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Author(s)
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Role of intestinal *Bifidobacterium pseudolongum* in dietary fructo-oligosaccharide inhibition of 2,4-dinitrofluorobenzene-induced contact hypersensitivity in mice

Naho Sasajima\(^1\), Toru Ogasawara\(^1\), Naoki Takemura\(^1\), Reiko Fujiwara\(^1\), Jun Watanabe\(^2\) and Kei Sonoyama\(^3\)*

\(^1\)Laboratory of Gastrointestinal Physiology, Graduate School of Life Science, Hokkaido University, Sapporo 060-8589, Japan
\(^2\)Creative Research Initiative Sousei, Hokkaido University, Sapporo 001-0021, Japan
\(^3\)Laboratory of Food Biochemistry, Research Faculty of Agriculture, Hokkaido University, Kita-9, Nishi-9, Kita-ku, Sapporo-shi, Hokkaido 060-8589, Japan

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Strategies to manipulate the gut microbiota have been explored for preventing allergy development. We previously showed that dietary supplementation with fructo-oligosaccharide (FOS) reduced 2, 4-dinitrofluorobenzene (DNFB)-induced contact hypersensitivity (CHS) in BALB/c mice. Because the CHS response was negatively correlated with the number of faecal bifidobacteria, particularly *Bifidobacterium pseudolongum*, the present study aimed to examine whether oral administration of *B. pseudolongum* affects CHS response. Viable *B. pseudolongum* was successfully isolated from mouse faeces. Female BALB/c mice were fed a synthetic diet with or without FOS supplementation, and *B. pseudolongum* (2 × 10\(^7\) cells) was administered daily throughout the experimental period. Two weeks after starting the test diets, mice received DNFB on the ear auricle twice at 7-d intervals. Conventional cultivation and molecular biological analyses based on 16S rRNA gene sequences showed that administration of FOS and *B. pseudolongum* resulted in higher excretion of viable bifidobacteria, mainly *B. pseudolongum*. Although dietary FOS reduced the CHS response as demonstrated by ear swelling, *B. pseudolongum* administration resulted in a reduction in the initial phase only of the CHS response. *B. pseudolongum* administration increased hapten-specific IgG1, while dietary FOS decreased IgG2a in sera. Administration of FOS and *B. pseudolongum* decreased interferon-γ production and increased IL-10 production in cervical lymph node cells restimulated with hapten in vitro. We conclude that *B. pseudolongum* proliferation in the intestinal tract is partially responsible for the reduction in DNFB-induced CHS response by dietary supplementation with FOS in mice, which may be mediated by the modulation of antigen-induced cytokine production.

**Prebiotics: Bifidobacteria: Contact hypersensitivity: Mice**

Commensal microbiota in the intestinal tract plays an important role in the normal development of the immune system\(^{1,2}\). Therefore, strategies for microbiota manipulation have been explored for the prevention of the onset of immune diseases such as allergy. This idea is supported by epidemiological data demonstrating that differences in the composition of gut microbiota in infancy precede the development of atopic dermatitis\(^3\). In addition, clinical trials showed that administration of probiotic bacterial strains, such as *Lactobacillus rhamnosus* GG, was beneficial in both the prevention\(^{4,5}\)and treatment\(^6\) of early allergic diseases. However, some studies reported that *L. rhamnosus* GG and *Lactobacillus acidophilus* did not have a preventative effect in infancy\(^7\)–\(^9\). Therefore, there is currently insufficient data to recommend probiotics as part of a standard therapy in the treatment or prevention of allergic conditions\(^10\).

