

**Table S1.** Effects of monosaccharide and disaccharide intake on gut microbiota

Sugar	Fermentation	Gut microbiota <sup>a)</sup>		Other metabolites	Ref
		Abundance up	Abundance down		
Glucose	Mice/ In vivo	<b>Genus:</b> <i>Enterobacteria</i>	<b>Genus:</b> <i>Lactobacillus</i>	<b>Fecal:</b> acetate↑, aspartate↓, formate↑, methanol↑, propionate↑, pyruvate↑	[1]
	Mice/ In vivo <sup>b)</sup>	<b>Phylum:</b> <i>Firmicutes</i> , <i>Verrucomicrobia</i> , <i>Proteobacteria</i>	<b>Phylum:</b> <i>Deferribacteres</i> , <i>Bacteroidetes</i>	<b>Serum:</b> total cholesterol↑, low-density lipoprotein (LDL)- cholesterol↑, endotoxin↑	[2]
Fructose	Mice/ In vivo	<b>Phylum:</b> <i>Firmicutes</i> , <i>Verrucomicrobia</i> , <i>Proteobacteria</i> , <i>Deferribacteres</i> <b>Family:</b> <i>Lachnospiraceae</i> <i>Ruminococcaceae</i>	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Family:</b> <i>Deferribacteraceae</i> , <i>Helicobacteraceae</i>	<b>Fecal:</b> total SCFAs↓, Acetate↓, propionate↓, butyrate↓ <b>Serum:</b> endotoxin↑	[3]
	Mice/ In vivo	<b>Genus:</b> <i>Enterobacteria</i>	<b>Genus:</b> <i>Lactobacillus</i>	<b>Fecal:</b> acetate↑, formate↑, aspartate↓, butyrate↓, xylose↑, pyruvate↑, glutamate↓, methanol↑, succinate↑, taurine↑	[1]
Sucrose	Rats/ In vivo	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Family:</b> <i>Bacteroidaceae</i> , <i>Erysipelotricgaceae</i> , <i>Turicibacteraceae</i>	<b>Phylum:</b> <i>Firmicutes</i> <b>Family:</b> <i>Ruminococcaceae</i> , <i>Clostridiales</i> <i>Lactobacillaceae</i>	—	[4]
	Mice/ In vivo	<b>Phylum:</b> <i>Firmicutes</i> , <i>Proteobacteria</i> <b>Genus:</b> <i>Alistipes</i> , <i>Bacteroides</i>	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Genus:</b> <i>Lactobacillus</i> , <i>Alloprevotella</i> , <i>Akkermansia</i>	—	[5]
	Mice/ In vivo	<b>Order:</b> <i>Clostridiales</i> , <i>Erysipelotrichales</i> <i>Lactobacillales</i>	<b>Order:</b> <i>Bacteroidales</i> <b>Genus:</b> <i>Alistipes</i> , <i>Ruminococcus</i> ,	—	[6]

			<i>Butyricicoccus</i>		
	Mice/ In vivo	<b>Phylum:</b> <i>Verrucomicrobia</i> <b>Family:</b> <i>Verrucomicrobiaceae</i> <i>Porphyromonadaceae</i>	<b>Phylum:</b> <i>Firmicutes, Tenericutes</i> <i>Proteobacteria</i> <b>Family:</b> <i>Prevotellaceae</i> <i>Lachnospiraceae, Anaeroplasmataceae</i>	<b>Fecal:</b> total SCFA↓ acetate↓, butyrate↓	[7]
Sucrose mimics <sup>c)</sup>	Rats/ In vivo	<b>Phylum:</b> <i>Firmicutes, Proteobacteria</i> <b>Genus:</b> <i>Sutterella Parabacteroides,</i> <i>Bacteroides, Lactobacillus, Oscillosoira</i>	<b>Phylum:</b> <i>Verrucomicrobia, Bacteroidetes</i> <b>Genus:</b> <i>Prevotella, Akkernansia,</i> <i>Paraprevotella, Mucisoirillum</i>	—	[8]
	Rats/ In vivo	<b>Family:</b> <i>Rikenellaceae, Bacteroidaceae</i> <i>Enterobacteriaceae, Bifidobacteriaceae</i> <i>Clostridiaceae. I, Lactobacillaceae</i> <b>Genus:</b> <i>Bacteroides, Clostridium sensu</i> <i>stricto, Alistipes, Lactobacillus,</i> <i>Parasutterella, Bifidobacteriaceae,</i>	<b>Family:</b> <i>Prevotellaceae, Ruminococcaceae</i> <i>Lachnospiraceae</i> <b>Genus:</b> <i>Prevotella,</i> <i>Lachnospiraceae incertae sedis</i>	—	[9]

**Notes:**

- a) This column only lists the level of discussion highlighted in the references.
  - b) In this study, both high glucose/fructose diets were fed, both of which caused the same trend of change compared to normal diet.
  - c) In some references, glucose and fructose are mixed in certain proportions, and such "mixed sugars" are classified as "sucrose mimics" in this table.
- : Not tested; ↑: increased; ↓: decreased.

