

Supplementary Table 1 Randomised trials of miscellaneous dietary fibres

Author/Year	Intervention	Metagenomic approach	Microbiota	Faecal SCFA concentration
Ampatzoglou et.al., 2015 [1]	15g/d Arabinogalactan product or Maltodextrin (n=30)	16S rRNA amplicon	Decreased alpha diversity. No change to beta diversity. Significant decrease in faecal Firmicutes to Bacteroidetes ratio	No change
An et. al., 2019 [2]	8g/d polydextrose powder or maltodextrin (n=31)	FISH and qPCR	significant increase in Ruminococcus intestinalis/bacteria of the Clostridium clusters I, II and IV. decrease in Lactobacillus-Enterococcus group.	No change
Elison et.al., 2016 [3]	HMOs	16S rRNA amplicon	increase in bifidobacteria	No change
Brandl et.al., 2020 [4]	15g/day of Galacto Oligosaccharides	qPCR 16S rRNA amplicon sequencing	Increased <i>bifidobacteria</i> ($P<0.001$); decreased microbial diversity ($p=0.023$)	No change

	or Maltodextrin (n=24)			
Vuholm et.al., 2017 [5]	14g/day oligofructose or maltodextrin (n=37)	16S rRNA amplicon sequencing	reduced <i>Bifidobacterium</i> ; Increased abundance of <i>Ruminococcaceae</i> in maltodextrin group; decreased <i>Lachnospiraceae</i> in the oligofructose group	No change
David et. al.,[6]	10,15, 20g/d of resistant dextrin or glucose (n=48)	RT-qPCR	increased <i>Bacteroides</i> . Inhibition of <i>Clostridium</i> <i>perfringens</i>	No change
Wu et. al., 2011 [7]	15 or 25 g Resistant Maltodextrin or maltodextrin (n= 51)	qPCR	bifidobacteria higher (P = .008)	n/a
FDA, 2018[8]	Three type IV resistant starchs	16S rRNA amplicon sequencing	Decreased alpha diversity Beta diversity increased	No change

	(RS4s) or digestible corn starch (n=40)		Dose dependent with plateau at 35g	
Phelps et.al., 1965 [9]	40g high-amylase resistant starch or digestible starch (n=19)	16S rRNA amplicon sequencing	not changed at the phylum level; increase in <i>Ruminococcaceae</i> UCG- 005; Bacteroides decreased	Increased Acetate
Alfa et.al, 2018 [10]	30g/d of resistant starch or placebo (n=42)	16S rRNA amplicon sequencing	Decreased alpha diversity and Firmicutes/Bacteroidetes ratio. Increased Bifidobacterium	No change
Finegold et.al, 2014 [11]	XOS in capsule form or placebo capsules	Culture based analysis	Increased bifidobacterium, anaerobes, bacteroides fragilis	No changes
Lecerf et. al, 2012 [12]	XOS/XOS Inulin mixture or maltodextrin as placebo (n=60)	qPCR	Increased bifidobacterium and moderately increased lactobacillus	Increased total SCFA

Supplementary Table 2 Randomised trials of miscellaneous fibre mixtures

Rrf.	Intervention	Method of analysis	Microbiota	Faecal SCFA concentration
Clarke et. al, 2016 [13]	5g/day thrice a day of beta 2 -1 fructan or maltodextrin (n=30)	qPCR	Increased bifidobacterium	Increased SCFAs
Healey et.al, 2016 [14]	16g/day of inulin type fructan or maltodextrin (n=34)	16S rRNA amplicon sequencing	Alpha diversity – decreased Shannon index, increased Increased bifidobacterium	No change
Fernando et. al, 2010 [15]	Usual diet + 200g/d canned chickpeas/ 5g/day raffinose for 3 weeks or usual diet	Terminal restriction fragment-length polymorphism (T-RFLP) analysis and qPCR	Decreased clostridium histolyticum/clostridium lituseburense	No change
Duysberg et. al, 2021 [16]	40g/day oats or cream of rice	qPCR	increase in lactobacilli; increased bifidobacteria	no change

	(n= 34)		(not significant)	
Carvelho-Wells et. al, [17]	48g/d whole grain maize or non-whole grain breakfast cereal (n=32)	FISH	Increased bifidobacterium	No changes
Connoly et.al, 2016 [18]	45g/d whole grain or non-whole grain oat granola breakfast cereal (n=30)	FISH	Increased bifidobacterium, lactobacilli and total bacteria	No change
Venegas et. al, 2017 [19]	Whole grain or Refined grain diet: 40g fibre	16S rRNA amplicon sequencing	Decrease Enterobacteriaceae, increased lachnospira	Increased acetate and total SCFAs
Alexander et. al, [20]	Orange or apple juice with pomace or without pomace	qPCR	No change in alpha or beta diversity	n/a
Benitez-Paez et. al, [21]	10 g day inulin + 10 g day resistant	Shotgun metagenomics	no change in alpha diversity.	n/a

maltodextrin milk or maltodextrin (n=80)	beta diversity increased ($p =$ 0.002)
--	--

