Supporting information for

Dietary fiber isolated from sweet potato residues promote healthy gut microbiome profile

Man Liu[ab¶], Xuezhi Li[b¶], Shengmin Zhou[c], Thomas T.Y. Wang[d], Sihan Zhou[b], Kunlong Yang[b], Yongxin Li[b], Jun Tian[ab*], Jing Wang[a*]

[a] Beijing Advanced Innovation Center for Food Nutrition and Human Health, Beijing Technology and Business University, Beijing 10048, China

[b] College of Life Science, Jiangsu Normal University, Xuzhou, Jiangsu Province, 221116, China

[c] Wilmar (Shanghai) Biotechnology Research & Development Center Co., Ltd., Shanghai, 200137, China

[d] Diet, Genomics and Immunology Lab, Beltsville Human Nutrition Research Center, ARS, USDA, Beltsville, MD 20705, USA

¶ These authors contributed equally to this work.

***Contact Information of the Corresponding Authors: (**Jing Wang) Ph.D. Tel: (86)-010-6898-5334, E-mail: wangjing@th.btbu.edu.cn (Jun Tian), Ph.D. Email: tj-085@163.com

Table S1 Identification of the main genera isolated from the in vitro batch culture system.

Microorganism identified	Description	Query Cover	Percent identity	Accession
Bifidobacterium	Bifidobacterium animalis subsp. lactis strain IDCC 4301 16S ribosomal RNA gene, partial sequence	99%	99.56%	EF589111.1
	Bifidobacterium animalis subsp. lactis strain 56 16S ribosomal RNA gene, partial sequence	99%	99.49%	MN435721.1
	Bifidobacterium animalis subsp. lactis strain 55 16S ribosomal RNA gene, partial sequence	99%	99.49%	MN435720.1
	Bifidobacterium animalis subsp. lactis strain 54 16S ribosomal RNA gene, partial sequence	99%	99.49%	MN435719.1
	Bifidobacterium animalis subsp. lactis strain 53 16S ribosomal RNA gene, partial sequence	99%	99.49%	MN435718.1
Lactobacillus	Lactobacillus reuteri strain LL7 chromosome, complete genome	99%	99.80%	CP041676.1
	Lactobacillus reuteri strain reuteri chromosome, complete genome	99%	99.73%	CP045049.1
	Select seq MK564724.1 Lactobacillus reuteri strain SKB1241 16S ribosomal RNA gene, partial sequence	99%	99.73%	MK564724.1
	Lactobacillus reuteri strain I49 16S ribosomal RNA gene, partial sequence	99%	99.73%	KR364776.1
	Lactobacillus reuteri strain 8.1 16S ribosomal RNA gene, partial sequence	99%	99.73%	JX272059.1
Escherichia	Escherichia coli strain 64-a pink 16S ribosomal RNA gene, partial sequence	99%	98.05%	MN208138.1

	Escherichia coli strain 1 16S ribosomal RNA gene, partial sequence	98%	98.19%	MK621229.1
	Escherichia coli strain S7-5 16S ribosomal RNA gene, partial sequence	98%	98.19%	KP716695.1
	Escherichia coli strain 145 16S ribosomal RNA gene, partial sequence	99%	98.04%	MH671465.1
	Escherichia coli strain DL1501 16S ribosomal RNA gene, partial sequence	99%	97.97%	MG736060.1
Bacteroides	Bacteroides fragilis strain CCUG4856T chromosome, complete genome	100%	98.75%	CP036555.1
	Bacteroides fragilis NCTC 9343, complete genome	100%	98.75%	CR626927.1
	Bacteroides fragilis strain DCMOUH0042B chromosome, complete genome	100%	98.42%	CP036550.1
	Bacteroides fragilis genome assembly BFBE1.1, chromosome : scaffold1	100%	98.42%	LN877293.1
	Bacteroides fragilis 638R genome	100%	98.42%	FQ312004.1
Clostridium perfringens	Clostridium perfringens strain DSM 106278 16S ribosomal RNA gene, partial sequence	99%	97.61%	MN537509.1
	Clostridium perfringens ATCC 13124 16S ribosomal RNA gene, partial sequence	99%	97.61%	MN326666.1
	Clostridium perfringens strain 4928STDY7387940 genome assembly, chromosome: 1	99%	97.61%	LR607374.1
	Clostridium perfringens strain P8-2 16S ribosomal RNA gene, partial sequence	99%	97.61%	MH828355.1

	Clostridium perfringens strain JXJA17 chromosome, complete genome	99%	97.61%	CP028149.1

Table S2

Absolute and relative organ weight of Wistar rats fed normal diet or with 3%SPDF or 15%SPDF.

