Human Gut Bacterial Communities Are Altered by Addition of Cruciferous Vegetables to a Controlled Fruit- and Vegetable-Free Diet1–3

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Abstract
In the human gut, commensal bacteria metabolize food components that typically serve as energy sources. These components have the potential to influence gut bacterial community composition. Cruciferous vegetables, such as broccoli and cabbage, contain distinctive compounds that can be utilized by gut bacteria. For example, glucosinolates can be hydrolyzed by certain bacteria, and dietary fibers can be fermented by a range of species. We hypothesized that cruciferous vegetable consumption would alter growth of certain bacteria, thereby altering bacterial community composition. We tested this hypothesis in a randomized, crossover, controlled feeding study. Fecal samples were collected from 17 participants at the end of 2 14-d intake periods: a low-phytochemical, low-fiber basal diet (i.e. refined grains without fruits or vegetables) and a high (“double”) cruciferous vegetable diet [basal diet + 14 g cruciferous vegetables/(kg body weight×d)]. Fecal bacterial composition was analyzed by the terminal restriction fragment length polymorphism (tRFLP) method using the bacterial 16S ribosomal RNA gene and nucleotide sequencing. Using blocked multi-response permutation procedures analysis, we found that overall bacterial community composition differed between the 2 consumption periods (d = 0.603; P = 0.011). The bacterial community response to cruciferous vegetables was individual-specific, as revealed by nonmetric multidimensional scaling ordination analysis. Specific tRFLP fragments that characterized each of the diets were identified using indicator species analysis. Putative species corresponding to these fragments were identified through gene sequencing as Eubacterium hallii, Phascolarctobacterium faecium, Burkholderiales spp., Alistipes putredinis, and Eggerthella spp. In conclusion, human gut bacterial community composition was altered by cruciferous vegetable consumption, which could ultimately influence gut metabolism of bioactive food components and host exposure to these compounds. J. Nutr. doi: 10.3945/jn.109.108191.

Introduction
Epidemiologic studies have shown that there is an inverse association between the consumption of cruciferous vegetables and risk of cancer, especially cancers of the digestive tract, bladder, prostate, and lung (1–3). In a meta-analysis, Kohlmeier et al. (4) concluded that cruciferous vegetables confer a protective benefit against cancer after controlling for the effects of overall vegetable intake. At least part of the protective effect of cruciferous vegetables is hypothesized to be due to their relatively high content of fiber and phytochemicals such as glucosinolates. Dietary fiber can be fermented by gut bacteria to yield SCFA and other metabolites that suppress the growth of tumor cells (5,6). Isothiocyanates (ITC),6 one group of hydrolysis products of glucosinolates, have been shown to have anticarcinogenic properties (7–9). The enzyme myrosinase (EC 3.2.1.147), which is present in Brassica plant cells, catalyzes the hydrolysis of glucosinolates to ITC. Plant myrosinases can be deactivated by cooking; however, certain bacteria residing in the human gut have myrosinase-like activity and can metabolize glucosinolates. Thus, humans depend on gut bacteria to convert glucosinolates to ITC when cooked cruciferous vegetables are consumed. The importance of gut bacteria in producing ITC was elucidated in a previous feeding study that showed that urinary ITC excretion after cruciferous vegetable consumption decreased significantly when participants were pretreated with

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3 Supplemental Figure 1 is available with the online posting of this paper at jn.nutrition.org.
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antibiotics and bowel cleansing (10). In in vitro incubations of fecal or bacterial samples with glucosinolates, several gut bacteria species have been found to degrade glucosinolates (11–17). Thus, not only the amount of cruciferous vegetables consumed but also gut bacterial composition may determine exposure to bioactive ITC and ultimately affect cancer risk.

