Nutrigenomic Effects of Fermented Milk Containing *Bifidobacterium longum* Bb536 on Hepatic Cholesterologenic Genes in Hypercholesterolemic Rats

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**Abstract**

The aim of this study was to investigate the effects of fermented milk contains *bifidobacteria* on plasma lipid levels and selected genes in hypercholesterolemic rats. Effects of *Bifidobacterium longum* BB536 with prebiotics on body weight of rats, level of bile acids and selected genes were studied. Sprague-Dawley rats were randomly divided into groups. Negative control group received standard diet, positive control group received high-cholesterol diet, and intervention groups received high-cholesterol diet added with fermented milk contains *Bifidobacterium longum* BB536 in presences of prebiotics. After 8 weeks, body weight, level of bile acids were measured and low density lipoprotein receptor and 3-hydroxy-3-methylglutaryl-coenzyme A reductase were investigated in rats’ liver using quantitative real-time polymerase chain reaction. Fermented milk contains *Bifidobacterium longum* BB536 increased weight of rats and level of bile acids over 8 weeks of intervention. Low density lipoprotein receptor gene level was increased significantly in fermented milk treated rats compared to positive control. Whereas, 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene level was decreased significantly in fermented milk treated compared to positive control. The present study showed that fermented milk contains *Bifidobacterium longum* BB536 effectively regulated the expression of low-density lipoprotein receptor and 3-hydroxy-3-methylglutaryl-coenzyme A reductase genes influencing the cholesterol metabolism in liver cells.

**Keywords:** Nutrigenomic; *Bifidobacteria*; Hypercholesterolemic; Fermented; Prebiotic

**Introduction**

Alhaj [1] have reported that the major cause of morbidity and mortality in the world is cardiovascular disease. Cholesterol is required for certain hormones and vitamin formation, being an essential component in the nerve cells and cell membranes. It is one of the risk factors in cardiovascular disease as well as other chronic health conditions including artherosclerosis. However, Manson [2] has shown that a percent decrease in serum cholesterol level may decrease cardiovascular disease risk to about 3%.

One of the intervention measures aimed at maintaining a disease free condition to manage and/or control triglycerides and blood cholesterol levels in our diet is with drug treatment, for example the use of statins [3]. Other intervention to reduce blood cholesterol consumption of food with low fat and cholesterol [4], probiotic bacteria [5] and dietary fibre [6].

Attention has focused on the use of probiotic bacteria in commercial and scientific fields as a result of the different beneficial effects of these bacteria on humans. Probiotics are living microorganisms, which after consumption to a certain amount is capable of promoting the host health beyond normal nutrition [7]. They form part of the food components in food products as supplements. However, probiotics bacteria have been used for years in food fermentation, examples include some strains of *lactobacillus* and *bifidobacteria*.

*Bifidobacteria* is one of human intestinal microflora which assists in maintenance of good health [8]. Research has assessed the probiotic bacteria effects on lipid profile. Although the mechanism about cholesterol reduction by probiotic bacteria is yet unclear; some hypotheses are suggested to determine the hypocholesterolemic activity of probiotic bacteria, and bioactive peptides produced by their proteolytic activities. Probiotic bacteria could ferment non-digestible carbohydrates in intestinal to produce short chain fatty acids (SCFAs) such as propionic acid which is capable of reducing hepatic cholesterol synthesis. Pereira, et al. [3,9-11] stated that probiotics are capable of inhibiting intestinal cholesterol absorption by binding bile acids and cholesterol to probiotic bacterial cells, absorption cholesterol by probiotic bacteria.

Different attempts have been adopted including supplementation with prebiotics ingredients, which are non-digestible by human gastrointestinal tract, to maintain required *bifidobacteria* levels. Promotion of growth in the colon and overall well-being of human health by *lactobacilli and bifidobacteria* have been reported [9]. Recently, the interest in prebiotics was to combine them with probiotic bacteria in food to improve the functional properties for special health importance [12].
**Materials and Methods**

**Materials**

The fibrous of *M. pajang* fruit was prepared by removing its skin, peel and separating the seed from the pulp. The pulp was wet-milled and the juice was separated. The pomace was dried and ground. Crude polysaccharide was extracted using hot water, deproteinated, dialysed, concentrated, precipitated and lyophilized.

