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

- 3
- 4 Cyril Raveschot ^{ab}, François Coutte ^a, Marc Frémont ^b, Maxime Vaeremans ^b, Jamyan
- 5 Dugersuren^c, Shirchin Demberel^c, Djamel Drider^a, Pascal Dhulster^a, Christophe
- 6 Flahaut ^a, Benoit Cudennec ^{a*}
- 7
- ^a Univ. Lille, INRA, ISA, Univ. Artois, Univ. Littoral Côte d'Opale, EA 7394 ICV Institut
- 9 Charles Viollette, F-59000 Lille, France
- 10 ^b VF Bioscience, Parc Eurasanté, F-59120 Loos-lez-Lille, France
- ^c Probiotic Research Center, Mongolian Veterinary Institute, 17024 Ulaanbaatar, Mongolia
 12
- 13 *Corresponding author:
- 14 Dr. Benoit Cudennec
- 15 Université de Lille, Institut Charles Viollette
- 16 Cité Scientifique, Bâtiment SN2
- 17 Avenue Mendeleiev
- 18 59655 Villeneuve d'Ascq, France
- 19 E-mail address: benoit.cudennec@univ-lille.fr
- 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

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

57

- 58 Keywords: Calcium intake; gut barrier; lactobacillus, probiotics, Caco-2 cells; HT29-MTX
 59 cells
- 60

61 **1. Introduction**

More than 99% of calcium in the human body is stored in the skeleton (Beto, 2015). 62 However, besides being the main mineral component of bones, calcium is also involved in 63 64 many physiological processes such as vascular contraction, vasodilation, muscle function, neuronal transmission, intracellular signaling and hormonal secretion (Pu et al., 2016). 65 Calcium deficiency or hypocalcemia is associated with the development of bone diseases, like 66 67 osteopenia and osteoporosis, but also arterial hypertension, insulin resistance, obesity and metabolic syndrome (Areco et al., 2015; Soto et al., 2014). Moreover, chronic hypocalcemia 68 is associated with neuropsychiatric symptoms, cataract formation, and sometimes increased 69 70 intracranial pressure (Hassan-Smith & Gittoes, 2017). These diseases occur predominantly in postmenopausal women, individuals with milk allergy or lactose intolerance, adolescents or 71 elders (Beto, 2015). 72

About 90% of the overall calcium absorption occurs in the small intestine via two different 73 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 calcium ions across the intestinal epithelium (Pérez et al., 2008). This transport mechanism is 76 not fully understood but recent report showed the involvement of tight junction proteins 77 78 claudin-2 and claudin-12 (Fujita et al., 2008). The second pathway is a transcellular saturable multistep process which first involves the uptake of calcium by epithelial intestinal cells via 79 the Ca²⁺ channel protein transient receptor potential vanilloid 6 (TRPV6), followed by 80 intracellular transport mediated by calbindin D9k proteins, and finally calcium extrusion 81 through plasma membrane involving Ca^{2+} -ATPase PMCA and sodium-calcium exchanger 82 83 NCX1 (Fleet & Schoch, 2010; Pu et al., 2016).

These Ca²⁺-transport systems both depend on the steroid hormone 1,25 dihydroxyvitamin D,
and its interaction with the nuclear vitamin D receptor (VDR). Vitamin D is thus crucial for

