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MASSEY UNIVERSITY  
TE KUNENGA KI PŪREHUROA  
UNIVERSITY OF NEW ZEALAND

Plant & Food  
**RESEARCH**  
RANGAHAU AHUMĀRA KAI



# The influence of habitual dietary intake on the responsiveness of the gut microbiota to a dietary intervention

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A thesis presented in partial fulfilment of the requirements for the degree

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Doctor of Philosophy

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Genelle Rose Healey

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## Abstract

Preliminary evidence suggests that inter-individual variability in gut microbiota response to a dietary intervention is influenced by baseline gut microbiota composition. Differing habitual dietary intakes lead to distinctions in baseline gut microbiota composition making it plausible that habitual dietary intake may also influence gut microbiota response. Prior to conducting this research no studies had been undertaken to determine whether habitual dietary intake has an impact on gut microbiota responsiveness. Therefore, the aim of this research was to investigate the influence habitual dietary intake has on gut microbiota response to a dietary intervention.

Initially, secondary data analysis was conducted to determine whether there was any support for the hypothesis that individuals with differing habitual dietary intakes would have gut microbiota that respond in a distinctive manner to a dietary intervention. The secondary data analysis results demonstrated that dietary groups rich in dietary fibre had the greatest impact on gut microbiota responsiveness. An *in vitro* three-stage colonic model system study was conducted to determine whether media with differing fermentable carbohydrate (i.e. dietary fibre) contents influenced gut microbiota response to an inulin-type fructan prebiotic. It was demonstrated that differing prebiotic driven changes in organic acids and bacterial taxa occurred between the low (LFC) and high fermentable carbohydrate (HFC) content media. The results of the secondary data analysis and *in vitro* study provided evidence to suggest that a human intervention study was warranted. A randomised, double-blind, placebo-controlled, cross-over, human intervention study in 34 healthy participants was undertaken to determine whether habitual dietary fibre intake influenced gut microbiota response to an inulin-type fructan prebiotic. The results of the human intervention study demonstrated that the low habitual

dietary fibre (LDF) group harboured gut microbiota that were less responsive to the inulin-type fructan prebiotic than the high habitual dietary fibre (HDF) group.

Future studies which aim to modulate the gut microbiota via dietary change or to determine the prebiotic potential of a novel fermentable substrate should take habitual dietary fibre intakes into consideration when recruiting participants or analysing the data. This will help reduce the confounding influence of inter-individual variability in gut microbiota responsiveness and ensure the true efficacy of a dietary intervention is demonstrated.

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## Table of Contents

Chapter 1 Introduction .....	2
1.1 Aim and objectives.....	2
1.1.1 Aim.....	2
1.1.2 Primary objectives.....	2
1.1.3 Secondary objectives.....	2
1.2 Hypotheses .....	4
1.2.1 Primary hypotheses .....	4
1.2.2 Secondary hypotheses .....	4
1.3 Thesis structure .....	5
Chapter 2 Literature review .....	8
2.1 Abstract .....	8
2.2 Introduction .....	9
2.3. “Healthy” gut microbiota .....	11
2.4 Metabolic functionality of the gut microbiota .....	14
2.5 Analysing gut microbiota communities .....	16
2.5.1 Culture-based methods.....	16
2.5.2 Culture-independent methods .....	16
2.6 Factors that influence gut microbiota composition.....	19
2.6.1 Genetics.....	19
2.6.2 Life stage and gender .....	19



2.6.3 Antibiotics .....	20
2.6.4 Human disease .....	21
2.6.5 Dietary intake .....	28
2.7 In vitro human GI tract model systems .....	39
2.8 The influence of gut microbiota on appetite regulation .....	43
2.9 Inter-individual variability in responsiveness to dietary interventions .....	46
2.9.1 Gut microbiota response to dietary change .....	46
2.9.2 Host response to dietary change .....	57
2.10 Conclusion .....	64
2.11 References .....	66
Chapter 3 Secondary data analysis .....	88
3.1 Abstract .....	88
3.2 Introduction .....	90
3.3 Methods .....	92
3.3.1 Intervention .....	92
3.3.2 Participants .....	92
3.3.3 Dietary intake analysis .....	94
3.3.4 Dietary groupings .....	94
3.3.5 Bacterial DNA extraction .....	95
3.3.6 16S rRNA bacterial gene sequencing .....	96
3.3.7 Bioinformatics .....	97

