Effects of food matrix on the prebiotic efficacy of inulin-type fructans: a randomised trial

Article

Supplemental Material

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Supplemental Data Table 1: Mean bacterial FLOW-FISH populations across the four interventions at Day 0 and Day 10

	Intervention Group												
	Pure inulin (*n* =24)			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
Probe	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Eub I-II-III	9.79 (.004)	9.83 (0.04)	**0.002**	9.78 (0.05)	9.82 (0.05)	**0.01**	9.62 (0.06)	9.69 (0.06)	≤ **0.001**	9.73 (0.04)	9.82 (0.04)	**0.00**	0.315
Bif164	8.49 (0.13)	9.12 (0.11)	≤ **0.001**	8.37 (0.11)	8.96 (0.11)	≤ **0.001**	8.24 (0.13)	8.89 (0.12)	≤ **0.001**	8.34 (0.12)	9.05 (0.07)	≤ **0.001**	0.641
Bac303	8.07 (0.09)	8.17 (0.10)	0.243	8.06 (0.03)	8.31 (0.04)	**0.001**	8.09 (0.06)	8.13 (0.08)	0.57	8.13 (0.05)	8.16 (0.09)	0.64	0.201
Erec482	9.20 (0.07)	9.13 (0.08)	0.582	9.18 (0.09)	9.27 (0.07)	0.25	9.11 (0.08)	9.2 (0.07)	0.35	9.18 (0.08)	9.23 (0.08)	0.53	0.291
Rrec584	8.32 (0.08)	8.33 (0.10)	0.923	8.39 (0.07)	8.61 (0.07)	**0.005**	8.18 (0.12)	8.16 (0.12)	0.82	8.29 (0.10)	8.4 (0.09)	0.17	**0.022**
Pro853	8.25 (0.08)	8.32 (0.07)	0.50	8.38 (0.09)	8.39 (0.09)	0.94	8.18 (0.13)	8.11 (0.11)	0.50	8.26 (0.11)	8.36 (0.12)	0.32	0.272
Fprau655	8.6 (0.10)	8.69 (0.10)	0.58	8.73 (0.07)	8.93 (0.07)	**0.004**	8.62 (0.10)	8.62 (0.10)	0.35	8.77 (0.08)	8.94 (0.08)	**0.012**	**0.029**

FLOW-FISH results for probes total bacteria (Eub338 I-II-III), *Bifidobacterium* spp. (Bif164), most *Bacteroidacae* and *Prevotellaceae* (Bac303), *Clostridium coccoides-Eubacterium rectale* group (Erec452), *Roseburia* (Rrec584), Clostridial cluster IX (Prop853) and *Faecalibacterium prausnitzii* (Fprau655). Reported as log10 Cells/gram wet faeces. Mean and standard error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons utilising Day 0 values as a baseline covariate (orange column)

Supplemental Data Table 2: Relative microbiome profiling (RMP) abundances recorded across all four interventions at Day 0 and Day 10

	Intervention												
Phylum	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
***Actinomycetota* (*Actinobacteria*)**	23.13 (2.84)	34.55 (4.05)	≤ **0.001**	17.57 (2.63)	27.72 (3.84)	≤ **0.001**	18.51 (2.37)	29.47 (3.39)	≤ **0.001**	16.16 (1.71)	28.92 (3.37)	≤ **0.001**	0.82
***Bacteroidota* (*Bacteroidetes*)**	3.07 (0.97)	4.80 (1.57)	0.96	1.97 (0.70)	2.80 (0.76)	0.42	2.53 (0.56)	3.29 (0.98)	0.46	1.97 (0.37)	2.47 (0.62)	0.34	0.62
***Pseudomonadota* (*Proteobacteria*)**	2.88 (1.42)	6.56 (3.48)	0.16	1.32 (0.48)	1.09 (0.36)	0.93	1.53 (0.74)	3.21 (1.74)	0.52	4.43 (1.94)	5.50 (2.78)	0.68	0.45
***Verrucomicrobiota* (*Verrucomicrobia*)**	2.69 (1.19)	2.79 (0.90)	≤ **0.001**	1.35 (0.53)	1.06 (0.31)	0.83	4.38 (1.27)	5.06 (1.99)	0.63	3.45 (1.31)	7.23 (3.26)	**0.01**	0.09
Euryarchaeota	0.89 (0.33)	0.90 (0.43)	0.97	1.63 (0.61)	0.84 (0.40)	**0.02**	1.05 (0.51)	0.32 (0.17)	**0.03**	1.30 (0.51)	1.37 (0.57)	0.83	0.09
Cyanobacteria	0.01 (0.01)	0.001 (0.001)	0.61	0.03 (0.01)	0.02 (0.02)	0.84	0.04 (0.04)	0.02 (0.02)	0.38	0.02 (0.01)	0.05 (0.04)	0.37	0.54
***Mycoplasmatota* (*Tenericutes*)**	0.25 (0.08)	0.24 (0.12)	0.99	1.08 (0.76)	1.26 (1.06)	0.60	1.05 (0.62)	0.09 (0.05)	**0.01**	0.44 (0.16)	0.38 (0.15)	0.86	0.11
***Bacillota* (*Firmicutes*)**	67.09 (3.19)	50.20 (3.55)	≤ **0.001**	72.97 (3.16)	59.05 (4.70)	≤ **0.001**	73.94 (2.14)	62.55 (3.26)	**0.002**	71.30 (3.26)	56.26 (4.03)	≤ **0.001**	0.40