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

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-

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

et al., 2004), and this is actually concomitant with a loss of microbiota diversity (Mello et al., 111 112 2016; Vaiserman et al., 2017). Calcium and vitamin D supplementations alone have failed to show any significant pharmacological effect in the treatment of osteoporosis (Brincat et al., 113 114 2015). However, probiotics may efficiently complement these supplementation strategies, by increasing calcium biodisponibility and absorption (Vaiserman et al., 2017). Consistent with 115 116 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). This study aimed to evaluate the probiotic capacity of Lactobacillus strains isolated in three 118 different areas of Mongolia (Raveschot et al., 2020). Production of dairies through 119 120 spontaneous milk fermentation has a long history in this country. Herders use different milks (mare, cow, yak, camel, sheep, and goat) to produce a variety of fermented food such as 121 yogurt, kefir, or airag (fermented horse milk). These products were reported to contain a wide 122 diversity of LAB, especially Lactobacillus species (Watanabe et al., 2008; Yu et al., 2011). It 123 was recently reported that calcium bioavailability in dairy products was not impacted by the 124 125 food structure or components but was more dependent on the calcium source and its solubility (Lorieau et al., 2018). Nevertheless, the presence of probiotics in these products could 126 increase the intestinal calcium absorption (Areco et al., 2015; Cavalcanti Neto et al., 2018; 127 128 Chugh & Kamal-Eldin, 2020). In this study, a screening of 174 LAB isolates was carried out based on different probiotic characteristics. Criteria like cell surface hydrophobicity, acid 129 tolerance, adhesion to intestinal cells, autoaggregation, and tolerance to gastrointestinal (GI) 130 digestion were assessed. Then, the main objective of this study was to assess the possible 131 impact of probiotic strains on intestinal calcium absorption. To achieve this goal, the selected 132 133 strains were studied for their capacity to modulate calcium absorption using both Caco-2 and HT-29 MTX intestinal cells. This study provides evidence for the beneficial impact of 134 Mongolian Lactobacillus probiotic strains on calcium metabolism and absorption. 135

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**

Cell surface hydrophobicity was determined by the Microbial Adhesion To Solvents (MATS) 147 test as described by Bellon-Fontaine et al., (1996). Briefly, strains were grown in 5 mL of 148 MRS medium for 24h at 37°C, washed twice, by successive centrifugation at $13,000 \times g$ for 149 10 min and resuspension in 10 mL of phosphate buffered saline (PBS) buffer. The culture was 150 151 finally resuspended in 10 mL of PBS buffer and the OD_{630nm} of the suspension was determined. One milliliter of the suspension was mixed with 100 µL of n-hexadecane (Acros 152 153 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 phase for OD_{630nm} determination. Cell surface hydrophobicity was determined using the 155 following formula: 156

157
$$\%$$
H = $\left(\frac{A0 - A}{A0}\right) \times 100$

Where A0 is the initial OD_{630nm} of the bacterial suspension and A the final OD_{630nm} of the mix 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

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

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

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

Autoaggregation was assessed as described by Kotzamanidis et al., (2010). Briefly, strains were grown in 5 mL of MRS medium for 24h at 37°C, centrifuged at 13,000 × g for 10 min and resuspended in PBS buffer at OD_{600nm} of 1. Four milliliters of the suspension were then vortexed for 10 seconds and let to rest at room temperature. One hundred microliters were carefully removed from the upper suspension at 0, 2.5h and 5h of incubation. Samples were then diluted (1/10) in PBS buffer and OD_{600nm} was measured. The autoaggregation percentage was calculated according to the following formula:

