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1 **Probiotic *Lactobacillus* strains from Mongolia improve calcium**
2 **transport and uptake by intestinal cells in vitro**

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20

21 **Abbreviations**

22 ATR: Acid Tolerance Response

23 CFU: Colony Forming Unit

24 Cld-2: Claudin-2

25 Cld-4: Claudin-4

26 Cld-12: Claudin-12

27 DMEM: Dulbecco's Modified Eagle's Medium

28 LAB: Lactic Acid Bacteria

29 LDH: Lactate Dehydrogenase

30 MATS: Microbial Adhesion To Solvents

31 MRS: De Man, Rogosa, Sharpe

32 OD: Optical Density

33 PBS: Phosphate Buffered Saline

34 TEER: Trans Epithelial Electrical Resistance

35 TRPV6: Transient Receptor Potential Vanilloid 6

36 VDR: Vitamin D Receptor

37 **ABSTRACT**

38 The aim of this study was to investigate the probiotic properties of 174 *Lactobacillus* strains
39 isolated from Mongolian dairy products, and particularly their impact on intestinal calcium
40 uptake and absorption. All isolates underwent a first screening based on cell surface
41 hydrophobicity, acid tolerance, tolerance to gastro-intestinal digestion, autoaggregation,
42 adhesion and cytotoxicity against intestinal cells. Six *Lactobacillus* strains from different
43 species (*L. casei*, *L. kefiranofaciens*, *L. plantarum*, *L. fermentum*, *L. helveticus* and *L.*
44 *delbrueckii*) were selected, and their impact on intestinal calcium uptake and transport was
45 investigated using Caco-2. Five strains were able to improve total calcium transport after 24h
46 contact with a differentiated Caco-2 cell monolayer. Concomitantly the *L. plantarum* strain
47 was able to increase cellular calcium uptake in Caco-2 cells by 10% in comparison to control
48 conditions. To determine which pathway(s) of calcium absorption was modulated by the
49 strains, a qPCR-based study on 4 genes related to calcium/vitamin D metabolism or tight
50 junction integrity was conducted on mucus-secreting intestinal HT-29 MTX cells. The *L.*
51 *plantarum* strain modulates the transcellular pathway by regulating the expression of vitamin
52 D receptor (1.79 fold of control) and calcium transporter (4.77 fold of control) while the *L.*
53 *delbrueckii* strain acts on the paracellular pathway by modulating claudin-2 expression (2.83
54 fold of control). This work highlights the impact of *Lactobacillus* probiotic strains on
55 intestinal calcium absorption and for the first time give some evidence about the cellular pathways
56 involved

57

58 **Keywords:** Calcium intake; gut barrier; lactobacillus, probiotics, Caco-2 cells; HT29-MTX
59 cells

60

61 **1. Introduction**

62 More than 99% of calcium in the human body is stored in the skeleton (Beto, 2015).

63 However, besides being the main mineral component of bones, calcium is also involved in
64 many physiological processes such as vascular contraction, vasodilation, muscle function,
65 neuronal transmission, intracellular signaling and hormonal secretion (Pu et al., 2016).

66 Calcium deficiency or hypocalcemia is associated with the development of bone diseases, like
67 osteopenia and osteoporosis, but also arterial hypertension, insulin resistance, obesity and
68 metabolic syndrome (Areco et al., 2015; Soto et al., 2014). Moreover, chronic hypocalcemia
69 is associated with neuropsychiatric symptoms, cataract formation, and sometimes increased
70 intracranial pressure (Hassan-Smith & Gittoes, 2017). These diseases occur predominantly in
71 postmenopausal women, individuals with milk allergy or lactose intolerance, adolescents or
72 elders (Beto, 2015).

73 About 90% of the overall calcium absorption occurs in the small intestine via two different
74 pathways (Areco et al., 2015). The first one is a non-saturable process that relies on the
75 electric gradient between lumen and intestinal mucosa, leading to the passive diffusion of
76 calcium ions across the intestinal epithelium (Pérez et al., 2008). This transport mechanism is
77 not fully understood but recent report showed the involvement of tight junction proteins
78 claudin-2 and claudin-12 (Fujita et al., 2008). The second pathway is a transcellular saturable
79 multistep process which first involves the uptake of calcium by epithelial intestinal cells via
80 the Ca^{2+} channel protein transient receptor potential vanilloid 6 (TRPV6), followed by
81 intracellular transport mediated by calbindin D9k proteins, and finally calcium extrusion
82 through plasma membrane involving Ca^{2+} -ATPase PMCA and sodium-calcium exchanger
83 NCX1 (Fleet & Schoch, 2010; Pu et al., 2016).

84 These Ca^{2+} -transport systems both depend on the steroid hormone 1,25 dihydroxyvitamin D,
85 and its interaction with the nuclear vitamin D receptor (VDR). Vitamin D is thus crucial for

86 both calcium absorption in the intestine and metabolism in bones (Brincat et al., 2015;
87 Bronner, 2003). Vitamin D-activated VDR acts as a transcription factor which regulates the
88 expression of TRPV6, or TRPV5 in kidney, calbindin D9k, claudin-2 and claudin-12
89 (Bronner, 2003; Fleet, 2017; Fujita et al., 2008; Haussler et al., 2010; Pu et al., 2016).
90 Generally, hypocalcemia results from vitamin D or parathyroid hormone deficiency (Hassan-
91 Smith & Gittoes, 2017). Deletion of VDR in mice causes disruption of calcium metabolism,
92 severe hypocalcemia and elevated plasma levels of parathyroid hormone and vitamin D (Van
93 Cromphaut et al., 2001).

94 Probiotics are defined as live microorganisms that, when administered in adequate amounts,
95 confer a health benefit on the host. Live cultures associated with fermented foods or
96 undefined fecal microbiota transplants are not include in this definition (Hill et al., 2014). The
97 most common probiotics are lactic acid bacteria (LAB) such as *Lactobacillus*, *Streptococcus*,
98 *Enterococcus*, *Bifidobacterium* (Roobab et al., 2020). The beneficial effects of probiotics are
99 numerous and include enhancement of intestinal epithelium barrier function, production of
100 antimicrobial substances, exclusion of pathogenic microorganisms, immunomodulation, anti-
101 inflammatory, antidiabetic and hypolipidaemic effects (Belguesmia et al., 2019; Bermudez-
102 Brito et al., 2012; Fernandez et al., 2011; Mousavi Khaneghah et al., 2020; Sarfraz et al.,
103 2019; Shafi et al., 2019; Vasconcelos et al., 2019). The impact of *Lactobacillus* species on
104 calcium metabolism was already evidenced *in vitro* (Gilman & Cashman, 2002) and *in vivo*
105 by animal or clinical studies (Areco et al., 2015; Kruger et al., 2009; McCabe &
106 Parameswaran, 2018; Nilsson et al., 2018; Parvaneh et al., 2014; Scholz-Ahrens et al., 2016),
107 but the mechanisms involved are still unclear, and there has been little investigation on the
108 impact of probiotics on calcium uptake.

109 The use of probiotics could be a safe and promising approach to treat elderly people suffering
110 from hypocalcemia. A decrease in calcium absorption is indeed observed upon aging (Nordin

111 et al., 2004), and this is actually concomitant with a loss of microbiota diversity (Mello et al.,
112 2016; Vaiserman et al., 2017). Calcium and vitamin D supplementations alone have failed to
113 show any significant pharmacological effect in the treatment of osteoporosis (Brincat et al.,
114 2015). However, probiotics may efficiently complement these supplementation strategies, by
115 increasing calcium biodisponibility and absorption (Vaiserman et al., 2017). Consistent with
116 this hypothesis, one publication previously reported that two strains of *L. plantarum* and *L.*
117 *rhamnosus* could increase VDR expression in mouse and human cells (Wu et al., 2015).

