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PII: S2405-6545(20)30134-7

DOI: https://doi.org/10.1016/j.aninu.2020.07.005

Reference: ANINU 381

To appear in: Animal Nutrition Journal

Received Date: 3 November 2019

Revised Date: 21 June 2020

Accepted Date: 12 July 2020

Please cite this article as: Noohi N, Papizadeh M, Rohani M, Talebi M, Pourshafie MR, Screening for probiotic characters in lactobacilli isolated from chickens revealed the intra-species diversity of *Lactobacillus brevis*, *Animal Nutrition Journal*, https://doi.org/10.1016/j.aninu.2020.07.005.

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Screening for Probiotic Characters in Lactobacilli Isolated from Chickens Revealed the Intra-Species Diversity of Lactobacillus brevis

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species diversity of Lactobacillus brevis
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15

16 Abstract

17 Considering the importance of the poultry industry and the increasing interest in alternative growth promoters, probiotics are considered as a potential candidate for use in the poultry 18 19 industry. In this study, Lactobacillus species were isolated from 21 rectal swabs of 11 healthy 6day-old and 10 healthy 21-day-old chickens and their fecal and feed samples. The isolates were 20 characterized and their probiotic characteristics, including resistance to gastric acid and bile salts, 21 biofilm formation and adherence to epithelium or mucus, amylase and protease activity and 22 production of inhibitory compounds, were assessed. From 31 acid and bile resistant lactobacilli, 23 only 2 Lactobacillus brevis and 1 Lactobacillus reuteri strains showed significant probiotic 24 properties. These isolates indicated detectable attachment to Caco-2 cells and significant 25 antibacterial activities against Gram-positive and Gram-negative pathogens. Additionally, 26 phenotypic and genotypic diversity of lactobacilli isolates were studied by Phene Plate (PhP) 27 system (PhP-LB) and random amplified polymorphic DNA (RAPD)-PCR, respectively. PhP-LB 28 results of 24 L. brevis isolates showed a high phenotypic variation among the isolates. In 29 comparison, results of RAPD-PCR highlighted a low diversity. Therefore, it seems that 30 31 combination of the 2 techniques (PhP and RAPD-PCR) could result in a significant discriminatory power than each of them used alone. 32

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34 Keywords: Probiotic; Lactobacilli; Poultry; Feed; Fecal

36 1. Introduction

The Iranian poultry industry is the largest in the Middle East with nearly 1.2 million tons of output (meat and eggs). Therefore, this industry has a special status in the Iranian industry (Shariatmadari, 2000). The significant concerns related to this industry are health issues that threaten not only animal production, but also the people using their products. (Griggs and Jacob, 2005; Nava et al., 2005; Zhang et al., 2018). Gastrointestinal diseases are one of the most important threats, as they lead to lost productivity, increased mortality, and contamination of poultry products for human consumption (Patterson and Burkholder, 2003).

The balance among the gastrointestinal microbiota plays a significant role in maintaining the 44 normal physiology of host animals. Gastrointestinal microbiota help direct the normal formation 45 or development of gut structure and morphology, support immune responses, offer protection 46 47 from intestinal pathogens, and play an active role in the digestion of nutrients (Slizewska, 2020; Rodrigues, 2020). In the past, using antibiotics to promote the growth of animals and manage gut 48 microbiota was a norm. Feeding of antibiotics to food animals has been recognized as one 49 leading cause of the spread of antimicrobial resistance in human populations. The gradual 50 emergence of populations of antibiotic resistant bacteria has become a major public health 51 52 problem of global proportions. Due to this concern, since 2006 the European Union banned the 53 use of antibiotics as growth promoters in animal feed (de Souza, 2018). Therefore, several alternative strategies have been proposed with some success that mimic the functions of 54 antibiotics. Probiotics have been widely studied because of their ability to modulate gut 55 microbiota and immunological systems in both humans and livestock. They have been used to 56 57 increase milk production and to reduce diarrhoea both in cattle and pigs, and to control the colonisation of the intestinal tract by pathogenic bacteria (Alayande, 2020). 58