$$180 \qquad \% \mathbf{A} = \left(1 - \frac{At}{A0}\right) \times 100$$

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

183

184 2.5. Tolerance to simulated gastro-intestinal digestion

The survivability of *Lactobacillus* strains was evaluated using a static *in vitro* digestion model 185 inspired by Belguesmia et al., (2016). This model simulates mouth, stomach and small 186 187 intestine steps of digestion by incubating the bacteria in fluids that mimic the physiological conditions encountered in these different compartments. Strains were grown in MRS for 24h 188 at 37°C, washed twice and resuspended with PBS buffer at 10⁹ CFU.mL⁻¹. One milliliter of 189 the bacterial suspension was used for digestion. Mouth step was simulated by adding 8 mL of 190 PBS buffer (pH 6.8) to the bacterial suspension and incubating for 5 minutes at 37°C at 191 constant agitation (200 rpm) in an incubation shaker (Infors HT, Basel, Switzerland). The 192 gastric step was simulated by adding 12 mL of PBS buffer (pH 3) containing 1.56 mg.mL⁻¹ of 193 porcine pepsin (Sigma-Aldrich, St Louis, USA). This step was conducted during 2h at 37°C 194 and 200 rpm, the pH being maintained with HCl (1 M) or NaOH (1 M) at values ranging from 195 3 to 3.5. Two milliliters of NaHCO₃ (1 M) were then added to raise the pH up to 7; finally, the 196 small intestine step was then simulated by adding 12 mL of PBS buffer (pH 8.2) containing 197 0.28 mg.mL⁻¹ of pancreatin from porcine pancreas (Sigma-Aldrich, St Louis, USA) and 6 mL 198 of PBS buffer (pH 8.1) containing 60 g.L⁻¹ of bile salts (Sigma-Aldrich, St Louis, USA). This 199 200 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 (pH 7.4). One hundred microliters of adequate dilutions were streaked on MRS plates and 202 incubated at 37°C for 48h under anaerobic conditions. The dilution factor varied from 10³ to 203 10⁸ depending on each strain and step of the digestion process. The number of CFU was then 204 calculated for each step of the simulated gastro-intestinal digestion. 205

206

207 **2.6. Cell lines and culture**

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

220

221 **2.7. Adhesion assay**

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

230

231 **2.8.** Cytotoxicity assay

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

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

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

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

negative control. After incubation for 24h at 37°C under 5% CO₂, 50 µL 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

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

240

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

Caco-2 cells were seeded on transwell permeable supports and grown for 15 days. Bacterial 242 243 suspensions were prepared as described in section 2.7. The Caco-2 cell monolayers were washed twice with PBS, then 300 µL of the bacterial suspension (or PBS buffer as control) 244 and 10 µL of CaCl₂ (250 mM) were added on the cells (apical chamber) which were then 245 incubated for 24h at 37°C under 5% CO₂. At 30 minutes, 7h and 24h of incubation, 100 µL of 246 the basolateral medium were taken and kept at -20°C until calcium quantification. At the 247 248 same time, transepithelial electrical resistance (TEER) value of Caco-2 monolayer was measured using a Voltmeter Ohmmeter MilliCell Electrical Resistance System (Merck 249 Millipore, Burlington, USA). Calcium quantification in samples taken from the basolateral 250 251 side of the Caco-2 cell monolayer was done using a Calcium Colorimetric Assay Kit (Sigma Aldrich, St Louis, USA) following manufacturers' instructions and a microplate reader 252

spectrofluorometer (Xenius, Safas, Monaco, France). Results for both TEER and calcium
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

Caco-2 cells were seeded in 96-well tissue culture plate and cultured for 15 days as described 257 in section 2.6. Bacterial suspensions were prepared as described in section 2.7. Cell 258 259 monolayer was washed with PBS buffer, 150 µL of bacterial suspension were added in each well and incubated for 24h under 5% CO₂. The supernatants were discarded and cells washed 260 261 three times with PBS buffer. Then, calcium uptake by Caco-2 cells was determined using the FluoForteTM Calcium Assay Kit (ENZ-51017, Enzo Life Sciences, Farmingdale, USA). 262 Briefly, the fluorogenic calcium binding dye FluoForte[™] was added on Caco-2 monolayer for 263 1 hour at room temperature until its integration in cells. Fluorescence was then monitored 264 every second for a period of 30 seconds in a microplate reader spectrofluorometer (Xenius, 265 Safas, Monaco, France). 25 µL of CaCl₂ (250 mM) were injected in the well at 10 seconds of 266 the kinetic. Fluorescence emission was expressed as fold of the basal fluorescence measured 267 between 0 and 9 seconds of the kinetic. 268