More than 800 species of bacteria reside in the human gut and 30–40 species dominate this community, comprising up to 99% of the total population (18). Additionally, individuals have their own distinct combination of predominant and subdominant bacteria species. This interindividual difference in community composition may ultimately contribute to differences in metabolism of dietary constituents and health status of the host. Several community fingerprinting techniques have been established to describe this interindividual difference in gut bacterial community profiles, because >70% of gut bacteria species are not cultivable (19). Most of these techniques are based on the sequence variation of the bacterial 16S ribosomal RNA (rRNA) gene, which is a phylogenetic marker (20). Terminal restriction fragment length polymorphism (tRFLP) analysis offers a rapid overview of interindividual differences in gut microbial communities (21). The method takes advantage of sequence variation of the 16S rRNA gene to generate sequence fragments. The pattern of the number and size of the sequence fragments is used to characterize the compositional differences in gut bacterial communities. Bacteria in fecal samples have long been used as a surrogate to study gut bacterial community, because the variation in gut bacterial community within a person has been shown to be less than the variation between individuals, although community composition differences do exist along the digestive tract and between different environments (e.g. between intestinal mucosa and lumen) (22).

Intervention studies have shown that diet can influence gut bacterial composition (23–28). A recent study demonstrated that Brussels sprouts, a cruciferous vegetable, altered the diversity and metabolic activities of gut bacteria in human fecal bacteria-associated rats (29). However, to our knowledge, the effect of cruciferous vegetable intake on gut bacterial composition in humans has not been studied to date. We hypothesized that cruciferous vegetables would have a selective effect on certain gut bacteria involved in metabolizing constituents of cruciferous vegetables (e.g. fiber, glucosinolates, etc.). The purpose of this study was to examine the extent to which cruciferous vegetable intake alters the gut bacterial composition in a randomized, crossover study of cruciferous vegetable supplementation.

### Materials and Methods

#### Human subjects.

This study was ancillary to a randomized, crossover, controlled feeding study, which was designed to test the response of selected biotransformation enzymes to cruciferous vegetable supplementation (30). Participants were healthy, nonsmoking men and women, 20–40 y old, and recruited on the basis of GSTM1, GSTT1, and CYP1A2 genotypes. There was an extensive list of exclusion criteria that determined participant eligibility for the parent study (30). Those relevant to the current study included: medical history of gastrointestinal disorders; known allergies/intolerances to any foods used in the feeding trial; antibiotic use within the past 3 mo; current use of prescription and over-the-counter medications; and severe and frequent constipation necessitating treatment by a health care professional and/or frequent medication. Demographic information [age, gender, race, body weight, and height] was collected and genotypes were measured at screening. All activities were approved by the Institutional Review Board of the Fred Hutchinson Cancer Research Center, and informed, written consent was obtained from the study participants.

#### Dietary intervention.

As part of the parent study, participants consumed 4 controlled diets in a randomized, crossover design: 1) a low-phytochemical basal diet devoid of fruits and vegetables and whole-grain, high-fiber foods [major food items consumed included bagels, pasta, white rice, ready-to-eat cereal, dairy, etc.; menu details in (31)]; 2) a “single-cruciferous” diet [i.e. basal diet + 7 g cruciferous vegetables/(kg body weight-d)]; 3) a “double-cruciferous” diet [i.e. basal diet + 14 g cruciferous vegetables/(kg body weight-d)]; and 4) a mixed diet [i.e. basal diet + 7 g cruciferous vegetables/(kg body weight-d) and 4 g apiaceous vegetables/(kg body weight-d)]. The supplemented cruciferous vegetables included broccoli (45.7% of the total cruciferous vegetables), cauliflower (34.6%), green and red cabbage (15.7%), and radish sprouts (4%). Cabbage and radish sprouts were provided raw whereas broccoli and cauliflower were fully cooked (one-half steamed, pureed, and prepared as a soup and the other one-half microwaved). We provided all food items to the participants during the diet periods and instructed them not to consume any other foods or beverages, except water. All diets were designed to provide similar proportions of macronutrients, except dietary fibers, by adjusting components of the basal diet to accommodate the addition of vegetables. Each diet period lasted 14 d. There was at least a 21-d washout period between each diet period.

#### Fecal sample collection.

Fecal samples were collected from 17 participants at 1 time point at the end of the basal and double-cruciferous vegetable diet periods. Participants were provided with fecal collection tubes with scoop in the lid (76 × 20 mm; Sarstedt) containing 5 mL RNAlater (Ambion). They were instructed to collect 2 pea-sized aliquots of stool immediately at the time of defecation and place the stool into the collection tubes and mix well by shaking. The samples were delivered to the laboratory within 24 h and stored at −80°C.

