

# **Anti‑adipogenic Effects of the Probiotic** *Lactiplantibacillus plantarum* **KU15117 on 3T3‑L1 Adipocytes**

**Kyoung Jun Han1 · Na‑Kyoung Lee<sup>1</sup> · Hyung‑Seok Yu1 · Hoon Park2 · Hyun‑Dong Paik[1](http://orcid.org/0000-0001-9891-7703)**

Accepted: 7 July 2021 / Published online: 15 July 2021

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## **Abstract**

In this study, we investigated the probiotic properties and anti-obesity efects of bacterial strains isolated from homemade kimchi. *Lactiplantibacillus plantarum* KU15117 was isolated using lactobacilli selective medium. *L. plantarum* KU15117 did not produce β-glucuronidase and showed high tolerance to artifcial gastric juice and bile salt, acceptable resistance to antibiotics, and high adhesion ability to HT-29 cells. The anti-adipogenic activity of *L. plantarum* KU15117 at 10<sup>9</sup> CFU/ well was confrmed by the reduction of oil red O staining and intracellular triglyceride level. Additionally, the expression levels of fatty acid synthase, CCAAT/enhance-binding protein-α, and peroxisome proliferator-activated receptor-γ, which are associated with the early stage of adipocyte diferentiation, were signifcantly lower in the probiotic-treated group than in the control group. These results suggest that *L. plantarum* KU15117 has probiotic properties and anti-obesity efects and could be used as a prophylactic probiotics.

**Keywords** Probiotics · Kimchi · *Lactiplantibacillus plantarum* · Anti-adipogenic efect · Obesity

## **Abbreviations**



# **Introduction**

Changes in lifestyles, such as reduction in physical activities and convenient lifestyles, may induce obesity, which is not only a cosmetic problem but also a major health issue. Obesity is associated with abnormal or excessive fat accumulation leading to various diseases, including non-alcoholic fatty liver disease, cardiovascular diseases, type 2 diabetes, cancer, and hypertension [[1,](#page-7-0) [2\]](#page-7-1). Particularly, obesity is caused by an imbalance between lipogenesis and lipolysis, which are complex processes regulated by various signaling molecules. Adipogenesis is characterized by changes in cell morphology, accumulation of triglycerides, and expression of related gene [\[3](#page-7-2), [4](#page-7-3)]. Peroxisome activated receptor-γ (PPAR-γ) and CCAAT/enhancer-binding protein-α (C/ EBP- $\alpha$ ) are involved in the early stage of adipocyte differentiation, and some enzymes, including adipose-specifc fatty acid-binding protein (aP2), fatty acid synthase (FAS), sterol regulatory element-binding protein-1c (SREBP-1c), and carnitine palmitoyltransferase-1 (CPT-1), are involved in the formation of mature adipocytes [[5,](#page-7-4) [6](#page-7-5)].

Probiotics are live bacteria, mainly lactic acid bacteria, which are beneficial to humans and animals by improving intestinal microbial balance [[7\]](#page-7-6). Common probiotics include representatives of *Lactobacillus acidophilus*, *Lacticaseibacillus casei*, *Lactiplantibacillus plantarum*, *Lacticaseibacillus rhamnosus*, *Bifdobacterium bifdum*, and *Bifdobacterium longum*. Some of these probiotics can be components of functional foods and may be sold as dietary supplements. Few studies have reported the pleiotropic effects of probiotics, including antimicrobial, anticancer, anti-infammatory, antioxidant, anti-biofilm, anti-obesity, antidiabetic, and cholesterol-lowering activities [\[8](#page-7-7), [9](#page-7-8)].