269

270 **2.11. Gene expression analysis**

271 HT-29 MTX cells were grown in 24-well tissue culture plate for 15 days. Bacterial

suspensions were prepared as described previously. The HT-29 MTX monolayer was washed

twice with PBS buffer and 300 μ L of bacterial suspension were added in each well. PBS

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 µL of Trizol reagent was added

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

302	TGCAGCGAGAGCACAAAGAT-3' for <i>ppia</i> 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	$2^{-\Delta\Delta Ct}$ method (Livak & Schmittgen, 2001) using <i>ppia</i> 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. Acid tolerance repartition was done in classes from 0 to 3 (non resistant to highly tolerant). 314 315 Among the 174 studied strains, 85 fell into class 0, 29 into class 1, 16 into class 2 and 44 into class 3 (Figure 1). 75% of the strains in class 0 were L. delbrueckii, highlighting the poor acid 316 317 tolerance of this species. In contrast, all L. fermentum and L. plantarum strains fell into class 3. For the 2 other species most represented in the Mongolian collection (L. helveticus and L. 318 319 *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 acid tolerance for all studied strains. For the rest of this study, 8 Lactobacillus strains were 321 322 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 strains selected were L. casei 9b, L. kefiranofaciens 15b, L. plantarum 46a, L. fermentum 48a, 324 L. helveticus 49d, L. delbrueckii 50b, L. delbrueckii 56a and L. fermentum 62b. 325

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

The 8 selected Lactobacillus strains were then tested for survivability upon simulated GI 328 digestion. At the beginning of the *in vitro* digestive process the bacterial cells were added at 329 10⁹ CFU.mL⁻¹. At the end of the first step (mouth conditions), the number of living bacterial 330 cells was about 10⁹ CFU.mL⁻¹ for all strains (Figure 2), which corresponds to the initial 331 amount: there was no decrease of viability at this stage. Depending on the strain, the number 332 of viable counts then decreased to various extents in subsequent digestion steps. The most 333 sensitive strains were L. plantarum 46a and L. delbrueckii 56a who went down to 10⁶ 334 CFU.mL⁻¹ at the end of the whole process. The other strains reached cell counts ranging from 335 10^8 to 10^7 CFU.mL⁻¹. 336

It is important to note that samples resulting from strain GI digestion were not used for the
further experiments in intestinal cells because bile acids are toxic for cultured cells. Thus, in
order to get closer to post-digestion conditions, the concentration of bacterial suspensions was
adjusted at the mean concentration reached at the end of the digestion process (10⁷ CFU.mL⁻
¹).

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

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

Lactobacillus strains were tested for their adhesion capacity on Caco-2 cells monolayer.
Percentages of adherent bacteria varied between 0.18 and 4.63% depending on the strain

350	(Table 1). The 3 less adherent strains were <i>L. casei</i> 9b, <i>L. delbrueckii</i> 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,
- 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
- between adhesion and autoaggregation, that were equal to -0.6 (autoaggregation values at
- 358 2.5h) and -0.75 (autoaggregation values at 5h).
- 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
- all tested *Lactobacillus* strains after 24h of contact with the 2 cell lines (**Table 2**).
- 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.
- The TEER of Caco-2 monolayer was measured at the same time. The TEER increased
- 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 effect374 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*

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*

Calcium uptake was assessed after contact for 24h between bacterial strains and fully
differentiated Caco-2 cells. After injection of CaCl₂, an increase in fluorescence emission
occurred showing the calcium incorporation by Caco-2 cells (Figure 4). In control condition
(PBS), the ratio of fluorescence emission increased from 1 to 1.3-1.4 after calcium injection.
The ratio increase was not significantly different upon contact with *L. casei* 9b, *L. 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

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

significantly from 1 to 1.4-1.5 after calcium injection. These results suggested that *L*.

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
- 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.