**Chemicals**

Bovine milk casein, alpha-cellulose, corn starch, lithocholic acid, and thiobarbituric acid (TBA) were purchased from Sigma-Aldrich (St. Louis, MO, USA). Butylated hydroxytoluene (BHT) was purchased from Sigma-Aldrich Fine Chemicals. Vitamin mixture, mineral mixture, choline chloride, DL-methionine, cholesterol, cholic acid, chenodeoxycholic acid and deoxycholic acid were purchased from MP Biomedicals, California, USA.

**Preparation of synbiotic yoghurt**

Yoghurt was prepared according to method described by [20] with some modifications. Skim milk powder instant (NZMP, Fonterra, Auckland, New Zealand) was weighed, dissolved in water to constitute 8.25% skim milk (w/v) and divided into three experimental lots; one lot was fortified with 0.75 g.L⁻¹ non-fat dried milk (YCBB), the second lot with 0.75 g.L⁻¹ inulin (YCBBI) and the third lot with 0.75 g.L⁻¹ MPFP (YCBBM). After mixing the mixtures were separately homogenised with an APV homogeniser (Alberslund, Denmark) until all ingredients were dissolved in the milk. The homogenates were then pasteurised at 85°C for 30 min and cooled by immersion of the flasks in an ice water bath until they reached temperatures of 40°C-43°C. Exactly 3% (v/v) yoghurt starter culture; *Lactobacillus delbrueckii* subsp. *bulgaricus* and *Streptococcus thermophilus* and *B. longum* BB 536 were added to each lot. The mixtures were distributed into 100 mL plastic cups and were then incubated at 40°C, until they reached a pH of 4.55, followed by cooling to 4°C and storage at that temperature no longer than 7 days before feeding. The number of all bacteria in all yoghurt products was enumerated to be as below:

| YCBB | 7.5 Log CFU/mL *Bifidobacterium longum* BB 536, 8.17 Log CFU/mL *Lactobacillus delbrueckii* spp. *Bulgaricus* and 8.45 Log CFU/mL *Streptococcus thermophilus*. YCBB contains 8.48 Log CFU/mL *Bifidobacterium longum* BB 536, 8.44 Log CFU/mL *Lactobacillus delbrueckii* spp. *Bulgaricus* and 8.44 Log CFU/mL *Streptococcus thermophilus*. YCBBM contains 8.39 Log CFU/mL *Bifidobacterium longum* BB 536, 8.18 Log CFU/mL *Lactobacillus delbrueckii* spp. *Bulgaricus* and 8.44 Log CFU/mL *Streptococcus thermophilus*. |

**Animal handling, feeding and induction of hypercholesterolemia**

Forty male Sprague-Dawley rats at 4 weeks of age were housed in stainless steel cages in a room with relative humidity 60% and temperature 20°C-25°C, with 12 h light exposure in a daily cycle from 6 am to 6 pm. Experiment was carried out according to the guidelines for the use of animals approved by the Animal Care and Use Committee (ACUC) of Faculty of Medicine and Health Sciences, Universiti Putra Malaysia with approval no. UPM/FPSK/PADS/BR-UUH/00362. All animals were fed on a basal diet for one week. After this acclimatization period, the rats were divided randomly into 5 experimental groups of 8 rats. First group was given a basal diet (cholesterol-free diet) and water during the experimental time of 8 weeks and considered as a negative control group (NC). The other four groups were nourished on the diet with cholesterol added at a level of 2.0% (w/w) (cholesterol-enriched diet), one of the 4 groups, which considered as a positive control group (PC), was nourished only on a cholesterol-enriched diet and tap water for an 8-week period. The other 3 groups were provided the cholesterol-enriched diet along with a variety of liquid yoghurt instead of normal water: group YCBB, milk fermented with 2% (v/v) *Lactobacillus delbrueckii* subsp. *Bulgaricus*, *Streptococcus thermophilus* (Chr. Hansen Laboratories, Copenhagen, Denmark) and 1% *B. longum* BB 536; group YCBBI, milk fermented with 2% (v/v) *L. delbrueckii* subsp. *Bulgaricus*, *S. thermophilus* and 1% *B. longum* BB 536; and group YCBBM, milk fermented with 2% (v/v) *L. delbrueckii* subsp. *Bulgaricus*, *S. thermophilus* and 1% *B. longum* BB 536. Throughout the feeding period, the environmental conditions were well controlled, and both diet and drink were available ad libitum.