Relative Microbiome Profiling 16S rRNA (phylum level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 values as a baseline covariate (orange column)

Genus	**Intervention**												***P* (b)**
	Pure inulin (*n* =24)			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Bifidobacterium	17.96 (3.04)	31.45 (3.97)	**≤ 0.001**	12.96 (2.53)	24.7 (3.90)	**≤ 0.001**	13.00 (2.24)	25.43 (3.52)	**≤ 0.001**	12.19 (1.79)	25.22 (3.21)	**≤ 0.001**	0.92
Bacteroides	1.59 (0.57)	3.62 (1.34)	0.18	1.20 (0.55)	1.78 (0.55)	0.44	1.48 (0.39)	1.97 (0.71)	0.52	1.06 (0.20)	1.37 (0.40)	0.69	0.28
Prevotella	0.16 (0.06)	0.22 (0.08)	0.70	0.26 (0.09)	0.25 (0.07)	0.96	0.41 (0.12)	0.73 (0.34)	**0.04**	0.32 (0.09)	0.45 (0.16)	0.40	0.64
Alistipes	1.12 (073)	0.48 (0.16)	0.10	0.43 (0.18)	0.42 (0.14)	0.97	0.49 (0.12)	0.55 (0.15)	0.87	0.4 (0.08)	0.37 (0.10)	0.95	0.82
Roseburia	2.96 (0.80)	2.10 (0.41)	0.29	2.61 (0.63)	3.94 (0.92)	0.10	2.80 (0.63)	2.57 (0.42)	0.77	2.48 (0.44)	3.91 (1.32)	0.08	0.64
Clostridium cluster IVXA + IVXB	0.77 (0.11)	0.44 (0.07)	**0.04**	0.76 (0.08)	0.65 (0.09)	0.46	1.07 (0.29)	0.54 (0.12)	**0.001**	0.85 (0.12)	0.52 (0.09)	**0.04**	0.31
Faecalibacterium prausnitziciand relatives	3.74 (1.10)	3.73 (1.20)	0.99	2.27 (0.74)	4.11 (1.30)	0.14	7.76 (2.44)	6.67 (1.89)	0.38	2.62 (0.76)	3.72 (1.31)	0.38	0.37
Ruminococcaceae (excluding Fprau)	12.04 (1.66)	8.59 (1.27)	**0.02**	14.02 (1.88)	10.73 (1.55)	**0.03**	13.89 (1.12)	11.21 (0.94)	0.08	18.01 (2.37)	11.86 (1.45)	**≤ 0.001**	0.21
Ruminococcus 2	2.06 (0.40)	1.86 (0.52)	0.66	2.83 (0.61)	2.41 (0.63)	0.35	3.20 (0.39)	2.19 (0.42)	**0.03**	2.68 (0.32)	1.90 (0.27)	0.09	0.41
Coprococcus	1.45 (0.29)	1.02 (0.20)	0.15	1.51 (0.22)	1.30 (0.25)	0.49	1.29 (0.19)	1.15 (0.18)	0.65	1.99 (0.35)	1.67 (0.27)	0.28	0.42
Blautia	16.33 (2.03)	9.36 (1.73)	**≤ 0.001**	17.54 (1.82)	10.92 (1.57)	**0.001**	18.37 (2.28)	14.85 (1.97)	0.08	16.21 (1.95)	11.70 (1.57)	**0.03**	0.24
Lactobacillus/Enterococcus	1.24 (0.51)	1.03 (0.70)	0.89	3.24 (1.25)	5.4 (2.13)	0.16	1.19 (0.51)	3.64 (1.23)	0.11	2.54 (1.18)	1.38 (0.77)	0.45	0.09