The microbes which are suitable for probiotic purposes in human and animals are mainly 59 members of a metabolically defined group of Gram-positive bacteria, known as lactic acid 60 bacteria (LAB) (Naidu et al., 1999). These microbes are widely distributed in the environment 61 and play a significant role in the gastrointestinal tract of a diverse array of animals (Bermudez-62 Brito et al., 2012; Butel, 2014). A main part of the candidate strains, which have been introduced 63 for probiotic purposes, fall into the genus Lactobacillus which is a major genus of LAB and 64 harbor more than 200 species (Goktepe et al., 2005). Lactobacillus species, with a record of safe 65 use as probiotics in humans and animals, are among the common inhabitants of the broiler 66 gastrointestinal tract (Lu et al., 2003). In poultry, administration of the probiotic Lactobacillus 67 68 strains improves not only the feed digestion, but also the nutrient uptake. In addition, probiotics increase the growth performance, neutralizing various enterotoxins and enhancing immune 69 responses (Ghadban, 2002; Al-Khalaifa, 2019). Additionally, probiotics reduce the risk of 70 71 gastrointestinal colonization by foodborne pathogens, such as *Campylobacter* (Ghareeb et al., 2012; Khan et al., 2019; Neal-McKinney et al., 2012), Clostridium (Li, 2017) and Salmonella 72 (Kizerwetter-Swida and Binek, 2009; Tellez et al., 2012), and increase the safety of poultry-73 based foods (Gaggia et al., 2010). Such antagonistic activities against the pathogens is highly 74 linked to lactic acid produced by Lactobacillus strains, which can be toxic for many bacteria, can 75 76 compete for nutrients, and affect cell attachment capabilities of the beneficial microbes to the 77 intestinal epithelium (Patterson and Burkholder, 2003).

Despite the importance of the poultry industry in Iran, little attention has been given to the isolation of probiotic bacteria and determination of their biological activities in this country. In this study, we aimed to isolate and characterize *Lactobacillus* species from indigenous poultry farms with a special focus on their probiotic properties.

83 2. Materials and methods

84 2.1 Isolation of lactic acid bacteria

85 A total of 21 rectal swabs of 11 healthy 6-day-old and 10 healthy 21-day-old chickens, their fecal and their feed samples, were collected from 2 poultry farms near Tehran, Iran. The chicken breed 86 was Ross and diets were standard according to the breed requirements, containing maize and 87 soybean balanced with minerals, vitamins, and amino acids without growth promoting 88 antibiotics. To isolate LAB from fecal samples, 6 chicken feces from 2 poultry farms (each 89 sample was 1 g) were collected randomly in Man Rogosa and Sharpe (MRS) broth (Merck, 90 Germany). The samples were serially diluted in phosphate-buffered saline (PBS) pH 7.4 and 91 aliquots of them were plated on MRS agar medium in 8-cm plates. The plates were incubated for 92 48 h at 37 °C in microaerobic conditions. From each sample, different morpho-type colonies 93 were selected for further purification and then the LAB isolates were cryopreserved at -80 °C in 94 MRS broth containing 20% glycerol under defined designations. 95

96 2.2 Resistance to low pH and bile salts

97 Tolerance of isolates to low acidity and bile salts were determined in triplicate experiments as described by Cano Roca et al (2014). Briefly, exponentially growing cells in MRS broth were 98 washed by centrifugation $(4,000 \times g \text{ at } 25 \text{ °C for } 10 \text{ min})$ and re-suspended in PBS. After serial 99 dilutions, an initial dilution of the bacterial suspension was prepared for plating on MRS agar. To 100 investigate the reaction of the isolates to low pH values, 100 μ L of the cell suspension (10⁸) 101 102 CFU/mL) was added to 900 μ L of sterile PBS (pH = 3) in a 1.5-mL microtube. The endurable 103 cell counts were measured after 3 h of incubation at 37 °C. A similar procedure was performed using PBS (pH = 7) as a control. To determine the tolerance of isolates to bile salts, 50 μ L of 104

bacterial suspension was added into tubes containing 4,950 μL of MRS broth (Merck, Germany)
with 0.4% (wt/vol) of bile salts (Merck, Germany) and incubate at 37 °C for 6 h.

107 The harvested cells from the acid in both bile salt stress experiments were washed in PBS (pH =108 7.4) and cultured on MRS agar and finally counting was performed. Based on 2, 2–4, 4–6 and > 109 6 log reduction in comparison to the initial suspension after 3 and 6 h of incubation in acid and 110 bile salts, isolates were grouped as strongly resistant, resistant, intermediate and susceptible, 111 respectively.