Prebiotics, such as indigestible oligosaccharides, have also been considered to promote immune health by selectively stimulating the growth and/or activity of beneficial bacteria, such as bifidobacteria and lactobacilli, in the intestinal tract\(^11\)–\(^14\). Indeed, a mixture of long-chain fructo-oligosaccharide (FOS) and short-chain galacto-oligosaccharide reportedly reduced the incidence of atopic dermatitis in formula-fed high-risk infants\(^15\)–\(^17\). In terms of experimental evidence, we demonstrated that dietary raffinose and α-linked galacto-oligosaccharide reduced allergic airway inflammation in ovalbumin-sensitised Brown Norway rats\(^17,18\). In addition, Fujitani et al.\(^19\) showed that dietary FOS reduced infiltration of inflammatory cells and oedema formation in duodenal mucosa using an ovalbumin-induced food allergy model of NC/jic mice. Furthermore, Vos et al.\(^20\) reported that consumption of a mixture of long-chain FOS and short-chain galacto-oligosaccharide suppressed allergic airway inflammation in an ovalbumin-induced allergic asthma model of BALB/c mice. These findings suggest that administration of indigestible oligosaccharides is effective in the prevention of allergic diseases.

**Abbreviations:** BIM, bifidobacterium iodoacetate medium; CHS, contact hypersensitivity; CLN, cervical lymph node; DGGE, denaturing-gradient gel electrophoresis; DNFB, 2,4-dinitrofluorobenzene; FOS, fructo-oligosaccharide; IFN, interferon; RT-qPCR, real-time quantitative PCR.

*Corresponding author:* Kei Sonoyama, fax +81 11 706 2496, email ksnym@chem.agr.hokudai.ac.jp
Allergic contact dermatitis is one of the most prevalent human skin diseases, causing moderate to severe inflammatory damage. This pathological condition arises after contact hypersensitivity (CHS)\(^{2+21}\). CHS is a T-cell-mediated, antigen-specific type of skin inflammation that is induced by topical skin contact with hapten in a previously sensitised host\(^{22,23}\). When the host is sensitised by application of the hapten, skin dendritic cells capture the hapten and migrate to draining lymph nodes, where they prime specific T cells. These cells differentiate into CHS effector cells, which recirculate through the blood. The second contact with the same hapten leads to a skin inflammatory response that peaks 24–48 h after the challenge. Avoidance of causal allergens is one of the emphasised therapeutic suggestions for CHS; however, avoidance is not practical in the majority of cases.

We previously reported that dietary supplementation with short-chain FOS reduced DNFB-induced CHS response in BALB/c mice\(^{24}\). Molecular biological analyses of gut microbiota in these mice, based on 16S rRNA gene sequences, showed that the CHS response, i.e. ear swelling, was negatively correlated with the numbers of bifidobacteria. Because sequence analysis revealed that Bifidobacterium pseudolongum was the most predominant bifidobacterium in the intestine of FOS-supplemented mice, we postulated that a reduction in the CHS response by feeding FOS was associated with the proliferation of B. pseudolongum in the intestinal tract. In the present study, therefore, we aimed to examine whether oral administration of B. pseudolongum, isolated from FOS-supplemented mice, affects the development of DNFB-induced CHS response in mice.

Materials and methods

Animals and diets

The following study was approved by the Hokkaido University Animal Use Committee, and animals were maintained in accordance with the Hokkaido University guidelines for the care and use of laboratory animals.

Female BALB/c mice (5 weeks old) were purchased from Japan SLC (Hamamatsu, Japan) and housed in standard plastic cages in a temperature-controlled (23 ± 2°C) room with a dark period from 20.00 to 08.00 hours. They were allowed free access to food and water. Mice were allocated to two groups of eleven mice and fed either a synthetic diet prepared according to AIN-93G guidelines\(^{25}\) or the same diet prepared by adding (50 g/kg diet) FOS to the FOS(+) diet at the expense of corn starch. In each dietary group, mice were further divided into two subgroups of five or six mice and intragastrically administered vehicle or 2 × 10\(^7\) cells of viable B. pseudolongum daily as described below. These treatments were referred to as BP(−) and BP(+), respectively. Thus, mice were divided into four groups: FOS(−)BP(−), FOS(−)BP(+), FOS(+)BP(−) and FOS(+)BP(+) (n 5, 6, 5 and 6, respectively). Mice were fed the test diets and administered B. pseudolongum throughout the experimental period. B. pseudolongum was isolated from the faeces of mice-fed FOS(+) in a separate experiment as described below.