Relative Microbiome Profiling 16S rRNA (genus level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 values as a baseline covariate (orange column)

	Intervention												
Genus (continued)	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Lactococcus	0.18 (0.10)	0.15 (0.06)	0.66	0.17 (0.09)	0.01 (0.01)	**0.04**	0.03 (0.02)	0.04 (0.03)	0.89	0.10 (0.03)	0.03 (0.02)	0.38	0.35
Dorea	2.51 (0.37)	2.08 (0.36)	0.32	3.88 (0.67)	2.61 (0.47)	**0.003**	3.75 (0.57)	3.14 (0.53)	0.16	4.54 (0.79)	3.09 (0.54)	**≤ 0.001**	0.57
Anaerostipes	4.54 (1.17)	4.68 (1.54)	0.85	4.23 (0.88)	3.85 (0.96)	0.61	2.73 (0.62)	3.25 (0.83)	0.50	2.75 (0.52)	2.99 (0.70)	0.75	0.90
Lachnospiraceae incertae sedi	5.77 (0.59)	3.89 (0.70)	**0.001**	5.21 (0.75)	3.10 (0.58)	**≤ 0.001**	3.91 (0.48)	3.6 (0.49)	0.60	4.00 (0.52)	2.95 (0.40)	0.07	0.42
Collinsella	3.00 (0.70)	1.61 (0.51)	**0.05**	2.11 (0.37	1.23 (0.25)	0.22	2.52 (0.61)	2.25 (0.53)	0.70	1.60 (0.27)	2.11 (1.02)	0.47	0.80

Relative Microbiome Profiling 16S rRNA (genus level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 values as a baseline covariate (orange column)

Supplemental Data Table 3: α-diversity measures recorded across all four interventions at Day 0 and Day 10

Measure	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* values Intervention (b)**
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Shannon Index	3.23 (0.08)	2.86 (0.14)	**0.003**	3.28 (0.11)	3.06 (0.13)	0.06	3.35 (0.09)	3.14 (0.07)	0.07	3.32 (0.12)	3.06 (0.13)	**0.03**	0.517
Richness (no. of species)	102.70 (6.58)	86.46 (7.33)	**0.01**	110.10 (8.12)	101.40 (7.37)	0.16	102.50 (6.80)	97.58 (4.07)	0.43	120.90 (7.63)	106.70 (6.92)	**0.03**	0.173
Simpson Index	0.08 (0.01)	0.14 (0.03)	**0.01**	0.08 (0.01)	0.11 (0.02)	0.12	0.07 (0.01)	0.10 (0.01)	0.28	0.09 (0.02)	0.12 (0.02)	0.20	0.631

α-diversity measures across the four interventions from samples collected at Day 0 and Day 10. Mean and Standard Error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons utilising Day 0 values as a baseline covariate (orange column)

Supplemental Data Table 4: Quantitative microbiome profiling (QMP) data recorded across all four interventions at Day 0 and Day 10