**Food intake and body weight**

The animals were fed for an 8-week period, during which time body weight was recorded every 2 weeks (AND, HR-200, Singapore), and food intake was recorded daily.
Faeces collection

Faeces were collected on the last 2 days of the feeding period and kept frozen at -20°C for the analysis of bile acids.

Determination of bile acids in faeces

Extraction of bile acids from faeces was carried out according to the method of Kikuchi-Hayakawa [22], in brief lyophilized ground feces were accurately weighed (0.25 g) into a 16 × 150 mm screw-capped test tube and extracted with 5 mL of ethanol at 80°C after that the ethanol was evaporated by pure nitrogengases, and then the residue was dissolved in methanol and passed through a 0.45 µm membrane filter.

The level of extracted bile acids was determined according to the method of Roda et al. using an Agilent series 1100 HPLC system (Agilent Technologies, Palo Alto, CA, USA) equipped with an auto sampling injector, solvent degasser and diode array detector (DAD). Thirty five microlitres of the extracted sample was injected on the Spherosorb BDS C18 column (250 mm × 4.6 mm, ID 5 µm particle size). The operating parameters were set as follows: column temperature, 35°C; flow rate 1.0 mL/ min; UV-detector, 210 nm. The isocratic elution was with methanol/ acetonitrile/ 0.01% M phosphate buffer pH 5.3 (50/25/25, v/v/v) as a mobile phase. The standard bile acids used were cholic acid, chenodeoxycholic acid, deoxycholic acid and lithocholic acid (Sigma Chemical Co., St Louis, MO, USA). Each sample was injected twice. The peak area of bile acids standard solution was used to prepare a standard curve. From these standard curves (Appendices D.7, D.8, D.9 and D.10), the concentration of bile acids in the test samples was calculated.

RNA isolation

Rats were sacrificed after 8 weeks of intervention and their livers preserved in RCL2® Solution (ALPHELYS, Toulouse, France) within 5-10 min of death. RNA was isolated from frozen liver samples using the RNeasy® Lipid Tissue Isolation Kit (QIAGEN GmbH, Hilden, Germany) according to the manufacturer's instructions. The purity of the extracted RNA was determined by measuring the ratio of the optical density at 260 and 280 nm using a spectrophotometer (BioRad, USA). The total RNA concentration was determined by measuring the absorbance at 260 nm. The integrity and size distribution of the total RNA was determined by using a 1.5 agarose gel. The 18s and 28s RNA bands on gel electrophoresis were visualized under UV light using gel image instrumentation.

cDNA synthesis

RNA samples were reverse transcribed into first-strand cDNA using QuantiTect® Reverse Transcription Kit (QIAGEN GmbH, Hilden, Germany). According to the manufacturer's instructions, 1 µg of total extracted RNA was mixed with 2 µl of gDNA and completed to 14 µl with RNase free water. The mixture was mixed gently and incubated at 70°C for 5 min. Then, the microcentrifuge tubes were placed on ice and the reverse-transcription rxn components were added: 1 µl of quantitscript reverse transcriptase, 4 µl of quantitscript RT Buffer, 1 µl of RT primer mix and the previous mixture (14 µl). The mixture was mixed gently and incubated for 15 min at 42°C Finally, the reaction was stopped by heating at 95°C for 3 min. cDNA samples were labeled and stored at -20°C for real time PCR work.

Primers and probes design

TaqMan Primers and probes specific for LDLR, HMG-COAR and β-actin genes were designed and synthesized by (Profligo France SAS) and supplied by First BASE Laboratories (Selangor, Malaysia) from the gene sequence of rat (rattus norvegicus) adopted from the NCBI (National Center for Biotechnology Information) GenBank Database (www.ncbi.nlm.nih.gov). GenBank accession number code for LDLR is NM-175762, for HMG-COAR is NM_013134 and β-actin gene is NM_031144.