118 This study aimed to evaluate the probiotic capacity of *Lactobacillus* strains isolated in three
119 different areas of Mongolia (Raveschot et al., 2020). Production of dairies through
120 spontaneous milk fermentation has a long history in this country. Herders use different milks
121 (mare, cow, yak, camel, sheep, and goat) to produce a variety of fermented food such as
122 yogurt, kefir, or airag (fermented horse milk). These products were reported to contain a wide
123 diversity of LAB, especially *Lactobacillus* species (Watanabe et al., 2008; Yu et al., 2011). It
124 was recently reported that calcium bioavailability in dairy products was not impacted by the
125 food structure or components but was more dependent on the calcium source and its solubility
126 (Lorieau et al., 2018). Nevertheless, the presence of probiotics in these products could
127 increase the intestinal calcium absorption (Areco et al., 2015; Cavalcanti Neto et al., 2018;
128 Chugh & Kamal-Eldin, 2020). In this study, a screening of 174 LAB isolates was carried out
129 based on different probiotic characteristics. Criteria like cell surface hydrophobicity, acid
130 tolerance, adhesion to intestinal cells, autoaggregation, and tolerance to gastrointestinal (GI)
131 digestion were assessed. Then, the main objective of this study was to assess the possible
132 impact of probiotic strains on intestinal calcium absorption. To achieve this goal, the selected
133 strains were studied for their capacity to modulate calcium absorption using both Caco-2 and
134 HT-29 MTX intestinal cells. This study provides evidence for the beneficial impact of
135 Mongolian *Lactobacillus* probiotic strains on calcium metabolism and absorption.

136

137 **2. Material and methods**

138 **2.1. Mongolian *Lactobacillus* collection**

139 The screening was performed on a collection of 174 LAB strains isolated from Mongolian
140 dairy products. Strain isolation and identification had been described previously (Raveschot et
141 al., 2020). More than 93% of the isolates are *Lactobacillus* strains with 3 major species: *L.*
142 *helveticus*, *L. delbrueckii* subsp. *bulgaricus* and *L. kefiranofaciens*. The other species in the
143 collection are *L. fermentum*, *L. plantarum*, *L. kefiri*, *L. acidophilus*, *L. casei*, *Lactococcus*
144 *lactis*, *Leuconostoc lactis* and *Streptococcus thermophilus*.

145

146 **2.2. Cell surface hydrophobicity determination**

147 Cell surface hydrophobicity was determined by the Microbial Adhesion To Solvents (MATS)
148 test as described by Bellon-Fontaine et al., (1996). Briefly, strains were grown in 5 mL of
149 MRS medium for 24h at 37°C, washed twice, by successive centrifugation at 13,000 × g for
150 10 min and resuspension in 10 mL of phosphate buffered saline (PBS) buffer. The culture was
151 finally resuspended in 10 mL of PBS buffer and the OD_{630nm} of the suspension was
152 determined. One milliliter of the suspension was mixed with 100 µL of n-hexadecane (Acros
153 Organics, Molinons, France). The final mix was vortexed for 1 minute and let to rest for 15
154 minutes at room temperature. One hundred microliters were then taken from the aqueous
155 phase for OD_{630nm} determination. Cell surface hydrophobicity was determined using the
156 following formula:

$$157 \%H = \left(\frac{A_0 - A}{A_0} \right) \times 100$$

158 Where A_0 is the initial OD_{630nm} of the bacterial suspension and A the final OD_{630nm} of the mix
159 with n-hexadecane.

160

161 **2.3. Acid tolerance assay**

162 For acid tolerance assay, each strain was grown in 5 mL of MRS medium for 24h at 37°C.

163 Two hundred microliters of each culture were then diluted 1/10 in either MRS pH 6.2 (tube

164 A), or in MRS pH 2 (tube B). The tubes were incubated at 37°C for 2h and 10 μ L were

165 streaked on MRS plates followed by incubation for 48h at 37°C in anaerobic conditions. Acid

166 tolerance was evaluated by comparing the number of colonies on plates between A and B.

167 Strains were grouped in classes according to their acid tolerance: class 0, no colony on B

168 (strain not resistant), class 1, B = 0 to 30% of colonies on A (sensitive strain), class 2, B = 30-

169 80% of colonies on A (moderately sensitive strain), class 3, B > 80% of colonies on A

170 (tolerant strain).

171

172 **2.4. Autoaggregation assay**

173 Autoaggregation was assessed as described by Kotzamanidis et al., (2010). Briefly, strains

174 were grown in 5 mL of MRS medium for 24h at 37°C, centrifuged at $13,000 \times g$ for 10 min

175 and resuspended in PBS buffer at OD_{600nm} of 1. Four milliliters of the suspension were then

176 vortexed for 10 seconds and let to rest at room temperature. One hundred microliters were

177 carefully removed from the upper suspension at 0, 2.5h and 5h of incubation. Samples were

178 then diluted (1/10) in PBS buffer and OD_{600nm} was measured. The autoaggregation percentage

179 was calculated according to the following formula:

$$180 \%A = \left(1 - \frac{At}{A_0}\right) \times 100$$

181 Where A_t is the OD_{600nm} measured at $t = 2.5$ or 5 hours and A_0 the initial OD_{600nm} measured at
182 $t = 0$ hour.

183

184 **2.5. Tolerance to simulated gastro-intestinal digestion**

185 The survivability of *Lactobacillus* strains was evaluated using a static *in vitro* digestion model
186 inspired by Belguesmia et al., (2016). This model simulates mouth, stomach and small
187 intestine steps of digestion by incubating the bacteria in fluids that mimic the physiological
188 conditions encountered in these different compartments. Strains were grown in MRS for 24h
189 at 37°C, washed twice and resuspended with PBS buffer at 10^9 CFU.mL⁻¹. One milliliter of
190 the bacterial suspension was used for digestion. Mouth step was simulated by adding 8 mL of
191 PBS buffer (pH 6.8) to the bacterial suspension and incubating for 5 minutes at 37°C at
192 constant agitation (200 rpm) in an incubation shaker (Infors HT, Basel, Switzerland). The
193 gastric step was simulated by adding 12 mL of PBS buffer (pH 3) containing 1.56 mg.mL⁻¹ of
194 porcine pepsin (Sigma-Aldrich, St Louis, USA). This step was conducted during 2h at 37°C
195 and 200 rpm, the pH being maintained with HCl (1 M) or NaOH (1 M) at values ranging from
196 3 to 3.5. Two milliliters of NaHCO₃ (1 M) were then added to raise the pH up to 7; finally, the
197 small intestine step was then simulated by adding 12 mL of PBS buffer (pH 8.2) containing
198 0.28 mg.mL⁻¹ of pancreatin from porcine pancreas (Sigma-Aldrich, St Louis, USA) and 6 mL
199 of PBS buffer (pH 8.1) containing 60 g.L⁻¹ of bile salts (Sigma-Aldrich, St Louis, USA). This
200 digestion step was conducted for 2h at 37°C and 200 rpm, the pH being maintained between 7
201 and 7.5. Samples were taken after each step of the digestion process and diluted in PBS buffer
202 (pH 7.4). One hundred microliters of adequate dilutions were streaked on MRS plates and
203 incubated at 37°C for 48h under anaerobic conditions. The dilution factor varied from 10^3 to
204 10^8 depending on each strain and step of the digestion process. The number of CFU was then
205 calculated for each step of the simulated gastro-intestinal digestion.

206

207 **2.6. Cell lines and culture**

208 Caco-2 human colorectal carcinoma (Sigma-Aldrich, St Louis, USA) and mucus-secreting
209 HT-29 MTX human adenocarcinoma (Sigma-Aldrich, St Louis, USA) cell lines were both
210 used between passages 10 to 25. Both cell lines were grown in Dulbecco's Modified Eagle's
211 Medium (DMEM) supplemented with 10% (v/v) fetal bovine serum, 5 mM L-glutamine and
212 100 U.mL⁻¹ each of penicillin and streptomycin (all from Dutscher, Brumath, France). For
213 cytotoxicity assay and calcium uptake measurement, cells were seeded at a density of 8,000
214 cells/well in 96-well tissue culture plate. For adhesion assay and gene expression analysis,
215 cells were seeded at 40,000 cells/well in 24-well tissue culture plate. For calcium transport
216 determination, cells were seeded at 50,000 cells/well on transwell permeable supports (0.4
217 µm, polyester membrane) in 12-well tissue culture plate. Plates were incubated at 37°C under
218 5% CO₂-95% air atmosphere for 7 days for cytotoxicity and adhesion assays and for 15 days
219 for the other experiments. Medium was replaced every 2 days after confluence (7 days).