	Intervention												
Phylum	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
	Day 0	**D 10**	***P* (a)**	**Day 0**	**D 10**	***P* (a)**	**Day 0**	**D 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Actinomycetota (Actinobacteria)	1.83 x 10^{9} (3.82 x 10^{8})	2.88 x 10^{9} (6.15 x 10^{8})	**0.003**	1.23 x 10^{9} (2.37 x 10^{8})	2.36 x 10^{9} (6.83 x 10^{8})	**0.001**	1.05 x 10^{9} (1.83 x 10^{8})	1.92 x 10^{9} (2.91 x 10^{8})	**0.02**	1.05 x 10^{9} (1.80 x 10^{8})	2.10 x 10^{9} (2.41 x 10^{8})	**0.003**	0.61
Bacteroidota (Bacteroidetes)	3.00 x 10^{8} (1.42 x 10^{8})	4.51 x 10^{8} (2.31 x 10^{8})	0.19	1.63 x 10^{8} (8.50 x 10^{7})	1.57 x 10^{8} (4.32 x 10^{7})	0.96	1.27 x 10^{8} (3.00 x 10^{7})	1.96 x 10^{8} (5.04 x 10^{7})	0.54	1.24 x 10^{8} (2.54 x 10^{7})	2.08 x 10^{8} (5.75 x 10^{7})	0.46	0.34
Pseudomonadota (Proteobacteria)	1.63 x 10^{8} (7780 x 10^{7})	3.92 x 10^{8} (2.15 x 10^{7})	0.24	8.15 x 10^{7} (3.18 x 10^{7})	5.51 x 10^{7} (1.87 x 10^{7})	0.89	6.39 x 10^{7} (2.77 x 10^{7})	1.00 x 10^{8} (7.00 x 10^{7})	0.27	2.31 x 10^{8} (1.17 x 10^{8})	4.49 x 10^{8} (2.69 x 10^{8})	0.65	0.40
Verrucomicrobiota (Verrucomicrobia)	1.35 x 10^{8} (5.38 x 10^{7})	1.37 x 10^{8} (4.60 x 10^{7})	0.90	2.06 x 10^{8} (7.55 x 10^{7})	4.22 x 10^{8} (1.66 x 10^{8})	0.03	6.56 x 10^{7} (2.69 x 10^{7})	6.25 x 10^{7} (2.38 x 10^{7})	0.97	2.58 x 10^{8} (7.18 x 10^{7})	4.12 x 10^{8} (1.79 x 10^{8})	0.11	**0.01**
Euryarchaeota	3.97 x 10^{7} (1.31 x 10^{7})	3.94 x 10^{7} (1.68 x 10^{7})	0.99	7.90 x 10^{7} (2.81 x 10^{7})	5.70 x 10^{7} (3.24 x 10^{7})	0.46	3.97 x 10^{7} (1.85 x 10^{7})	1.49 x 10^{7} (7.71 x 10^{6})	0.40	6.90 x 10^{7} (2.88 x 10^{7})	1.35 x 10^{8} (6.49 x 10^{7})	**0.03**	0.13
Cyanobacteria	9.25 x 10^{5} (4.84 x 10^{5})	4.52 x 10^{5} (4.52 x 10^{5})	0.46	1.62 x 10^{6} (8.06 x 10^{5})	9.57 x 10^{6} (7.11 x 10^{5})	0.57	1.54 x 10^{6} (1.49 x 10^{6})	9.50 x 10^{5} (8.72 x 10^{5})	0.62	2.09 x 10^{6} (1.38 x 10^{6})	1.73 x 10^{6} (1.30 x 10^{6})	0.76	0.59
Mycoplasmatota (Tenericutes)	1.36 x 10^{9} (5.00 x 10^{8})	9.45 x 10^{8} (4.17 x 10^{8})	0.85	3.60 x 10^{9} (2.38 x 10^{9})	4.26 x 10^{9} (3.32 x 10^{9})	0.77	5.82 x 10^{9} (4.03 x 10^{9})	5.28 x 10^{8} (3.10 x 10^{8})	**0.02**	2.63 x 10^{9} (8.04 x 10^{8})	3.87 x 10^{9} (1.71 x 10^{8})	0.58	0.38
Bacillota (Firmicutes)	4.64 x 10^{9} (5.87 x 10^{8})	3.78 x 10^{9} (5.69 x 10^{8})	**0.02**	5.26 x 10^{9} (7.83 x 10^{8})	3.97 x 10^{9} (4.79 x 10^{9})	**≤0.001**	4.26 x 10^{9} (6.41 x 10^{8})	4.44 x 10^{9} (6.21 x 10^{8})	0.61	4.78 x 10^{9} (6.51 x 10^{8})	4.55 x 10^{9} (5.87 x 10^{8})	0.51	0.74

Quantitative Microbiome Profiling 16S rRNA (phylum level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). Numbers are expressed as cells per gram of faeces. **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 counts as a baseline covariate (orange column)

