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<td>Author(s)</td>
<td>Sonoyama, Kei; Ogasawara, Toru; Goto, Haruka; Yoshida, Tomoyo; Takemura, Naoki; Fujiwara, Reiko; Watanabe, Jun; Ito, Hiroyuki; Morita, Tatsuya; Tokunaga, Yoshinari; Yanagihara, Tetsuji</td>
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<tr>
<td>Citation</td>
<td>British Journal of Nutrition, 103(2): 218-226</td>
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<tr>
<td>Issue Date</td>
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Comparison of gut microbiota and allergic reactions in BALB/c mice fed different cultivars of rice

Kei Sonoyama1*, Toru Ogasawara2, Haruka Goto2, Tomoyo Yoshida2, Naoki Takekura2, Reiko Fujiwara2, Jun Watanabe3, Hiroyuki Ito4, Tatsuya Morita4, Yoshinari Tokunaga5 and Tetsuji Yanagihara6

1Research Faculty of Agriculture, Hokkaido University, Sapporo, Hokkaido 060-8589, Japan
2Graduate School of Life Science, Hokkaido University, Sapporo, Hokkaido 060-8589, Japan
3Creative Research Initiative ‘Sousei’, Hokkaido University, Sapporo, Hokkaido 001-0021, Japan
4Department of Applied Biological Chemistry, Faculty of Agriculture, Shizuoka University, Shizuoka 422-8529, Japan
5Chinobeikokuten Co., Ltd, Sapporo, Hokkaido 065-0032, Japan
6Hokkaido Prefectural Kamikawa Agricultural Experiment Station, Pippu, Hokkaido 078-0397, Japan

(Received 3 April 2009 – Revised 13 July 2009 – Accepted 13 July 2009 – First published online 22 September 2009)

Our preliminary clinical trial showed that consumption of cooked rice of a Japanese common cultivar Yukihikari improved atopic dermatitis associated with a suspected rice allergy, although the underlying mechanisms remain unclear. We hypothesised that the ameliorating effect of Yukihikari on atopic dermatitis is associated with the gut microbiota. BALB/c mice were fed a synthetic diet supplemented with uncooked and polished white rice powder prepared from one of four different cultivars: Yukihikari, rice A (common rice), rice B (brewery rice) and rice C (waxy rice). Denaturing gradient gel electrophoresis of PCR-amplified 16S rRNA gene fragments showed that the composition of faecal microbiota was different between mice fed Yukihikari and those fed rice A. Analysis of the 16S rRNA clone library and species-specific real-time PCR showed that the abundance of Akkermansia muciniphila, a mucin degrader, tended to be lower in mice fed Yukihikari. The incidence of allergic diarrhoea induced by oral administration of ovalbumin in systemically immunised mice was lower in mice fed Yukihikari, albeit with no difference in serum antibodies specific to ovalbumin. In a separate experiment, serum antibody levels specific to orally administered ovalbumin were lower in mice fed Yukihikari. Additionally, the translocation of horseradish peroxidase in isolated segments of ileum and colon tended to be lower in mice fed Yukihikari, suggesting a reduction in gut permeability in mice fed Yukihikari. These data indicate that changes in the gut microbiota of mice fed Yukihikari could be advantageous in the prevention of food allergy.

Rice: Allergy: Gut microbiota: Mice

Rice seed is a cereal consumed in large quantities around the world and is a staple foodstuff in most countries in South and East Asia. So far, several clinical studies have shown that IgE-mediated allergy against rice was associated with a subset of patients with atopic dermatitis (AD) in Japan1–3. Additionally, since Shibasaki et al.4 first described that a high degree of allergenicity was found in a globulin fraction of rice seed proteins4,5, many studies have reported on rice allergenic proteins5–9. Although avoidance of the intake of allergens is generally one of the emphasised therapeutic suggestions for allergy, it is impractical to strictly remove rice and its products from Asian diets, including that of Japan. Therefore, attempts have been made to eliminate allergenic rice proteins by protease treatment10, high-pressure treatment11 and antisense transgene expression12.