**Table S2.** Effects of starch with different digestive properties intake on gut microbiota

Type	Starch origin	Fermentation	Gut microbiota		SCFA	Ref
			Abundance up	Abundance down		
RDS	Maltodextrin	Mice/ In vivo	cecal bacterial loads↑ chronic inflammation↑ disease susceptibility↑ gut microbes dysbiosis suppressed intestinal anti-microbial defense mechanisms			[10,11]
	Pregelatinized maize starch	Mice/ In vivo	<b>Phylum:</b> <i>Proteobacteria, Firmicutes</i> <b>Genus:</b> <i>Alistipes, Oscillibacter, Ruminiclostridium-9</i>	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Genus:</b> <i>bacteroides, Streptococcus</i>	isovalerate↓ valerate↓	[12]
SDS	Starch yields modified with 1,4-α-glucan branching enzyme	Mice/ In vivo	<b>Phylum:</b> <i>Verrucomicrobia</i> <b>Genus:</b> <i>Lactobacillus, Lachnodpiraceae, Akkermamsia, Mucispirillum, Bifidobacterium</i>	<b>Phylum:</b> <i>Proteobacteria</i> <b>Genus:</b> <i>Enterococcus, Alistipes, Odoribacter, Ruminiclostridium</i>	acetate↑ butyrate↑ valerate↑	[12]
	Starch-entrapped microspheres	Mice/ In vivo	<b>Phylum:</b> <i>Firmicutes</i>	<b>Phylum:</b> <i>Bacteroidetes</i>	total SCFAs↑ acetate↓ butyrate↓	[13]
			(compared with RSII, raw potato starch)			
RMD <small>a)</small>	Cassava starch modified with α-amylase and branching enzyme	Human Feces/ In vitro	<b>Genus:</b> <i>Bifidobacteria, Lactobacillus</i>	<b>Genus:</b> <i>Clostridia, Bacteroids</i>	Acetic↑ Butyric↑	[14]
	(compared with glucose)					
	Resistant maltodextrin	Mice/ In vivo	<b>Phylum:</b> <i>Firmicutes, Proteobacteria, Actinobacteria</i>	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Genus:</b> <i>Bacteroides,</i>	—	[15]

			<b>Genus:</b> <i>Lactobacillus, Bifidobacterium</i>	<i>Oscillibacter, Alistipes, Prevotella, Prevotellaceae Ruminococcaceae, Ruminococcus</i>		
RSI	Isolated intact cotyledon cells from pinto bean seeds	Human Feces/ In vitro	<b>Phylum:</b> <i>Firmicutes</i> <b>Family:</b> <i>Lachnospiraceae, Ruminococcaceae,</i> <b>Genus:</b> <i>Clostridiales</i>	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Family:</b> <i>Faecalibacterium</i> <b>Genus:</b> <i>Megamonas</i>	total SCFAs↓ acetate↓ pyruvate↓ butyrate↓	[16]
	Intact cotyledon cells isolated from red kidney beans	human intestinal microbial ecosystem	<b>Phylum:</b> <i>Actinobacteria</i> <b>Family:</b> <i>Coriobacteriaceae, Bifidobacteriaceae</i>	<b>Phylum:</b> <i>Firmicutes, Bacteroidetes</i> <b>Family:</b> <i>Bacteroidaceae, Selenomonadaceae</i>	butyrate↑	[17]
			(compared with microbiota taken before the application of bean treatment)			
RSII	High-amylose maize starch	Mice/ In vivo	<b>Phylum:</b> <i>Verrucomicrobia, Bacteroidetes, Actinobacteria</i> <b>Genus:</b> <i>Bifidobacterium, Akkermansia, Allobaculum</i>	<b>Phylum:</b> <i>Firmicutes</i> <b>Genus:</b> <i>Butyrivibrio, Turicibacter</i>	—	[18]
	Highly resistant starch rice	Feces/ In vitro	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Genus:</b> <i>Prevotellacea Faecalibacterium</i>	<b>Phylum:</b> <i>Firmicutes, Proteobacteria</i> <b>Genus:</b> <i>Escherichia, Megamonas</i>	Acetate↑ propionate↑ butyrate↑ isobutyric↓ isovaleric↓	[19]
	High amylose maize starch	Human/ In vivo	<b>Phylum:</b> <i>Bacteroidetes, Actinobacteria</i> <b>Family:</b> <i>Ruminococcaceae, Porphyromonadaceae</i>	<b>Phylum:</b> <i>Firmicutes</i> <b>Family:</b> <i>Erysipelotrichaceae</i> <b>Genus:</b> <i>Faecalibacterium,</i>	—	[20]