Genus	**Intervention**												**P (b)**
	Pure inulin (*n* =24)			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			
	Day 0	**Day 10**	**P (a)**	**Day 0**	**Day 10**	**P (a)**	**Day 0**	**Day 10**	**P (a)**	**Day 0**	**Day 10**	**P (a)**	
Bifidobacterium	1.48 x 10^{9} (3.85 x 10^{8})	2.68 x 10^{9} (6.16 x 10^{8})	**0.004**	9.48 x 10^{8} (2.27 x 10^{8})	2.41 x 10^{9} (7.9 x 10^{8})	**≤ 0.001**	7.86 x 10^{8} (1.67 x 10^{8})	1.64 x 10^{9} (2.92 x 10^{8})	**0.04**	7.76 x 10^{8} (1.69 x 10^{8})	1.81 x 10^{9} (2.07 x 10^{8})	**0.01**	0.47
Bacteroides	1.42 x 10^{8} (7.57 x 10^{7})	3.63 x 10^{7} (1.92 x 10^{8})	0.38	1.15 x 10^{8} (7.54 x 10^{7})	1.08 x 10^{8} (3.10 x 10^{7})	0.93	7.63 x 10^{7} (2.13 x 10^{7})	1.08 x 10^{8} (3.06 x 10^{7})	0.69	6.41 x 10^{7} (1.46 x 10^{7})	1.10 x 10^{8} (3.24 x 10^{7})	0.56	0.19
Prevotella	9.85 x 10^{6} (4.04 x 10^{6})	1.99 x 10^{7} (1.18 x 10^{7})	0.54	1.28 x 10^{7} (4.62 x 10^{7})	1.41 x 10^{7} (4.44 x 10^{6})	0.93	1.84 x 10^{7} (3.80 x 10^{6})	5.65 x 10^{7} (2.99 x 10^{7})	**0.02**	2.83 x 10^{7} (1.33 x 10^{7})	4.51 x 10^{7} (2.08 x 10^{7})	0.31	0.36
Alistipes	1.38 x 10^{8} (1.12 x 10^{8})	4.65 x 10^{7} (2.66 x 10^{7})	0.12	2.93 x 10^{7} (1.27 x 10^{7})	2.58 x 10^{7} (9.39 x 10^{6})	0.95	2.40 x 10^{7} (5.88 x 10^{6})	3.32 x 10^{7} (7.80 x 10^{6})	0.87	2.43 x 10^{7} (5.82 x 10^{6})	3.03 x 10^{7} (8.84 x 10^{6})	0.92	0.80
Roseburia	1.89 x 10^{8} (5.00 x 10^{7})	2.02 x 10^{8} (6.15 x 10^{7})	0.89	1.88 x 10^{8} (6.40 x 10^{7})	3.12 x 10^{8} (9.37 x 10^{7})	**0.03**	2.24 x 10^{8} (6.51 x 10^{7})	2.16 x 10^{8} (5.11 x 10^{7})	0.88	1.54 x 10^{8} (3.09 x 10^{7})	2.46 x 10^{8} (6.23 x 10^{7})	0.10	0.68
Clostridium cluster IVXA + IVXB	5.88 x 10^{7} (1.15 x 10^{7})	3.71 x 10^{7} (8.45 x 10^{6})	**0.01**	5.33 x 10^{7} (8.37 x 10^{6})	4.69 x 10^{7} (7.66 x 10^{6})	0.42	5.40 x 10^{7} (1.13 x 10^{7})	3.70 x 10^{7} (9.08 x 10^{6})	**0.03**	5.43 x 10^{7} (8.70 x 10^{6})	3.90 x 10^{7} (6.16 x 10^{6})	0.06	0.79
Faecalibacterium prausnitzii and relatives	2.73 x 10^{8} (7.37 x 10^{7})	3.83 x 10^{8} (1.18 x 10^{7})	0.27	1.36 x 10^{8} (3.50 x 10^{7})	2.54 x 10^{8} (5.96 x 10^{7})	0.23	4.61 x 10^{8} (1.20 x 10^{8})	4.94 x 10^{8} (1.44 x 10^{8})	0.74	2.03 x 10^{8} (5.69 x 10^{7})	3.09 x 10^{8} (8.04 x 10^{7})	0.23	0.42
Ruminococcaceae (excluding Fprau)	7.78 x 10^{8} (1.25 x 10^{8})	6.64 x 10^{8} (1.34 x 10^{7})	0.43	1.02 x 10^{9} (2.51 x 10^{8})	7.16 x 10^{8} (1.03 x 10^{8})	**0.04**	7.74 x 10^{8} (1.19 x 10^{8})	7.73 x 10^{8} (1.27 x 10^{8})	0.99	1.28 x 10^{9} (2.28 x 10^{8})	1.00 x 10^{8} (1.63 x 10^{7})	0.06	0.30
Ruminococcus 2	1.60 x 10^{8} (4.56 x 10^{7})	1.61 x 10^{8} (5.74 x 10^{7})	1.00	2.53 x 10^{8} (9.56 x 10^{7})	1.97 x 10^{8} (5.48 x 10^{7})	0.25	2.03 x 10^{8} (4.31 x 10^{7})	1.57 x 10^{8} (3.83 x 10^{7})	0.34	1.67 x 10^{8} (2.31 x 10^{7})	1.41 x 10^{8} (1.96 x 10^{7})	0.59	0.85