3.3.8 Statistics .....	97
3.4 Results .....	98
3.4.1 Differences in baseline gut microbiota .....	98
3.4.2 Differences in gut microbiota response to high-dose Actazin™ .....	99
3.5 Discussion .....	105
3.6 References .....	107
Chapter 4 In vitro three-stage colonic model system.....	112
4.1 Abstract .....	112
4.2 Introduction .....	113
4.3 Methods.....	117
4.3.1 In vitro three-stage continuous colonic model system.....	117
4.3.2 Faecal donors .....	118
4.3.3 Dietary intake analysis .....	120
4.3.4 Media vessel sampling .....	120
4.3.5 Bacterial DNA extraction.....	120
4.3.6 16S rRNA bacterial gene sequencing and bioinformatics .....	121
4.3.7 Quantitative PCR .....	122
4.3.8 Organic acid analysis .....	123
4.3.9 Statistical analysis .....	124
4.4 Results .....	125
4.4.1 Donor characteristics and dietary intake .....	125

4.4.2 Baseline differences in gut microbiota.....	125
4.4.3 Media vessel contamination.....	126
4.4.4 Prebiotic driven changes in gut microbiota and organic acid concentrations .....	127
4.4.5 Individual donor pre-intervention differences in gut microbiota and organic acid concentrations between media types .....	131
4.4.6 Individual donor prebiotic driven changes in gut microbiota and organic acid concentrations .....	133
4.5 Discussion .....	137
4.6 References .....	141
Chapter 5 Validation study .....	148
5.1 Abstract .....	148
5.2 Introduction.....	149
5.3 Methods.....	150
5.3.1 Subjects .....	150
5.3.2 Development of the DFI-FFQ.....	150
5.3.3 DFI-FFQ Scoring Sheet .....	151
5.3.4 Dietary Fibre Classification .....	151
5.3.5 Dietary Assessment Method Used for Comparison.....	152
5.3.6 Statistical analysis.....	152
5.4 Results.....	153
5.5 Discussion .....	155

5.6 References .....	158
Chapter 6 Study Protocol .....	162
6.1 Abstract .....	162
6.2 Introduction .....	164
6.3 Methods and Analysis .....	168
6.3.1 Study design .....	168
6.3.2 Primary objective .....	168
6.3.3 Secondary objectives .....	168
6.3.4 Primary hypothesis .....	169
6.3.5 Secondary hypotheses .....	169
6.3.6 Study setting .....	169
6.3.7 Exclusion criteria .....	169
6.3.8 Study duration .....	170
6.3.9 Sample size calculations .....	171
6.3.10 Participant recruitment .....	172
6.3.11 Participant screening .....	172
6.3.12 Interventions .....	174
6.3.13 Outcome measures .....	177
6.3.14 Statistical analysis .....	178
6.4 Ethics and Dissemination .....	180
6.4.1 Research ethics approval .....	180

6.4.2 Dissemination.....	180
6.5 Discussion.....	181
6.6 References.....	182
Chapter 7 Human intervention study.....	188
7.1 Abstract.....	188
7.2 Introduction.....	189
7.3 Methods.....	191
7.3.1 Participants.....	191
7.3.2 Interventions.....	193
7.3.3 Study design.....	193
7.3.4 Dietary intake analysis.....	195
7.3.5 Appetite rating analysis.....	196
7.3.6 Bacterial DNA extraction.....	196
7.3.7 16S rRNA bacterial gene sequencing.....	196
7.3.8 Quantitative PCR.....	198
7.3.9 Faecal short-chain fatty acid analysis.....	199
7.3.10 Sample size calculations.....	200
7.3.11 Statistical analysis.....	200
7.4 Results.....	202
7.4.1 Participants.....	202
7.4.2 Baseline dietary intake and participant characteristic differences.....	202