220

221 **2.7. Adhesion assay**

222 *Lactobacillus* strains were grown in MRS for 24h at 37°C and washed in PBS buffer. Strain
223 density was then adjusted to 10⁷ CFU.mL⁻¹ in DMEM medium. After 7 days of culture, Caco-
224 2 cells were washed twice with PBS buffer. Three hundred microliters of bacterial suspension
225 were then added on confluent Caco-2 monolayer. After incubation for 2h at 37°C under 5%
226 CO₂, cells were washed twice with PBS buffer to remove non-adherent bacteria. Cells were
227 then lysed by adding 100 µL of Triton X-100 in PBS 0.1% (v/v) and incubated for 15
228 minutes. The lysate containing adherent bacteria was then diluted and streaked on MRS plates
229 for CFU determination.

230

231 **2.8. Cytotoxicity assay**

232 *Lactobacillus* strain cytotoxicity was assessed on both Caco-2 and HT-29 MTX cell lines.

233 Bacterial suspensions were prepared as described in section 2.7. Cells were grown until

234 confluence (7 days) in 96-well tissue culture plate, washed twice in PBS buffer, then 150 μ L

235 of the different bacterial suspensions were added on cell monolayers. PBS buffer was used as

236 negative control. After incubation for 24h at 37°C under 5% CO₂, 50 μ L of cell supernatant

237 were taken and lactate dehydrogenase (LDH) activity was determined using In Vitro

238 Toxicology Assay Kit, LDH Based (Sigma-Aldrich, St Louis, USA). Results were expressed

239 in percentage of the LDH activity of non-treated cells.

240

241 **2.9. Transepithelial calcium transport across Caco-2 monolayer**

242 Caco-2 cells were seeded on transwell permeable supports and grown for 15 days. Bacterial

243 suspensions were prepared as described in section 2.7. The Caco-2 cell monolayers were

244 washed twice with PBS, then 300 μ L of the bacterial suspension (or PBS buffer as control)

245 and 10 μ L of CaCl₂ (250 mM) were added on the cells (apical chamber) which were then

246 incubated for 24h at 37°C under 5% CO₂. At 30 minutes, 7h and 24h of incubation, 100 μ L of

247 the basolateral medium were taken and kept at -20°C until calcium quantification. At the

248 same time, transepithelial electrical resistance (TEER) value of Caco-2 monolayer was

249 measured using a Voltmeter Ohmmeter MilliCell Electrical Resistance System (Merck

250 Millipore, Burlington, USA). Calcium quantification in samples taken from the basolateral

251 side of the Caco-2 cell monolayer was done using a Calcium Colorimetric Assay Kit (Sigma

252 Aldrich, St Louis, USA) following manufacturers' instructions and a microplate reader

253 spectrofluorometer (Xenius, Safas, Monaco, France). Results for both TEER and calcium
254 quantification were expressed as fold or percentage of the initial sample (t = 30 min).

255

256 **2.10. Measurement of calcium uptake in Caco-2 cells**

257 Caco-2 cells were seeded in 96-well tissue culture plate and cultured for 15 days as described
258 in section 2.6. Bacterial suspensions were prepared as described in section 2.7. Cell
259 monolayer was washed with PBS buffer, 150 μ L of bacterial suspension were added in each
260 well and incubated for 24h under 5% CO₂. The supernatants were discarded and cells washed
261 three times with PBS buffer. Then, calcium uptake by Caco-2 cells was determined using the
262 FluoForte™ Calcium Assay Kit (ENZ-51017, Enzo Life Sciences, Farmingdale, USA).

263 Briefly, the fluorogenic calcium binding dye FluoForte™ was added on Caco-2 monolayer for
264 1 hour at room temperature until its integration in cells. Fluorescence was then monitored
265 every second for a period of 30 seconds in a microplate reader spectrofluorometer (Xenius,
266 Safas, Monaco, France). 25 μ L of CaCl₂ (250 mM) were injected in the well at 10 seconds of
267 the kinetic. Fluorescence emission was expressed as fold of the basal fluorescence measured
268 between 0 and 9 seconds of the kinetic.

269

270 **2.11. Gene expression analysis**

271 HT-29 MTX cells were grown in 24-well tissue culture plate for 15 days. Bacterial
272 suspensions were prepared as described previously. The HT-29 MTX monolayer was washed
273 twice with PBS buffer and 300 μ L of bacterial suspension were added in each well. PBS
274 buffer was used as negative control (non-treated cells). After incubation for 24h at 37°C under
275 5% CO₂, cells were washed twice with PBS buffer and RNA extraction was performed using
276 Trizol reagent (Sigma-Aldrich, St Louis, USA). Briefly, 100 μ L of Trizol reagent was added

277 in each well for cell lysis, the obtained lysates were then transferred in new sterile tubes.
278 Twenty microliters of chloroform were added and the tubes were centrifuged 13,000 × g for
279 15 minutes at 4°C. The RNA-containing fraction was taken and 50 µL of isopropanol were
280 added followed by incubation at -20°C for 24h for RNA precipitation. Centrifugation for 20
281 minutes at 13,000 × g at 4°C was then performed and the supernatants were discarded. The
282 pellet was washed with ethanol 70% (v/v) and centrifuged for 20 minutes at 13,000 × g at
283 4°C. RNAs were then air dried for 3h at room temperature and finally dissolved in water.
284 Extracted total RNA were kept at -80°C. Concentration and purity of each sample was
285 assessed on a NanoDrop Lite (ThermoScientific, Waltham, USA). cDNA was obtained by
286 reverse transcription on a Mastercycler gradient (Eppendorf, Hambourg, Germany) using the
287 RevertAid H Minus First Strand cDNA Synthesis Kit (ThermoScientific, Waltham, USA).
288 Four genes were studied: vitamin D receptor (*vdr*), claudine-2 (*cld-2*), claudine-4 (*cld-4*) and
289 transient receptor potential selective for calcium (*trpv6*). The peptidylprolyl isomerase A
290 (*ppia*) gene was used as reference gene (Domenger et al., 2018). For each gene, reverse
291 transcribed cDNA was quantified by comparative Ct experiment on a CFX Connect Real
292 Time Detection System (Bio-Rad, Hercules, USA) using the Power SYBR Green PCR Master
293 Mix (Applied Biosystems, Life Technologies, Foster City, USA). Specific primers were used:
294 forward 5'-GCCACCTGCTCTATGCCAAG-3' and reverse 5'-
295 CAGGCTGTCCTAGTCAGGAGAT-3' for *vdr* gene; forward 5'-
296 TGATGCGGCTCATCAGTGCCAGC-3' and reverse 5'-
297 GTAGAAGTGGCCTAGCTCCTCG-3' for *trpv6* gene; forward 5'-
298 TGGCCTCTCTTGGCCTCCAACCTTGT-3' and reverse 5'-
299 TTGACCAGGCCTTGGAGAGCTC-3' for *cld-2* gene; forward 5'-
300 CCACTCGGACAACCTTCCCAA-3' and reverse 5'-ACTTCCGTCCCTCCCCAATA-3' for
301 *cld-4* gene; forward 5'-TGCTGACTGTGGACAACCTCG-3' and reverse 5'-

302 TGCAGCGAGAGCACAAAGAT-3' for *ppia* gene. Thermocycler conditions were 10
303 minutes at 95°C, 40 cycles of 15 seconds at 95°C, 30 seconds at 60°C and 30 seconds at
304 72°C, followed by a melting curve step. mRNA fold induction was calculated according to the
305 $2^{-\Delta\Delta C_t}$ method (Livak & Schmittgen, 2001) using *ppia* as reference gene. Results were
306 expressed as fold of control (non-treated cells).

307

308 **3. Results**

309

310 **3.1. Strain selection based on cell surface hydrophobicity and acid tolerance**

311 The first step of selection was conducted by assessing cell surface hydrophobicity and acid
312 tolerance. The cell surface hydrophobicity of the Mongolian strains ranged from 0 to 74%
313 (**Figure 1**). 50% of the studied strains showed less than 10% cell surface hydrophobicity.
314 Acid tolerance repartition was done in classes from 0 to 3 (non resistant to highly tolerant).
315 Among the 174 studied strains, 85 fell into class 0, 29 into class 1, 16 into class 2 and 44 into
316 class 3 (**Figure 1**). 75% of the strains in class 0 were *L. delbrueckii*, highlighting the poor acid
317 tolerance of this species. In contrast, all *L. fermentum* and *L. plantarum* strains fell into class
318 3. For the 2 other species most represented in the Mongolian collection (*L. helveticus* and *L.*
319 *kefiranofaciens*), acid tolerance appeared to be strain-dependent, as the isolates were more
320 equally distributed between classes. **Figure 1** represents cell surface hydrophobicity versus
321 acid tolerance for all studied strains. For the rest of this study, 8 *Lactobacillus* strains were
322 selected i) with cell surface hydrophobicity more than 30%, ii) preferentially in class 3 for
323 acid tolerance and iii) belonging to different *Lactobacillus* species. The 8 *Lactobacillus*
324 strains selected were *L. casei* 9b, *L. kefiranofaciens* 15b, *L. plantarum* 46a, *L. fermentum* 48a,
325 *L. helveticus* 49d, *L. delbrueckii* 50b, *L. delbrueckii* 56a and *L. fermentum* 62b.