112 **2.3 Phenotypic classification**

All of the acid-bile resistant isolates were subjected to a biochemical fingerprinting with the 113 114 PhPlate system according to the manufacturer's instructions (PhPlate Micro-plate Techniques AB, Stockholm, Sweden) which was modified for isolates typing (PhP-LB). The microplates 115 contained 4 sets of dehydrated reagents (23 different sugars including arabinose, xylose, 116 117 galactose, maltose, cellobiose, trehalose, palatinose, sucrose, lactose, melibiose, manose, melezitose, inosin, mannitol, arbutin, sorbitool, gallac, sorbose, rhamnose, taghatose, amigdalin, 118 gluconate, salicin), which have been specifically selected for phenotypic typing of *Lactobacillus* 119 species. After the incubation of PhP-LB plates at 37 °C, the utilization of the substrates in each 120 well was measured by scanning the images after 24, 48, and 72 h. Scanned images were analyzed 121 by software package PhPWIN (PhPlate micro-plate techniques AB, Sweden). The mean 122 similarity between duplicate assays of all strains ± 2 SD was calculated as the identification level 123 (ID), which was 0.975 and strains with > 0.975 similarities were grouped into the same Phene 124 Plate (PhP) type. 125

126 **2.4 Molecular identification**

127 Total DNA of the acid-bile resistant isolates was extracted using a peqGOLD Bacterial DNA Kit (peQlab, Germany) according to the manufacturer's instruction. Preliminary characterization of 128 lactobacilli was performed based on the phenotype. Then, molecular identification of the 129 Lactobacillus spp. was performed using primers which were specific for amplification of a 247 130 bp region of the 16S rRNA gene in the genus Lactobacillus (McOrist et al., 2002). The PCR 131 amplification program was as follows: a single initial denaturation cycle (5 min at 94 °C) 132 followed by 30 cycles (30 s at 94 °C [denaturation], 30 s at 57 °C [annealing], and 30 s at 72 °C 133 [elongation]), with a final extension of 7 min at 72 °C. As the next step, multiplex PCR 134 amplifications were used for *Lactobacillus* species identification. Hence, the previously designed 135 136 species specific primer pairs which were already confirmed for detection of Lactobacillus acidophilus, Lactobacillus casei, Lactobacillus delbrueckii, Lactobacillus gasseri, Lactobacillus 137 rhamnosus, Lactobacillus plantarum, and Lactobacillus reuteri were used to identify the 138 139 Lactobacillus isolates (Kwon et al., 2004). Multiplex PCR reactions for amplifications entailed a cycle of 94 °C for 5 min, followed by 40 cycles (94 °C for 30 s, 51 °C for 40 s and 72 °C for 30 140 s), plus one additional cycle with a final 7 min chain elongation at 72 °C. The amplified genomic 141 regions of Lactobacillus brevis strains were sequenced. Additionally, species specific primers 142 were used for identification of L. brevis strains as described by Guarneri et al (2001). The 143 thermo-cycling conditions for the L. brevis specific PCR reaction was as follows: after one cycle 144 at 94 °C for 2 min, 25 cycles of 94 °C for 1 min, 40 °C for 1 min and 72 °C for 1 min, followed 145 by an additional 10 min cycle of extension (Table 1). 146

147 2.5 RAPD-PCR genotypic classification

Acid-bile resistant isolates, which were identified as lactobacilli, were subjected to
Random amplified polymorphic DNA (RAPD)-PCR using a previously designed oligonucleotide

by Tilsala et al (1998) with some modifications. The PCR amplification conditions were as follows: 2 min at 94 °C for initial denaturation followed by 40 cycles of 30 s at 94 °C for denaturation, 30 s at 37 °C for annealing, and 2 min at 72 °C for elongation. The final extension at 72 °C was prolonged to 10 min. PCR reaction was performed for each primer in a separate tube and run in the same well in 1.5% agarose gel to increase the discrimination. The UPGMA method using the software Gel compare II version 4.0 was used to compare banding patterns (Applied Maths, Sint-Martens-Latem, Belgium).

157 **2.6 Biofilm assay**

Biofilm formation of lactobacilli was studied as previously described by Lebeer et al (2007) 158 159 with minor modifications. For each strain, 200 µL aliquots of a modified tryptic soy broth (TSB) medium (15 g/L TSB enriched with 20 g/L Bacto proteose peptone), which was already 160 inoculated by approximately 3×10^7 CFU of a *Lactobacillus* isolate, were added into 96-well 161 162 plates (8 wells for each strain) and incubated at 37 °C. After 72 h of incubation, the wells were washed with PBS and stained for 30 min with 200 µL crystal violet (0.1%) in an isopropanol-163 methanol-PBS solution (1:1:18). After washing with double distilled water, the wells were air-164 dried for 30 min at room temperature. Extraction of the dye bound to the adherent cells was done 165 with 200 µL ethanol-acetone (80:20) solution. The optical density of 135 µL of each well was 166 167 measured at 570 nm. Data were normalized to the indicated positive control, which was taken as 168 100% to compare different experiments. The results are presented as means \pm SD. Additionally, the sterile medium and *Pseudomonas aeruginosa* were used as negative and positive controls, 169 respectively. 170

