATTGGTATTTGCTATCTGCCCATTAAGCTCGGTTCCAACCGCTAATATCTCCGCATTCATATTGAAAGACC CCTTAAATTTAACTTTTTGTAACCTATTATATCAATTAGTGTTATAAAAATAAAAGGGAAAAAGAATTTAAATCAAAGGTTTCAAGAGCAGCCGTATC ACCCGTAAAAGTTTCAGCCGATTCAACCTTTTTACACATAAAAACCTTTCAAAAATTGATGACTTACAATTATCAAGTAGGATATAATATTACTAATGCTA AACAGTTATTGATAAAGGAGGAAGGAATGATAAACAAAGGACGGTTCAGGGCTTCTGCTCATCCTACTCTGCATTGAAAAAGGTAGGATGAATTTT <u>TATTTTTAATCTTATTGAAAAAATTTTTGAAAATCGGTTTTATAAAAAAAAGTGGGTATATTTATAATAGTCAATTGATTGGTTAAAAAATTTAAA</u> <u>TAAGCAAACAGAATAATAACAAAAGTAAGGAGGAATTTGTTATGAACAATAACAAAGTAATTTAAAAAAGTAACCGTAGTTGGTGCAGGCTTTGTAG</u>

		GTTCCACCACAGCTTATACATTGATGCTCAGCGGACTTATATCTGAAATTGTAAGTACTGATAGACATAAATGCAAAAAAGCCGACGGAGAAGTCATGGACTTAAATCACGGCATGCCTTTTGTAAAGCCCGTTGAAATTTATCGTGGTACTACAAAGACTGTGCCGGATCCGACATAGTAATCATTACCGCCGGTCCAACCAAAAAGAAGGCGAAACGAGAATAGATCTTGTTAAAAGAAACACGGAAGTATTCAAAAATATCATAAATGAAATTGTAAGTACAACAACGATTGTATTCTTCTGGTAGTCACAAATCCGGTGGATATTTAACCTATGTAACCTACAAACTATCCGGATTCCCGAAAAACAAAGTAATAGGTTCCGGAACGGTTTTGGACACAGCCAGGTTCCGTTATCTTTAAGCGAACATGTAAAAGTGGACTGCTAATAGTAGTGAAAAA
XD904 (1203 bp)	insertion of promoter P _{Thl}	TACCTGGCCCAGTAGTTCAGCTTTTTCCCAAAACTTCCGCAACAGTCTCCTTTGTAAGGTCATCCTGCGTGGGGCCGAGTCCTCCGGTCATAATAACAAGGTCGCACCTTTCCAAAGCTGCAAGAAGACATTTTTTCAGCCGAACGGAATTGTCCCCACCACACTGTGATAATACACATTCACACCAATGTCATGAGCCTTTTGGATATATACTGGGCATTGGTATTTGCTATCTGCCCATTAAGCTCGGTTCCAACCGCTAATATCTCCGCATTCATATTGAAAGACCCTTAAATTTAACTTTTTGTAACCTATTATATCAATTAGTGTATAAAAATAAAAGGGAAAAAGAATTAATCAAAGGTTTCAAGAGCAGCCGTATCACCCGTAAAAGTTTCAGCCGATTCAACCTTTTTACACATAAACTTTCAAAAATTGATGACTTACAATTATCAAGTAGGATATAATATACTAATGCTAACAGTTATTGATAAAGGAGGAAGGAATTCGACTTTTTAACAAAATATATTGATAAAAATAATAATAGTGGGTATAATTAAGTTGTTAGAGAAAACGTATAAATTAGGGATAAACTATGGAACCTATGAAATAGATTGAAATGGTTTTATCTGTTACCCCGTAGGATCCAGAATTTAAAAGGAGGGATTAAAATGACAATAACAAAGTAATTAAGTAACCGTAGTTGGTGCAGGCTTTGTAGGTTCCACCACAGCTTATACATTGATGCTCAGCGGACTTATATCTGAATTGTAAGTACTGATAGACATAAATGCAAAAAAGCCGACGGAGAAGTCATGGACTTAAATCACGGCATGCCTTTTGTAAAGCCCGTTGAAATTTATCGTGGTACTACAAAGACTGTGCCGGATCCGACATAGTAATCATTACCGCCGGTGCCAACCAAAAAGAAGGCGAAACGAGAATAGATCTTGTTAAAAGAACACGGAAGTATTCAAAAATATCATAAATGAAATTGTAAGTACAACAACGATTGTATTCTTCTGGTAGTCACAAATCCGGTGGATATTTAACCTATGTAACCTACAAACTATCCGGATTCCCGAAAAACAAAGTAATAGGTTCCGGAACGGTTTTGGACACAGCCAGGTTCCGTTATCTTTAAGCGAACATGTAAAAGTGGACTGCTAATAGTAGTGAAAAA