	Control	3%SPDF	15%SPDF
BW(g)	369.15±17.59	354.18±30.91	365.75±31.80
Absolute weight(g)			
Liver	13.0023±1.3842	16.6820±2.3376	16.2120±2.2782
Kidney	2.6593±0.1801	2.6672±0.2829	2.8290±0.1894
Spleen	0.7723±0.0931	0.8165±0.1014	0.7408±0.1152
Thymus	0.7019±0.1365	0.7147±0.0503	0.7972±0.1807
Relative weight(g)			
Liver	0.0352±0.0038	0.0473±0.0066	0.0443±0.0062
Kidney	0.0072±0.0005	0.0076±0.0008	0.0077±0.0005
Spleen	0.0021±0.0003	0.0023±0.0003	0.0020±0.0003
Thymus	0.0019±0.0004	0.0020±0.0001	0.0022±0.0005

Data are expressed as mean ± SD(n = 6).

Table S3

Richness and diversity indexes from fecal samples of each group (OUT cutoff of 0.03)

	Control	3%SPDF	15%SPDF
reads	40814±1936ab	50245±2192b	38838±5553a
OTUs	30847±1835a	39534±2055a	31321±5281a
coverage	0.9987±0.0002a	0.9991±0.0002a	0.9989±0.0003a
Ace	357±9ab	365±12b	321±17a
Chao	363±9a	367±16a	324±22a
Shannon	3.96±0.12a	3.72±0.27a	3.85±0.32a
Simpson	0.045±0.006a	0.095±0.053a	0.054±0.021a

Data are expressed as mean ± SD (n = 3).

Table S4

Colon SCFA content for the rats fed 0, 3% or 15% SPDF after 28-day feeding study (mg/kg).

	Control	3%SPDF	15%SPDF
Formic acid	246.35±0.65a	154.40±45.30b	183.53±39.39b
Acetic acid	7754.06±1108.58a	9644.62±2571.23a	7602.18±1186.56a
Propionic acid	993.74±75.24a	1244.43±199.17b	1401.78±192.31b
Butyric acid	513.68±167.26a	1571.25±259.16ab	2793.27±1445.31b
Total SCFAs	9507.83±1606.55a	12614.70±509.6a	11543.86±939.12a

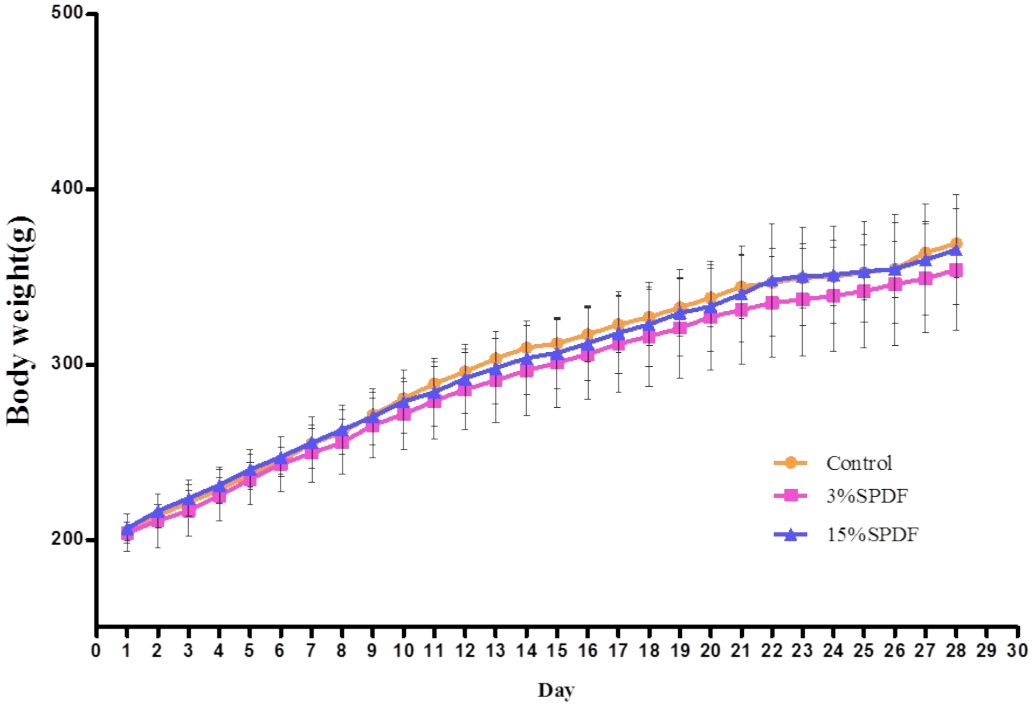

Fig. S1 Body weight changes for the rats in the control or 3% and 15% SPDF groups.