We previously performed a small-scale prospective open clinical trial to examine the effects of consuming Yukihikari, a common rice cultivar developed by the Hokkaido Central Agricultural Experiment Station in Japan, on AD patients with a suspected rice allergy. A total of thirty-eight patients with a mean age of 50.91 (range 0–38) years were enrolled in the trial and fed Yukihikari as their staple food for 4 weeks. The clinical skin score was improved in twenty-six patients (68.4 %), unchanged in eleven patients (29.0 %) and exacerbated in one patient (2.6 %) after consuming Yukihikari (T Yanagihara, unpublished results). However, the contents of the salt-soluble fraction of rice proteins in Yukihikari did not differ from those in other rice cultivars, and the binding capacities of these proteins in Yukihikari to IgE antibodies in the sera of AD patients were also comparable with other cultivars (T Yanagihara, unpublished results). Therefore, not only rigorously controlled clinical trials, but also mechanistic studies are needed to clarify the ameliorating effect of Yukihikari on AD associated with rice allergy.

Abbreviations: AD, atopic dermatitis; DGGE, denaturing gradient gel electrophoresis; HRP, horseradish peroxidase; OVA, ovalbumin; rice A, common rice; rice B, brewery rice; rice C, waxy rice.

*Corresponding author: Dr Kei Sonoyama, fax +81 11 706 2496, email ksnym@chem.agr.hokudai.ac.jp
The commensal microbiota in the intestinal tract plays an important role in the normal development of the immune system\(^{(13)\,\,14}\). Therefore, strategies to manipulate the microbiota have been explored in the prevention of the onset of immune diseases such as allergy. Indeed, several clinical interventions showed that administration of probiotic bacterial strains, such as *Lactobacillus rhamnosus* GG, was beneficial in both the prevention\(^{(15)}\) and treatment\(^{(16)}\) of early allergic diseases. Additionally, prebiotics, such as indigestible oligosaccharides, have also been shown to promote immune health by selectively stimulating the growth and/or activity of beneficial bacteria, such as *bifidobacteria* and *lactobacilli*, in the intestinal tract\(^{(17–20)}\). A mixture of long-chain fructo-oligosaccharide and short-chain galacto-oligosaccharide reportedly reduced the incidence of AD in formula-fed high-amylose maize starch\(^{(21)}\). These findings suggest that dietary resistant starch potentiates the intestinal mucosal barrier. Therefore, an alternation of gut microbiota by consuming Yukihikari may be involved in the AD-reducing effect of Yukihikari.

### 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 (aged 5 weeks) were purchased from Japan SLC (Hamamatsu, Japan) and housed in standard plastic cages in a temperature-controlled (23 ± 2°C) room under a 12 h light–dark cycle. They were allowed free access to food and water. Mice were randomly allocated to four groups and fed a synthetic diet supplemented with uncooked and polished white rice seed powder from the four different cultivars named Yukihikari, rice A, rice B and rice C (Table 1). Rice A, rice B and rice C are cultivars of common rice, brewery rice and waxy rice, respectively.

#### Experimental design for allergic diarrhoea model

After feeding the test diets for 3 weeks, allergic diarrhoea was induced in systemically immunised mice according to Kweon *et al.*\(^{(34)}\). Mice were immunised subcutaneously with 1 mg OVA (grade V; Sigma, St Louis, MO, USA) in 100 μl of complete Freund adjuvant (Difco Laboratories, Detroit, MI, USA). At 2 weeks after immunisation, mice were repeatedly

<table>
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<th>Ingredient</th>
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<tr>
<td>Rice seed powder*</td>
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</tr>
<tr>
<td>Casein</td>
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<tr>
<td>Soyabean oil</td>
<td>70.0</td>
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<td>Cellulose</td>
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<td>Mineral mixture (AIN-93G-MX)</td>
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<td>Vitamin mixture (AIN-93-VX)</td>
<td>10.0</td>
</tr>
<tr>
<td>L-Cystine</td>
<td>3.0</td>
</tr>
<tr>
<td>Choline bitartrate</td>
<td>2.5</td>
</tr>
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</table>

* Each of the four kinds of rice cultivars, i.e. Yukihikari, common rice (rice A), brewery rice (rice B), and waxy rice (rice C), was used individually.
given 10 mg OVA dissolved in 100 µl PBS by intragastric administration every other day. Fresh faeces were obtained before immunisation and subjected to molecular biological analyses of the microbiota as described below. Before immunisation and after the last (10th) oral administration of OVA, blood samples were obtained from the submandibular vein and subjected to ELISA for measurement of OVA-specific antibody titres as described below.