171 2.7 Attachment to Caco-2 cells

Detection of adhesion ability in lactobacilli isolates was performed according to Jacobsen et al 172 (1999). A monolayer of Caco-2 cells was cultured in Roswell Park Memorial Institute (RPMI) 173 medium (Gibco, Carlsbad, CA, USA), supplemented with 20% (vol/vol) fetal calf serum (Gibco, 174 Life Technology, USA), penicillin (100U/mL) and streptomycin (100 mg/mL), and incubated at 175 37 °C in 5% CO₂ atmosphere. At first, 3 mL of Caco-2 cells containing 1.5×10^5 cells/mL were 176 seeded on a 6-well cell culture plate and after confluency, the cells were washed twice with 3 mL 177 PBS. After adding 2 mL of RPMI (without antibiotics) to each well, the plates were incubated 178 for 3h at 37 °C. Overnight cultures of the isolates (cell concentration of approximately 10⁹ 179 CFU/mL) were suspended in 1 mL RPMI1640 medium (without antibiotics) and added to 180 181 different wells and incubated for 1 h at 37 °C. The wells were washed 4 times with PBS to remove the unbound bacteria. Then, the cells were fixed with 3 mL of methanol and incubated 182 for 5 to 10 min at room temperature for the removal of methanol. Staining was made with 3 mL 183 184 of Giemsa stain solution (1:20) (Sigma-Aldrich Co., Mo, USA) and incubated for 30 min at room temperature. After washing the plates with distilled water, the air-dried plates were examined 185 microscopically under oil immersion. Adherent isolates were counted in 20 random microscopic 186 fields. Cells showing < 40, between 40 and 100, and > 100 attached bacteria were regarded as 187 non-adhesive, adhesive, and strongly adhesive, respectively. 188

189 **2.8 Detection of amylase and protease activities**

Enzymatic activity of 31 acid-bile resistant lactobacilli was determined according to the method described by Taheri et al (2009) with minor modifications. For assessment of the amylase activity, the selected *Lactobacillus* strains were cultured on modified MRS broth described by Taheri et al (2009) (0.25% starch instead of glucose), and inoculated on a medium containing starch (2%), meat peptone (0.5%), yeast extract (0.7%), NaCl (0.2%), and agar (1.5%). After 48 h of incubation at 37 °C, lugol's solution (5 g iodine [Merck, Germany] and 10 g potassium
iodide [KI] [Merck, Germany] in 100 mL distilled water) was poured over the agar for detection
of any clear zones as indicative of amylolytic activities.

For detection of proteolytic activity, *Lactobacillus* strains were inoculated into MRS broth and were incubated at 37 °C for 24 h. Bacterial suspension (30 μ L) was moved onto a disc placed over a MRS agar containing 1% skim milk. Finally, the halo zone surrounding each disc was measured.

202 2.9 Antimicrobial activity

The antimicrobial activity of the lactobacilli, which showed a detectable attachment to Caco-2 203 204 cells, was studied against Shigella soneii (ATCC 12022), Pesudomonas aeruginosa (ATCC 27853), Salmonella typhi (ATCC 19430), Proteus mirabilis (ATCC 25933), Yersinia 205 enterocolitica (ATCC 23715), Streptococcus agalactiea (ATCC 12386), 206 Listeria 207 monocytogenes (ATCC 19113), wild types of *Escherichia coli* strains belonging to 3 pathotypes i.e. enteropathogenic E. coli (EPEC) (ATCC 43887), enterotoxigenic E. coli (ETEC) and 208 enteroaggregative E. coli (EAEC). These strains were provided by the Microbial Collection of 209 Iran (Davoodabadi et al., 2015; Shahrokhi et al., 2011). The antimicrobial activity was observed 210 based on the well diffusion method as described by Fernandez et al (2003). Suspensions 211 containing approximately10⁸ CFU/mL of the abovementioned pathogens were poured on Muller 212 213 Hinton agar medium in 8-cm plates, except for L. monocytogenes where brain heart infusion (BHI) agar medium was used. Then, 100 μ L of an overnight culture of the selected *Lactobacillus* 214 strains in MRS broth was poured into 6 mm agar wells created by punching in 8-cm plates. After 215 24 h of incubation at 37 °C, the antimicrobial activity was measured as the zone of growth 216 inhibition around the wells. The inhibition zones of 1, 2, 2 to 5 mm, and more than 5 mm were 217

classified as strains of no (-), mild (+), strong (++), and very strong (+++) inhibition,
respectively.