Two weeks after starting the test diets and B. pseudolongum administration, fresh faeces were collected, and CHS was induced as described below. At 25 d after the first application of DNFB, mice were anaesthetised by inhalation of diethyl ether and blood was drawn from the carotid artery. Cervical lymph node (CLN) was excised for primary cell culture as described below.

Isolation of Bifidobacterium pseudolongum

Fresh faeces were collected from female BALB/c mice-fed FOS(+) for 3 weeks. Faecal samples were homogenised in 450 μl of 50 mM anaerobic phosphate buffer (pH 6.8) that contained 0.05 % (w/v) l-cystein, 0.05 % (w/v) Tween 80 and 0.1 % (w/v) agar. The samples were diluted, and aliquots were plated on bifidobacteria-selective Bifidobacterium lactic acid and 25 mg/l 2,3,5-triphenyltetrazolium chloride, and incubated at 37°C for 5 d under anaerobic condition (N₂−CO₂–H₂, 8:1:1, Coy anaerobic chamber, Coy Laboratory Products, Grass Lake, MI, USA). After incubation, a single colony was picked with a platinum loop and streaked onto an agar plate. Following incubation at 37°C for 5 d under anaerobic conditions, a number of single colonies were picked and suspended in BIM broth. After incubation at 37°C for 3 d under anaerobic conditions, the medium was removed by centrifugation (8000 g 10 min), and the resultant pellet was resuspended in BIM broth that contained 20 % glycerol medium and stored at −80°C. In addition, aliquots of the pellet were used for isolation of DNA, followed by sequencing analysis as described below. Light microscopic observation following Gram staining was also performed.

Oral administration of Bifidobacterium pseudolongum

A frozen stock sample of isolated B. pseudolongum was thawed, washed twice with PBS and adjusted to 10⁶ cells/ml with PBS before use. Mice were intragastrically administered 200 μl of the bacterial suspension (2 × 10⁷ cells) daily throughout the experimental period. Before administration, viability of bacteria was checked by flow cytometry according to Ben-Amor et al.\(^{27}\). In brief, approximately 10⁶ cells were suspended in 1 ml anaerobic PBS containing 1 mM dithiothreitol, 0.01 % (w/v) Tween 20, 10⁴ particles/ml fluorospheres (Flow-Check fluorospheres, Beckman Coulter, Tokyo Japan), 1 μg/ml propidium iodide (Wako Pure Chemical Industries, Osaka, Japan) and 5 mM SYTO-BC (Molecular Probes, Eugene, OR, USA). After 5 min incubation at room temperature, samples were analysed by flow cytometry (Epics XL, Beckman Coulter). The viability was routinely greater than 80 %.

Species-specific PCR and DNA sequencing for Bifidobacterium pseudolongum

B. pseudolongum subsp. pseudolongum (JCM1264) was obtained from the Japan Collection of Microorganisms of the Institute of Physical and Chemical Research, and used as a positive control. DNA was isolated from bacterial samples isolated from mouse faeces and B. pseudolongum subsp.
pseudolongum (JCM1264) using PrepMan Ultra reagent (Applied Biosystems Japan, Tokyo, Japan), according to the manufacturer’s instructions. Bacterial DNA samples were used as a template to amplify the 16S rRNA gene fragments with a primer pair specific to B. pseudolongum (forward: IDB41F, CCC TTT TTC CGG GTC CTG T; reverse: IDBC1R, ATC CGA ACT GAG ACC GGT TY)[28]. PCR was performed in a reaction volume of 25 μl that contained 500 nM each of primers, 1 μl PCR buffer, 0.2 mM dNTP and 1.25 U Taq-HS polymerase (Takara, Otsu, Japan). The reaction conditions were 96°C for 2 min, followed by 35 cycles at 94°C for 30 s, 53°C for 40 s and 72°C for 30 s, and a final extension at 72°C for 5 min. The size of the amplicon (471 bp) was checked by agarose gel electrophoresis. In addition, the nearly complete 16S rRNA gene was sequenced (471 bp) was checked by agarose gel electrophoresis. In addition, the nearly complete 16S rRNA gene was sequenced (471 bp) was checked by agarose gel electrophoresis.