Quantitative Microbiome Profiling 16S rRNA (genus level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). Numbers are expressed as cells per gram of faeces**. (a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 as a baseline covariate (orange column)

	Intervention												
Genus (continued)	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Coprococcus	1.10 x 10^{8} (3.17 x 107)	6.74 x 10^{7} (1.25 x 10^{7})	0.11	8.76 x 10^{7} (1.27 x 10^{7})	8.69 x 10^{7} (1.71 x 10^{7})	0.98	6.72 x 10^{7} (1.25 x 10^{7})	8.12 x 10^{7} (1.76 x 10^{7})	0.60	1.16 x 10^{8} (2.18 x 10^{7})	1.56 x 10^{8} (3.65 x 10^{7})	0.13	0.36
Blautia	1.15 x 10^{9} (2.04 x 108)	7.08 x 10^{8} (1.65 x 10^{8})	**0.01**	1.39 x 10^{9} (2.83 x 10^{8})	8.93 x 10^{7} (1.72 x 10^{8})	**0.003**	1.11 x 10^{9} (2.57 x 10^{8})	1.11 x 10^{9} (2.33 x 10^{8})	0.98	1.00 x 10^{9} (1.41 x 10^{8})	9.35 x 10^{8} (1.62 x 10^{8})	0.83	0.50
Lactobacillus/Enterococcus	1.00 x 10^{8} (5.37 x 10^{7})	4.77 x 10^{7} (2.60 x 10^{7})	0.71	2.50 x 10^{8} (1.02 x 10^{8})	4.56 x 10^{8} (2.16 x 10^{8})	0.15	6.87 x 10^{7} (3.21 x 10^{7})	2.70 x 10^{8} (1.12 x 10^{7})	0.16	2.41 x 10^{8} (1.46 x 10^{8})	1.00 x 10^{8} (5.41 x 10^{7})	0.32	0.10
Lactococcus	1.29 x 10^{7} (7.92 x 10^{6})	1.29 x 10^{7} (5.91 x 10^{6})	1.00	1.18 x 10^{7} (7.14 x 10^{6})	8.13 x 10^{5} (3.82 x 10^{5})	0.09	1.03 x 10^{6} (6.61 x 10^{5})	2.74 x 10^{6} (1.75 x 10^{6})	0.80	7.27 x 10^{6} (3.18 x 10^{6})	1.72 x 10^{6} (8.50 x 10^{5})	0.39	0.21
Dorea	2.11 x 10^{8} (6.31 x 10^{7})	1.70 x 10^{8} (3.58 x 10^{7})	0.18	2.89 x 10^{8} (6.85 x 10^{7})	2.25 x 10^{8} (5.28 x 10^{7})	0.05	2.03 x 10^{8} (4.52 x 10^{7})	2.06 x 10^{8} (4.46 x 10^{7})	0.95	2.57 x 10^{8} (4.32 x 10^{7})	2.40 x 10^{8} (4.15 x 10^{7})	0.44	0.68
Anaerostipes	3.20 x 10^{8} (8.06 x 10^{7})	2.86 x 10^{8} (7.38 x 10^{7})	0.59	2.90 x 10^{8} (5.92 x 10^{7})	3.16 x 10^{8} (9.73 x 10^{7})	0.67	1.47 x 10^{8} (3.90 x 10^{7})	2.05 x 10^{8} (5.46 x 10^{7})	0.34	1.84 x 10^{8} (5.19 x 10^{7})	2.46 x 10^{8} (7.32 x 10^{7})	0.31	0.80
Lachnospiraceae incertae sedi	4.19 x 10^{8} (8.89 x 10^{7})	2.76 x 10^{8} (6.58 x 10^{7})	**≤0.001**	3.56 x 10^{8} (6.87 x 10^{7})	2.42 x 10^{8} (5.01 x 10^{7})	**0.01**	2.13 x 10^{8} (3.90 x 10^{7})	2.41 x 10^{8} (4.57 x 10^{7})	0.49	2.53 x 10^{8} (4.27 x 10^{7})	2.26 x 10^{8} (3.69 x 10^{7})	0.52	0.91
Collinsella	1.99 x 10^{8} (5.77 x 10^{7})	1.00 x 10^{8} (3.50 x 10^{7})	**0.04**	1.25 x 10^{8} (2.14 x 10^{7})	8.52 x 10^{7} (1.65 x 10^{7})	0.41	1.22 x 10^{8} (2.75 x 10^{7})	1.52 x 10^{8} (4.56 x 10^{7})	0.53	1.18 x 10^{8} (3.06 x 10^{7})	1.60 x 10^{8} (6.33 x 10^{7})	0.39	0.54