220 **2.10** Antibiotic susceptibility testing

The susceptibility of isolates to different antibiotics including penicillin G (10 µg), gentamicin 221 (120 µg), erythromycin (15 µg), tetracycline (30 µg), amoxicillin (25 µg), ciprofloxacin (5 µg), 222 chloramphenicol (30 µg), oxacillin (1 µg), and streptomycin (10 µg) (MAST Diagnostics, U.K.) 223 224 was determined by the agar disc diffusion method on MRS agar plates instead of the Muller 225 Hinton agar. Lactic acid bacteria require special growth conditions and conventional media, as Mueller Hinton agar are not uniformly suitable for to susceptibility test them (Klare et al., 2005). 226 227 After incubation of plates at 37 °C for 48 h, the diameter of the inhibition zones was measured and the results were expressed as sensitive or resistant according to CLSI standard (Institute, 228 229 2009).

230 2.11 Plasmid profiles

The isolation of plasmid DNA from the selected bacterial strains was performed by GF-1 plasmid DNA extraction kit (Vivantis, Malaysia). *E. coli* V517 was used as a positive control. Electrophoresis of the extracted plasmids was performed in a 1% agarose gel and the plasmids were visualized with UV trans-illumination in a Gel Doc apparatus.

235 **3. Results**

236 **3.1 Isolation and identification**

A total of 168 LAB were isolated from rectal swabs, fecal and feed samples, among which 89
(53%) and 79 (47%) isolates were from 21 days and 6 days old chickens, respectively.
Furthermore, out of 168 LAB isolates, 51 (30.3%) isolates were resistant to low pH (pH 3.00)

and bile salts (0.4%), among which 20 and 31 isolates were identified as members of the genera *Pediococcus* and *Lactobacillus*, respectively.

The results of the molecular identification showed that 31 isolates belonged to the genus *Lactobacillus*. Out of these, 24 (77.4%), 3 (9.6%), 2 (6.4%), and 2 (6.4%) were identified as *L. brevis*, *L. plantarum*, *L. reuteri* and *L. vaginalis*, respectively (Table 2). Interestingly, a considerable part of the isolates which originated from the rectal-swabs were identified as *L. brevis*. The same results were observed in fecal samples.

247 **3.2 Phenotypic and genotypic classification**

Acid-bile resistant lactobacilli were typed using Phene Plate system (PhP-LB) followed by genotype-based identification using RAPD-PCR. PhP-LB results of 24 *L. brevis* isolates showed a high phenotypic diversity and most of the isolates gave unique phenotypes, denoted as single types (3 common types with 10 isolates and 14 single types) (Fig. 1). On the other hand, the results of RAPD-PCR showed a low genetic diversity in *L. brevis* species (3 common types with 20 isolates and 4 single types) (Fig. 2).

254 3.3 Biofilm and Attachment to Caco-2 cells assay

Out of the 31 acid-bile resistant lactobacilli strains examined in this study, *L. brevis* L2, L6, L31, and *L. reuteri* L26 had the biofilm formation capability. Adhesion to Caco-2 cells showed that 22 (71%) isolates were non-adhesive (with less than 40 bacteria attached in 20 microscopic fields), 7 (22.5%) isolates (*L. brevis* L3, L29, L30, L31, *L. reuteri* L26, L27, and *L. vaginalis* L25) were adhesive (with 41 to 100 bacteria) and 2 (6.4%) isolates (*L. brevis* L2 and L6) were strongly adhesive (>101 bacteria) (Fig. 3).

261 **3.4 Antibacterial activity**

The assay of antagonistic activity of lactobacilli with an acceptable ability of attachment to Caco-2 cells showed that *L. brevis* strains L2, L6, L31 and *L. reuteri* strains L26 and L27 have a strong inhibitory effect against different serotypes of *E. coli* (EAEC, EPEC, and ETEC) (Table 3). *L. brevis* strains L2 and L6 had antibacterial activities against all the tested pathogenic bacteria with the exception of *L. monocytogenes* and *Staphylococcus aureus*.

267 **3.5 Detection of amylase and protease activities**

Measuring the size of the halo zones surrounding the colonies as an indicative of extracellular enzyme level showed that all 31 lactobacilli isolates investigated here were protease positive but extracellular-amylase negative.