One software (version 4.6.0; Bio-Rad, Hercules, CA, USA) was used for band identification and normalisation of band patterns from DGGE gels. Subsequently, a dendrogram of the DGGE band profile was constructed using Pearson’s curve-based correlation and the unweighted pair-group method using the arithmetic average clustering method in Quantity One software as previously described[32].

Quantification of bifidobacteria in faeces

Populations of bifidobacteria in faecal samples were determined by conventional culture method. Briefly, the fresh samples were diluted tenfold with anaerobic phosphate buffer, and then 50 μl of each dilution were inoculated onto bifidobacteria-selective BIM agar[26]. Anaerobic incubation was performed at 37°C for 72 h using the AnaeroPack system (Mitsubishi gas, Tokyo, Japan). The number of colonies was counted after incubation and is represented as logarithm of colony-forming units.

Additionally, populations of bifidobacteria were quantified by real-time quantitative PCR (RT-qPCR) as previously described[26]. Amplification and detection of faecal DNA were performed with the Thermal Cycler Dice Real Time System (Takara). Bifidobacterium genus-specific primer pairs (forward: TCG CGT C(T)/G TGA TGA AAG; reverse: CCA CAT CCA GC(A/G) TCC AC)[33] and B. pseudolongum species-specific (IDB41F and IDBC1R as described above)[28] primer pairs were used. RT-qPCR was performed in a reaction volume of 25 μl, containing 12.5 μl SYBR Premix Ex Taq (Takara), 200 nM each of the forward and reverse primers and 1 μl of the faecal DNA samples. The reaction conditions were: 95°C for 10 s, followed by forty cycles at 95°C for 5 s, 64°C for 30 s for the quantification of bifidobacteria; and 95°C for 10 s, followed by forty cycles at 95°C for 5 s, 60°C for 30 s for the quantification of B. pseudolongum. The fluorescent products were detected at the last step of each cycle. A melting curve analysis was performed after amplification to distinguish the targeted PCR product from the non-targeted PCR product. All samples were analysed in duplicate.

B. pseudolongum subsp. pseudolongum (JCM1264) was cultured in BIM broth, and the genomic DNA was extracted by PrepMan Ultra reagent according to the manufacturer’s instructions. The 16S rRNA gene fragment was amplified by PCR with the B. pseudolongum species-specific primer pair (IDB41F and IDBC1R as described above)[28]. The amplicons were purified by QIAquick PCR purification kit (Qiagen, Tokyo, Japan) and cloned in pGEM-Easy T vectors (Promega, Madison, WI, USA). Transformation was performed with competent Escherichia coli XL-1 Blue cells, and the cells were plated onto Luria-Bertani agar plates supplemented with 25 μg/ml ampicillin, 30 μg/ml X-gal and 20 μg/ml IPTG, and incubated overnight at 37°C. White transformants were picked and grown in Luria-Bertani broth. Plasmid DNA was extracted with a QIAprep Spin Miniprep kit (Qiagen) and used as a standard for RT-qPCR.

Antibody ELISA

Serum levels of IgG1 and IgG2a specific to the hapten were determined by ELISA as previously described[24]. In brief, each well of the ninety-six-well microtitre plates was coated with dinitrophenol-bovine serum albumin (Calbiochem, San Diego, CA, USA). After blocking the wells, serial dilutions of serum were added and then incubated for 2 h at room temperature. After washing, each well was incubated with a 1:5000 dilution of rabbit anti-mouse IgG1 and IgG2a antibody (The Binding Site) for 1 h at 37°C. During the incubation, horseradish peroxidase-conjugated goat anti-rabbit IgG (Jackson Immunoresearch) at a 1:2000 dilution was added to each well. After subsequent washing, each well was incubated with a solution of 0.1 mg/ml o-phenylenediamine in 0.05 M citrate buffer at 37°C for 30 min. When the reaction was complete, 0.1 M sulfuric acid was added to each well. The absorbance of each well was measured at 490 nm using a microtitre plate reader (Molecular Devices).
temperature. Horseradish peroxidase-conjugated rat anti-
mouse IgG1 (clone LO-MG1-2, Zymed Laboratories, South
San Francisco, CA, USA) or rat anti-mouse IgG2a (clone
LO-MG2a-3, Zymed Laboratories) was added and incubated
at 37°C for 2 h. Plates were developed at room temperature
after the addition of o-phenylenediamine (0.4 mg/ml) and
hydrogen peroxide (0.016%).