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414

415 **4. Discussion**

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

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

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

460 Resistance to GI digestion is an important criteria for probiotic selection (Shewale et al., 2014). In addition to the acid tolerance assay, a static in vitro digestion model was used 461 (Belguesmia et al., 2016), mimicking the impact of different GI digestion effectors (digestive 462 463 enzymes, bile salt and electrolytes). The tested *Lactobacillus* strains displayed good tolerance abilities, reaching a high number of viable cells after the intestinal phase (at least 10⁶ 464 CFU.mL⁻¹. The most deleterious step was the gastric phase with the combined effect of low 465 pH and gastric enzymes except L. casei 9b, that was unaffected by all steps of GI digestion, 466 and L. plantarum 46a for which a significant decrease was only observed at the end of the 467 468 whole process. Protocols used to simulate GI digestion (pH, enzyme concentrations, incubation times) differ between studies, comparing our findings with published results is 469 therefore difficult. In most studies however, a loss 1 to 3 points of log(CFU/mL) was seen 470

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

Finally, no cytotoxic effect was reported for the tested Lactobacillus strains on both Caco-2 473 474 and HT-29 MTX intestinal cells. This is in agreement with previous reports, supporting the recognition of *Lactobacillus* strains as safe bacteria (Er et al., 2015; Messaoudi et al., 2012). 475 Based on the results obtained, 6 Lactobacillus strains were kept for further studies on calcium 476 transport modulation: L. casei 9b, L. kefiranofaciens 15b, L. plantarum 46a, L. fermentum 477 48a, L. helveticus 49d and L. delbrueckii 50b. Two isolates were eliminated, L. delbrueckii 478 56a for its poor tolerance to GI digestion and L. fermentum 62b for its adhesion ability lower 479 than L. fermentum 48a. 480

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

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

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).

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

concentration in the basal side of the monolayer was assessed. Except for L. fermentum 48a, 495 496 all strains increased calcium concentration in the basal compartment after 24h of incubation, suggesting an improvement of total calcium transport by Caco-2 cells. However, calcium 497 uptake by Caco-2 was only improved significantly by L. plantarum 46a strain. Calcium 498 uptake by enterocytes is the first step of the saturable pathway of calcium absorption (Pérez et 499 al., 2008). It has been observed that a strain of *Lactobacillus salivarius* improved calcium 500 501 uptake in Caco-2 cells (Gilman & Cashman, 2002) but to our knowledge, this is the first report showing an impact of probiotic Lactobacillus on intestinal calcium transport in vitro. 502 503 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 or tight junction integrity was assessed on HT-29 MTX cells. HT-29 MTX cells, because of 505 their growth characteristics, are not well suited for experiments requiring monolayer 506 formation; but the presence of a mucus layer on differentiated cells, which mimics the 507 508 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 tight junctions, drives the selective paracellular transport of calcium through the intestinal 513 514 mucosa (Amasheh, 2002; Fujita et al., 2008). Claudin-4 is involved in tight junction integrity and plays a critical role in regulating paracellular permeability (Lu et al., 2013). 515 All tested strains lead to an increase of *cld-4* mRNA level, suggesting improvement of 516 517 membrane integrity (Lechuga & Ivanov, 2017), which is consistent with the TEER results on Caco-2 cells. L. fermentum 48a did not modulate any of the other genes, which is in 518 accordance with its absence of effect on total calcium transport. L. casei 9b, L. 519

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

vitro by modulation of the paracellular pathway.

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

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

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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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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 Ω .cm⁻² at time t=30 min (\bullet), 7h (\blacksquare) and 24h (\blacktriangle). (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 ± 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.





Fig. 4. Change in the intracellular calcium concentration in Caco-2 cells after injection of 25 μ L of CaCl₂ (250 mM) at 9 seconds of the kinetic (arrow). Modulation of the fluorescent Ca²⁺ sensitive molecule is assessed for 30 seconds after the CaCl₂ 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).





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.

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

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

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 \pm 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).

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

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

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 \pm 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).