271 **3.6 Plasmid profiles and antibiotic susceptibility testing**

No plasmid was found in *L. brevis* strain L6 but *L. brevis* L2 and *L. reuteri* L26 harbored a single plasmid. Antibiotic susceptibility tests showed that the *Lactobacillus* isolates were sensitive to augmentin, amoxicillin, erythromycin, penicillin G, chloramphenicol, and rifampin and were resistant to ciprofloxacin, amikacin, tobramycin, oxacillin and streptomycin. *L. reuteri* L26 was sensitive to tetracycline but *L. brevis* L2 and L6 were resistant to this antibiotic.

277 **4. Discussion**

Probiotics have been emerging as a safe alternative to antibiotics for increasing performance in livestock. Administration of probiotic strains may have a significant effect on absorption and utilization of feed, and increase the body weight of various animals, including chicken, piglets, sheep and cattle (Markowiak et al, 2018). Lactobacillus species with a record of safe use as a probiotic in humans and animals is regarded as a significant part of chicken-GIT (Gastrointestinal Tract) microbiota. (Wei et al., 2013; Yadav, 2019). Among such a diverse array of *Lactobacillus* species, some defined species have been frequently reported as chicken-GIT

inhabitants. L. reuteri, L. salivarius and L. johnsonii are among the most detected lactobacilli in 285 chicken-GIT samples (Adhikari and Kwon, 2017; Dec et al., 2016; Pan and Yu, 2014). 286 Interestingly, L. reuteri, L. salivarius and L. johnsonii have been repeatedly isolated from the 287 GIT samples of a wide range of hosts and this harsh environment is among their preferred 288 ecological niches (Lebeer et al., 2008; Walter, 2008; Pokorná, 2019). However, L. brevis have 289 also been found in GIT samples in a diverse range of warm-blooded animals (Feyereisen, 2019, 290 291 Fraunhofer, 2018). Considering the results of this study, 3 lactobacilli strains were isolated, which showed promising probiotic characteristics. Those strains fall into L. brevis (L2 and L6) 292 and L. reuteri (L26) species. L. brevis shows a significant prevalence in the GIT of chickens 293 294 although the GIT is not the preferred ecological niche for this species. The species L. brevis falls into a Lactobacillus phylogenetic group which harbors mostly foodborne species (Papizadeh et 295 al., 2017). Strains of this species have been isolated from a diverse array of samples, including 296 297 water, feces of various animals, and various food-associated samples (Feyereisen, 2019). Hence, the findings of this study shed more light on the ecological distribution of L. brevis. 298

299 Considering the results, *L. brevis* species were isolated from the rectal swabs of both 21- and 6-300 day-old chickens and also from their feed and fecal samples. Hence, it can be inferred that this 301 species has the ability to survive on a wide range of substrates (Ramos et al., 2013).

Phenotypic characterization of the isolates indicated a high intra-species diversity among *L. brevis* isolates. In comparison, results of RAPD-PCR highlighted a low diversity. Therefore, it seems that combination of 2 techniques (PhPlate and RAPD-PCR) could result in a more significant discriminatory power than each of them used alone. In this study, biochemical fingerprinting of lactobacilli was used primarily for the screening of biodiversity in lactobacilli strains to reduce their number for the next tests; a significant number of single types indicated

that PhP system alone cannot serve as a method for determining relationships between *Lactobacillus* strains (Skelin et al., 2012).

Adhesion to mucosal surfaces has been used as a criterion for the selection of probiotic bacteria 310 because this character has a major role in the colonization of the gastrointestinal tract (GIT) by 311 these bacteria (Broderick and Duong, 2016; Kosin and Rakshit, 2006). Additionally, mucosal 312 adhesion is important for pathogenic antagonism, modulation of the immune system and healing 313 of damaged gastric mucosa (Oelschlaeger, 2010; Ohland and MacNaughton, 2010; Monteagudo-314 315 Mera, 2019). In this study, 2 strongly adhesive strains (L. brevis strains L2 and L6) showed the highest biofilm formation capacity. Furthermore, we observed specific correlation between 316 317 adhesion to Caco-2 cells and biofilm formation by lactobacilli isolates.

Antimicrobial resistance poses a serious global threat of growing concern to human, animal and 318 environmental health. This is due to the consumption of antibiotics in animals (raised for food or 319 320 kept as pets) and humans (Aslam et al., 2018). Therefore, probiotics with antibacterial activity against pathogens are a promising alternative to antibiotics (Baldwin et al., 2018). The strong 321 antibacterial activity of L. brevis strains L2, L6, L31 and L. reuteri strains L26 and L27 against 322 various serotypes of *E. coli* (EAEC, EPEC and ETEC), which is shown in Table 3, have 323 highlighted the probiotic capabilities of these strains. Interestingly, such a capability among the 324 isolates of this study was highly detectable in cases of L. brevis strains L2 and L6, which showed 325 326 significant antibacterial activities against all the tested pathogenic bacteria (except for L. monocytogenes and S. aureus). Such an antibacterial activity of Lactobacillus isolates is 327 essentially associated with the production of bacteriocins, H₂O₂, lactic acid and other metabolites 328 which inhibit the growth of pathogens (Vieco Saiz, 2019). Considering the fact that various 329 serotypes of E. coli (EAEC, EPEC, and ETEC) are considered as the most important cause of 330