7.4.3 Baseline SCFA concentration and gut microbiota differences .....	205
7.4.4 Gastrointestinal symptoms .....	206
7.4.5 Prebiotic driven changes in appetite ratings.....	206
7.4.6 Prebiotic driven changes in SCFA concentrations and gut microbiota.....	207
7.4.7 Correlation between baseline bifidobacteria concentrations and change in bifidobacteria.....	212
7.4.8 Bifidogenic response during the prebiotic intervention phase .....	213
7.5 Discussion .....	218
7.6 References .....	224
Chapter 8 Discussion, conclusion and areas of future research .....	230
8.1 Discussion .....	230
8.2 Conclusion .....	235
8.3 Areas of future research .....	236
8.4 References .....	238

## List of Appendices

Appendix 2-1. Figure permission for figure 2-1 .....	240
Appendix 2-2. Figure permission for figure 2-2 .....	242
Appendix 2-3. Figure permission for figure 2-4 .....	244
Appendix 4-1. Media rationale .....	246
Appendix 4-2. <i>In vitro</i> three-stage colonic model system publication .....	256
Appendix 4-3. Statement of contribution to doctoral thesis containing publications..	268
Appendix 4-4. Media recipes table .....	269
Appendix 4-5. Medium contamination table .....	270
Appendix 5-1. Validation study protocol.....	271
Appendix 5-2. Validation study publication .....	277
Appendix 5-3. Statement of contribution to doctoral thesis containing publications..	284
Appendix 5-4. Validation study advertising .....	285
Appendix 5-5. Validation study participant information .....	287
Appendix 5-6. Validation study consent form .....	291
Appendix 5-7. Validation study screening questionnaire .....	293
Appendix 5-8. Validation study SurveyMonkey DFI-FFQ.....	297
Appendix 5-9. Validation study DFI-FFQ scoring sheet.....	300
Appendix 5-10. Validation study Bland-Altman plots .....	301
Appendix 6-1. Study protocol publication .....	302
Appendix 6-2. Statement of contribution to doctoral thesis containing publications..	311
Appendix 7-1. Human intervention study advertisement .....	312
Appendix 7-2. Human intervention study consent form.....	313
Appendix 7-3. Human intervention study information sheet.....	314
Appendix 7-4. Human intervention study screening questionnaire.....	322

Appendix 7-5. Human intervention study participant questionnaire .....	328
Appendix 7-6. Human intervention 3-day diet record and appetite questionnaire .....	333
Appendix 7-7. Human intervention study fructan intake food frequency questionnaire .....	360
Appendix 7-8. Human intervention daily diary .....	363
Appendix 7-9. Human intervention faecal sample collection instructions .....	385
Appendix 7-10. Dietary intake comparison table .....	387
Appendix 7-11. Alpha diversity table .....	388
Appendix 7-12. Gastrointestinal symptom table.....	389
Appendix 7-13. Appetite rating table- Whole cohort.....	390
Appendix 7-14. Appetite rating table- Low dietary fibre .....	391
Appendix 7-15. Appetite rating table- High dietary fibre.....	392
Appendix 7-16. Washout phase table.....	393
Appendix 7-17. Placebo intervention phase table.....	394
Appendix 7-18. PICRUSSt analysis table.....	395
Appendix 7-19. Change in <i>Bifidobacterium</i> table.....	396
Appendix 7-20. Poster presented at conference .....	397



## List of Tables

Table 2-1. The observed differences in baseline gut microbiota composition and function and/or dietary intake and host characteristics between responders (R) and non-responders (NR) in studies which have demonstrated differing gut microbiota responses to a dietary intervention .....	54
Table 2-2. The observed differences in baseline gut microbiota composition and function and/or dietary intake and host characteristics between responders (R) and non-responders (NR) in studies which have demonstrated differing host responses to a dietary intervention .....	62
Table 3-1. Comparison of baseline bacterial taxa (% relative abundance) and change in bacterial taxa after the dietary intervention between constipated and healthy participants <sup>1</sup> .....	93
Table 3-2. Mean nutrient and food group intakes of the entire cohort, and for low, moderate and high consumers compared to mean intakes in New Zealand and the Ministry of Health Food and Nutrition guidelines .....	95
Table 3-3. Dietary groups that had significantly different baseline bacterial taxa (% relative abundance) between low versus high, or low versus moderate versus high consumers <sup>1</sup> .....	98
Table 3-4. Dietary groups with significantly different baseline alpha diversity (PD <sub>whole tree</sub> index) between low versus moderate versus high consumers <sup>1</sup> .....	99
Table 3-5. Dietary groups that had bacterial taxa (% relative abundance) that changed in response to the high-dose Actazin™ in a significantly different way between low versus high, or low versus moderate versus high consumers <sup>1</sup> .....	99
Table 4-1. Donor characteristics, nutrient intakes and food group serves .....	126