Measurement of in vitro cytokine production in
 cervical lymph node cells

The excised CLN was gently homogenised with RPMI-1640
medium (GIBCO-BRL, Tokyo, Japan) supplemented with 2 %
heat-inactivated fetal calf serum (GIBCO-BRL), 100 U/ml
penicillin, 100 μg/ml streptomycin and 50 μg/ml gentamycin,
and cells were filtered through nylon mesh (Nippon Rikagaku
Kikai, Tokyo, Japan) and centrifuged for 5 min at 300 g.
To remove erythrocytes, the cell pellet was resuspended
in 10 mm 2-amino-2-(hydroxymethyl)propane-1,3-diol–HCl
buffer (pH 7.4) supplemented with 0.24 M NH₄Cl and incu-
bated for 5 min at room temperature, followed by washing
twice with RPMI-1640 medium supplemented with 2 % fetal
calf serum. Thereafter, cells were counted by a Z1 coulter
particle counter (Yamato Scientific, Tokyo, Japan), and an
equal number of cells isolated from each mouse were
pooled in each group. The cells (2 x 10⁵ cells in 0.2 ml) were
cultured in round-bottomed ninety-six-well plates
(Greiner Bio-One, Tokyo, Japan) in RPMI-1640 medium sup-
plemented with 10 % fetal calf serum and 500 μg/ml dinitroben-
zene sulphonic acid sodium salt at 37°C in a 5 % CO₂
atmosphere. Following 3-d-culture, the conditioned medium
was collected and subjected to ELISA for cytokines. ELISA
was performed in ninety-six-well microtitre plates. Wells
were coated overnight at 4°C with primary antibodies (clones
XMG1.2 and JES5-16E3 for IFN-γ and IL-10, respectively,
eBioscience, San Diego, CA, USA). After blocking with
RPMI-1640 medium supplemented with 10 % fetal calf serum
at room temperature for 1 h, serial dilutions of conditioned
medium, recombinant mouse interferon (IFN)-γ (eBioscience)
and recombinant mouse IL-10 (eBioscience) were added and
incubated for 2 h at room temperature. Thereafter, biotin-con-
jugated secondary antibodies (clones R4-6A2 and JES5-2A5
for IFN-γ and IL-10, respectively, eBioscience) were added
and incubated for 1 h at room temperature. Streptavidin-horse-
radish peroxidase (Zymed Laboratories) was then added
and incubated for 30 min at room temperature. Plates were devel-
oped at room temperature after the addition of 0.2 m citrate
buffer (pH 4.0) containing 0.0123 mg/ml 3,3′,5,5′-tetramethyl-
benzidine and 0.01 044 % hydrogen peroxide. Finally, 1 m
H₂SO₄ was added, and absorbance was measured at 450 nm
with a microplate reader.
Statistical analysis

Results are presented as means with their standard errors. Tukey–Kramer’s test following two-way ANOVA was used to compare mean values. Data analysis was performed with StatView for Macintosh (version 5.0, Statistical Analysis Systems Institute Inc., Spring Valley, CA, USA). \( P \) values less than 0.05 were considered statistically significant.

Results

Isolation of Bifidobacterium pseudolongum from mouse faeces

A Gram-positive obligate anaerobe, in the shape of a club or jelly bean, was isolated from the faeces of mice-fed FOS. DNA isolated from this bacterial sample and \( B. \) pseudolongum subsp. pseudolongum (JCM1264) were subjected to PCR with \( B. \) pseudolongum-specific primers. Fig. 1 shows the PCR amplicons separated on 3% agarose gel. The size of the amplicons was consistent with the predicted size (471 bp). In addition, the nearly complete 16S rRNA gene sequence (1420 bp) exhibited 99% similarity to \( B. \) pseudolongum subsp. pseudolongum (GenBank accession number, AY174106; Supplementary Fig. 1; the supplementary material for this article can be found at http://www.journals.cambridge.org/bjn). These findings indicate that the isolated bacterium is identical to \( B. \) pseudolongum.