326

327 **3.2. Strains were resistant to simulated GI digestion**

328 The 8 selected *Lactobacillus* strains were then tested for survivability upon simulated GI
329 digestion. At the beginning of the *in vitro* digestive process the bacterial cells were added at
330 10^9 CFU.mL⁻¹. At the end of the first step (mouth conditions), the number of living bacterial
331 cells was about 10^9 CFU.mL⁻¹ for all strains (**Figure 2**), which corresponds to the initial
332 amount: there was no decrease of viability at this stage. Depending on the strain, the number
333 of viable counts then decreased to various extents in subsequent digestion steps. The most
334 sensitive strains were *L. plantarum* 46a and *L. delbrueckii* 56a who went down to 10^6
335 CFU.mL⁻¹ at the end of the whole process. The other strains reached cell counts ranging from
336 10^8 to 10^7 CFU.mL⁻¹.

337 It is important to note that samples resulting from strain GI digestion were not used for the
338 further experiments in intestinal cells because bile acids are toxic for cultured cells. Thus, in
339 order to get closer to post-digestion conditions, the concentration of bacterial suspensions was
340 adjusted at the mean concentration reached at the end of the digestion process (10^7 CFU.mL⁻¹).
341

342 **3.3. Autoaggregation, adhesion capacity and cytotoxicity**

343 An increase of strain autoaggregation was observed for all isolates between 2.5h and 5h of
344 incubation in PBS, except for *L. casei* 9b which had already reached its maximal value at
345 2.5h. This strain showed the highest capacity of autoaggregation with about 95% of cells
346 aggregated at the end of the test; for the other strains, autoaggregation scores at 5h ranged
347 from 7.86% to 67.44% (**Table 1**).

348 *Lactobacillus* strains were tested for their adhesion capacity on Caco-2 cells monolayer.

349 Percentages of adherent bacteria varied between 0.18 and 4.63% depending on the strain

350 (Table 1). The 3 less adherent strains were *L. casei* 9b, *L. delbrueckii* 50b and 56a whereas
351 the 3 most adherent strains were *L. kefiranofaciens* 15b, *L. plantarum* 46a and *L. fermentum*
352 48a.

353 Interestingly, adhesion and autoaggregation results were negatively correlated. For instance,
354 *L. casei* 9b strain presented a high aggregation percentage but a weak adhesion capacity
355 whereas *L. kefiranofaciens* 15b showed a poor aggregation capacity but a high adhesion
356 potential. This negative correlation was confirmed by the calculation of Pearson's coefficients
357 between adhesion and autoaggregation, that were equal to -0.6 (autoaggregation values at
358 2.5h) and -0.75 (autoaggregation values at 5h).

359 In parallel the cytotoxicity of the isolates was evaluated on both Caco-2 and HT-29 MTX
360 cells (LDH assay). No significant cytotoxicity (one way ANOVA, $p < 0,05$) was observed for
361 all tested *Lactobacillus* strains after 24h of contact with the 2 cell lines (Table 2).

362 Based on these results, 6 *Lactobacillus* strains were kept for the rest of this study: *L. casei* 9b,
363 *L. kefiranofaciens* 15b, *L. plantarum* 46a, *L. fermentum* 48a, *L. helveticus* 49d and *L.*
364 *delbrueckii* 50b.

365

366 3.4. Modification of calcium uptake and transport in Caco-2 cells

367 3.4.1. Modification of total calcium transport across Caco-2 monolayer

368 Modulation of total calcium transport was assessed by determination of calcium flux across
369 fully differentiated Caco-2 monolayer upon contact with the selected *Lactobacillus* strains.

370 The TEER of Caco-2 monolayer was measured at the same time. The TEER increased
371 significantly (two way ANOVA) during the experiment (Figure 3A); however there was no
372 statistical difference between cells that were put in contact with the bacterial suspensions and

373 cells treated with PBS. This suggested that none of the tested strains had a detrimental effect
374 on Caco-2 monolayer integrity.

375 None of the strains was found to increase total calcium transport through the Caco-2
376 monolayer after 7h of contact (**Figure 3B**). However, after 24h of contact, 4 strains
377 significantly increased the basal side calcium concentration compared to control condition
378 (PBS buffer): *L. casei* 9b, *L. kefiranofaciens* 15b, *L. helveticus* 49d and *L. delbrueckii* 50b.
379 Moreover, a tendency for calcium increase at the basal side was observed for *L. plantarum*
380 46a strain (P value = 0.052). There was no increase of calcium transport for cells treated with
381 *L. fermentum* 48a.

382

383 3.4.2. *Lactobacillus* strains could modulate calcium uptake by Caco-2 cells

384 Calcium uptake was assessed after contact for 24h between bacterial strains and fully
385 differentiated Caco-2 cells. After injection of CaCl₂, an increase in fluorescence emission
386 occurred showing the calcium incorporation by Caco-2 cells (**Figure 4**). In control condition
387 (PBS), the ratio of fluorescence emission increased from 1 to 1.3-1.4 after calcium injection.
388 The ratio increase was not significantly different upon contact with *L. casei* 9b, *L.*
389 *kefiranofaciens* 15b, *L. helveticus* 49d and *L. delbrueckii* 50b. A significant diminution of
390 calcium uptake was observed after contact with *L. fermentum* 48a strain compared to control
391 condition. In contrast, calcium uptake was higher in Caco-2 cells monolayer incubated with *L.*
392 *plantarum* 46a bacteria, than in the control monolayer: the ratio of fluorescence increased
393 significantly from 1 to 1.4-1.5 after calcium injection. These results suggested that *L.*
394 *fermentum* 48a and *L. plantarum* 46a modulate calcium uptake by Caco-2 cells.

395

396 3.6. Change in *vdr*, *trpv6*, *cld-2* and *cld-4* RNA levels on HT-29 MTX cells

397 The effect of the 6 selected *Lactobacillus* strains on the expression of 4 genes related to
398 calcium/vitamin D metabolism or tight junction integrity (*vdr*, *trpv6*, *cld-2* and *cld-4*) were
399 evaluated on HT-29 MTX cells. Only 2 strains modulated the expression of *vdr* in HT-29
400 MTX cells: *L. plantarum* 46a and *L. delbrueckii* 50b (**Figure 5A**). *vdr* mRNA level increased
401 by 1.8 fold compared to control condition (PBS buffer). Four strains significantly increased
402 the level of *trpv6* mRNA: *L. casei* 9b, *L. kefiranofaciens* 15b, *L. plantarum* 46a and *L.*
403 *helveticus* 49d (**Figure 5B**). Only *L. delbrueckii* 50b lead to a significant increase of *cld-2*
404 mRNA level (**Figure 5C**), reaching 3 fold the level seen in control condition. However, all
405 *Lactobacillus* strains induced a significant increase of *cld-4* mRNA level (at least 2 fold of
406 control). The highest *cld-4* mRNA level was observed by treatments with *L. casei* 9b, *L.*
407 *kefiranofaciens* 15b and *L. helveticus* 49d strains (**Figure 5D**).

408 In summary, 4 patterns of mRNA level changes could be distinguished among the 4 tested
409 genes. *L. fermentum* 48a modulated only *cld-4* gene. Three *Lactobacillus* strains modulated
410 *cld-4* and *trpv6* mRNA levels: *L. casei* 9b, *L. kefiranofaciens* 15b and *L. helveticus* 49d. *L.*
411 *delbrueckii* 50b lead to an increase of *vdr*, *cld-2* and *cld-4* gene expressions. Finally, *L.*
412 *plantarum* 46a strain modulated expression of *vdr*, *trpv6* and *cld-4* genes.

