

**Effects of whole-grain cereals on fecal microbiota and short-chain fatty acids in dogs -
A comparison of rye, oats and wheat**

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Supplementary Table S1: Demographics of dogs participating in an experimental study on diets containing whole grain of rye, oats or wheat.

Dog nr	Breed	Age (years)	Sex	Weight (kg)	BCS
1	Lagotto romagnolo	9.7	F	11.4	4
2	Lagotto romagnolo	5	F	11.2	5
3	Mixed breed	8.4	MC	41.5	5
4	Mixed breed	5.2	MC	8.7	6
5	Border Collie	5.2	F	15.2	5
6	Lhasa Apso	9.7	MC	8.5	6
7	Nederlandse Kooikerhondje	1.5	M	9.9	5
8	Poodle medium size	8.1	F	7.5	5
9	Australian Kelpie	4.5	MC	18.9	5
10	Weimaraner, short-haired	7.5	FS	25.1	6
11	Nova Scotia Duck Tolling Retriever	2.6	M	20.2	5
12	Mixed breed	3.2	MC	29	4
13	Whippet	3.6	FS	14.4	5
14	Samoyed	6.2	F	29.4	5
15	Mixed breed	7.2	F	30	6
16	Labrador Retriever	3	FS	19.4	5
17	Xoloitzcuintle	3.4	F	10	5
18	Mixed breed	8.4	FS	20.7	6

Sex: F= female, FS= female spayed, M= male, MC= male castrated. BCS= body condition score.

Supplementary Table S2. Relative abundance, in % (means \pm SEM), of operational taxonomic units (OTU) with average relative abundance $\geq 0.1\%$ and significant difference in main diet effect and genera with relative abundance $\geq 3\%$ or significant difference in main diet effect.

Phylum	Family	Genus	Species	Relative abundance			<i>p</i> diet effect	<i>q</i> -value	
				Wheat diet	Oat diet	Rye diet			
Firmicutes									
Lachnospiraceae		Lachnospiraceae uncl.	Lachnospiraceae uncl.	0.37 \pm 0.1 ^a	0.23 \pm 0.04 ^{ab}	0.18 \pm 0.05 ^b	0.0009	0.062	
			Lachnospiraceae NK4A136 group	0.63 \pm 0.1 ^a	0.41 \pm 0.1 ^b	0.37 \pm 0.1 ^b	0.008	0.16	
		Blautia	Lachnospiraceae NK4A136 group	0.57 \pm 0.1 ^a	0.35 \pm 0.1 ^b	0.31 \pm 0.05 ^b	0.005	0.14	
			Coprococcus sp. HPP0074	1.5 \pm 0.3 ^a	1.1 \pm 0.2 ^{ab}	0.95 \pm 0.2 ^b	0.028	0.20	
		Megamonas	Blautia	5.6 \pm 0.6	4.8 \pm 0.8	4.6 \pm 0.6	0.10	0.22	
			Blautia uncl.	1.9 \pm 0.4 ^a	1.1 \pm 0.2 ^b	1.2 \pm 0.2 ^{ab}	0.013	0.15	
			Blautia uncl.	0.87 \pm 0.1 ^a	0.56 \pm 0.1 ^b	0.65 \pm 0.1 ^{ab}	0.035	0.20	
	Veillonellaceae	Erysipelotrichaceae	Megamonas	2.9 \pm 0.5	2.8 \pm 0.6	4.9 \pm 1.0	0.046	0.22	
	Megamonas uncl.		2.8 \pm 0.5	2.7 \pm 0.6	4.7 \pm 0.9	0.044	0.22		
	Erysipelotrichaceae	Catenibacterium	Erysipelotrichaceae UCG-003	0.39 \pm 0.2 ^a	1.3 \pm 0.5 ^b	0.59 \pm 0.3 ^{ab}	0.014	0.19	
	Erysipelotrichaceae UCG-003 uncl.		0.39 \pm 0.2 ^a	1.3 \pm 0.5 ^b	0.58 \pm 0.3 ^{ab}	0.015	0.15		
	Catenibacterium		4.7 \pm 1.6 ^a	8.7 \pm 2.7 ^{ab}	9.4 \pm 1.8 ^b	0.032	0.22		
	Catenibacterium uncl.		4.6 \pm 1.6 ^a	8.7 \pm 2.7 ^{ab}	9.3 \pm 1.7 ^b	0.033	0.20		
Peptostreptococcaceae Peptoclostridium				8.4 \pm 1.1	6.3 \pm 1.1	6.8 \pm 1.2	0.08	0.22	
Bacteroidetes									
Bacteroidaceae	Bacteroides	Bacteroides	Bacteroides	11.0 \pm 0.9 ^a	11.8 \pm 1.9 ^a	6.8 \pm 1.2 ^b	0.003	0.11	
			Bacteroides uncl.	0.79 \pm 0.3 ^a	0.23 \pm 0.1 ^b	0.21 \pm 0.1 ^b	0.006	0.14	
			Bacteroides coprocola	0.64 \pm 0.1 ^a	0.44 \pm 0.1 ^{ab}	0.33 \pm 0.1 ^b	0.014	0.15	
		Prevotellaceae	Bacteroides stercoris	0.87 \pm 0.6 ^a	0.87 \pm 0.6 ^{ab}	0.18 \pm 0.04 ^b	0.026	0.20	
			Bacteroides vulgatus	0.85 \pm 0.3 ^{ab}	2.7 \pm 1.3 ^a	0.29 \pm 0.1 ^b	0.031	0.20	
			Bacteroides caecigallinarum	0.30 \pm 0.1 ^a	0.13 \pm 0.03 ^{ab}	0.06 \pm 0.01 ^b	0.04	0.21	
	Prevotella_9			11.4 \pm 2.3	9.5 \pm 2.2	14.1 \pm 3.0	0.098	0.22	

	Alloprevotella		3.6±0.5	4.7±1.0	3.7±0.7	0.81	0.93
Fusobacteria							
Fusobacteriaceae	Fusobacterium		13.7±1.9	14.5±2.0	13.4±2.7	0.58	0.70
		Fusobacteriales uncl.	7.0±1.3 ^a	10.9±1.6 ^b	6.0±1.2 ^a	0.008	0.14
Proteobacteria							
Alcaligenaceae	Sutterella		3.2±0.5	3.0±0.6	4.4±0.9	0.20	0.34

Values on the same row without common superscript letters differ significantly ($p < 0.05$) in post-hoc pairwise comparisons. q -value obtained from correction with false discovery rate (FDR) according to Benjamini-Hochberg.