The gut microbiome infuences human health and con-sists of more than 100 trillion bacterial species [[10\]](#page-7-9). They include the commensal bacteria, which are involved in digestion related to metabolic disorders [\[11](#page-7-10)]. The cell-free extract (CFE) of *Lactobacillus fermentum* MG4231 and

 $\boxtimes$  Hyun-Dong Paik hdpaik@konkuk.ac.kr

<sup>&</sup>lt;sup>1</sup> Department of Food Science and Biotechnology of Animal Resource, Konkuk University, Seoul 05029, Republic of Korea

Department of Food Science, Sun Moon University, Asan 31460, Republic of Korea

MG4244 strains showed anti-obesity efects through the inhibition of adipogenesis and lipid accumulation in 3T3- L1 preadipocytes. The anti-obesity effects of CFE also involved the downregulation of FAS, aP2, PPAR-γ, and C/ EBP-α expression, as well as upregulating of AMP-activated protein kinase (AMPK) and hormone-sensitive lipase (HSL) phosphorylation [[4,](#page-7-3) [12](#page-7-11)]. The adjustment of the gut microbiome has been suggested as a therapeutic approach against obesity and metabolic disorders. Therefore, in this study, we determined the probiotic properties and anti-adipogenic efects of *Lactobacillus* strains isolated from homemade kimchi.

# **Materials and Methods**

# **Bacterial Strains and Culture Conditions**

*Lactiplantibacillus plantarum* KU15117 (KCCM 12212P) and *Latilactobacillus curvatus* KU15031 were isolated using Lactobacillus Selective Medium (BD BBL, Franklin Lakes, NJ, USA) from Korean homemade diced-radish kimchi and cabbage kimchi. The commercial probiotic strain *Lacticaseibacillus rhamnosus* GG (KCTC 5033) was used as the reference strain. *Lactobacillus* strains were cultured in MRS broth at 37 °C for 24 h.

## **Tolerance of Bacterial Strains to Artificial Acid and Bile Salt**

The tolerance of bacterial strains to artifcial acid and bile salt conditions was determined as previously described by Lee et al. [\[9\]](#page-7-8) and Son et al. [[13\]](#page-7-12). To determine the tolerance of the strains to artifcial acid, overnight cultures of bacterial strains were resuspended in artifcial gastric acid (pH 2.5) (MRS medium containing 0.3% (w/v) of pepsin (Sigma-Aldrich, St. Louis, MO, USA)), followed by incubation at 37 °C for 3 h. To determine tolerance to bile acid, overnight cultures were resuspended in MRS medium containing 0.3% (w/v) of oxgall (BD BBL), followed by incubation at 37 °C for 24 h. Viable cells were counted after plating and incubated on MRS agar at 48 °C for 24 h. The survival rate was calculated as follows:

$$
Survival rate (\%) = \frac{Cell \text{ no. of after reaction (CFU)}}{\text{Initial cell no. (CFU)}} \times 100
$$

## **Enzyme Production**

Enzyme production was measured using the API ZYM kit (BioMerieux, Lyon, France). Bacterial strains were centrifuged  $(12,000\times g, 4\degree C, 10\text{ min})$ , and the harvested cells were resuspended in PBS at  $10^5$  CFU/mL. The resuspended cultures were inoculated in each well and incubated at 37 °C for 4 h. Next, ZYM reagents A and B were added to the cupules. The enzyme activity was determined as  $0$  to  $\geq 40$  nM based on the color change.

## **Adhesion of Bacterial Strains to HT‑29 Cells**

HT-29 (human colon adenocarcinoma, KCLB 30038) cell line was cultivated in RPMI 1640 (HyClone Laboratories, Inc., Logan, UT, USA) with 10% fetal bovine serum (FBS; HyClone Laboratories, Inc.) and 1% streptomycin/penicillin solution at 37 °C in 5% CO<sub>2</sub> atmosphere.

The adherence of bacterial strains to HT-29 cells was performed according to the method of Son et al. [[13](#page-7-12)]. HT-29 cells were seeded by  $1 \times 10^5$  cells/well in a 24-well plate and cultured at 37 °C for 24 h. Bacterial strains were inoculated into each well at approximately  $10^7$  CFU and cultured at 37 °C for 2 h. Non-adhered bacteria were removed by washing thrice with PBS, followed by the addition of 1 mL Triton X-100 (1% (v/v); Sigma-Aldrich) into each well and incubation at 37  $^{\circ}$ C for 10 min. Incubated cells were harvested from each well, and adherent bacterial cells were plated on MRS plates. Adhesion activity was calculated as follows:

Adhesion activity (%) =  $\frac{\text{Adhered cell no. (CFU)}}{\text{Initial cell no. (CFU)}} \times 100$ 

## **Antibiotic Sensitivity of Bacterial Strains**

The sensitivity of the bacterial strains was measured according to the guidelines of the Clinical and Laboratory Standards Institute [\[15](#page-7-13)]. Each bacterial strain, at a concentration of 10<sup>7</sup> CFU/mL, was dispersed on MRS agar, and paper discs containing the antibiotics were placed on the plate after a few minutes. The antibiotics used were ampicillin (10 μg/disc), chloramphenicol (30 μg/disc), ciprofloxacin (5 μg/disc), doxycycline (30 μg/disc), gentamicin (10 μg/disc), kanamycin (30 μg/disc), streptomycin (10 μg/disc), and tetracycline (30  $\mu$ g/disc). The plates were cultured at 37 °C for 24 h, and the inhibition zones were measured.

#### **Anti‑adipogenic Effect of Bacterial Strains**

#### **Preparation of Heat‑Killed Bacteria**

Bacterial strains were grown in MRS broth and washed twice with PBS by centrifugation at  $12,000 \times g$  at 4 °C for 10 min. The washed bacteria were resuspended in PBS at a final concentration of  $10^8$  and  $10^9$  CFU/mL, respectively, and the cells were plated to confrm the number of viable

cells. Each bacterial sample was heated in a water bath at 80 °C for 30 min.

# **Cell Culture and Differentiation of 3T3‑L1 cells**

3T3-L1 preadipocytes (ATCC CL-173) were cultured in Dulbecco's modifed Eagle's medium (DMEM; HyClone Laboratories, Inc.) supplemented with 10% bovine calf serum (HyClone Laboratories, Inc.) and 1% streptomycin/penicillin solution at 37 °C at 5%  $CO<sub>2</sub>$ . For adipocyte diferentiation, the cells were seeded in 6-cm cell culture dishes at a density of  $1.5 \times 10^4$  cells/dish and cultured until confuence (approximately 3 days). After confuence, the growth medium was replaced with the differentiation medium (MDI), consisting of DMEM, 10% FBS, 0.5 mM 3-isobutyl-1-methylxanthine (IBMX; Sigma-Aldrich), 10 μM dexamethasone (Sigma-Aldrich), and 5 μg/mL insulin (Sigma-Aldrich), and the cells were cultured for 2 days. Next, the medium was changed to insulin media containing DMEM, 10% FBS, and 5 μg/mL insulin, which was replaced at 2, 4, and 6 days.

#### **Cell Viability of 3T3‑L1**

The effect of bacterial strains on the viability of 3T3-L1 cells was evaluated using 3-(4,5-dimethylthiazol-2-yl)- 2,5-diphenyltetrazolium bromide (MTT; Sigma-Aldrich) assay. 3T3-L1 cells were plated at  $1 \times 10^4$  cells/well in 24-well plates until confuence. Next, the *Lactobacillus* strains were added at  $10^8$  and  $10^9$  CFU/well and incubated at 37 °C for 48 h in an incubator (5% CO<sub>2</sub>). The supernatant was aspirated, and the cells were incubated with MTT solution (2.5 mg/mL) for 1 h. After discarding the supernatant, DMSO (Sigma-Aldrich) was added to each well to dissolve the generated formazan. The dissolved solution was measured at 570 nm using a microplate reader, and cell viability was calculated.

#### **Oil Red O Staining and Intracellular Triglyceride Contents**

The effects of bacterial strains on oil red O-stained differentiated 3T3-L1 were determined as described by Park et al. [[16](#page-7-14)]. Diferentiated 3T3-L1 cells were fxed with 10% formaldehyde solution for 20 min, followed by the addition of 0.5% oil red O solution (Sigma-Aldrich) to each dish and incubation at room temperature for 20 min. After staining, the cells were washed twice with PBS and isopropanol was added to each dish, and the absorbance was measured at 520 nm.