Experimental design for oral sensitisation model

After feeding the test diets for 3 weeks, mice were subjected to oral immunisation with OVA according to Yamaguchi et al. (35). PBS (0.2 ml) containing 0.1 mg OVA was intragastrically administered five times per week for 11 weeks. Blood samples were obtained from the submandibular vein at weekly intervals and subjected to ELISA for measurement of OVA-specific antibody titres as described below. On the last day of the experiment, mice were anaesthetised by diethyl ether and killed by exsanguination from the carotid artery. Following a laparotomy, a 5 cm section of ileum and colon was excised and subjected to an in vitro permeation experiment as described below.

Profile analysis of faecal microbiota by PCR-denaturing gradient gel electrophoresis

DNA was isolated from fresh faeces using a faecal DNA isolation kit (MO Bio Laboratories, Carlsbad, CA, USA) according to the manufacturer’s instructions. DNA samples were used as a template to amplify the 16S rRNA gene fragments with the universal primers U968-GC (CGC CCG GGG GCC GCC CCG GGC GGG GCG GGG GCA CCG GCC CCG GAA GAA CCT TAC) and L1401 (CGG TGT GTA CAA GAC CC) (36). Denaturing gradient gel electrophoresis (DGGE) analysis of the amplicon was performed as previously described (25). Quantity 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 with arithmetic mean clustering method in Quantity One software as previously described (37).

Analysis of the 16S rRNA gene sequences in faecal bacteria

Faecal DNA samples isolated from individual mice as described above were pooled in each group and used as a template to amplify the 16S rRNA gene fragments with the universal primers U968 (AAC GCG AAG AAC CTT AC) and L1401. PCR was performed in a reaction volume of 25 µl that contained 500 mM each of primers, 1 × PCR buffer, 0.2 mM each of dNTPs and 1.25 U of Taq DNA polymerase (Takara, Ohtsu, Japan). The reaction conditions were 94°C for 5 min, followed by twenty cycles of 94°C for 30 s, 56°C for 20 s, and 68°C for 40 s, and a final extension at 68°C for 7 min. The amplicons were purified by a QIAquick PCR purification kit (Qiagen, Tokyo, Japan) and cloned into pGEM-Easy T vectors (Promega, Madison, WI, USA). Transformation was performed with competent Escherichia coli XL-1 Blue cells, and the transformants were spread on Luria–Bertani agar plates supplemented with ampicillin (25 µg/ml), 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (30 µg/ml) and iso-propyl-β-D-thiogalactopyranoside (20 µg/ml) and incubated overnight at 37°C. White colonies were randomly picked from each sample and grown on Luria–Bertani agar. Clones carrying inserts were identified by colony PCR using a Colony PCR M13 set (Nippongene, Tokyo, Japan). Plasmid DNA in the positive clones were amplified for sequencing with an Illustra TempliPhi DNA amplification Kit (GE Healthcare Bioscience, Tokyo, Japan) according to the manufacturer’s instructions. Resultant amplicons were sequenced using an ABI3730XL or ABI3730 (Applied Biosystems, Carlsbad, CA, USA) with M13-F (GTT TTC CCA GTC CAG CAA GAC CC) and L1401 (CGG TGT GTA CAA GAC CC) as a sequencing primer. Sequence data were aligned with the CLUSTAL W package (38) and corrected by manual inspection. The sequences were compared with the public Ribosomal Database Project (http://rdp.cme.msu.edu/). Naive Bayesian rRNA classifier version 2.0 from Ribosomal Database Project was used to assign 16S rRNA gene sequences to the taxonomical hierarchy proposed in Bergey’s Manual of Systematic Bacteriology, release 6.0 (39), with a setting threshold value of 90%. Analysis of the 16S rRNA gene sequences was also performed using the GenBank DNA database and the Basic Local Assignment Search Tool (BLAST) algorithm.