			<b>Genus:</b> <i>Parabacteroides</i> , <i>Bifidobacterium</i>	<i>Dorea</i>		
	Buckwheat-resistant starch	Mice/ In vivo	<b>Phylum:</b> <i>Bacteroidetes</i> <b>Genus:</b> <i>Bacteroides</i> , <i>Ruminiclostridium</i> , <i>Blautia</i>	<b>Phylum:</b> <i>Firmicutes</i> , <i>Proteobacteria</i> <b>Genus:</b> <i>Turicibacter</i> , <i>Erysipelatoclostridium</i> , <i>Escherichia-Shigella</i>	Propionate↑ Butyrate↑	[21]
RSIII	Lotus seed resistant starch	Mice/ In vivo	<b>Family:</b> <i>Lachnospiraceae</i> , <i>Clostridium</i> , <i>Ruminococcaceae</i> <b>Genus:</b> <i>Lactobacillus</i> , <i>Bifidobacterium</i>	<b>Family:</b> <i>Rikenellaceae</i> , <i>Porphyromonadaceae</i>	Formic acid↑ Acetic acid↑ Propionic acid↓ Butyrate↑	[22]
	Buckwheat-resistant starch	Mice/ In vivo	<b>Genus:</b> <i>Lactobacillus</i> , <i>Bifidobacterium</i> , <i>Enterococcus</i>	<b>Genus:</b> <i>Escherichia Coli</i>	Acetic acid↑ Butyrate↑ Propionic acid↑	[23]
	Retrograded tapioca starch	Young pigs/ In vivo	<b>Family:</b> <i>Strptococcaceae</i> , <i>Bacteroidales</i> <b>Family:</b> <i>Ruminococcaceae</i>	<b>Family:</b> <i>Lachnospiraceae</i>	—	[24]
RSIV	Chemically modified phosphorylated cross-linked RSIV	Human/ In vivo	<b>Phylum:</b> <i>Actinobacteria</i> , <i>Bacteroidetes</i> <b>Genus:</b> <i>Veillonellaceae</i> , <i>Lachnospiraceae</i> , <i>Erysipelotrichaceae</i>	<b>Phylum:</b> <i>Firmicutes</i> <b>Family:</b> <i>Ruminococcaceae</i>	—	[20]
		Human Feces/ In vitro	<b>Genus:</b> <i>Clostridiales</i> , <i>Bacteroides</i> <i>Ruminococcus</i>	<b>Genus:</b> <i>Blautia</i> , <i>Roseburia</i> , <i>Faecalibacterium</i>	total SCFAs↓ acetate↓ propionic↓ butyrate↓	[25]
			(compared with high-amylose maize starch, which is the raw material of RSIV)			
			Human/ In vivo	<b>Species:</b> <i>Ruminococcus lactaris</i> , <i>Bacteroides acidifaciens</i> , <i>Blautia glucerasea</i> , <i>Christensenella minuta</i> , <i>Eubacterium</i>	<b>Species:</b> <i>Enterococcus casseliflavus</i> , <i>Streptococcus cristatus</i>	butyric↑ propionic↑ valeric↑

			<i>oxidoreducens, Parabacteroides distasonis</i>		isovaleric↓	
RSV	Debranched high-amylose starch and palmitic acid	Human Feces/ In vitro	<b>Phylum:</b> <i>Actinobacteria, Firmicutes</i> <b>Genus:</b> <i>Blautia, Anaerostipes, Holdemanella, Bifidobacterium, Streptococcus, Collinsella, Dialister, Megamonas, Faecalibacterium</i>	<b>Phylum:</b> <i>Proteobacteria, Bacteroidetes</i> <b>Genus:</b> <i>Parasutterella, Alistipes, Barnesiella, Clostridiales, Bilophila, Parabacteroides, Sutterella, Dorea, Lachnoclostridium, Flavonifractor, Phascolarctobacterium</i>	acetic acid↑ butyric acid↑ lactic acid↑ valeric acid↓	[27]
			(compared with high-amylose maize starch, which is the raw material of RSII)			
	High-amylose maize starches complexed with saturated fatty acids	Human Feces/ In vitro	<b>Phylum:</b> <i>Bacterioidetes</i> <b>Genus:</b> <i>Prevotella, Megamonas, Bacteroides</i>	<b>Phylum:</b> <i>Firmicutes</i> <b>Genus:</b> <i>Roseburia, Lachnospiraceae, Ruminococcus</i>	total SCFAs↑ acetate↑ butyrate↑ propionate↑	[28]
			(compared with high-amylose maize starch, which is the raw material of RSII)			

**Notes:**

a) RMD: Resistant maltodextrin

Unless otherwise noted, any upward or downward adjustments that appear in the table are compared to the normal diet or normal corn starch.

—: Not tested; ↑: increased; ↓: decreased.

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