Quantitative real-time PCR

Real-time PCR was performed using the QuantiFast™ SYBR® Green PCR Kit (QIAGEN GmbH, Hilden, Germany). According to the manufacturer's instructions, a reaction (25 µl) containing 12.5 µl of QuantiFast SYBR Green PCR master mix with 2 µl of 400 nM of each forward and reverse primer, 1 µl of the probe (200 nM) and 1 µl of the template cDNA (10 ng/µl). Real-time PCR amplification of cDNA was performed for 40 cycles. After an initial incubation for 15 min at 95°C the PCR cycle consisted of a denaturation period for 10 s at 95°C and an annealing period for 30s at 60°C. Analysis of the gene expression data was performed using a ΔΔ CT method of relative quantification, according to a previous report by Kenneth et al. (2001). RotorGene analysis software (version 6.0) was used to analyze all the results from the PCR assays.

Statistical analysis

All the data are presented as the mean ± standard deviation (SD). Group differences were analysed using a one-way ANOVA (SPSS version 19.0., SPSS, Inc., Chicago, IL, USA) followed by a least significant difference (LSD) test. Significance was set at p<0.05.

Results and Discussion

Body weight gain, total food intake and food efficiency of rats

Table 1 shows the changes of body weight gain, total food intake, and food efficiency of rats between the baseline and in the week 8 of the treatment. At the beginning of experiment the body weight of all groups was between 133, 136 g and there is no difference between all groups, after that the body weights of all treatment groups showed increases from the beginning until the end of the experiment period it reached 428 g (NC), 406 g (PC), 392 g (YCBB), 415 g (YCBBI), and 472 g (YCBBM).

<table>
<thead>
<tr>
<th>Group</th>
<th>Weight at baseline (g)</th>
<th>Weight at 8 weeks (g)</th>
<th>Body weight gain (g)</th>
<th>Food intake (g)</th>
<th>Food efficiency (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC</td>
<td>135.88 ± 21.98a</td>
<td>428.13 ± 27.59c</td>
<td>282.25 ± 26.29c</td>
<td>1029.84 ± 13.27d</td>
<td>27.10 ± 2.4d</td>
</tr>
<tr>
<td>PC</td>
<td>133.75 ± 12.08a</td>
<td>406.50 ± 36.80ab</td>
<td>272.75 ± 33.29bc</td>
<td>1040.48 ± 16.16d</td>
<td>27.10 ± 2.1b</td>
</tr>
<tr>
<td>YCBB</td>
<td>135.09 ± 14.85a</td>
<td>392.88 ± 19.29a</td>
<td>257.79 ± 16.80a</td>
<td>861.28 ± 12.24a</td>
<td>29.11 ± 1.4c</td>
</tr>
</tbody>
</table>
The food was taken by rats throughout the experiment. The highest amount of food intake was by PC (1040 g) followed by NC (1029 g). However, the lowest amount was in YCBB (861 g). Also the average of food intake by YCBB and YCBBM is 957 g and 932 g respectively. Results showed food intake of treated rats with different yoghurt significantly lower compared to control groups. Although food intake of treated rats with different yoghurt was significantly lower than other groups, however, the percentage of body weight gain of these groups was significantly higher than other groups at the end of the study maybe due to consumption of yoghurt that contains nutrient/ calorie more than the positive and negative control. The findings are in agreement with those found by [22] Kikuchi-Hayakawa, [23] Suzuki et al., mentioned that no significant (p>0.05) difference in body weight gain in rats treated with L. acidophilus or bifidobacteria.

### Faecal bile acid excretion of experimental rats at the end of study

As tabulated in Table 2, there was no significant (p>0.05) difference in the levels of total bile acids between rats in NC and PC, however rats fed on YCBB, YCBBI and YCBBM diets excreted significantly higher level of bile acids than those PC and NC. It is noteworthy that the excretion of bile acids in rats fed on the YCGB1, YCGBM and YCBBM diets was significantly higher than those fed on YCG4 diet. This result demonstrates an opposite relationship between the level of bile acids excreted in the faeces and the total levels of TC, LDL-C or VLDL-C in rats fed with YCG4, YCGBM and YCBBM diets.