To determine the intracellular triglyceride level, a triglyceride quantifcation kit (BioVision, Milpitas, CA, USA) was used. Diferentiated 3T3-L1 cells were harvested and centrifuged at  $14,000 \times g$  for 25 min at 4 °C. Triglyceride levels were determined according to the manufacturer's protocol.

#### **Semi‑Quantitative RT‑PCR Analysis**

The 3T3-L1 cells were seeded in 6-cm cell culture dishes  $(1.5 \times 10^4 \text{ cells/dish})$  and differentiated into mature adipocytes. This was followed by the addition of bacterial strains  $(10^8 \text{ and } 10^9 \text{ CFU/well})$ . RNA was isolated from the treated 3T3-L1 cells using the RNeasy Mini Kit (Qiagen, Germany), and cDNA was synthesized using the Revert Aid First Strand cDNA Synthesis Kit (ThermoFisher Scientifc, MA, USA). The expression of adipogenesis-related genes was measured by RT-PCR using synthesized cDNA, primers (shown in Table [1](#page-2-0)), and SYBR Green PCR Master Mix (PikoReal 96, ThermoFisher Scientifc). The RT-PCR conditions were 95 °C for 2 min, 40 cycles of 95 °C for 5 s, and 60 °C for 15 s. Gene expression was determined by relative quantifcation with *β-*actin as the house-keeping gene.

#### **Western Blot Analysis**

The expression of obesity-related proteins was investigated by western blotting. Diferentiated 3T3-L1 adipocytes treated with bacterial strains  $(10^8 \text{ and } 10^9 \text{ CFU/well})$ were harvested by using RIPA lysis and extraction bufer with Halt™ Protease and Phosphatase Inhibitor Cocktail (ThermoFisher Scientifc), and the cell lysates were sonicated (5 AMP; pulse on, 3 s; pulse of  $3$  s) for a total period of 9 s and placed on ice. The sonicated cell lysate was harvested, and the supernatant was obtained by centrifugation at  $14,000 \times g$  at  $4^{\circ}$ C for 25 min. The protein concentration of the supernatant was measured using a DC™ protein assay kit (Bio-Rad Laboratories Inc., Hercules, CA, USA). Each protein was separated using sodium dodecylsulfate–polyacrylamide gel electrophoresis gel. The separated proteins were transferred onto a polyvinylidene fuoride membrane (Millipore, Bedford, MA, USA). The membrane was blocked with 5% skim milk for 30 min and reacted with a specifc primary antibody at 4 °C for 20 h.

<span id="page-2-0"></span>**Table 1** Primer sequences for semiquantitative reverse-transcription polymerase chain reaction analysis

| Gene           | Primer sequence $(5' \rightarrow 3')$ |   |  |
|----------------|---------------------------------------|---|--|
| $\beta$ -Actin | Sense                                 | 5'-TGT CCA CCT TCC AGC AGA TGT-3'                   |  |
|                |                                       | Antisense 5'-AGC TCA GTA ACA GTC CGC CTA<br>$GA-3'$ |  |
| <i>FAS</i>     | Sense                                 | 5'-AGG GGT CGA CCT GGT CCT CA-3'                    |  |
|                |                                       | Antisense 5'-GCC ATG CCC AGA GGG TGG TT-3'          |  |
| $C/ERP\alpha$  | Sense                                 | 5'-GGA ACT TGA AGC ACA ATC GAT C-3'                 |  |
|                |                                       | Antisense 5'-TGG TTT AGC ATA GAC GTG CAC A-3'       |  |
| $PPAR\gamma$   | Sense                                 | 5'-TTG ATT TCT CCA GCA TTT CT-3'                    |  |
|                |                                       | Antisense 5'-RTG TTG TAG AGC TGG GTC TTT-3'         |  |

*FAS* fatty acid synthase, *C/EBP-α* CCAAT/enhancer-binding protein-α, *PPAR-γ* peroxisome proliferator-activated receptor-γ

The membrane was then incubated with a horseradish peroxidase–conjugated secondary antibody for 2 h. The protein bands were visualized using a chemiluminescence detection kit (Thermo FisherScientifc), and the thickness was analyzed using ImageJ software (National Institutes of Health, Bethesda, MD, USA).