Quantitative Microbiome Profiling 16S rRNA (genus level) from samples collected at Day 0 and Day 10 of the intervention phase. Mean and standard error (SE). Numbers are expressed as cells per gram of faeces**. (a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 as a baseline covariate (orange column)

Supplemental Data Table 5: Gastrointestinal sensation and bowel habit scores across the four interventions

	Intervention Group												
GI Sensation/ bowel habit	**Pure inulin (*n* =24)**			**Shortbread (*n* =24)**			**Milk Chocolate (*n* =24)**			**Rice Drink (*n* =24)**			***P* (b)**
	Day 0	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	**Day 0**	**Day 10**	***P* (a)**	
Flatulence	0.80 (0.11)	0.81 (0.12)	0.0923	0.88 (0.10)	0.88 (0.13)	0.99	0.78 (0.11)	0.66 (0.10)	0.21	0.81 (0.12)	0.95 (0.14)	0.18	0.262
Intestinal Bloating	0.37 (0.09)	0.32 (0.11)	0.625	0.53 (0.10)	0.58 (0.14)	0.70	0.44 (0.11)	0.39 (0.10)	0.62	0.34 (0.08)	0.39 (0.10)	0.63	0.657
Abdominal Pressure	0.27 (0.10)	0.23 (0.07)	0.657	0.37 (0.08)	0.34 (0.11)	0.75	0.21 (0.06)	0.18 (0.05)	0.69	0.26 (0.07)	0.31 (0.08)	0.54	0.655
Abdominal Pain	0.19 (0.08)	0.17 (0.05)	0.744	0.26 (0.07)	0.26 (0.09)	0.93	0.08 (0.02)	0.10 (0.05)	0.79	0.13 (0.05)	0.23 (0.07)	0.15	0.576
Feeling of Fullness	0.65 (0.10)	0.38 (0.07)	**0.002**	0.72 (0.11)	0.65 (0.15)	0.39	0.63 (0.12)	0.58 (0.12)	0.56	0.77 (0.10)	0.77 (0.11)	0.96	0.058
Stool Consistency	3.74 (0.22)	4.29 (0.21)	0.001	3.69 (0.16)	3.76 (0.22)	0.60	3.60 (0.21)	3.69 (0.21)	0.57	3.18 (0.22)	3.35 (0.21)	0.31	**0.017**
Stool Frequency	1.62 (0.13)	1.77 (0.15)	0.08	1.58 (0.12)	1.52 (0.10)	0.45	1.55 (0.12)	1.57 (0.11)	0.84	1.50 (0.15)	1.54 (0.15)	0.58	0.759

Mean and Standard Error (SE). **(a)** *P* values are as a result of planned Day 0 vs Day 10 comparisons (grey columns). **(b)** *P* values are as a result of Day 10 group comparisons using Day 0 as a baseline covariate (orange column)