### Table 1: Body weight gain, total food intake, and food efficiency of rats fed a high- cholesterol diet for 8 weeks.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Body weight gain (g)</th>
<th>Total food intake (g)</th>
<th>Food efficiency (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC</td>
<td>31.85 ± 2.3a</td>
<td>1040 ± 14.0b</td>
<td>76.2 ± 3.9a</td>
</tr>
<tr>
<td>PC</td>
<td>31.62 ± 0.59c</td>
<td>1039 ± 14.6b</td>
<td>76.1 ± 3.8a</td>
</tr>
<tr>
<td>YCBB</td>
<td>31.62 ± 0.59c</td>
<td>997 ± 14.8b</td>
<td>77.7 ± 3.4a</td>
</tr>
<tr>
<td>YCBBI</td>
<td>31.62 ± 0.59c</td>
<td>974 ± 15.1b</td>
<td>78.0 ± 3.6a</td>
</tr>
<tr>
<td>YCBBM</td>
<td>31.62 ± 0.59c</td>
<td>957 ± 15.3b</td>
<td>78.2 ± 3.5a</td>
</tr>
</tbody>
</table>

### Table 2: Faecal bile acid excretion.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Cholic acid (mg/g)</th>
<th>Chenodeoxycholic acid (mg/g)</th>
<th>Deoxycholic acid (mg/g)</th>
<th>Lithocholic acid (mg/g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC</td>
<td>28.67 ± 0.25a</td>
<td>21.78 ± 0.26a</td>
<td>05.82 ± 0.13c</td>
<td>05.72 ± 0.41a</td>
</tr>
<tr>
<td>PC</td>
<td>28.67 ± 0.25a</td>
<td>21.78 ± 0.26a</td>
<td>05.82 ± 0.13c</td>
<td>05.72 ± 0.41a</td>
</tr>
<tr>
<td>YCBB</td>
<td>31.62 ± 0.59c</td>
<td>27.90 ± 0.37c</td>
<td>10.57 ± 0.37c</td>
<td>07.29 ± 0.17b</td>
</tr>
<tr>
<td>YCBBI</td>
<td>31.62 ± 0.59c</td>
<td>27.90 ± 0.37c</td>
<td>10.57 ± 0.37c</td>
<td>07.29 ± 0.17b</td>
</tr>
<tr>
<td>YCBBM</td>
<td>35.04 ± 0.40d</td>
<td>51.81 ± 0.76c</td>
<td>12.37 ± 0.27c</td>
<td>08.85 ± 0.56d</td>
</tr>
</tbody>
</table>

**NC**: Negative Control; **PC**: Positive Control; **YCBB**: Group Treated with Yoghurt Culture+*B. longum* BB536; **YCBBI**: Group Treated with Yoghurt Culture+*B. longum* BB536+inulin and **YCBBM**: Group Treated with Yoghurt Culture+*B. longum* BB536+MPFP. Each value represents means of 8 rats ± SD. Means with different small letter superscripts in the same column are significantly different (p<0.05).

### Regulation of LDLR mRNA level by *Bifidobacterium longum* BB536 in presence of prebiotic

From the amplification plot for LDLR gene, the β-actin gene had CT values ranging from 18 - 19 cycles and LDLR gene had CT values between 19-23 cycles. The effects of *Bifidobacterium longum* BB536 in presence of prebiotic on the regulation of LDLR gene are shown in Table 3. When cells were incubated with HLPDS and treated with *Bifidobacterium longum* BB536 in presence of prebiotics, LDLR mRNA level was increased significantly by 4.11, 7.46 and 8.45 fold in group treated with yoghurt culture+*B. longum* BB536, group treated with yoghurt culture+*B. longum* BB536+inulin and group treated with yoghurt culture+*B. longum* BB536 + MPFP respectively, compared to untreated cells. The effect of *B. longum* BB536 was significantly increased in presence of either inulin or MPFP as. LDLR activity was significantly upregulated by *Bifidobacterium longum* BB536 in presence of inulin.
presence of prebiotic. Although inhibition of LDL oxidation by a range of different plant sources has been widely reported [25]. The LDLR modulation effects have not been described previously for the

Bifidobacterium longum BB536 in presence of prebiotics which used in this study.

