

Supplemental Material

Table 1. Comparison of gut microbiota and SCFA changes in humans after feeding interventions with specific foods.

Substrate	Study design*	No of individuals	Microbiota technique	Microbiota changes	SCFA changes	Reference
Maize-based whole grain breakfast cereals	<ul style="list-style-type: none"> • Healthy • 3 weeks • Cross-over 	32 (women and men)	FISH	<ul style="list-style-type: none"> ↑ <i>Bifidobacterium</i> spp. <i>Atobobium cluster</i> spp. 	No changes in lactic, acetic, propionic, butyric, valeric acid and branched-chain fatty acids	(1)
Whole grain wheat cereals or wheat bran	<ul style="list-style-type: none"> • Healthy • 3 weeks (wash-out 2 weeks) • Cross-over 	31 (16 women, 15 men)	FISH	<ul style="list-style-type: none"> ↑ <i>Bifidobacteria</i> (whole grain) <i>Lactobacilli/Enterococci</i> (both products) <i>Clostridium</i> (wheat bran) 	No changes in acetic, propionic or caproic acid	(2)
Whole grain barley, brown rice or mix	<ul style="list-style-type: none"> • Healthy • 4 weeks (wash-out 2 weeks) • Cross-over 	28 (17 women 11 men)	pyrosequencing	<ul style="list-style-type: none"> ↑ <i>Firmincutes</i> (all treatments) <i>Blautia, Roseburia, Bifidobacterium, Dialister</i> (whole grain barley) ↓ <i>Bacteroidetes</i> (all treatments) <i>Bacteroides</i> (mix) <i>Odoribacter</i> (whole grain barley) 	n.d.	(3)
Rye bread	<ul style="list-style-type: none"> • Metabolic syndrome • 12 weeks • Parallel 	51 (26 women, 25 men)	HITChip and qPCR	<ul style="list-style-type: none"> ↓ <i>Bryantella formatexigans</i> 	n.d.	(4)
Wild blueberry drink	<ul style="list-style-type: none"> • Healthy • 6 weeks (wash-out 6 weeks) • Cross-over 	20 men	Real-time PCR	<ul style="list-style-type: none"> ↑ <i>Bifidobacterium</i> spp., <i>Lactobacillus acidophilus</i> 	n.d.	(5)
Wild blueberry drink	<ul style="list-style-type: none"> • Healthy • 6 weeks (wash-out 6 weeks) • Cross-over 	20 men	Real-time qPCR	<ul style="list-style-type: none"> ↑ <i>B. longum</i> subsp. <i>infantis</i> 	n.d.	(6)
Red wine, dealcoholized red wine, gin	<ul style="list-style-type: none"> • Healthy • 20 days (no wash-out between intervention periods) • Cross-over 	10 men	PCR-DGGE Sequencing qPCR	<ul style="list-style-type: none"> ↑ <i>Bacteroidetes, Firmicutes, E.rectale group, Bacteroides, B. uniformis Prevotella</i> (red wine) <i>Fusobacteria, Proteobacteria, Bifidobacterium, Eggerthella lenta Enterococcus</i>(both wines) 	n.d.	(7)

Almonds and pistachios (2 studies)	<ul style="list-style-type: none"> • Healthy • 18 days (wash-out 2 weeks) • Cross-over 	18	DGGE, qPCR, pyrosequencing	<ul style="list-style-type: none"> ↑ Butyrate-producing bacteria (Pistachio) ↓ Lactic acid bacteria (pistachio) 	n.d.	(8)
almonds and almond peel Positive control: Fructo-oligosaccharides	<ul style="list-style-type: none"> • Healthy • 6 weeks • Parallel 	48 (24 women, 24 men)	Culturing	<ul style="list-style-type: none"> ↑ <i>Bifidobacterium</i> spp. <i>Lactobacillus</i> spp. ↓ <i>Clostridium perfringens</i> (FO and almond peel) 	n.d.	(9)
Apple	<ul style="list-style-type: none"> • Healthy • 2 weeks • Compared with baseline 	8 men	Culturing	<ul style="list-style-type: none"> ↑ <i>Bifidobacteria</i> ↓ <i>Clostridia</i> 	↑ Acetic acid (tendency)	(10)
Banana or banana drink (Control: water)	<ul style="list-style-type: none"> • Healthy • 60 days • Parallel 	34 women	Culturing	↑ <i>Bifidobacterium</i> (banana)	No changes in acetic, propionic, butyric acids and branched-chain fatty acids	(11)
Chickpea or raffinose	<ul style="list-style-type: none"> • Healthy • 3 weeks • Cross-over 	12 (5 women, 7 men)	T-RFLP, qPCR	↓ <i>Clostridium</i> cluster XI, <i>Clostridium</i> cluster I/II	No changes in, acetic, propionic, butyric, valeric, caproic, heptanoic, lactic acid, branched-chain fatty acids	(12)
Soy milk low-glycinin soy milk, bovine milk	<ul style="list-style-type: none"> • Overweight • 3 month • parallel 	64 men	qPCR, bTEFAP .	<ul style="list-style-type: none"> ↑ <i>Bacteroid-Prevotella</i>(low glycinin soy milk), <i>Lactobacillus</i> (bovine milk) ↓ <i>Bifidobacterium</i> (both soymilks) 	n.d.	(13)

n.d.: not determined

Studies which are marked with blue have been excluded from the review due to flaws in study design or due to a targeted approach.