413

414

415 **4. Discussion**

416 The first objective of this study was to evaluate the probiotic characteristics of 174 LAB
417 strains isolated from Mongolian dairy products. Before looking at biological effects *per se*,
418 the screening focused on the analysis of parameters related to the capacity of the strains to
419 settle and survive in the GI tract, and interact with intestinal epithelial cells without exerting
420 any cytotoxicity.

421 Acid tolerance determination was used as a first evaluation of the bacterial cell capacity to
422 resist GI digestion (particularly the gastric step) and reach the intestine in a viable and active
423 state (Angmo et al., 2016; Lo Curto et al., 2011). The acid tolerance response (ATR) of
424 *Lactobacillus* is known to be variable (Sengupta et al., 2013). The differences observed in our
425 study were, to some extent, species-specific. All *L. fermentum* and *L. plantarum* strains tested
426 were tolerant to acid condition. These species were already reported to be tolerant to pH 2
427 (Ramos et al., 2013). In contrast, all *L. delbrueckii* isolates were weakly tolerant, which is also
428 consistent with previous reports (Charteris et al., 1998; Vinderola & Reinheimer, 2003).

429 Cell surface hydrophobicity was also analyzed. It is thought to be a determinant of cell
430 adhesion capacity (Van Loosdrecht et al., 1987). Adherence to intestinal cells is considered as
431 a major criteria for the selection of probiotic strain (Vinderola et al., 2004), as it may in some
432 cases mediate the biological activities observed (Di Cerbo et al., 2016; Sengupta et al., 2013).

433 A high variability was observed between the Mongolian isolates, even within the same
434 species. Such variability was already observed; it reflects the fact that hydrophobicity depends
435 on a complex pattern of cell wall components (peptidoglycan, teichoic acids, cell wall
436 polysaccharides, cell surface proteins) (Angmo et al., 2016; Sengupta et al., 2013).

437 Isolates presenting the highest hydrophobicity values (29.2% for *L. fermentum* 62b, up to
438 69.1% for *L. casei* 9b), and showing strong acid tolerance, were further considered for the
439 screening (*L. casei* 9b, *L. kefiranofaciens* 15b, *L. plantarum* 46a, *L. fermentum* 48a, *L.*
440 *helveticus* 49d and *L. fermentum* 62b). Two *L. delbrueckii* strains (50b, 56a) were also kept
441 owing to their high cell surface hydrophobicity (36.3% and 48.9%, respectively).

442 Consistent with the high hydrophobicity values, most of the selected strains showed a good
443 percentage of adhesion to Caco-2 cells, ranging from 1.48 to 4.63%. These values are in
444 agreement with Tuomola and Salminen (1998) which obtained adhesion percentages ranging
445 from 2.6 to 14.4%. Both *L. delbrueckii* strains (50b and 56a) make a notable exception, with

446 low adhesion percentages (0.18% and 0.22%). Adhesion to intestinal cells depends on the
447 strain cell wall composition which varies between *Lactobacillus* strains and species (Dimitrov
448 et al., 2014; Sengupta et al., 2013).

449 Another parameter analyzed was autoaggregation. This trait is also thought to relate to the
450 capacity of the bacteria to interact with intestinal cells (Abushelaibi et al., 2017; Kotzamanidis
451 et al., 2010). Autoaggregation results were highly variables between the strains. Six of the 8
452 tested strains showed high autoaggregation percentages after 5h incubation in PBS, the values
453 were similar in range to those obtained by Kotzamanidis et al., (2010). Surprisingly, a
454 negative correlation was observed between autoaggregation and adhesion percentage. This
455 observation was not in agreement with a previous report of a positive correlation
456 (Kotzamanidis et al., 2010). However, other authors did not find any correlation between
457 aggregation abilities and adhesion, suggesting that interaction of probiotic bacteria with
458 intestinal cells involves more complex mechanisms (García-Cayuela et al., 2014; Ramos et
459 al., 2013).

460 Resistance to GI digestion is an important criteria for probiotic selection (Shewale et al.,
461 2014). In addition to the acid tolerance assay, a static *in vitro* digestion model was used
462 (Belguesmia et al., 2016), mimicking the impact of different GI digestion effectors (digestive
463 enzymes, bile salt and electrolytes). The tested *Lactobacillus* strains displayed good tolerance
464 abilities, reaching a high number of viable cells after the intestinal phase (at least 10^6
465 CFU.mL⁻¹). The most deleterious step was the gastric phase with the combined effect of low
466 pH and gastric enzymes except *L. casei* 9b, that was unaffected by all steps of GI digestion,
467 and *L. plantarum* 46a for which a significant decrease was only observed at the end of the
468 whole process. Protocols used to simulate GI digestion (pH, enzyme concentrations,
469 incubation times) differ between studies, comparing our findings with published results is
470 therefore difficult. In most studies however, a loss 1 to 3 points of log(CFU/mL) was seen

471 following simulated GI digestion (Belguesmia et al., 2016; Fernandez et al., 2003; Pitino et
472 al., 2010), which is consistent with our results.

473 Finally, no cytotoxic effect was reported for the tested *Lactobacillus* strains on both Caco-2
474 and HT-29 MTX intestinal cells. This is in agreement with previous reports, supporting the
475 recognition of *Lactobacillus* strains as safe bacteria (Er et al., 2015; Messaoudi et al., 2012).

476 Based on the results obtained, 6 *Lactobacillus* strains were kept for further studies on calcium
477 transport modulation: *L. casei* 9b, *L. kefiranofaciens* 15b, *L. plantarum* 46a, *L. fermentum*
478 48a, *L. helveticus* 49d and *L. delbrueckii* 50b. Two isolates were eliminated, *L. delbrueckii*
479 56a for its poor tolerance to GI digestion and *L. fermentum* 62b for its adhesion ability lower
480 than *L. fermentum* 48a.

481 Modulation of calcium metabolism by probiotic bacteria was mostly studied *in vivo* on bones;
482 usually probiotic treatment resulted in increased bone calcium content and reduced rate of
483 bone loss (Areco et al., 2015; Kruger et al., 2009; McCabe & Parameswaran, 2018; Parvaneh
484 et al., 2014; Scholz-Ahrens et al., 2016). In this study, the effect of *Lactobacillus* strains on
485 intestinal total calcium transport was assessed *in vitro* using Caco-2 cells. The Caco-2
486 monolayer is considered as a relevant model for calcium transport experiments (Giuliano et
487 al., 1991); indeed, these cells possess an enterocyte like phenotype after differentiation, a
488 functional vitamin D receptor and both saturable and non-saturable calcium transport
489 pathways (Fleet & Wood, 1999).

490 Assessment of TEER values confirmed that contact with the bacteria for 24h did not affect the
491 integrity of the Caco-2 membrane, nor impact the paracellular transport of nutrients. Actually,
492 a reinforcement of membrane integrity was observed for all tested conditions. In previous
493 studies, *Lactobacillus* strains improved or did not change TEER values on Caco-2 cells (Alard
494 et al., 2018; Belguesmia et al., 2019; Ramos et al., 2013). In the same experiment, calcium

495 concentration in the basal side of the monolayer was assessed. Except for *L. fermentum* 48a,
496 all strains increased calcium concentration in the basal compartment after 24h of incubation,
497 suggesting an improvement of total calcium transport by Caco-2 cells. However, calcium
498 uptake by Caco-2 was only improved significantly by *L. plantarum* 46a strain. Calcium
499 uptake by enterocytes is the first step of the saturable pathway of calcium absorption (Pérez et
500 al., 2008). It has been observed that a strain of *Lactobacillus salivarius* improved calcium
501 uptake in Caco-2 cells (Gilman & Cashman, 2002) but to our knowledge, this is the first
502 report showing an impact of probiotic *Lactobacillus* on intestinal calcium transport *in vitro*.