Table 4-2. Pre- and post-intervention organic acid concentrations, phylum and genus level relative abundance for vessels 1, 2 and 3 of the high fermentable carbohydrate medium (LFC) gut models (A) and low fermentable carbohydrate medium (HFC) gut models (B) <sup>1</sup> .....	129
Table 4-3. Pre-intervention differences in organic acid concentrations, phylum and genus level relative abundance between donors in vessel 1 (V1), 2 (V2) and 3 (V3) for the low and high fermentable carbohydrate medium.....	130
Table 5-1. The dietary fibre intake cut-offs used to classify individuals as low, moderate and high dietary fibre consumers .....	152
Table 5-2. Characteristics, dietary fibre intakes and classifications for the study participants .....	153
Table 5-3. Comparison in dietary fibre classification (low, moderate and high) between the comprehensive nutrition assessment questionnaire (CNAQ) and the dietary fibre intake food frequency questionnaire (DFI-FFQ) .....	154
Table 5-4. Correlation and test–retest repeatability statistical analysis .....	154
Table 7-1. Baseline dietary intake differences between the low and high dietary fibre groups <sup>1</sup> .....	203
Table 7-2. Participant characteristic comparison between the low and high dietary fibre groups <sup>1</sup> .....	204
Table 7-3. Baseline differences in short-chain fatty acid concentrations and bacterial taxa between low and high dietary fibre groups <sup>1</sup> .....	205
Table 7-4. Short-chain fatty acid concentration and bacterial taxa changes during the placebo and prebiotic intervention phases in the whole cohort <sup>1</sup> .....	207
Table 7-5. Short-chain fatty acid concentration and bacterial taxa changes during the placebo and prebiotic intervention phases in the low dietary fibre group <sup>1</sup> .....	208

Table 7-6. Short-chain fatty acid concentration and bacterial taxa changes during the placebo and prebiotic intervention phases in the high dietary fibre group<sup>1</sup> ..... 210

Table 7-7. Short-chain fatty acid concentrations and bacterial taxa before and after the prebiotic intervention in low and high dietary fibre groups<sup>1</sup> ..... 211

Table 7-8. Participant characteristic comparison between the bifidogenic responders and non-responders<sup>1</sup> ..... 214

Table 7-9. Baseline dietary intake differences between bifidogenic responders and non-responders<sup>1</sup> ..... 215

Table 7-10. Baseline differences in short-chain fatty acid concentrations and bacterial taxa between bifidogenic responders and non-responders<sup>1</sup> ..... 217

## List of Figures

Figure 2-1. Representation of the microbiota content (cells/g) of a healthy human GI tract including the pH, nutrient utilisation and fermentation products associated with each section (figure from reference <sup>35</sup> ).....	11
Figure 2-2. An overview of the microbial groups (indicated in grey) and by-products formed as a result of dietary polysaccharide fermentation within the human GI tract (figure from reference <sup>55</sup> ) .....	15
Figure 2-3. In vitro three-stage continuous colonic model system .....	41
Figure 2-4. Hypothetical response in relative abundance of a number of gut microbiota genera (represented by vertical bars) to differences in habitual dietary fibre intake (A+C) and the addition of a prebiotic in the presence of the differing habitual dietary fibre intakes (B+D). This figure depicts that the abundance of certain bacterial genera will significantly differ between individuals with low versus high dietary fibre intakes (the ▒ bars indicate a significant difference in bacterial relative abundance between low and high dietary fibre consumers) (A+C). The figure also illustrates that certain bacterial genera may respond in a distinctive manner to a prebiotic as a result of differing baseline gut microbiota profiles and habitual dietary fibre intakes (B+D). Hypothetically individuals with low habitual dietary fibre intakes (B) may have a higher proportion of gut microbiota genera which significantly change in relative abundance in response to a prebiotic (the ▒ bars indicate a significant increase in relative abundance from baseline and the ▒ bars indicate a significant decrease from baseline) when compared to individuals with high habitual dietary fibre intakes (D) (adapted from reference <sup>201</sup> )....	52
Figure 3-1. Bacterial taxa that responded in a significantly different way after the high-dose Actazin™ for the low- versus high-dietary fibre consumers.....	101