Real-time quantitative PCR for Akkermansia muciniphila in faeces

Abundance of Akkermansia muciniphila in faecal DNA samples isolated from individual mice as described above was determined by real-time quantitative PCR (RT-qPCR) according to Collado et al. (40). In brief, amplification and detection of faecal DNA were performed with the Thermal Cycler Dice Real Time System (Takara). An A. muciniphila species-specific primer pair was 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 (AM1, CAG CAC GTG AAG GTG CGG GAC; AM2, CCT TGC GGT TGG CTT CAG AT) and 1 µl of faecal DNA samples. The reaction conditions were 95°C for 5 min, followed by forty cycles at 95°C for 15 s, 60°C for 40 s, and 72°C for 30 s, and a final extension at 72°C for 5 min. Collado et al. (40) reported that the primer pair is specific for A. muciniphila at 60°C. The fluorescent products were detected at the last step of each cycle. A melting curve analysis was made after amplification to distinguish the targeted PCR product from the non-targeted PCR product. All samples were analysed in duplicate. Using a pooled faecal DNA sample from mice fed rice A as a template, a fragment of 16S rDNA was amplified by PCR with the A. muciniphila species-specific primer pair (AM1 and AM2 as described above). The size of the amplicon, estimated by agarose gel electrophoresis, was identical to the expected size (327 bp) (40), and the sequence was completely identical to A. muciniphila (data not shown). The amplicon was purified and subcloned into a bacterial plasmid as described above. The plasmid DNA was extracted with the QIAprep Spin Miniprep kit (Qiagen) and used as a standard for RT-qPCR.
ELISA for antibody measurements

The serum titres of antibodies specific to OVA were determined by ELISA as previously described (35). In brief, IgG, IgG1 and IgG2a were captured with OVA-coated wells and detected with horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG polyclonal antibody (Zymed Laboratories, South San Francisco, CA, USA), rat anti-mouse IgG1 monoclonal antibody (mAb) (clone LO-MG1-2; Zymed Laboratories) and rat anti-mouse IgG2a mAb (clone LO-MG2a-3; Zymed Laboratories), respectively. IgE was captured with rat anti-mouse IgE mAb (LO-ME-2; Zymed Laboratories) and detected with digoxigenin (DIG)-conjugated OVA followed by HRP-conjugated sheep anti-DIG Fab fragments (Roche Diagnostics, Tokyo, Japan). Pre-immunised serum was used as a negative control. The average extinction in negative control wells, to which three times the standard deviation was added, provided the reference for determination of the titre in the test sera. Antibody titres were expressed as the reciprocal of the last dilution yielding an extinction value higher than the reference value.

Permeation of horseradish peroxidase in the ileum and colon in vitro

Gut permeability was measured using translocation of HRP in isolated segments of ileum and colon, according to Enomoto et al. (41). Briefly, 5 cm segments of ileum and colon were everted, filled with 200 μl Tris buffer (125 mM-NaCl, 10 mM-fructose, 30 mM-2-amino-2-hydroxymethyl-propane-1,3-diol; pH 7.5), and ligated at both ends. The filled gut segments were incubated in Tris buffer containing HRP (40 μg/ml) (Sigma) at 37°C. After 30 min, gut sacs were removed and the contents of each sac were collected. HRP activity in the contents of each sac was determined spectrophotometrically from the rate of oxidation of 3,3′,5,5′-tetramethylbenzidine (Sigma).

Statistical analysis

Results are presented as mean values with their standard errors or as individual values for each mouse. We assessed statistical significance using a P value calculated with the Kruskal–Wallis non-parametric test, while the χ² test was used to compare the frequencies of diarrhoea. Data analysis was performed with StatView for Macintosh (version 5.0; SAS Institute, Inc., Cary, NC, USA). P < 0.05 was considered statistically significant.