503 In order to understand the mechanism by which *Lactobacillus* strains improved calcium
504 uptake and/or transport, the expression of four genes related to calcium/vitamin D metabolism
505 or tight junction integrity was assessed on HT-29 MTX cells. HT-29 MTX cells, because of
506 their growth characteristics, are not well suited for experiments requiring monolayer
507 formation; but the presence of a mucus layer on differentiated cells, which mimics the
508 conditions of the intestinal mucosa, makes them an excellent model to study bacteria/gut cell
509 interactions. The four genes investigated were the genes coding for VDR and TRPV6, which
510 are directly involved in the saturable transcellular pathway of calcium transport (Bronner,
511 2003; Wood et al., 2001), and the genes coding for claudin-2 and claudin-4. Although the
512 paracellular pathway is not completely elucidated, it seems that claudin-2, as a component of
513 tight junctions, drives the selective paracellular transport of calcium through the intestinal
514 mucosa (Amasheh, 2002; Fujita et al., 2008). Claudin-4 is involved in tight junction integrity
515 and plays a critical role in regulating paracellular permeability (Lu et al., 2013).

516 All tested strains lead to an increase of *cld-4* mRNA level, suggesting improvement of
517 membrane integrity (Lechuga & Ivanov, 2017), which is consistent with the TEER results on
518 Caco-2 cells. *L. fermentum* 48a did not modulate any of the other genes, which is in
519 accordance with its absence of effect on total calcium transport. *L. casei* 9b, *L.*

520 *kefiranofaciens* 15b and *L. helveticus* 49d, all of which improved total calcium transport, had
521 a moderate effect on *trpv6* gene expression but did not modulate the expression of *vdr* or *cld-*
522 2. Based on these results, it is difficult to identify the pathway(s) by which these 3 strains
523 were able to improve intestinal calcium absorption. One possibility is the reduction of apical
524 (luminal) pH, by production of lactic acid or short chain fatty acids (mostly acetate,
525 propionate and butyrate), which contributes to increase calcium solubility and absorption
526 (Pérez et al., 2008; Scholz-Ahrens et al., 2007). Experiments should be conducted to analyze
527 the metabolites produced by these strains in intestinal condition. *L. delbrueckii* 50b improved
528 total calcium transport and upregulated both *vdr* and *cld-2* mRNA levels. Claudin-2 serves as
529 transport channel for ions and water (Lu et al., 2013). Together with claudin-12, it plays a role
530 in paracellular calcium diffusion under the control of vitamin D (Fujita et al., 2008).
531 Therefore, our results suggested that *L. delbrueckii* 50b strain improves calcium absorption *in*
532 *vitro* by modulation of the paracellular pathway.

533 The last strain tested in this study was *L. plantarum* 46a. This strain increased both *vdr* and
534 *trpv6* mRNA levels, and there was a tendency for improvement of calcium transport.
535 Interestingly it was the only strain tested which significantly increased calcium uptake by
536 Caco-2 cells. These two results are consistent, because TRPV6 is responsible for calcium
537 uptake by the cell; the suggested mechanism is therefore a modulation of the transcellular
538 calcium absorption pathway, involving upregulation of TRPV6 (Pérez et al., 2008). It is
539 important to note that the involvement of a calcium transporter (TRPV6) makes the
540 transcellular pathway a saturable pathway. This actually prevents intracellular calcium
541 concentration to reach unacceptable levels (Bronner, 2003; Fleet & Schoch, 2010). In the
542 meantime, this may also explain why the increase of total calcium transport by Caco-2 cells
543 upon contact with *L. plantarum* 46a was relatively moderate.

544 In conclusion, by screening a collection of 174 Mongolian LAB isolates, we were able to
545 identify 5 *Lactobacillus* strains displaying good probiotic characteristics, and able to modulate
546 calcium absorption by intestinal cells. The calcium absorption pathway actually modulated
547 appeared to depend on the tested strain. *L. casei* 9b, *L. kefiranofaciens* 15b and *L. helveticus*
548 49d were able to increase total calcium transport by Caco-2 cells most probably through an
549 improvement of calcium solubility. *L. delbrueckii* 50b impacted the paracellular pathway of
550 calcium absorption by up-regulation of the *cld-2* gene. Finally, *L. plantarum* 46a seemed to
551 improve intestinal calcium uptake and absorption through the transcellular pathway involving
552 VDR and TRPV6. This work provides new insights regarding the effects of probiotics on
553 calcium absorption, and their potential use in the prevention or treatment of hypocalcemia.
554 These results will be confirmed by *in vivo* experiments.

555

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563

564 **Conflict of interest**

565 CR, MF and MV are affiliated with VF Bioscience SAS, France, a company commercializing
566 lactic acid bacteria strains for use as probiotics or dairy starters.

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817

Figure 1:

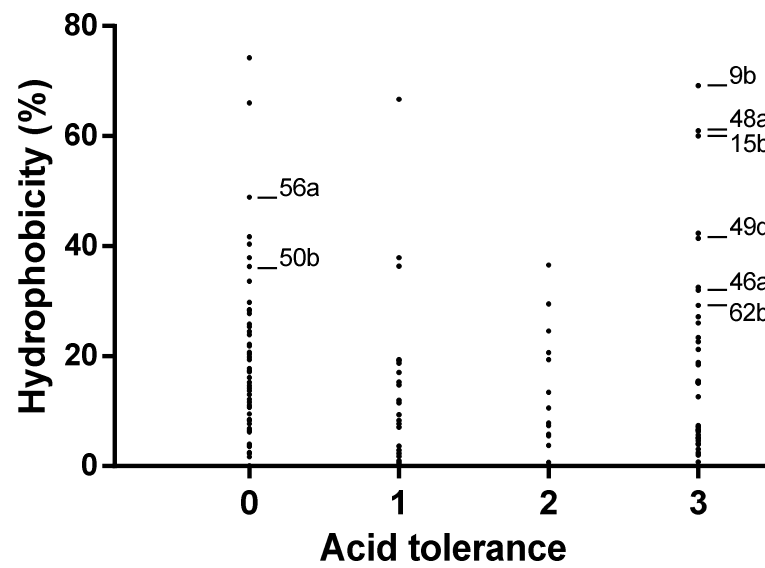


Fig. 1. Percentage of hydrophobicity versus acid tolerance for each Lactobacilli strain. Each strain is represented by a plot according to hydrophobicity and acid tolerance. Classes of acid tolerance: 0, strain not resistant, 1, sensitive strain, 2, moderately sensitive strain and 3, tolerant strain. The eight selected strains are reported on the graph: *L. casei* 9b, *L.kefiranofaciens* 15b, *L. plantarum* 46a, *L. fermentum* 48a, *L. helveticus* 49d, *L. delbrueckii* 50b, *L. delbrueckii* 56a and *L. fermentum* 62b. Values are means of three replicates.

Figure 2:

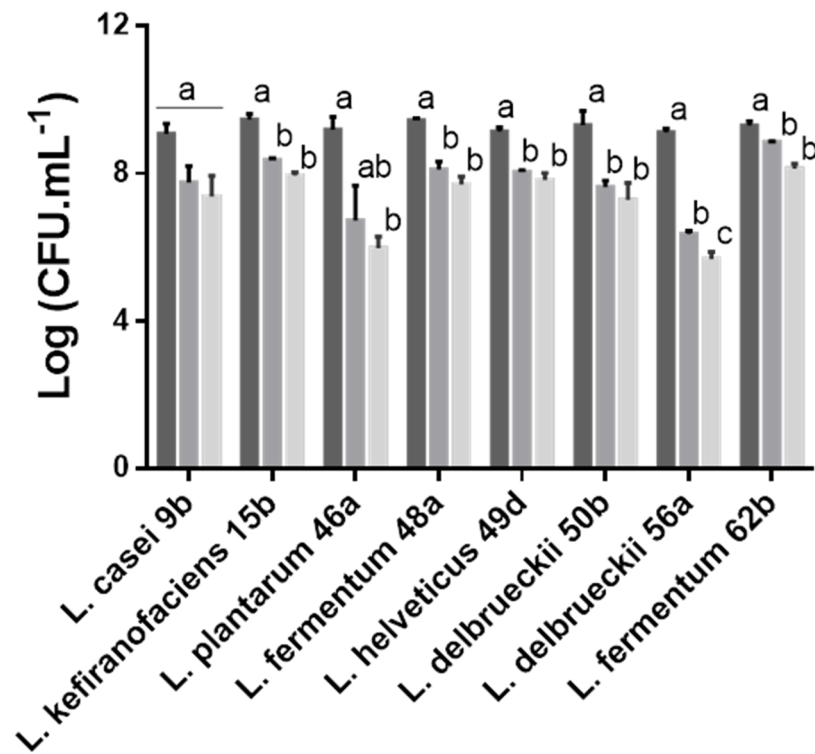


Fig. 2. Number of *Lactobacillus* after incubation in simulated GI tract compartments (static *in vitro* digestion model): mouth (dark grey), stomach (medium grey) and duodenum (light grey). Samples were taken after each step and the number of CFU.mL⁻¹ was evaluated by plating on MRS medium. Values are means \pm SD. *Statistical analysis using one way ANOVA and Tukey's post-hoc test for each strain. Mean with different letter differed significantly (P value < 0.05).