Figure 3-2. Bacterial taxa that responded in a significantly different way after the high-dose Actazin™ for the low- versus high-wholegrain consumers ..... 101

Figure 3-3. Bacterial taxa that responded in a significantly different way after the high-dose Actazin™ for the low- versus high-vegetable consumers ..... 102

Figure 3-4. Bacterial taxa that responded in a significantly different way after the high-dose Actazin™ for the low- versus high-plant protein consumers ..... 103

Figure 3-5. Bacterial taxa that responded in a significantly different way after the high-dose Actazin™ between low- versus moderate- versus high-Carbohydrate:Protein ratio consumers. Bars with differing superscripts are significantly different from each other (within each bacterial taxa) ..... 104

Figure 4-1. Diagram of the study design of the in vitro three-stage continuous colonic model system (“gut model”). Fresh faeces from each donor was used to inoculate each gut model twice through-out the experiment. The gut models were cleaned and autoclaved between each media type run. Samples were taken at baseline (after inoculation), pre-intervention (after steady state 1 [SS1] was reached) and post-intervention (after steady state 2 [SS2] was reached) for the high fermentable carbohydrate medium (HF) gut models and low fermentable carbohydrate medium (LF) gut models. D: day. .... 119

Figure 4-2. Principal co-ordinate analysis graphs (unweighted UniFrac distances) illustrating the differences and similarities in the bacterial communities between donors and media types at baseline (post inoculation) (A) and within vessel 1 comparing the pre- and post-intervention samples (B). LFC data from donor 2 was not included in Figure 4-2B. Samples that cluster together are more similar in bacterial composition and samples that are further apart have a more distinctive bacterial composition. Key: Donor 1 ★ , Donor 2 ▲ and Donor 3 ● . High fermentable carbohydrate medium ○ and low

fermentable carbohydrate medium □ . Black shapes- pre-intervention samples (or baseline samples in Figure 4-2A), Grey shapes- post-intervention samples. PC: principal co-ordinate.....	127
Figure 4-3. Stacked column graphs illustrating the inter- and intra-donor differences in pre-intervention organic acid concentrations (A), phylum level relative abundance (B) and genus level relative abundance (C) (16S rRNA bacterial gene sequencing) for each vessel (1, 2 and 3) and media type (high fermentable carbohydrate medium [HF] and low fermentable carbohydrate medium [LF]).	132
Figure 4-4. Bubble plot illustrating the distinctive changes in organic acid concentrations and bacterial relative abundance that occurred between donors (1, 2 and 3) and media types (high fermentable carbohydrate medium [HF] and low fermentable carbohydrate medium [LF]) in vessel 1, vessel 2 and vessel 3 in response to the prebiotic. The black circles represent increases in organic acid concentrations and bacterial relative abundance. The white circles represent decreases in organic acid concentrations and bacterial relative abundance. The X represents a less than $\pm 1 \mu\text{mol/mL}$ change in organic acid concentrations or a less than $\pm 1\%$ change in bacterial relative abundance. LF data from donor 2 was not included.....	135
Figure 4-5. Baseline, pre- and post-intervention bifidobacteria concentrations (gene copies/mL) for each vessel (1, 2 and 3), media type (high fermentable carbohydrate medium [HF] and low fermentable carbohydrate medium [LF]) and donor (1, 2 and 3). Bifidobacteria concentrations analysed using qPCR. LF data from donor 2 was not included.....	136

Figure 6-1. Flow diagram summarising the four separate study phases including the two possible intervention orders. The intervention orders may not be as described within the figure as they are blinded to the lead researcher, analysts and participants..... 171