Effect of fructo-oligosaccharide and \( B. \) pseudolongum on faecal microbiota

The diversity of faecal microbiota in mice was compared by PCR–DGGE analysis based on 16S rRNA gene sequences. A representative DGGE band profile is shown in Fig. 2(a). The intensity and position of detected bands were subjected to cluster analysis. The dendrogram shows two large clusters of FOS(+) and FOS(−) groups (Fig. 2(b)). The results indicate that dietary supplementation with FOS modulated the composition of gut microbiota in mice, being consistent with our previous study(24). In contrast, BP(−) and BP(+) groups showed no clear cluster. Thus, it appears that administration of \( B. \) pseudolongum had no influence on the global composition of gut microbiota in mice.

Effect of fructo-oligosaccharide and \( B. \) pseudolongum on faecal bifidobacteria

Faecal bifidobacteria were quantified using a conventional cultivation method (Fig. 3(a)). Two-way ANOVA showed that

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**Fig. 3.** Populations of bifidobacteria in the faeces of BALB/c mice-fed fructo-oligosaccharide (FOS) and \( B. \) pseudolongum (BP). Bifidobacteria (charts (a) and (b)) and \( B. \) pseudolongum (chart (c)) were quantified by a conventional culture method (chart (a)) and real-time quantitative PCR (charts (b) and (c)). Each symbol represents the value for an individual mouse, and horizontal bars represent mean values. In chart (a), \( P \) values estimated by two-way ANOVA were 0.0281, 0.0281 and 0.0618 for FOS, BP and their interaction, respectively. Similarly, \( P \) values in chart (b) were 0.0016, 0.0016 and 0.6903 for FOS, BP and their interaction, respectively. \( P \) values in chart (c) were 0.0002, 0.0017 and 0.4095 for FOS, BP and their interaction, respectively. Mean values with unlike letters were significantly different (\( P < 0.05 \)), as estimated by Tukey–Kramer’s test.
both FOS \((P=0.0281)\) and \(B.\) pseudolongum \((P=0.0281)\) increased the faecal excretion of bifidobacteria. The faecal bifidobacterial levels were significantly lower in the FOS\((-)\)BP\((-)\) group than in the other three groups. Only one out of the five mice in the FOS\((-)\)BP\((-)\) group had a detectable level of bifidobacteria in the faeces. There were no significant differences among the other three groups. In addition, RT-qPCR with \(Bifidobacterium\) genus-specific primers showed that both FOS \((P=0.0016)\) and \(B.\) pseudolongum \((P=0.0016)\) increased the faecal excretion of bifidobacteria (Fig. 3(b)). The bifidobacterial levels were significantly lower in the FOS\((-)\)BP\((-)\) group than in the other three groups, and the levels were significantly higher in the FOS\((+)\)BP\((+)\) group than in the FOS\((-)\)BP\((+)\) and FOS\((+)\)BP\((-)\) groups. There was no significant difference between the FOS\((-)\)BP\((+)\) group and the FOS\((+)\)BP\((-)\) group. Furthermore, faecal \(B.\) pseudolongum levels quantified by RT-qPCR with species-specific primers in each group were roughly comparable with the respective levels of bifidobacteria quantified by RT-qPCR with \(Bifidobacterium\) genus-specific primers (Fig. 3(c)).