#### Urinary ITC analysis.

Twenty-four-hour urine collections were obtained from participants on d 13 of each diet period. The urinary total ITC excretion (estimated as total dithiocarbamates) was determined by HPLC as described previously (32).

#### Total fecal bacterial DNA extraction.

Fecal samples in RNAlater were homogenized using an OMNI tissue homogenizer 115 and aliquoted into 300-μL aliquots. Fecal bacterial genomic DNA was extracted using a QIAamp DNA stool minikit (Qiagen) with 1 min of bead beating (21).

#### tRFLP.

The tRFLP analysis was conducted using a modification of methods described previously (21). The bacterial 16S rRNA gene was amplified using a fluorescent-labeled primer. PCR products were purified and then treated with 0.025 mmol/L of each dNTP and 2 U of Klenow (exo−) (New England BioLabs) to fill up the 5′-overhangs at 37°C for 30 min (33). The Klenow enzyme was deactivated at 70°C for 10 min and the DNA was digested overnight at 37°C with 5 U Alu I in a 20-μL reaction volume. Digested DNA (20 ng) from each sample was used for tRFLP analysis. Fragment analysis was conducted using capillary electrophoresis on an ABI 3100 (Applied Biosystems) at the Genomics Shared Resource of the Fred Hutchinson Cancer Research Center. GeneScan ROX-labeled GS500 (Applied Biosystems) was used as the internal size standard.

The tRFLP profiles were analyzed by DAx software (Van Mierlo Software Consultancy). Fragments that differed ≥2 base pairs in size were considered identical and were clustered together, being within the error of the instrument for fragment-size determination. Total peak area was summed across all fragments in each profile; peaks <1% of the total peak area were excluded as noise.

#### Bacterial 16S rRNA gene clone library.

A bacterial 16S rRNA gene clone library was established based on the bacterial genomic DNA from 1 participant during the double-cruciferous vegetable intake period to relate the tRFLP fragments to their taxonomic information. This participant was chosen because the fecal bacterial community as examined by tRFLP analysis showed a substantial difference between the 2 controlled diets and included 3 of the 4 tRFLP fragments that were significantly associated with cruciferous vegetable consumption. The library was created using Invitrogen TOPO TA cloning kit (Invitrogen).
following the manufacturer's protocol. A total of 96 white bacterial colonies were picked randomly and grown in Luria-Bertani broth (Invitrogen). The inserted 16S rRNA gene sequences were partially sequenced at the Marine Biological Laboratory (Woods Hole, MA) using an ABI 373 sequencer (Applied Biosystems), dye terminator chemistry, and the 700r primer (34).

16S rRNA sequence alignment, BLAST, and phylogenetic inference. 16S rRNA gene sequences were edited and assembled into consensus sequences using PHRED and PHRAP software packages (CodonCode) based on PHRAP quality scores of 20. The final data set containing 79 sequences was compared with the GenBank sequences using the program BLAST (35). Consensus sequences were aligned to the 16S rRNA sequence database in the ARB software package (36). Phylogenetic relationships of bacterial 16S rRNA gene sequences (based on the Escherichia coli 16S rRNA gene nucleotide position 68–644; the rest of the positions were masked) were inferred using the neighbor joining method with Kimura 2-parameter genetic distances (2:1 transition-transversion ratio) with bootstrap proportions calculated using PAUP 4.0 from 100 resampled data sets on the aligned sequences (37). Selected bacteria species were included in the phylogenetic tree for reference. These sequences were further digested in silico by Fragment Finder (38) to match the specifically sized rRFLP fragments.