References

- 1 **Ampatzoglou A**, Atwal KK, Maidens CM, Williams CL, Ross AB, Thielecke F, Jonnalagadda SS, Kennedy OB, Yaqoob P. Increased whole grain consumption does not affect blood biochemistry, body composition, or gut microbiology in healthy, low-habitual whole grain consumers. *J Nutr* 2015; **145**: 215-221 [PMID: 25644340 DOI: 10.3945/jn.114.202176]
- 2 **Costabile A**, Fava F, Röyttö H, Forssten SD, Olli K, Klievink J, Rowland IR, Ouwehand AC, Rastall RA, Gibson GR, Walton GE. Impact of polydextrose on the faecal microbiota: a double-blind, crossover, placebo-controlled feeding study in healthy human subjects. *Br J Nutr* 2012; **108**: 471-481 [PMID: 22099384 DOI: 10.1017/S0007114511005782]
- 3 **Elison E**, Vigsnaes LK, Rindom Krogsgaard L, Rasmussen J, Sørensen N, McConnell B, Hennet T, Sommer MO, Bytzer P. Oral supplementation of healthy adults with 2'-O-fucosyllactose and lacto-N-neotetraose is well tolerated and shifts the intestinal microbiota. *Br J Nutr* 2016; **116**: 1356-1368 [PMID: 27719686 DOI: 10.1017/S0007114516003354]

4 Wilms E, An R, Smolinska A, Stevens Y, Weseler AR, Elizalde M, Drittij MJ, Ioannou A, van Schooten FJ, Smidt H, Masclee AAM, Zoetendal EG, Jonkers DMAE. Galacto-oligosaccharides supplementation in prefrail older and healthy adults increased faecal bifidobacteria, but did not impact immune function and oxidative stress. *Clin Nutr* 2021; **40**: 3019-3031 [PMID: 33509667 DOI: 10.1016/j.clnu.2020.12.034]

5 Sloan TJ, Jalanka J, Major GAD, Krishnasamy S, Pritchard S, Abdelrazig S, Korpela K, Singh G, Mulvenna C, Hoad CL, Marciani L, Barrett DA, Lomer MCE, de Vos WM, Gowland PA, Spiller RC. A low FODMAP diet is associated with changes in the microbiota and reduction in breath hydrogen but not colonic volume in healthy subjects. *PLoS One* 2018; **13**: e0201410 [PMID: 30048547 DOI: 10.1371/journal.pone.0201410]

6 Lefranc-Millot C, Guérin-Deremaux L, Wils D, Neut C, Miller LE, Saniez-Degrave MH. Impact of a resistant dextrin on intestinal ecology: how altering the digestive ecosystem with NUTRIOSE®, a soluble fibre with prebiotic properties, may be beneficial for health. *J Int Med Res* 2012; **40**: 211-224 [PMID: 22429361 DOI: 10.1177/147323001204000122]

7 Burns AM, Solch RJ, Dennis-Wall JC, Ukhanova M, Nieves C Jr, Mai V, Christman MC, Gordon DT, Langkamp-Henken B. In healthy adults, resistant maltodextrin produces a greater change in fecal bifidobacteria counts and increases stool wet weight: a double-blind, randomized, controlled crossover study. *Nutr Res* 2018; **60**: 33-42 [PMID: 30527258 DOI: 10.1016/j.nutres.2018.09.007]

8 Deehan EC, Yang C, Perez-Muñoz ME, Nguyen NK, Cheng CC, Triador L, Zhang Z, Bakal JA, Walter J. Precision Microbiome Modulation with Discrete Dietary Fiber Structures Directs Short-Chain Fatty Acid Production. *Cell Host Microbe* 2020; **27**: 389-404.e6 [PMID: 32004499 DOI: 10.1016/j.chom.2020.01.006]

9 **Zhang L**, Ouyang Y, Li H, Shen L, Ni Y, Fang Q, Wu G, Qian L, Xiao Y, Zhang J, Yin P, Panagiotou G, Xu G, Ye J, Jia W. Metabolic phenotypes and the gut microbiota in response to dietary resistant starch type 2 in normal-weight subjects: a randomized crossover trial. *Sci Rep* 2019; **9**: 4736 [PMID: 30894560 DOI: 10.1038/s41598-018-38216-9]

10 **Alfa MJ**, Strang D, Tappia PS, Graham M, Van Domselaar G, Forbes JD, Laminman V, Olson N, DeGagne P, Bray D, Murray BL, Dufault B, Lix LM. A randomized trial to determine the impact of a digestion resistant starch composition on the gut microbiome in older and mid-age adults. *Clin Nutr* 2018; **37**: 797-807 [PMID: 28410921 DOI: 10.1016/j.clnu.2017.03.025]