Results

Comparison of faecal microbiota in mice fed different rice cultivars

The 16S rRNA gene profiles of the bacterial collections in the faecal samples were generated by PCR coupled with DGGE. Fig. 1 shows the DGGE band profile of all mice subjected to the experiment. The intensity and position of detected bands were subjected to cluster analysis. The dendrogram shows two large clusters of mice fed rice A and those fed the other three cultivars (Fig. 1(B)). In the latter cluster, mice fed Yukihikari constituted a sub-cluster. Thus, it appears that the gut microbiota composition was different between mice fed Yukihikari and those fed rice A. To further investigate the difference, 16S rRNA clone libraries were constructed from DNA samples pooled in each dietary group, and eighty-four and seventy-seven sequences were analysed for the Yukihikari group and rice A group, respectively (Table 2). The phylum Firmicutes was the most abundant taxonomic group in both the Yukihikari and rice A groups (60.9 and 41.6 %, respectively). In the Yukihikari group, the phylum Proteobacteria was the second most predominant group (29.5 %). Although the phylum Verrucomicrobia was the second most abundant group in the rice A group (24.6 %), the Yukihikari group contained small numbers of bacteria.
belonging to the phylum Verrucomicrobia (2·4 %). Because all sequences in the phylum Verrucomicrobia were classified to the genus *Akkermansia* (similarity 100 %), RT-qPCR with a species-specific primer pair was used to estimate the abundance of *A. muciniphila* in the faecal samples of each mouse (Fig. 2). Although there was no significant difference among the groups, the levels tended to be lower in mice fed Yukihikari than those fed rice A, rice B and rice C.

**Comparison of allergic diarrhoea in mice fed different rice cultivars**

Fig. 3 shows the time course of changes in the number of mice affected with diarrhoea. The total number of mice subjected to the experiment was five, six, six and six in the Yukihikari, rice A, rice B and rice C groups, respectively. Diarrhoea was observed after three to five oral administrations of OVA to the systemically immunised mice. Repeated oral administration of OVA in mice without systemic immunisation did not induce any change in the gross appearance of faeces (data not shown). As described by Kweon *et al.* (34), diarrhoea was observed within 30 min after oral OVA administration and the effect decayed within 2 h, suggesting that an acute allergic response had occurred in these mice. In mice fed rice A, rice B and rice C, the incidence of diarrhoea roughly continued to increase by the end of the experiment, whereas mice fed Yukihikari showed a lower incidence of diarrhoea throughout the induction period. In particular, mice fed rice A showed a significantly higher incidence of diarrhoea as compared with mice fed Yukihikari after the 7th and 10th oral administration of OVA. Likewise, the incidence after the 8th administration was significantly higher in mice fed rice B than in those fed Yukihikari.

**Comparison of oral sensitisation in mice fed different rice cultivars**

Fig. 4 shows serum antibody titres specific to OVA before starting oral OVA administration and after the last administration. In both IgG (Fig. 4(A)) and IgE (Fig. 4(B)), the titres tended to be increased by oral administration of OVA. However, there was no significant difference in both IgG and IgE titres among the groups. Mice without systemic immunisation showed undetectable levels of both IgG and IgE antibodies specific to OVA (data not shown).

### Table 2. Taxonomic distribution of 16S rRNA gene sequences in faeces of BALB/c mice fed different cultivars of rice

<table>
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<tr>
<th>Sequences</th>
<th>Yukihikari</th>
<th>Rice A</th>
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<tbody>
<tr>
<td>Phylum Actinobacteria</td>
<td>2 (2·4)</td>
<td>3 (3·9)</td>
</tr>
<tr>
<td>Class Actinobacteria</td>
<td>2 (2·4)</td>
<td>3 (3·9)</td>
</tr>
<tr>
<td>Phylum Bacteroidetes</td>
<td>3 (3·6)</td>
<td>11 (14·3)</td>
</tr>
<tr>
<td>Class Bacteroidetes</td>
<td>3 (3·6)</td>
<td>11 (14·3)</td>
</tr>
<tr>
<td>Phylum Firmicutes</td>
<td>51 (60·9)</td>
<td>32 (41·6)</td>
</tr>
<tr>
<td>Class Bacilli</td>
<td>2 (2·4)</td>
<td>12 (15·6)</td>
</tr>
<tr>
<td>Class Clostridia</td>
<td>45 (53·7)</td>
<td>12 (15·6)</td>
</tr>
<tr>
<td>Unclassified Firmicutes</td>
<td>4 (4·8)</td>
<td>8 (10·4)</td>
</tr>
<tr>
<td>Phylum Proteobacteria</td>
<td>25 (29·5)</td>
<td>8 (10·4)</td>
</tr>
<tr>
<td>Class Delta proteobacteria</td>
<td>20 (23·9)</td>
<td>5 (6·5)</td>
</tr>
<tr>
<td>Class Epsilon proteobacteria</td>
<td>5 (5·6)</td>
<td>3 (3·9)</td>
</tr>
<tr>
<td>Phylum Verrucomicrobia</td>
<td>2 (2·4)</td>
<td>19 (24·6)</td>
</tr>
<tr>
<td>Class Verrucomicrobiae</td>
<td>2 (2·4)</td>
<td>19 (24·6)</td>
</tr>
<tr>
<td>Unclassified bacteria</td>
<td>1 (1·2)</td>
<td>4 (5·2)</td>
</tr>
<tr>
<td>Total</td>
<td>84 (100·0)</td>
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Rice A, common rice.
in mice fed rice B were intermediate. In particular, there was a significant difference between mice fed Yukihikari and those fed rice C at 6 weeks after starting OVA administration. Additionally, the levels were significantly lower in mice fed Yukihikari than in those fed rice C and rice A at 7 weeks after starting OVA administration. After the last oral administration of OVA, the anti-OVA IgE titres tended to be lower in mice fed Yukihikari and rice B than in those fed rice A and