Table 3: Regulation of LDLR mRNA level by Bifidobacterium longum BB536 in presence of prebiotic.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Average CT of LDLR</th>
<th>Average CT of β-actin</th>
<th>ΔCT</th>
<th>ΔΔ CT</th>
<th>2 –ΔΔ CT (Fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC</td>
<td>29.24 ± 1.05</td>
<td>26.91 ± 0.91</td>
<td>2.33</td>
<td>-1.65</td>
<td>3.14b</td>
</tr>
<tr>
<td>PC</td>
<td>29.34 ± 0.93</td>
<td>25.36 ± 0.57</td>
<td>3.98</td>
<td>0</td>
<td>1.00a</td>
</tr>
<tr>
<td>YCBB</td>
<td>29.63 ± 0.57</td>
<td>27.69 ± 0.87</td>
<td>1.94</td>
<td>-2.04</td>
<td>4.11c</td>
</tr>
<tr>
<td>YCBBI</td>
<td>30.29 ± 1.12</td>
<td>29.22 ± 0.79</td>
<td>1.07</td>
<td>-2.9</td>
<td>7.46d</td>
</tr>
<tr>
<td>YCBBM</td>
<td>28.31 ± 0.92</td>
<td>27.41 ± 0.86</td>
<td>0.9</td>
<td>-3.08</td>
<td>8.45e</td>
</tr>
</tbody>
</table>

Δ CT: CT of target gene (LDLR) - CT of reference gene (β-actin), ΔΔCT: ΔCT of experimental cells- Δ CT of control. NC: Negative Control; PC: Positive Control; YCBB: Group treated with yoghurt culture+B. longum BB536; YCBBI: Group Treated with Yoghurt Culture+B. longum BB536+inulin and YCBBM: Group Treated with Yoghurt Culture+B. longum BB536 + MPFP. Each value represents the mean ± SD of 4 rats.

Table 4: Regulation of HMG-COAR mRNA level by Bifidobacterium longum BB536 in presence of prebiotics.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Average CT of HMG-COAR</th>
<th>Average CT of β-actin</th>
<th>ΔCT</th>
<th>ΔΔ CT</th>
<th>2 –ΔΔ CT (Fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NC</td>
<td>27.05 ± 1.05</td>
<td>25.77 ± 0.41</td>
<td>1.28</td>
<td>0.51</td>
<td>1.49d</td>
</tr>
<tr>
<td>PC</td>
<td>26.70 ± 0.49</td>
<td>25.93 ± 0.95</td>
<td>0.77</td>
<td>0</td>
<td>1.00c</td>
</tr>
<tr>
<td>YCBB</td>
<td>26.76 ± 0.50</td>
<td>24.91 ± 0.21</td>
<td>1.85</td>
<td>1.08</td>
<td>0.92b</td>
</tr>
<tr>
<td>YCBBI</td>
<td>26.30 ± 2.60</td>
<td>24.22 ± 0.12</td>
<td>2.08</td>
<td>1.31</td>
<td>0.69a</td>
</tr>
<tr>
<td>YCBBM</td>
<td>27.01 ± 0.87</td>
<td>24.72 ± 0.45</td>
<td>2.29</td>
<td>1.52</td>
<td>0.48a</td>
</tr>
</tbody>
</table>

ΔCT: CT of target gene (HMG-COAR) - CT of reference gene (β-actin), ΔΔCT: ΔCT of experimental cells- Δ CT of control. NC: Negative Control; PC: Positive Control; YCBB: Group Treated with Yoghurt Culture+B. longum BB536; YCBBI: Group Treated with Yoghurt Culture+B. longum BB536+inulin, and YCBBM: Group Treated with Yoghurt Culture+B. longum BB536 + MPFP. Each value represents the mean ± SD of 4 rats.

References

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