11 **Finegold SM**, Li Z, Summanen PH, Downes J, Thames G, Corbett K, Dowd S, Krak M, Heber D. Xylooligosaccharide increases bifidobacteria but not lactobacilli in human gut microbiota. *Food Funct* 2014; **5**: 436-445 [PMID: 24513849 DOI: 10.1039/c3fo60348b]

12 **Lecerf JM**, Dépeint F, Clerc E, Dugenet Y, Niamba CN, Rhazi L, Cayzeele A, Abdelnour G, Jaruga A, Younes H, Jacobs H, Lambrey G, Abdelnour AM, Pouillart PR. Xylo-oligosaccharide (XOS) in combination with inulin modulates both the intestinal environment and immune status in healthy subjects, while XOS alone only shows prebiotic properties. *Br J Nutr* 2012; **108**: 1847-1858 [PMID: 22264499 DOI: 10.1017/S0007114511007252]

13 **Clarke ST**, Green-Johnson JM, Brooks SP, Ramdath DD, Bercik P, Avila C, Inglis GD, Green J, Yanke LJ, Selinger LB, Kalmokoff M. β 2-1 Fructan supplementation alters host immune responses in a manner consistent with increased exposure to microbial components: results from a double-blinded, randomised, cross-over study in healthy adults. *Br J Nutr* 2016; **115**: 1748-1759 [PMID: 26987626 DOI: 10.1017/S0007114516000908]

- 14 **Healey G**, Murphy R, Butts C, Brough L, Whelan K, Coad J. Habitual dietary fibre intake influences gut microbiota response to an inulin-type fructan prebiotic: a randomised, double-blind, placebo-controlled, cross-over, human intervention study. *Br J Nutr* 2018; **119**: 176-189 [PMID: 29307330 DOI: 10.1017/S0007114517003440]
- 15 **Fernando WM**, Hill JE, Zello GA, Tyler RT, Dahl WJ, Van Kessel AG. Diets supplemented with chickpea or its main oligosaccharide component raffinose modify faecal microbial composition in healthy adults. *Benef Microbes* 2010; **1**: 197-207 [PMID: 21831757 DOI: 10.3920/BM2009.0027]
- 16 **Duysburgh C**, Van den Abbeele P, Kamil A, Fleige L, De Chavez PJ, Chu Y, Barton W, O'Sullivan O, Cotter PD, Quilter K, Joyce SA, Murphy M, DunnGalvin G, Dinan TG, Marzorati M. In vitro-in vivo Validation of Stimulatory Effect of Oat Ingredients on Lactobacilli. *Pathogens* 2021; **10** [PMID: 33669689 DOI: 10.3390/pathogens10020235]
- 17 **Carvalho-Wells AL**, Helmolz K, Nodet C, Molzer C, Leonard C, McKeivith B, Thielecke F, Jackson KG, Tuohy KM. Determination of the in vivo prebiotic potential of a maize-based whole grain breakfast cereal: a human feeding study. *Br J Nutr* 2010; **104**: 1353-1356 [PMID: 20487589 DOI: 10.1017/S0007114510002084]
- 18 **Connolly ML**, Tzounis X, Tuohy KM, Lovegrove JA. Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population. *Front Microbiol* 2016; **7**: 1675 [PMID: 27872611 DOI: 10.3389/fmicb.2016.01675]
- 19 **Vanegas SM**, Meydani M, Barnett JB, Goldin B, Kane A, Rasmussen H, Brown C, Vangay P, Knights D, Jonnalagadda S, Koecher K, Karl JP, Thomas M, Dolnikowski G, Li L, Saltzman E, Wu D, Meydani SN. Substituting whole grains for refined grains in a 6-wk

randomized trial has a modest effect on gut microbiota and immune and inflammatory markers of healthy adults. *Am J Clin Nutr* 2017; **105**: 635-650 [PMID: 28179226 DOI: 10.3945/ajcn.116.146928]

20 **Alexander C**, Brauchla M, Sanoshy KD, Blonquist TM, Maloney GN, Mah E, Kelley-Garvin K, Chen O, Liska DJ, Shin JE, Boileau TW, Swanson KS. Bowel habits, faecal microbiota and faecal bile acid composition of healthy adults consuming fruit pomace fibres: two-arm, randomised, double-blinded, placebo-controlled trials. *Br J Nutr* 2023; **130**: 42-55 [PMID: 36102329 DOI: 10.1017/S0007114522002951]

21 **Benítez-Páez A**, Hess AL, Krautbauer S, Liebisch G, Christensen L, Hjorth MF, Larsen TM, Sanz Y; MyNewGut consortium. Sex, Food, and the Gut Microbiota: Disparate Response to Caloric Restriction Diet with Fiber Supplementation in Women and Men. *Mol Nutr Food Res* 2021; **65**: e2000996 [PMID: 33629506 DOI: 10.1002/mnfr.202000996]