enteric bacterial infections in poultry, the use of such isolates with functional probiotic competence can significantly reduce the infection rate. Another finding was that all 31 lactobacilli isolates investigated in this study, were protease positive with no extracellular amylase activity and this has shed light on the importance of these isolates since amylase, lipase, and protease enzymes play very important roles in the digestion of nutrient materials.

The probable existence of transferable resistant genes in the 3 probiotic *Lactobacillus* strains was observed by the determination of antibiotic resistance patterns and plasmid profiling, but no plasmid was detected in *L. brevis* strains L2 and L6 and only a single plasmid was detected in *L. reuteri* strain L26. Furthermore, *L. reuteri* L26 was sensitive to tetracycline, but *L. brevis* L2 and L6 were resistant to this antibiotic. The properties of antibiotic resistance in various Lactobacillus species seem to be associated with drug resistant genes which are mainly located on the chromosome.

According to the criteria, the potential probiotic strains, which are assumed for animal or human applications, have to be non-pathogenic and from the same origin (host). Additionally, such strains should resist intestinal tract, gastric and bile acids, adhere to the epithelium or mucus, and produce inhibitory compounds. Among the lactobacilli isolated in this study, we found 3 lactobacilli strains with probiotic characteristics, L. brevis (L2 and L6) and L. reuteri (L26), which could be considered probiotic strains for use in the poultry industry.

349 **5.** Conclusion

In this study, the most common acid and bile resistant lactobacilli strains isolated from chickens belonged to the *L. brevis* species, with a high intra-species phenotypic diversity. In vitro evaluation in this study showed that 4 Lactobacillus strains (3 *L. brevis* strains and 1 *L. reuteri* strain) could be considered as probiotic. Further in vivo evaluation for determination of the

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355 poultry industry.

356 Author contributions

Nasrin Noohi: writing - original draft, visualization, investigation, formal analysis; Moslem
Papizadeh: writing - review & editing; Mahdi Rohani: investigation; Malihe Talebi: project
administration, methodology; Mohammad R. Pourshafie: conceptualiza, supervision.

- **360** Conflict of interest
- 361 The authors declare that there is no conflict of interest.

362 Acknowledgements

363 This study was support by a grant (No. 90007454) from Iran National Science Foundation.

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523	

Figures and tables

Table 1. Sequence of primers used to identify different species of *Lactobacillus* bacteria.

Target bacteria	Sequence (5' to 3')	References
All Lactobacillus	5' TGGAAACAGGTGCTAATACCG 3'	McOrist et al., 2002
	5' CCATTGTGGAAGATTCCC 3'	
L. casei-group	5' CCACCTTCCTCCGGTTTGTCA 3'	Kwon et al., 2004
L. acidophilus	5' AGGGTGAAGTCGTAACAAGTAGCC 3'	
L. delbrueckii	5' TGGTCGGCAGAGTAACTGTTGTCG 3'	
L. gasseri	5' AACTATCGCTTACGCTACCACTTTGC 3'	
L. reuteri	5' CTGTGCTACACCTAGAGATAGGTGG 3'	
L. plantarum	5' ATTTCAAGTTGAGTCTCTCTCTC 3'	
L. rhamnosus	5' ACCTGATTGACGATGGATCACCAGT 3'	
L. rnamnosus	5' CTAGTGGTAACAGTTGATTAAAACTGC 3'	
	5' GCCAACAAGCTATGTGTTCGCTTGC 3'	
L. brevis	5' CTTGCACTGATTTTAACA 3'	Guarneri et al., 2001
	5' GGGCGGTGTGTACAAGGC 3'	