Table 2. Comparison of gut microbiota and SCFA changes in humans after intake of dietary fibres with varying chemical characteristics.

Substrate	Study design*	No of individuals	Microbiota technique	Microbiota changes	SCFA changes	Reference
Resistant starch (type 3)	<ul style="list-style-type: none"> Overweight 10 weeks Cross-over 	14 men	Denaturing-gradient gel electrophoresis (DGGE)	↑ <i>Ruminococcus bromii</i> <i>Oscillibacter</i> (unclassified species) <i>Eubacterium rectale</i>	n.d.	(14)
Resistant starch (type 2 and 4)	<ul style="list-style-type: none"> Healthy 3 weeks Cross-over 	10	16S rRNA pyrosequencing	RS4: ↑ <i>Bifidobacterium adoloscentis</i> <i>Parabacteroides distasonis</i> RS2: ↑ <i>Ruminococcus bromii</i> <i>Eubacterium rectale</i>	n.d.	(15)
Inulin and partially hydrolyzed guar gum	<ul style="list-style-type: none"> Constipated 3 weeks Parallel 	60 women	RT-PCR	↓ <i>Clostridium</i>	No differences	(16)
Inulin and fructo-oligosaccharide	<ul style="list-style-type: none"> Radiotherapy patients 29 days Parallel 	31 women	Culturing	↑ <i>Lactobacillus</i> <i>Bifidobacterium</i>	n.d.	(17)
Inulin and oligofructose	<ul style="list-style-type: none"> Obese 3 months Parallel 	30 women	Microarray and qPCR	↑ <i>Faecalibacterium prausnitzii</i> <i>Bifidobacterium</i> ↓ <i>Bacteroides intestinalis</i> <i>Bacteroides vulgatus</i> <i>Propionibacterium</i>	n.d.	(18)
Long-chain inulin	<ul style="list-style-type: none"> Healthy 3 weeks (3 weeks wash-out) Cross-over 	32 18 women, 14 men	FISH and RT-PCR	↑ <i>Bifidobacterium</i> Lactobacilli/Enterococci <i>Atopobium</i> ↓ <i>Bacteroides/Prevotella</i>	No differences	(19)

Fructo-oligosaccharides and pea fibre	<ul style="list-style-type: none"> • Healthy • 14 days (wash-out 6 weeks) • Cross-over 	10 (6 women, 4 men)	FISH	↑ <i>Bifidobacterium</i>	n.d.	(20)
Xylo-oligosaccharides and inulin	<ul style="list-style-type: none"> • Healthy • 4 weeks • Cross-over 	60 (34 women, 26 men)	qPCR	↑ <i>Bifidobacterium</i>	Butyrate	(21)
Galacto-oligosaccharides	<ul style="list-style-type: none"> • Overweight • 12 weeks • Cross-over 	45 (29 women, 16 men)	FISH	↑ <i>Bifidobacterium</i> ↓ <i>Bacteroides spp.</i> <i>Clostridium histolyticum</i>	n.d.	(22)
Galacto-oligosaccharides, fructo-oligosaccharides	<ul style="list-style-type: none"> • Healthy infants • 4 months • Parallel 	224	FISH	↑ <i>Bifidobacteria</i>	n.d.	(23)
Polydextrose and soluble corn fibre	<ul style="list-style-type: none"> • Healthy • 21 days • Parallel 	20 men	16S rRNA pyrosequencing	↑ <i>Clostridiaceae</i> <i>Faecalibacterium prausnitzii</i> <i>Phasolarcibacterium</i> <i>Dialister</i> <i>Lactobacillus (corn fibre)</i> ↓ <i>Eubacteriaceae</i> <i>Actinobacteria</i>	n.d.	(24)
Polydextrose	<ul style="list-style-type: none"> • Healthy • 3 weeks • Parallel 	31 (16 women, 15 men)	qPCR	↑ <i>Ruminococcus intestinalis</i> <i>Clostridium clusters I, II and IV</i> ↓ <i>Lactobacillus/Enterococcus</i>	n.d.	(25)

Resistant maltodextrin	<ul style="list-style-type: none"> • Healthy • 24 days/treatment, 3 treatments • Cross-over 	15 men	16S rRNA pyrosequencing	<ul style="list-style-type: none"> ↑ <i>Ruminococcus</i> <i>Eubacterium</i> <i>Lachnospiraceae</i> <i>Bacteroides</i> <i>Holdemania</i> <i>Faecalibacterium</i> 		(26)
Arabinoxylans	<ul style="list-style-type: none"> • Healthy • 21 days/treatment, 5 treatments (21 days wash-out) • Cross-over 	40 (20 women, 20 men)	FISH	<ul style="list-style-type: none"> ↑ <i>Eubacterium rectale</i> <i>Roseburia/Eubacterium</i> <i>Faecalibacterium prausnitzii</i> <i>Bacteroides</i> 	<ul style="list-style-type: none"> ↑ Butyrate ↓ Iso-butyrate Iso-valerate 	(27)
Arabinoxylans	<ul style="list-style-type: none"> • Healthy • 3 weeks (4 weeks wash-out) • Cross-over 	20 (14 women, 6 men)	RT-PCR	<ul style="list-style-type: none"> ↑ <i>Bifidobacterium</i> 		(28)

n.d. not determined

Studies which are marked with blue have been excluded from the review due to flaws in study design or due to a targeted approach.

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