Statistical analysis. Paired t tests were used to compare any differences in urinary ITC excretion and dietary fiber intake for the participants between the basal and double-crusiferous vegetable diet periods. Peak area data from tRFLP profiles were exported from DAx. For each tRFLP fragment identified, the arcsin transformed square root of the peak area ratio (i.e. \( \sin^{-1}\sqrt{P}; P = \text{individual peak area}/\text{total peak area} \)) was calculated and used for further statistical analysis. The mean and SD of transformed \( P \) for individual peaks of each triplicate extraction were calculated after the binning process. Nonmetric multidimensional scaling ordination (NMDS) analysis, blocked multi-response permutation procedures (MRBP), indicator species analysis (ISA), and cluster analysis were performed based on PHRED quality scores of 20. The results from the Monte Carlo test showed that the solutions for each axis differed from solutions found by chance (\( P = 0.02 \)). The final solution showed that 3 axes explained a cumulative variation in the data set of 82%, with 45, 15, and 22% explained by axes 1, 2, and 3, respectively. Pearson correlations of each ordination axis and selected anthropometry and dietary variables (age, body weight, BMI, total cruciferous vegetable consumption per day, daily fiber intake, and urinary total ITC/24 h) were not significant. NMDS analysis of tRFLP profiles showed differences in bacterial community structure among individuals and within individuals for the 2 dietary periods (Supplemental Fig. 1). Two patterns emerged from the data. First, each participants had a unique gut bacterial community pattern. Most triplicate points originating from 1 stool sample clustered together in the plot, which indicated good reproducibility of the technique. Second, within a person, the community structure

### Results

Demographic and dietary information. The age of the 17 participants (12 women and 5 men) was 28.5 ± 4.8 y. There were 6 Asians, 10 Caucasians, and 1 Asian-Caucasian participant. Body weight and BMI at baseline were 66.0 ± 12.6 kg and 23.2 ± 2.9 kg/m², respectively. Because cruciferous vegetables were fed on the basis of body weight, cruciferous vegetable intake during the double-crusiferous vegetable diet period was 819 ± 144 g/d and ranged from 660 to 1080 g/d. The diets were designed so that daily energy, carbohydrate, fat, and protein intakes were similar during the basal and the double-crusiferous vegetable diet periods; however, fiber intake was higher during the latter (\( P < 0.01 \)) (Table 1).

#### Urinary ITC excretion after dietary intervention.

Daily total urinary ITC excretions on d 13 of the basal diet and double-crusiferous vegetable diet periods were 0.546 ± 1.41 and 200 ± 148 \( \mu \)mol/24 h, respectively (\( P < 0.01 \)). There was substantial individual variation in ITC excretion after cruciferous vegetable consumption (range, 1.1–378 \( \mu \)mol/24 h).

#### NMS analysis of bacterial community structure. Using NMDS analysis of the tRFLP profiles in the fecal samples after 500 iterations, the stress of the final solution was 14.9 and stable. The results from the Monte Carlo test showed that the solutions for each axis differed from solutions found by chance (\( P = 0.02 \)). The final solution showed that 3 axes explained a cumulative variation in the data set of 82%, with 45, 15, and 22% explained by axes 1, 2, and 3, respectively. Pearson correlations of each ordination axis and selected anthropometry and dietary variables (age, body weight, BMI, total cruciferous vegetable consumed per day, daily fiber intake, and urinary total ITC/24 h) were not significant. NMDS analysis of tRFLP profiles showed differences in bacterial community structure among individuals and within individuals for the 2 dietary periods (Supplemental Fig. 1). Two patterns emerged from the data. First, each participants had a unique gut bacterial community pattern. Most triplicate points originating from 1 stool sample clustered together in the plot, which indicated good reproducibility of the technique. Second, within a person, the community structure

### Table 1

<table>
<thead>
<tr>
<th>Macronutrient</th>
<th>Basal diet</th>
<th>Double-crusiferous vegetable diet</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total energy, kJ/d</td>
<td>9577 ± 2138</td>
<td>9556 ± 1858</td>
</tr>
<tr>
<td>Carbohydrate, g/d</td>
<td>319 ± 75</td>
<td>330 ± 68</td>
</tr>
<tr>
<td>Fat, g/d</td>
<td>74 ± 19</td>
<td>72 ± 14</td>
</tr>
<tr>
<td>Protein, g/d</td>
<td>87 ± 22</td>
<td>93 ± 17</td>
</tr>
<tr>
<td>Fiber, g/d</td>
<td>8.9 ± 2.3</td>
<td>28.6 ± 5.8*</td>
</tr>
</tbody>
</table>

1 Data are means ± SD, n = 17. *Different from basal diet, \( P < 0.01 \).
shifted noticeably after cruciferous vegetable consumption. Additionally, the bacterial community structure differences between the basal diet and double-cruciferous vegetable diet periods varied from individual to individual.