**Effect of fructo-oligosaccharide and \(Bifidobacterium\) pseudolongum on contact hypersensitivity**

Ear swelling began to be detected 5 d after the first application of DNFB (Fig. 4). At that time, two-way ANOVA showed that both FOS and \(B.\) pseudolongum significantly affected ear swelling (Table 1). Thus, ear swelling was significantly higher in the FOS\((+)\)BP\((+)\) group than in the FOS\((-)\)BP\((-)\) group and FOS\((+)\)BP\((-)\) groups. There was no significant difference between the FOS\((-)\)BP\((+)\) group and the FOS\((+)\)BP\((-)\) group. Furthermore, faecal \(B.\) pseudolongum levels quantified by RT-qPCR with species-specific primers in each group were roughly comparable with the respective levels of bifidobacteria quantified by RT-qPCR with \(Bifidobacterium\) genus-specific primers (Fig. 3(c)).

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**Effect of fructo-oligosaccharide and \(Bifidobacterium\) pseudolongum on contact hypersensitivity**

Ear swelling began to be detected 5 d after the first application of DNFB (Fig. 4). At that time, two-way ANOVA showed that both FOS and \(B.\) pseudolongum significantly affected ear swelling (Table 1). Thus, ear swelling was significantly higher in the FOS\((+)\)BP\((+)\) group than in the FOS\((-)\)BP\((-)\) group and FOS\((+)\)BP\((-)\) groups. There was no significant difference between the FOS\((-)\)BP\((+)\) group and the FOS\((+)\)BP\((-)\) group. Furthermore, faecal \(B.\) pseudolongum levels quantified by RT-qPCR with species-specific primers in each group were roughly comparable with the respective levels of bifidobacteria quantified by RT-qPCR with \(Bifidobacterium\) genus-specific primers (Fig. 3(c)).
FOS(+)BP(+) mice showed reduced ear swelling in response to topical application of DNFB when compared with vehicle-administered mice-fed FOS(−) diet (i.e. FOS(−)BP(−)). Although FOS(+)BP(−) mice also showed a similarly reduced extent of ear swelling as FOS(+)BP(+) mice, the inhibitory action of *B. pseudolongum* administration without FOS feeding (i.e. FOS(−)BP(+) was limited largely to the initial phase of the CHS response (i.e. on day 5 after the first application of DNFB). Because faecal excretion levels of bifidobacteria, mainly *B. pseudolongum*, in FOS(−)BP(+) group were comparable with those in FOS(+)BP(−) group as described above, we suppose that *B. pseudolongum* proliferation in the gastrointestinal tract might be partially responsible for the inhibitory effect of dietary FOS on DNFB-induced CHS response in mice. In other words, the proliferation of other bacterial species than bifidobacteria in the intestinal tract of mice-fed FOS might also contribute to the reduction in DNFB-induced CHS response. Indeed, PCR–DGGE analysis of faecal 16S rRNA gene indicated that dietary supplementation with FOS, but not administration of *B. pseudolongum*, influenced the global composition of gut microbiota in mice. Therefore, it is of interest to search for the bacterial species or strains that prevent the CHS response. Chapat et al. (34) demonstrated that oral administration of *Lactobacillus casei* DN-114 001, a strain used for the preparation of fermented milk, reduced the DNFB-induced CHS response in C57BL/6 mice.