530	Table 2.	Determination of acid and bile resistant Lactobacillus species isolated from different
531	samples.	

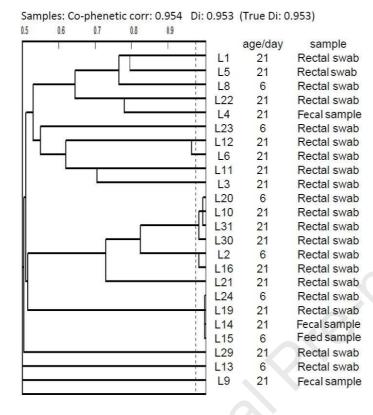
Item	L. brevis		L. plantarum		L. reuteri		L. vaginalis		
	21-day-	6-day-	21-day-	6-day	21-day-	6-day-	21-day-	6-day-	
	old	old	old	old	old	old	old	old	
Feed sample	0	1	3	0	0	0	0	0	
Rectal swab	14	6	0	0	1	1	0	2	
Fecal sample	3	0	0	0	0	0	0	0	

534

535	Table 3. Spectrum of antimicrobial activit	y exhibited b	v Lactobacillus strains L2.	L3, L6	6, L25, L2	26, L 27, L 29	9. L 30 and L 31.
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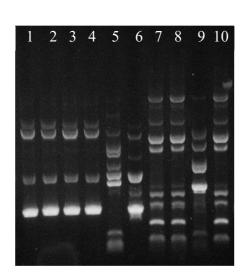
Item	L2 (<i>L</i> .	L3 (<i>L</i> .	L6 (<i>L</i> .	L25 (L.	L26 (L.	L27 (L.	L29	L30	L31
Item							(<i>L</i> .		
	brevis)	brevis)	brevis)	vaginalis)	reuteri)	reuteri)	(L. brevis)	(L. brevis)	(L. brevis
ETEC	+		+	+	+	+	Drevis)	Drevis)	+
EPEC		-		+			-	-	
	++	-	++	-	++	++	-	-	++
EAEC	++	-	++	-	+	+	-	-	++
Salmonella entritidis	++	-	++	+	+	+	-	-	+
Salmonella typhi	+	-	+	-	- 2	-	-	-	-
Pseudomonas aeruginosa	+	-	+	-	-2	-	-	+	-
Shigella flexneri	+	-	+	- 26	+	+	-	-	-
Klebsiella pneumonia	+	-	+	-	-	-	-	-	-
Citrobacter freundii	+	-	+	<u>O</u>	-	-	+	+	-
Proteus mirabilis	+	-	+	-	-	-	+	+	-
Yersinia. enterocolitica	+	- 5	+	-	-	-	-	-	-
Listeria monocytogenes	-	-	-	-	-	-	-	-	-
Staphylococcus aureus	-	-	-	-	-	-	-	-	-
Staphylococcus saprophyticus	+	-	+	-	-	-	-	-	-
Streptococcus group A	+	-	+	-	-	-	-	-	-
ETEC = enterotoxigenic E. coli	EPEC = e	nteropath	nogenic H	E. coli; \overline{EAE}	C = enter	roaggrega	tive E. c	oli.	
•),	mild	2	(+),	and	22 0	strong		(++)

inhibition.



540 Fig. 1. Cluster analysis of Phene plate (PhP) assay of 24 bile and acid resistant Lactobacillus

brevis.



546 Fig. 2. Agarose gel electrophoreses of RAPD-PCR products of Lactobacillus brevis strains.

547 RAPD = random amplified polymorphic DNA.

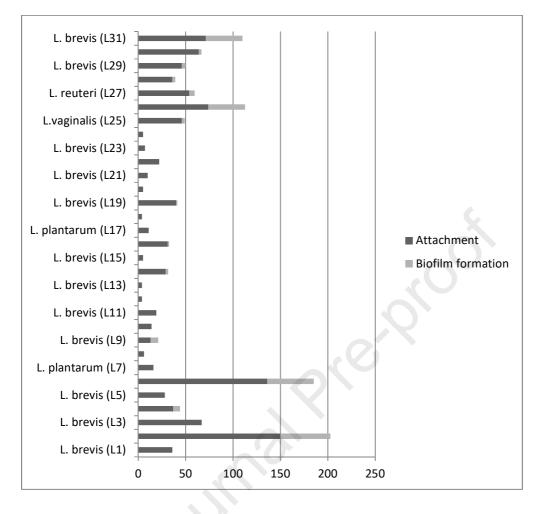


Fig. 3. Biofilm formation and attachment in 31 bile and acid resistant lactobacilli. Dark gray bars show the number of attached lactobacilli in 20 microscopic fields to Caco-2 cell line and light gray bars show the percentage of biofilm formation.

Nasrin Noohi: Writing - Original Draft, Visualization, Investigation, Formal analysis Moslem Papizadeh: Writing - Review & Editing, Mahdi Rohani: Investigation, Malihe Talebi: Project administration, Methodology, Mohammad R. Pourshafie: Conceptualiza, Supervision.

Journal Prevention