## **Statistical Analysis**

All experiments were performed in triplicate and presented as the mean  $\pm$  standard deviation using one-way analysis of variance (ANOVA) and Duncan's multiple range test. Values were considered significant at  $P < 0.05$ . All analyses were conducted using the Statistical Package for the Social Sciences (SPSS), version 24 (IBM, Chicago, IL, USA).

# **Results**

# **Gastric Acid and Bile Tolerance, Enzyme‑Production Ability, Antibiotic Susceptibility, and Adhesion Ability of Bacterial Strains**

The tolerance of *L. rhamnosus* GG, *L. curvatus* KU15031, and *L. plantarum* KU15117 to gastric acids and bile salts is shown in Table [2](#page-3-0). All bacterial strains exhibited high resistance with over 96% of survival rate in gastric conditions (0.3% pepsin, pH 2.5). *L. rhamnosus* GG (102.88%) exhibited higher resistance than *L. curvatus* KU15031 (92.33%) and *L. plantarum* KU15117 (84.70%) in bile conditions (0.3% oxgall).

The enzymes produced by the diferent bacterial strains are shown in Table [3.](#page-3-1) The tested bacterial strains did not produce α-galactosidase (diabetes-related enzyme) or β-glucuronidase. However, *L. rhamnosus* GG and *L. plantarum* KU15117 produced β-galactosidase.

The antibiotic sensitivity of bacterial strains is presented in Table [4](#page-4-0). *L. curvatus* KU15031 had a similar sensitivity to *L. rhamnosus* GG, except for ampicillin (10 μg). *L.* 

<span id="page-3-1"></span>**Table 3** Enzymatic activities of bacterial strains



*plantarum* KU15117 was resistant to ampicillin (10 μg) and doxycycline (30 μg).

The bacterial strains showed a high adhesion rate to HT-29 cells (Fig. [1](#page-4-1)). *L. rhamnosus* GG exhibited a higher adhesion (6.37%) than *L. curvatus* KU15031 (1.33%) and *L. plantarum* KU15117 (2.34%).

## **Effects of Bacterial Strains on Lipid Accumulation during Adipogenesis**

The viability of 3T3-L1 cells treated with *L. plantarum* KU15117 and *L. rhamnosus* GG at  $10^8$  and  $10^9$  CFU/well

<span id="page-3-0"></span>



All values are expressed as mean $\pm$ standard deviation. Values with different letters in the same row are significant different for each characteristic  $(P < 0.05)$ 

<span id="page-4-0"></span>**Table 4** Antibiotic susceptibility of bacterial strains

| Antibiotics                  | sus GG | L. rhamno- L. curvatus<br>KU15031 | L. plan-<br>tarum<br>KU15117 |
|------------------------------|--------|-----------------------------------|------------------------------|
| Ampicillin $(10 \mu g)$      | S      | R                                 | S                            |
| Gentamycin $(10 \mu g)$      | R      | R                                 | R                            |
| Kanamycin $(30 \mu g)$       | R      | R                                 | R                            |
| Streptomycin $(10 \mu g)$    | R      | R                                 | R                            |
| Tetracycline $(30 \mu g)$    | S      | S                                 | R                            |
| Ciprofloxacin $(30 \mu g)$   | R      | R                                 | R                            |
| Chloramphenicol $(30 \mu g)$ | S      | S                                 | R                            |
| Doxycycline $(30 \mu g)$     | S      | S                                 | S                            |

Resistant according to the CLSI breakpoints [\[15\]](#page-7-13)

*S* susceptible, *I* intermediate, *R* resistant

was over 96% (Fig. [2](#page-4-2)). However, the viability of the cells treated with *L. curvatus* KU15031 was 34.58% and 26.79% at 10<sup>8</sup> and 10<sup>9</sup> CFU/well, respectively. Therefore, *L. plantarum* KU15117 and *L. rhamnosus* GG were used to determine lipid accumulation.