![Fig. 4. Serum IgG (A) and IgE (B) antibody titres specific to ovalbumin (OVA) in BALB/c mice fed different rice cultivars (common rice (rice A); brewery rice (rice B); waxy rice (rice C); Yukihikari rice) in the allergic diarrhoea experiment. (–), Values of individual mice before immunisation; (●), values of individual mice after the last oral administration of OVA; (—), mean values.](image)

![Fig. 5. (A) Changes in time course of serum antibody titres specific to ovalbumin (OVA) in BALB/c mice fed different rice cultivars (rice A; –●–); brewery rice (rice B; –×–); waxy rice (rice C; –○–); Yukihikari rice (–○○–) in the oral sensitisation experiment. Values are means, with standard errors represented by vertical bars. **a,b** Mean values with unlike letters were significantly different (P<0.05). (B) Serum IgE, (C) serum IgG1 and (D) serum IgG2a titres specific to OVA. (●), Values of individual mice; (—), mean values.](image)
Fig. 6. In vitro gut permeability in BALB/c mice fed different rice cultivars: common rice (rice A; □); brewery rice (rice B; △); waxy rice (rice C; ■); Yukihikari rice (□). Gut permeability was estimated using translocation of horseradish peroxidase (HRP) in isolated segments of ileum and colon. Values are means, with standard errors represented by vertical bars.

Consumption of different rice cultivars modulates the gut microbiota in mice, even though this effect might not be attributed to resistant starch. Therefore, it remains to be elucidated which rice constituents modulate the gut microbiota. Additionally, we should be cautious in extrapolating such mice data to humans because of difference in the composition of gut microbiota between mice and humans. Furthermore, mice were fed the uncooked rice seed powder in the present study, while humans usually consume cooked rice which naturally contains smaller amounts of resistant starch as compared with uncooked rice. Therefore, further studies are needed to clarify the relationship between rice consumption and gut microbiota.

Although the present study showed that the phylum Firmicutes and the phylum Proteobacteria in faeces were more abundant in mice fed Yukihikari than in mice fed rice A, it remains unclear whether these changes are related to allergic reactions and/or immune responses. However, it is noteworthy that the abundance of A. muciniphila tended to be lower in faeces of mice fed Yukihikari than in those fed the three other cultivars, because A. muciniphila is a mucin-degrading bacterium in the intestine. Mucins are high-molecular mass glycoproteins and the main constituents of the mucus covering the epithelial surface of the gastrointestinal tract, and thus contribute to the epithelial protective barrier against pathogenic micro-organisms, as well as chemical, physical or enzymic damage. Therefore, degradation of intestinal mucins possibly results in reduced barrier function, which in turn may cause increased uptake of allergenic proteins in the gastrointestinal tract. The present study showed that the translocation of HRP in isolated segments of ileum and colon tended to be lower in mice fed Yukihikari than in those fed the other three cultivars, suggesting that lower abundance of A. muciniphila in the gut of mice fed Yukihikari are accompanied by higher integrity of intestinal barrier function and lower intestinal permeation of food antigens.