Figure 6-2. Participant flow through the study including measurements, questionnaires and samples taken at each Human Nutrition Research Unit visit. BodPod: air displacement plethysmography, FI-FFQ: fructan intake food frequency questionnaire, IP: intervention phase..... 176

Figure 7-1. Consolidated Standards of Reporting Trials (CONSORT) flow diagram. 192

Figure 7-2. Participant flow through the study including measurements, questionnaires and samples taken at each research unit visit. IP: intervention phase, Fructan-FFQ: fructan food frequency questionnaire, BodPod: air displacement plethysmography .. 194

Figure 7-3. Baseline differences in the average number of food group serves consumed per day (as assessed using four 3-day diet records) between the low and high dietary fibre groups. Changes that are significantly different ( $p < 0.05$ ) between dietary fibre groups are indicated with an asterisks (\*) as analysed by a Mann-Whitney test. .... 204

Figure 7-4. Genus level changes after the prebiotic intervention between the low and high dietary fibre groups. A significant change ( $p < 0.05$ ) is indicated with an asterisk (\*) as analysed by a two-way repeated-measures ANOVA (blocked by participant) and least significant difference test ..... 212

Figure 7-5. The correlation between baseline bifidobacteria concentrations (Before [log]) and change in bifidobacteria concentrations (After over before [log]) during the prebiotic intervention between the low and high dietary fibre groups. Bifidobacteria concentrations were determined using quantitative PCR. P values  $<0.05$  are considered significant as analysed by a Pearson’s rank correlation test ..... 213

Figure 7-6. Average inulin (A) and oligofructose (OF; B) intake differences between bifidogenic responders and non-responders.....216

Figure 7-7. The correlation between baseline bifidobacteria concentrations (Before [log]) and change in bifidobacteria concentrations (After over before [log]) during the prebiotic intervention between bifidogenic responders and non-responders. Bifidobacteria concentrations were determined using quantitative PCR. P values <0.05 are considered significant as analysed by a Pearson’s rank correlation test .....217



## List of Abbreviations

AA	African Americans
AC	African children
AMER	Typical American style dietary pattern
ANOVA	Analysis of variance
BMI	Body mass index
BodPod	Air displacement plethysmography
CD	Crohn's disease
CHO	Carbohydrate
CNAQ	Comprehensive nutrition assessment questionnaire
CRON	Plant-rich, calorie-restricted diet with optimal nutrient composition
D	Donor
DFI-FFQ	Dietary fibre intake short food frequency questionnaire
DNA	Deoxyribonucleic acid
EC	European children
EI:BMR	Energy intake: basal metabolic rate
FFQ	Food frequency questionnaire
FI-FFQ	Fructan intake food frequency questionnaire
FISH	Fluorescence <i>in situ</i> hybridisation
FMP	Fermented milk product
FODMAP	Fermentable Oligosaccharides, Disaccharides, Monosaccharides and Polyols
GC	Gas chromatography
GI	Gastrointestinal
GLP-1	Glucagon-like peptide-1
HFC	High fermentable carbohydrate medium
HDF	High habitual dietary fibre
HMP	Human Microbiome Project
HNRU	Human Nutrition Research Unit
IBD	Inflammatory bowel disease
IBS	Irritable bowel syndrome
IP1	Intervention phase 1

IP2	Intervention phase 2
LFC	Low fermentable carbohydrate medium
LDF	Low habitual dietary fibre
LPS	Lipopolysaccharide
MetaHIT	Metagenomics of the Human Intestinal Tract
MGC	Microbial gene count
MoH	Ministry of Health
NA	Native Africans
NCD	Non-communicable disease
NS	Not specified
NZ	New Zealand
OTU	Operational taxonomic units
PANDASeq	Paired-end assembler for DNA sequencing
PCR	Polymerase chain reaction
PICRUSt	Phylogenetic investigation of communities by reconstruction of unobserved states
PS	Prudent style
PYY	Peptide YY
QIIME	Quantitative Insights Into Microbial Ecology
qPCR	Quantitative real-time polymerase chain reaction
SCFA	Short-chain fatty acid
SD	Standard deviation
T2DM	Type 2 diabetes mellitus
TE	Total energy
UC	Ulcerative colitis
VAS	Visual analogue scales
WS	Western style