*L. plantarum* KU15117 and *L. rhamnosus* GG inhibited lipid accumulation, as shown by oil red O staining (Fig. [3](#page-5-0)A). In comparison with that of the positive control (100.81%), the oil red stain contents was as follows: *L. plantarum* KU15117 (31.88%) at  $10^9$  CFU/well < *L. rhamnosus* GG (45.02%) at 10<sup>9</sup> CFU/well<*L. plantarum* KU15117 (86.95%) at  $10^8$  CFU/well  $\lt L$ . *rhamnosus* GG  $(96.78%)$  at  $10<sup>8</sup>$  CFU/well (Fig. [3B](#page-5-0)). In addition, triglyceride contents of positive control were 5.661 mM, while *L. plantarum* KU15117 and *L. rhamnosus* GG showed



0.399 mM and  $1.684$  mM at  $10^9$  CFU/well, respectively (Fig. [3](#page-5-0)C).

# **Effects of Bacterial Strains on the mRNA and Protein Levels of Adipogenesis‑Related Genes in Differentiated 3T3‑L1 Adipocytes**

Figure [4](#page-6-0) shows the regulation of *FAS*, *C/EBP-α*, and *PPAR-γ* mRNA levels in diferentiated 3T3-L1 adipocytes. *L. rhamnosus* GG and *L. plantarum* KU15117 at 10<sup>9</sup> CFU/well signifcantly decreased the mRNA levels of the genes in 3T3- L1 cells. Particularly, *L. plantarum* KU15117 at 10<sup>9</sup> CFU/ well decreased the expression of *FAS* (92.96%), *C/EBP-α* (99.41%), and *PPAR-γ* (95.26%) (Fig. [4](#page-6-0)A–C). *L. rhamnosus* GG at 10<sup>8</sup> CFU increased the expression of *FAS*, *C/EBP-α*, and *PPAR-γ* mRNA.

The protein expression of adipogenic transcription factors and enzymes, including FAS,  $C/EBP-\alpha$ , and PPAR-γ (Fig. [4](#page-6-0)D) was confirmed by western blot analysis. In the positive control, the expression levels of FAS, C/EBP- $\alpha$ , and PPAR- $\gamma$  proteins were 3.28, 6.29, and 3.67, respectively. *L. rhamnosus* GG at 10<sup>9</sup> CFU/well decreased the protein expression by 0.96, 1.33, and 0.24, respectively. *L. plantarum* KU15117 at 10<sup>8</sup> CFU/well and L. *plantarum* KU15117 at 10<sup>9</sup> CFU/well significantly decreased the expression levels of FAS (3.08 and 0.91, respectively), C/EBP- $\alpha$  (2.74 and 1.15, respectively), and PPAR- $\gamma$  (1.97 and 0, respectively). The expression of FAS, C/EBP-α, and PPAR-γ proteins following treatment with LGG-8 was 3.32, 6.36, and 2.64, respectively. These results display a similar trend to those of mRNA expression levels.



<span id="page-4-1"></span>**Fig. 1** Adhesion activity of bacterial strains to HT-29 cells. LGG, *L. rhamnosus* GG; KU15031, *L. curvartus* KU15031; KU15117, *L. plantarum* KU15117. Error bars indicate standard deviation of three independent experiments. All values are expressed as mean  $\pm$  standard deviation. Letters denote statistical significance  $(P<0.05)$  as determined by Duncan's multiple range test

<span id="page-4-2"></span>Fig. 2 Effects of bacterial strains on the viability of 3T3-L1 adipocytes. LGG, *L. rhamnosus* GG; KU15031, *L. curvartus* KU15031; KU15117, L. plantarum KU15117. Filled square, 10<sup>8</sup> CFU/ well; empty square,  $10^9$  CFU/well. All values are expressed as mean $\pm$ standard deviation. Letters denote significance ( $P < 0.05$ ) as determined by Duncan's multiple range test