**MRBP, cluster analysis, and ISA.** MRBP analysis showed that there was a difference between the gut bacterial community structure in an individual consuming the basal diet compared with consuming the double-cruciferous vegetable diet in all 17 participants (δ = 0.603; P = 0.011).

Cluster analysis showed that whereas triplicates of the same sample always clustered together with >90% similarity, the samples from the basal and the double-cruciferous vegetable diet periods from the same participant did not always cluster closely. Gut bacterial community structure of the same participant consuming the basal and the double-cruciferous vegetable diets varied considerably (Fig. 1).

The ISA suggested that there were 5 tRFLP fragments significantly associated with the diet periods (Table 2). Four of them were significantly associated with cruciferous vegetable consumption and one was associated with the basal diet. Through the in silico digestion of the sequenced bacterial 16S rRNA genes, we identified the putative taxonomic affiliation and closest relatives of these tRFLP fragments (Table 2).

**Phylogenetic analysis of the gut bacterial 16S rRNA gene clone library.** Sequence data obtained from the fecal bacterial 16S rRNA gene clone library have been submitted to the GenBank databases under accession numbers FJ227596 to FJ227683. Members of the Firmicutes, Bacteroidetes, and Actinobacteria were represented in this clone library (Fig. 2). A large proportion (74%) were in the Clostridia class, with 54% in Cluster XIVa and 19% in Cluster IV. Another 6% of the clones belonged to the class Bacilli of the Firmicutes. The other 19% of the clones were Bacteroidetes, whereas the Actinobacteria clone represented only 1% of the clones in the library.

**Discussion**

In this study, we examined the effects of a high-cruciferous vegetable diet and a diet devoid of fruits and vegetables on the gut bacterial community profile as part of a randomized, crossover feeding study. We showed that: 1) each participant had a unique gut bacterial composition even when all individuals received the same controlled diet; 2) the gut bacterial composition differed significantly when participants consumed a basal diet devoid of fruits and vegetables compared with that diet supplemented with cruciferous vegetables; 3) specific bacteria species were associated with cruciferous vegetable intake; and 4) the response of the gut bacterial community to cruciferous vegetable consumption was unique for each individual but not directly related to the amount of cruciferous vegetables consumed.

Generally, the gut bacterial community of healthy adults is relatively stable with minor fluctuation over a short period of time. However, short-term dietary shifts, such as those found in controlled dietary interventions, have been shown to alter this community. Using MRBP, we showed that there was a significant difference in the overall gut bacterial community structure between the basal diet and the cruciferous vegetable diet periods in the 17 participants. Cruciferous

**Table 2** tRFLP fragments that are significantly associated with the 2 controlled diets in the ISA1

<table>
<thead>
<tr>
<th>tRFLP fragments, base pair</th>
<th>Indicator value2</th>
<th>Associated diet</th>
<th>Taxonomic affiliation3</th>
<th>Clone name</th>
<th>Closest relatives</th>
<th>Similarity to closest relatives</th>
</tr>
</thead>
<tbody>
<tr>
<td>159</td>
<td>40.1</td>
<td>Double4</td>
<td>Firmicutes</td>
<td>E06, F05, G01</td>
<td>Eubacterium hallii</td>
<td>98%5</td>
</tr>
<tr>
<td>219</td>
<td>17.6</td>
<td>Double</td>
<td>Firmicutes</td>
<td>C04, C08</td>
<td>Phascolarctobacterium faecium</td>
<td>99%</td>
</tr>
<tr>
<td>222</td>
<td>38.8</td>
<td>Basal4</td>
<td>Proteobacteria</td>
<td>N</td>
<td>Burkholderiales</td>
<td>N</td>
</tr>
<tr>
<td>241</td>
<td>48.3</td>
<td>Double</td>
<td>Bacteroidetes</td>
<td>B03</td>
<td>Alistipes putredinis</td>
<td>98%</td>
</tr>
<tr>
<td>468</td>
<td>23.5</td>
<td>Double</td>
<td>Actinobacteria</td>
<td>N</td>
<td>Eggerthella spp.</td>
<td>N</td>
</tr>
</tbody>
</table>

1 ISA showed that 5 tRFLP fragments were significantly associated with either basal or double-cruciferous diet (P < 0.01). P value of each fragment was calculated from Monte Carlo tests of significance using 1000 randomizations. Type I error (0.01) indicates the proportion of these 1000 times an indicator value was equal or larger than the indicator value from the actual data.