Aberrant regulation between IFN-γ-producing Th1 cells and IL-4-producing Th2 cells is considered important in the development of immune diseases (35). For example, CHS responses are coupled with excessive Th1 cells and also IFN-γ-producing CD8+ (Tc1) cells (36,37). In CHS responses, allergen re-exposure in the sensitised tissue results in the production of inflammatory cytokines by epidermal cells, which recruit hapten-specific T cells. Infiltrating T cells releases inflammatory cytokines such as IFN-γ that stimulate keratinocytes to produce chemokines. This in turn results in further recruitment of inflammatory cells, including monocytes and non-antigen-specific T cells. Ultimately, inflammation reaches its maximum, characterised by (epi)dermal infiltrates, oedema and spongiosis (38). In order to elucidate whether CHS-reducing action of dietary FOS is mediated by altered response of T cells that produce inflammatory cytokines, the present study examined the IFN-γ production in CLN cells in *vivo*. Dietary FOS reduced the IFN-γ production in CLN cells in response to hapten restimulation. Because oral administration of *B. pseudolongum* also reduced the IFN-γ production, these results suggest that CHS-reducing action of dietary FOS is associated with reduced response of IFN-γ-producing T cells, which might be mediated, at least in part, by increased proliferation of *B. pseudolongum* in the gastrointestinal tract. In addition, serum levels of IgG2a (i.e. the prototypic antibody of Th1-driven B-cell responses in mice) and IgG1 (i.e. the prototypic antibody of Th2-driven B-cell responses in mice)
were also measured as indicative parameters for Th1/Th2 balance. Dietary supplementation with FOS reduced Th1 response as indicated by reduced IgG2a levels, while administration of \textit{B. pseudolongum} increased Th2 response as indicated by increased IgG1 levels. The data suggest that dietary FOS and administration of \textit{B. pseudolongum} differently influence the Th1/Th2 balance. In other words, other bacterial species than bifidobacteria might contribute to the modulation of cytokine production. Furthermore, the present results are consistent with Chapat \textit{et al.} \cite{34} who reported that hapten-specific IgG2a levels in sera and IFN-\( \gamma \) production in splenic CD8\(^+\) T cells \textit{in vitro} were lower in mice-fed \textit{L. casei} DN-114 001. These findings suggest that probiotics and prebiotics exert immunoregulatory actions influencing hapten-specific T cells in DNFB-induced CHS response in mice.

\textit{de Waard} \textit{et al.} \cite{39,40} reported that administration of \textit{L. casei} Shirota YIT9029 up-regulated Th1-type immune responses including IgG2b (i.e. the prototypic antibody of Th1-driven B-cell responses in rats) production and delayed-type hypersensitivity reaction in response to infection with \textit{Trichinella spiralis} and \textit{Listeria monocytogenes} in rats and mice. Additionally, Vos \textit{et al.} \cite{41} reported that dietary supplementation with a mixture of galacto-oligosaccharide and FOS promoted Th1-type immune responses in a murine vaccination model. In terms of Th1/Th2 balance, these studies are contradictory to Chapat \textit{et al.} \cite{34} and the present results as described above. Thus, probiotics and prebiotics may have both adjuvant properties on immune defence, via up-regulating Th1 responses, and anti-inflammatory actions that prevent CHS responses, via down-regulating Th1 responses. Furthermore, the direction of the immune responses may depend on the bacterial strains relevant to the actions.

However, more recent studies have proposed novel Th cell subsets, i.e. IL-17-producing Th cells (Th17 cells) and regulatory T cells, as key players in the regulation of immune responses and the development of immune diseases\cite{42}. In particular, Nakae \textit{et al.} \cite{43} demonstrated that IL-17-producing T cells rather than IFN-\( \gamma \)-producing Th1 cells are important for the development of CHS in mice. Additionally, He \textit{et al.} \cite{44} showed that IL-17-producing CD8\(^+\) (Tc17) cells, but not IFN-\( \gamma \)-producing Tc1 cells, are a central player in effector functions at the elicitation of CHS responses in mice. In the present study, however, CLN cells produced undetectable levels of IL-17 in response to hapten stimulation \textit{in vitro} (data not shown). In contrast, IL-10 is a cytokine produced by regulatory T cells and reportedly associated with termination of CHS responses by suppressing the response of inflammatory cytokines such as IFN-\( \gamma \)\cite{35}. The present study showed a higher production of IL-10 in CLN cells isolated from FOS(–)BP(+) and FOS(+)BP(+) mice, suggesting that CHS-reducing action of dietary FOS is associated with increased production of IL-10, which might be mediated, at least in part, by increased proliferation of \textit{B. pseudolongum} in the gastrointestinal tract. Thus, modulation of antigen-induced production of inflammatory and regulatory cytokines might be involved in the inhibitory effect of gut microbiota on CHS response, although further studies remain to be performed, especially regarding IL-17, a possible key player in CHS responses.

In conclusion, we propose that \textit{B. pseudolongum} proliferation in the gastrointestinal tract is partially responsible for the reduction in DNFB-induced CHS response by dietary supplementation with FOS in mice.

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