<span id="page-5-0"></span>**Fig. 3** Anti-obesity efects of bacterial strains on 3T3-L1 adipocytes. **A** Photograph of oil red O staining, **B** related absorbance of oil red O staining, and **C** triglyceride content. A, NC (negative control, nontreated with MDI in adipocytes); B, PC (positive control, treated with MDI in adipocytes); C, *L. rhamnosus* GG (108 CFU/well); D, *L. rhamnosus* GG (109 CFU/well); E, *L. plantarum* KU15117 (108 CFU/ well); F, *L. plantarum* KU15117  $(10^9 \text{ CFU/well})$ ; gray square, 10<sup>8</sup> CFU/well; white square, 109 CFU/well, LGG, *L. rhamnosus* GG; KU15117, *L. plantarum* KU15117. All values are expressed as mean±standard deviation. Letters denote signifcance  $(P<0.05)$  as determined by Duncan's multiple range test



## **Discussion**

Probiotics are used as food formulations for prophylactic therapy against metabolic syndrome. In this study, the antiobesity efects of lactic acid bacteria isolated for probiotic use were investigated. Tolerance to gastric conditions is an essential characteristic, which infuences the probiotic properties of bacterial strains in the intestine [[14](#page-7-15)]. Under strongly acidic and bile salt conditions, the survival rate of *Levilactobacillus brevis* KU15153 reduced by 70.79% and increased by>104.47%, respectively [\[17](#page-7-16)]. *L. curvatus* KU15031 and *L. plantarum* possessed probiotic properties, as indicated by the resistance to gastric conditions.

Some probiotic bacteria produce useful β-galactosidase, which decreases lactose intolerance [[18](#page-7-17)]. However, some probiotic bacteria also produce deleterious enzymes, such as β-glucuronidase, which have been associated with the induction of carcinogenesis, mutagenesis, and toxicity [\[19](#page-7-18)]. Son et al. [\[13\]](#page-7-12) indicated that probiotic *L. plantarum* FI10604 and *L. brevis* FI10700 do not produce β-glucuronidase. *Lactococcus lactis* KC24 produces various enzymes, including acid phosphatase, β-galactosidase, and naphthol-AS-BI-phosphohydrolase, but not β-glucuronidase [[14](#page-7-15)]. Similarly, we showed that *L. curvatus* KU15031 and *L. plantarum* KU15117 do not produce α-galactosidase and β-glucuronidase.

The sensitivity of probiotic bacteria to antibiotics is a fundamental factor because antibiotic-resistant strains may not be easily eliminated if required, and the antibiotic resistance may be transmitted to pathogenic or potentially pathogenic bacteria [[20](#page-8-0)]. *L. plantarum* Ln4 is sensitive to commercial antibiotics, such as chloramphenicol, doxycycline, ampicillin, and tetracycline [[13](#page-7-12)]. *Lactobacillus* spp. have intrinsic resistance to aminoglycosides (kanamycin and streptomycin) or quinolones (ciprofoxacin) [[21](#page-8-1)]. Therefore, these results confrm that *L. curvatus* KU15031 and *L. plantarum* KU15117 are safe in accordance with the CLSI guidelines [[15\]](#page-7-13).





<span id="page-6-0"></span>**Fig. 4** Anti-adipogenic efects of bacterial strains in MDI-induced diferentiation of 3T3-L1 preadipocytes. **A** FAS, **B** C/EBPα, **C** PPAR-γ gene expression of lipid metabolism-related genes, and **D** adipogenic protein expression. NC (Negative control), not treated with MDI in adipocytes; PC (Positive control), treated with MDI in adipocytes; LGG, *L. rhamnosus* GG; KU15117, *L. plantarum* KU15117. Gray square,  $10^8$  CFU/well; white square,  $10^9$  CFU/well;

The adhesion of bacterial strains to intestinal cells is the most important factor associated with their probiotic properties [\[22\]](#page-8-2). Song et al. [[23\]](#page-8-3) showed that *L. brevis* KCCM 12203P (6.84%) and *L. rhamnosus* GG (6.21%) have similar adhesion rates. Zhang et al. [[24](#page-8-4)] and Jeon et al. [\[25\]](#page-8-5) showed that *L. plantarum* strains (<2%) and *B. subtilis* P223 (1.33%) have diminished adhesion to intestinal epithelial cells, respectively. Therefore, *L. curvatus* KU15031 (1.33%) and *L. plantarum* KU15117 (2.34%) have acceptable adhesion rates to HT-29 cells.