Figure 3:

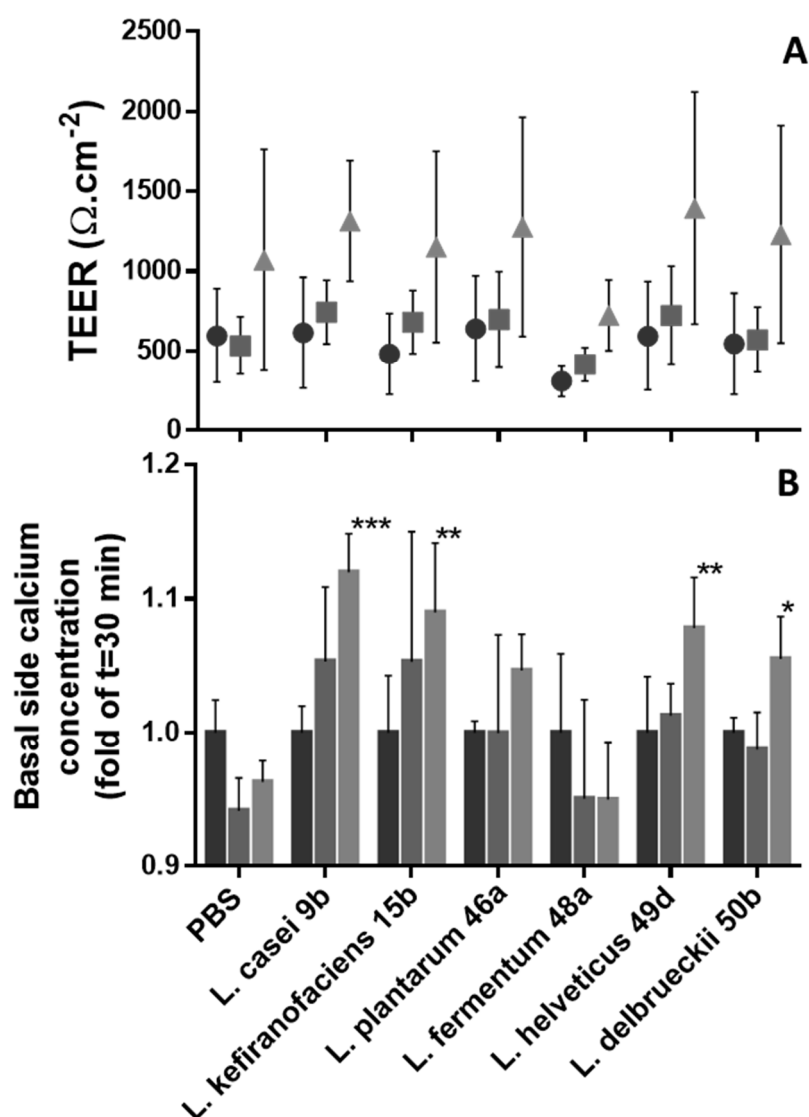


Fig. 3. Change in trans-epithelial electrical resistance (TEER) across Caco-2 cell monolayers, and in calcium concentration at the basal side of the monolayer, following contact with *Lactobacillus* strains for 24h. (A) Evolution of TEER in $\Omega.cm^{-2}$ at time t=30 min (●), 7h (■) and 24h (▲). (B) Change in calcium concentration at the basal side of Caco-2 membrane monolayers. Samples were taken at time t=30 min (dark grey), 7h (medium grey) and 24h (light grey) from the basal side of Caco-2 cell monolayers. Results are expressed as a fold ratio compared to t=30 min values. Values are means \pm SD of three repeated measurements. Means without a common symbol are different (*** P value < 0.001, ** P value < 0.01, * P value < 0.05) using one way ANOVA with Dunnet's post-hoc test vs PBS condition as reference.

Figure 4:

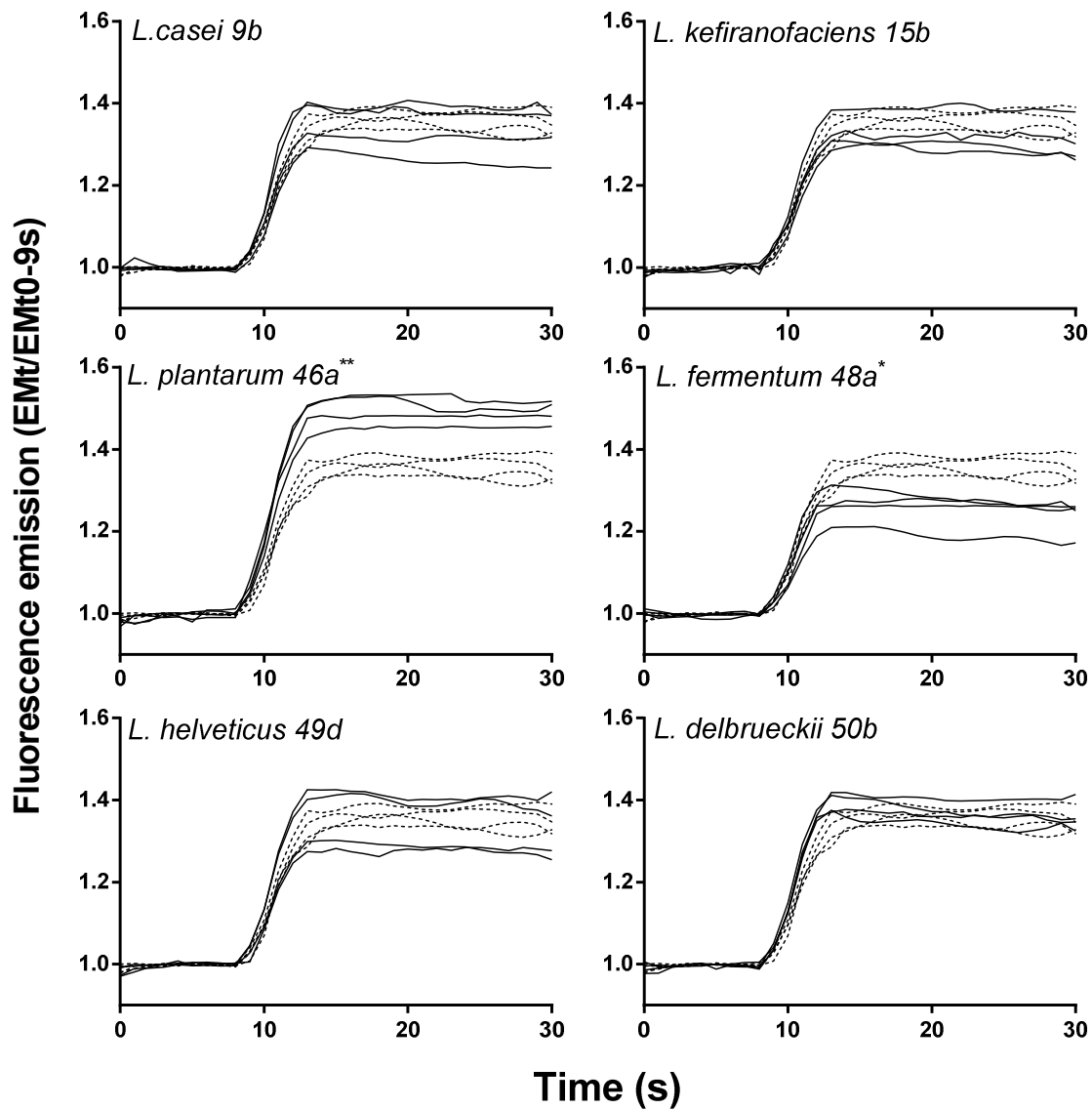


Fig. 4. Change in the intracellular calcium concentration in Caco-2 cells after injection of 25 μ L of CaCl_2 (250 mM) at 9 seconds of the kinetic (arrow). Modulation of the fluorescent Ca^{2+} sensitive molecule is assessed for 30 seconds after the CaCl_2 injection. Caco-2 cells were incubated with *Lactobacillus* strains for 24h before the experiment. Each graph represent experiments for one tested strain (full line) compared to control condition (PBS) (dotted line) (N=4). Values are expressed as ratio of emission (EMIt) by emission mean from 0 to 9 seconds of kinetic (EMIt0-9s). Statistical analysis between 15 and 30 seconds of kinetic using one way ANOVA with Dunnet's post-hoc test with PBS condition as reference (** P value < 0.01, * P value < 0.05).