Additionally, the present study initially assumed that resistant starch in Yukihikari potentiates intestinal barrier function, because Toden et al. and our previous study showed that consumption of resistant starch potentiates intestinal barrier function as a result of an increased mucus layer in rats. However, the resistant starch contents in the rice seed powders in the present study (approximately 0.1–0.2 %) were much lower as compared with those in high-amylose maize starch used in Toden et al. and our previous study (approximately 30–40 %). Therefore, lower intestinal permeability in mice fed Yukihikari may be attributed to not resistant starch but rather lower abundance of A. muciniphila.

Given that the gut microbiota influences normal development of the immune system, and in turn affects the development of allergic diseases, the ameliorating effect of Yukihikari on AD might be not limited to rice allergy. Indeed, the present study showed that the incidence of OVA-induced allergic diarrhea was lower in mice fed Yukihikari than in those fed rice A, rice B and rice C. The results suggest that consumption of different rice cultivars modulates the gut microbiota in mice, even though this effect might not be attributed to resistant starch. Therefore, it remains to be elucidated which rice constituents modulate the gut microbiota. Additionally, we should be cautious in extrapolating such mice data to humans because of difference in the composition of gut microbiota between mice and humans. Furthermore, mice were fed the uncooked rice seed powder in the present study, while humans usually consume cooked rice which naturally contains smaller amounts of resistant starch as compared with uncooked rice. Therefore, further studies are needed to clarify the relationship between rice consumption and gut microbiota.
with OVA. Additionally, the present study revealed that the increase in serum antibody titres specific to orally administered OVA was lower in mice fed Yukihikari than in those fed the other three cultivars. The data suggest that consumption of Yukihikari protects against oral sensitisation in mice. In our preliminary experiments, however, there were no differences in contact hypersensitivity induced by topical application of 2,4-dinitrofluorobenzene in BALB/c and C57BL/6 mice fed the four cultivars (K Sonoyama, S Honma, T Ogasawara, N Sasajima, Y Tokunaga and T Yanagihara, unpublished results). These findings suggest that consumption of Yukihikari might affect the intestinal uptake of orally administered antigen, but not systemic immune responses. Thus, it is possible that a lower incidence of OVA-induced allergic diarrhoea and lower antibody responses against orally administered OVA are attributed to higher integrity of intestinal barrier function, which is associated with a lower abundance of A. muciniphila. In the present study, however, we observed no significant correlation between the faecal excretions of A. muciniphila and the frequency of allergic diarrhoea in individual mice (data not shown). Therefore, further studies are needed to clarify the relationship between A. muciniphila in the gut and allergic reactions. Alternatively, the reduction of antibody responses against orally administered OVA in mice fed Yukihikari might be attributed, in part, to the induction of oral tolerance. Oral tolerance is characterised by a state of systemic immune non-responsiveness towards antigens present in the gastrointestinal tract(3), and this mechanism presumably prevents the development of food allergy. As several studies have reported that the gut microbiota plays a crucial role in the induction of oral tolerance(44–46), it is likely that the gut microbiota in mice fed Yukihikari might be advantageous in the induction of tolerance against orally administered OVA. Therefore, we are now conducting experiments that investigate the effect of different rice cultivars on the induction of oral tolerance in mice.

Taken together, the present study indicated that the composition of gut microbiota was modulated by the consumption of different rice cultivars, and that mice fed Yukihikari showed a lower incidence of OVA-induced allergic diarrhoea and lower antibody responses against orally administered OVA in mice. These results suggest that the gut microbiota in mice fed Yukihikari is beneficial in the prevention of food allergy. In particular, it is interesting to note that lower abundance of the mucin-degrader A. muciniphila in the gastrointestinal tract is associated with the consumption of Yukihikari in mice. In addition to rigorously controlled clinical trials, however, mechanistic studies are required to further elucidate the allergy-preventing and/or -ameliorating effect of Yukihikari.

Acknowledgements
The present study was partly supported by Special Coordination Funds for Promoting Science and Technology, by a Grant-in-Aid for Scientific Research from The Ministry of Education, Science, Sports and Culture of Japan, and by The Iijima Memorial Foundation.

K. S. and T. Yanagihara were involved in designing the study. K. S. wrote the manuscript. T. O., H. I. and T. M. were involved in the animal experiments. H. G. and T. Yoshida performed the in vitro permeation experiment. N. T., R. F. and J. W. performed the molecular biological analyses of gut microbiota. Y. T. was involved in the preparation of rice seed powder.

None of the authors has a conflict of interest.

References