Obesity is related to the diferentiation, expansion, and lipid accumulation of adipocytes [\[4\]](#page-7-3). *L. brevis* B151, *L. fermentum* KCCM 200060, and *L. plantarum* Ln4 exhibited reduced lipid accumulation in both heat-killed cells and freeze-dried broth [[11\]](#page-7-10). During the diferentiation

β-actin, loading control; LGG-8, 10<sup>8</sup> CFU/well of *L. rhamnosus* GG; LGG-9, 10<sup>9</sup> CFU/well of *L. rhamnosus* GG; 117–8, 10<sup>8</sup> CFU/well of *L. plantarum* KU15117; 117–9, 109 CFU/well of *L. plantarum* KU15117. All values are expressed as the mean $\pm$ standard deviation and standardized against the β-actin housekeeping gene. Values with diferent letters in the same row indicate signifcant diferences for each characteristic ( $P < 0.05$ )

period, *L. plantarum* Q180 dose-dependently inhibited 3T3-L1 adipogenesis in terms of lipid accumulation by 14.63% compared with that by control cells [\[26](#page-8-6)]. Park et al. [[27\]](#page-8-7) reported that the addition of *L. brevis* OPK-3 (40 μg/mL) showed 40% reduction in triglyceride accumulation. In our data, *L. plantarum* KU15117 (92.95%) and *L. rhamnosus* GG (68.93%) inhibited lipid accumulation by triglyceride accumulation.

In the early stage of adipocyte diferentiation, adipocytespecific FAS, C/EBP- $\alpha$ , and PPAR- $\gamma$  are regulated [[28](#page-8-8)]. *Weissella koreensis* OK1-6 signifcantly reduced the mRNA expression levels of *SREBP1*, *aP2*, *FAS*, and *C/EBP-α* [\[29](#page-8-9)]. *L. brevis* OPK-3 signifcantly downregulated the mRNA expression of *C/EBP-α* and *PPAR-γ* in diferentiating 3T3-L1 adipocytes [[27\]](#page-8-7). Similarly, *L. plantarum* KY1032 decreased the expression of PPAR-γ, C/EBP-α, FAS, and A-FABP proteins [[30](#page-8-10)]. *L. acidophilus* and cocktail of *Lactobacillus delbrueckii* subsp. *bulgaricus* and *Streptococcus thermophilus* were reduced adipogenesis genes (*PPAR-γ*, *CD36*, and *aP2*) expression [[31\]](#page-8-11). These results showed that the mRNA and protein expression levels of heat-killed *L. plantarum* KU15117 at  $10^8$  CFU/well and  $10^9$  CFU/well might have been downregulated during adipocyte diferentiation. Therefore, *L. plantarum* KU15117 could be infuenced in the early stage of adipocyte diferentiation in animal models.

In conclusion, we demonstrated the probiotic properties and anti-obesity efects of *L. plantarum* KU15117. *L. plantarum* KU15117 showed high tolerance to gastric conditions, safe enzyme activity, high adhesion rate to intestinal cells, and safe antibiotic sensitivity. Additionally, the anti-adipogenic activity of *L. plantarum* KU15117 was demonstrated by reduced lipid accumulation, low level of intercellular triglyceride, and suppressed expression of adipocyte-specifc genes and proteins that are associated with the early stage of adipocyte diferentiation. Therefore, *L. plantarum* KU15117 is a probiotic strain with anti-obesity efects. In addition, this study should be confrmed in animal model for further study.

**Author Contribution** Kyoung Jun Han: investigation, methodology, writing—original draft, validation. Na-Kyoung Lee: conceptualization, investigation, methodology, validation, writing—review and editing. Hyung-Seok Yu: investigation, methodology. Hoon Park: writing review and editing, validation. Hyun-Dong Paik: conceptualization, supervision, writing—review and editing, validation.

**Data Availability Statement** All data generated or analyzed during this study are included in this article.

## **Declarations**

**Conflict of Interest** The authors declare no competing interests.

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