Figure 5:

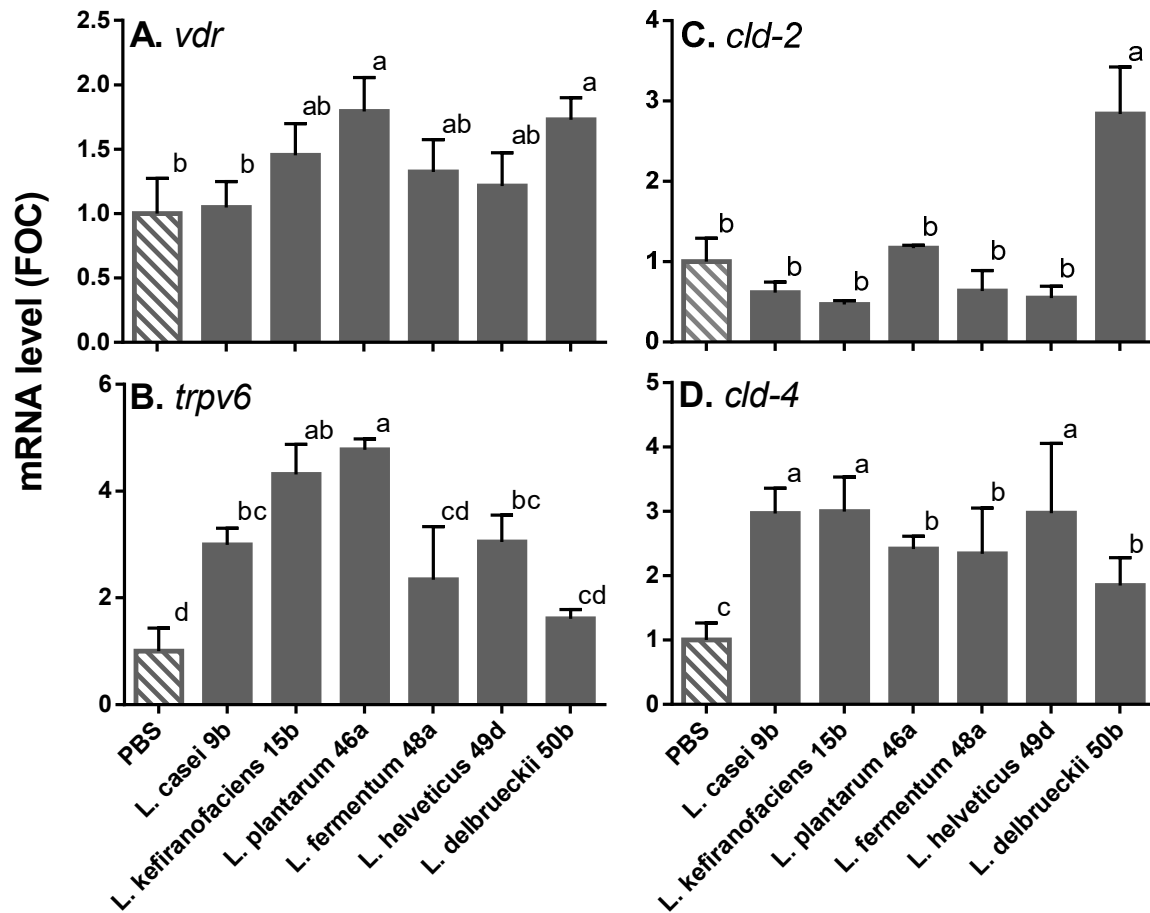


Fig. 5. mRNA expression levels of four genes in HT-29 MTX cells following 24h contact with *Lactobacillus* strains. (A) Vitamin D Receptor (*vdr*), (B) transient receptor potential selective for calcium (*trpv6*), (C) claudin-2 (*cld-2*) and (D) claudin-4 (*cld-4*). Results are reported in mean fold of control (FOC, PBS buffer) \pm SD of three replicates. Within the same graph, means with a different letter are significantly different (P value < 0.05) using one way ANOVA and Tukey's post-hoc test for pairwise comparisons.

Table 1. Percentage of autoaggregation in PBS buffer and percentage of *Lactobacillus* cells showing adhesion to Caco-2 cell monolayer.

| <i>Lactobacillus</i> strains | Autoaggregation (%) | | Adherent cells (%) |
|-------------------------------|----------------------------|-----------------------------|---------------------------|
| | 2,5 hours | 5 hours | 2 hours |
| <i>L. casei</i> 9b | 95,25 ± 2,23 ^d | 95,23 ± 0,92 ^d | 0,95 ± 0,53 ^{ab} |
| <i>L. kefiranofaciens</i> 15b | 3,53 ± 5,12 ^a | 7,86 ± 3,57 ^a | 4,11 ± 2,2 ^c |
| <i>L. plantarum</i> 46a | 12,74 ± 3,15 ^{ab} | 28,27 ± 9,7 ^{ac} | 4,63 ± 1,22 ^c |
| <i>L. fermentum</i> 48a | 1,97 ± 6,28 ^a | 22,49 ± 3,19 ^{ab} | 4,39 ± 0,33 ^c |
| <i>L. helveticus</i> 49d | 5,83 ± 5,24 ^a | 67,44 ± 6,99 ^{cd} | 1,48 ± 0,41 ^{ab} |
| <i>L. delbrueckii</i> 50b | 33,33 ± 14,8 ^{bc} | 66,67 ± 17,97 ^{cd} | 0,18 ± 0,13 ^a |
| <i>L. delbrueckii</i> 56a | 39,29 ± 6,97 ^c | 46,73 ± 22,13 ^{ac} | 0,22 ± 0,09 ^a |
| <i>L. fermentum</i> 62b | 11,72 ± 2,22 ^{ab} | 18,04 ± 9,94 ^{ab} | 2,76 ± 0,81 ^{bc} |

For autoaggregation assay, samples were taken at 2.5h and 5h of incubation from the top of the *Lactobacillus* suspensions for OD_{600nm} determination. For adhesion test, the percentage of *Lactobacillus* cells adhering to Caco-2 monolayer was assessed after contact with bacterial suspension for 2h. Values are expressed as percentage of OD_{600nm} or number of CFU.mL⁻¹ at 0h and are means ± SD of three replicates. *Statistical analysis using one way ANOVA and Tukey's post-hoc test. Mean values in the same column without a common letter differ significantly (P value < 0.05).

Table 2. Survival percentage of Caco-2 and HT-29 MTX cells after contact with PBS buffer or *Lactobacillus* strains for 24h.

| | Caco-2 | HT-29 MTX |
|-------------------------------|---------------|------------------|
| PBS | 100.00 ± 8.07 | 100.00 ± 4.16 |
| <i>L. casei</i> 9b | 91.99 ± 9.07 | 93.67 ± 7.50 |
| <i>L. kefiranofaciens</i> 15b | 95.74 ± 10.91 | 107.63 ± 4.34 |
| <i>L. plantarum</i> 46a | 101.34 ± 2.95 | 105.49 ± 8.37 |
| <i>L. fermentum</i> 48a | 98.66 ± 21.04 | 107,91 ± 6.57 |
| <i>L. helveticus</i> 49d | 97.58 ± 7.96 | 103.07 ± 1.05 |
| <i>L. delbrueckii</i> 50b | 97.16 ± 4.84 | 90.42 ± 4.84 |
| <i>L. delbrueckii</i> 56a | 93.84 ± 8.21 | 97.84 ± 2,93 |
| <i>L. fermentum</i> 62b | 85.80 ± 6.04 | 95.80 ± 2,68 |

The survival of Caco-2 and HT-29 MTX cells was assessed by determination of lactate dehydrogenase activity. Values are expressed in percentage of control (PBS) and are means ± SD of six replicates. No significant differences were observed between treatments after statistical analysis using one way ANOVA and Tukey's post-hoc test (P value < 0.05).