2 Indicator values showed how well the specific fragments pointed to a particular dietary period within the data set. The values range from zero (no indication) to 100 (perfect indication).

3 Taxonomic affiliations of the bacteria corresponding to some of these tRFLP fragments were identified through the 96 sequenced clones and from other established clone libraries.

4 Basal, Basal diet; Double, double-cruciferous vegetable diet.

5 Percentages of sequence similarity between the cloned 16S rRNA gene sequences and those of their closest relatives using BLAST.

6 N, No match found in the 96 sequenced clones of this study; fragment was matched with sequences from other studies.
Bifidobacterium spp. and Enterococcus faecalis, including E. coli in in vitro studies to be utilized by several gut bacteria species, isolated from feces (45). Glucosinolates have been shown to these specific components but was most likely due to the growth of certain bacteria in the human gut bacterial community and ultimately modify the community composition.

FIGURE 2 Phylogenetic analysis of the 16S rRNA gene amplified from the fecal bacterial community of 1 participant after cruciferous vegetable intake. Selected bacteria species were included in the phylogenetic tree for reference. Bootstrap values > 95 are indicated on the tree and the number of clones is shown in parentheses if there is more than one. *, Actinobacteria group.
associated with the community changes during dietary interventions. Additionally, after combining the clone library data and in silico digestion predictions of tRFLP fragments based on sequence data, we were able to link specific candidate bacteria species to specific tRFLP fragments (Table 2). Although 16S rRNA gene sequencing can be considered the gold standard to determine bacterial taxonomy, it is very costly, which limits its application in large-scale epidemiologic studies. tRFLP analysis applied in this study offered rapid yet reliable data for a picture of overall community composition in response to cruciferous vegetable consumption.

There are also limitations in this study. The small sample size limited our power to stratify by demographic or genetic factors in statistical tests. Each participant consumed different amounts of cruciferous vegetables based on their body weight, an approach that was used to normalize intakes for body weight. Therefore, the intake of fiber and glucosinolates varied from person to person during the double-cruciferous vegetable diet period. Nonetheless, we observed significant overall effects of the controlled diets despite not detecting significant correlations among the NMS axes and daily cruciferous vegetable intake, fiber intake, or urinary ITC excretion when participants consumed the cruciferous diet. Because many factors influence glucosinolate metabolism (e.g. cooking method, gut transit time, ITC absorption rate, further gut bacterial degradation of ITC, GST genotype, etc.), the lack of an association between the NMS axes and urinary ITC excretion is not surprising. Each diet period lasted 2 wk; therefore, the bacterial community changes detected reflected short-term effects of intensive cruciferous vegetable consumption. Similarly, other studies have shown that 1–4 wk of dietary intervention was sufficient to elicit a gut microbiota shift (23–28). However, whether this community shift is steady for a longer period of time is unknown. There are also limitations of the tRFLP technique in analyzing bacterial community structure, which has been discussed previously (21). We had only 96 rRNA genes sequenced, which were derived from 1 fecal sample after cruciferous vegetable intake. Considering the hundreds of bacteria species residing in the human gut, it was possible that only the dominant species in the community were selected for the phylogenetic analysis, plus species presented in other participants might not exist in this person. This could limit our ability to confirm the relationship between tRFLP fragments and bacteria species.

In summary, we showed that there was a significant difference in gut bacterial community after 14 d of consuming a cruciferous vegetable-rich diet compared with a fruit- and vegetable-free basal diet. This bacterial community difference was unique to individuals. We also identified several putative gut bacteria species that were associated with the specific diets, offering additional evidence that gut bacteria can be modified rapidly by dietary components. This study also showed that tRFLP analysis is a useful approach for evaluating gut bacterial community composition and to monitor community structure changes due to dietary intervention. Further studies are needed to identify the in vivo gut bacteria response to specific cruciferous vegetable components, such as glucosinolates.

Literature Cited


