Alginate Oligosaccharide and Gut Microbiota: Exploring the Key to Health

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Supplementary Material

Table S1. Influences of AOS on Gut Microbiota associated with beneficial functions.

Influenced Gut microbiota			Functions & Therapeutics	Involved Proteins/ Cytokine/Pathway	Changes of Metabolites	Reference
Family	Genus	Species				
Firmicutes (Bacillota)						
Lactobacillaceae (+)	*Lactobacillus* (+)	*L. rhamnosus* *L. gasseri* *L. reuteri* *L. johnsonii*	Intestinal barrier function (+) Lipid metabolism (+) Glucose metabolism (+) Metabolic syndrome (−) Neuroprotection (+) Inflammation (−) Oxidative Stress (−) IBD (−)	Nrf2 (+) AhR (+) TLR4 (−) GSH (+) SOD (+) CAT (+) MDA (−) TG (−) LDL-C (−) TNF-α(−) IL-1β(−) IL-6 (−)	Acetate (+) Propionate (+) Butyrate (+) Valerate (+)	[1–6]
	Ligilactobacillus (+)		Oxidation (−)			
Lachnospiraceae (+)	*Dorea*		growth performance (+)	Ghrelin	SCFAs (+)	[7]
	Lachnoclostridium (+)		Immunity (+)			[8]
	Roseburia (+)					
	Coprococcus (+)	*C. catus*	Reproduction (+)	CatSper (+) PKA gelsolin (+) zinc-α2-glycoprotein (+)		[9]
	Blautia (−)		Lipid metabolism (+) Diabetes (−) Insulin resistance (−) Inflammation (−)		LPS (−)	[3,10,11]
Leuconostocaceae	*Leuconostoc*	*L. mesenteroides*	IBD (−)		Blood metabolites (+)	[12]
Ruminococcaceae (+)	*Ruminococcus*	*R. albus*	Immunity (+) Gut barrier function (+) Uric acid excretion (+) Neuroprotection (+) Intestinal mucosal damage (−) Intestinal inflammation (−)	TLR4/MyD88/NF-κB GSH (+) ABCG2 (+) URAT1 (−) SMCT (−) GLUT9 (−)	SCFAs (+)	[8,13–16]
	Faecalibacterium (+)	*F. prausnitzii*				

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Family	Genus	Species				
			Pancreatitis (−) Cardiovascular disease (−) Hyperuricemia (−)	TNF-α(−) IL-1β(−) IL-6 (−) IL-12 (−) IL-18 (−)		
Bacillaceae	*Butyricicoccus*		skin aging (-)		Butyric acid (+)	[17]
	Bacillus		Neuroprotection (+)		Noradrenalin (+) Acetylcholine (+) Dopamine (+)	[18]
Eubacteriaceae	*Eubacterium*		Colonic mucosal immunity (+)		SCFAs (+)	[5]
Clostridiaceae	*Clostridium*	*C. difficile*	Infection (−) IBD (−)			[19]
			Intestinal inflammation (−) Skin aging (−) Colorectal cancer (−)			[20–23]
	Butyribacterium	*B. methylotrophicum*			Butyrate (+)	[24]
Staphylococcaceae	*Staphylococcus* (−)	*S. aureus* *S. epidermidis*	Inflammation (−) Infection (−) Bacteremia (−) Gut microenvironment homeostasis (+)	IL-6 (−) IL-10 (+) TNF-α (−)		[25,26]
Enterococcaceae	*Enterococcus* (−)	*E. faecalis* *E. faecium*	Infection (−)			[7,25]
Peptostreptococcaceae	*Peptostreptococcus*	*P. anaerobius*	Immunity (+) Gut barrier function (+) Infection (−)	TLR4 (−) TNF-α(−) IL-1β(−)	SCFAs (+)	[27–30]
	Romboutsia (+/−)	*R. ilealis*	Gut barrier function (+) IBD (−)	IL-6 (−)		
Peptoniphilaceae	*Parvimonas*		Inflammation (−) Colorectal cancer (−)			[31]
Erysipelotrichaceae	*Faecalibaculum* (+)		Immunity (+) Oxidation (−) Inflammation (−) Uric acid excretion (+) Hyperuricemia (−) Diabetes (−) Neuroprotection (+)	ABCG2 (+) URAT1 (−) SMCT (−) GLUT9 (−) IL-1β(−) IL-12 (−) IL-18 (−)	Acetate (+) Propionate (+) Isovalerate (+)	[11,13,16,29,32–34]

Influenced Gut microbiota			Functions & Therapeutics	Involved Proteins/ Cytokine/Pathway	Changes of Metabolites	Reference
Family	Genus	Species				
				SOD (+) CAT (+) MDA (−)		
	Dubosiella (+)		Intestinal barrier function (+) Gut inflammation (−) Immunity (+)	IL-1β (−) IL-6 (−) TNF-α (−)	Acetic acid (+) Propionic acid (+) Valeric acid (+)	[29]
Streptococcaceae	*Streptococcus*	*S. pyogenes*	Reproduction (+) Infection (−)		Serotonin	[35]
Veillonellaceae	*Veillonella (+)*		Supply energy (+) Gut microenvironment homeostasis (+) Inflammation (−) oxidative stress (−) Intestinal barrier function (+)	TLR4 (−) IL-1β (−) IL-6 (−) TNF-α (−) COX-2 (−) MDA (−) T-SOD (+) CAT (+)	Propionate (+)	[27,33]
	Megasphaera		Hypertension (−)			[36]
Turicibacteraceae	*Turicibacter* (+/−)		Inflammation (−) Immunity (+) Intestinal barrier function (+)	SIgA (+) IL-6 (−) IL-1β (−) IL-10 (+) IL-22 (−) TNF-α (−)	SCFAs (+)	[29,32]
Bacteroidetes (Bacteroidota)						
Bacteroidaceae	*Bacteroides*	*B. fragilis* *B. uniformis* *B. acidifaciens*	Colitis (−) Glucose metabolism (+) Intestinal barrier function (+) Lipid metabolism (+) Intestinal mucositis (−) Alzheimer's disease (−) Cardiovascular disease (−) Hypertension (−) Hyperuricemia (−)	IL-6 (−) IL-10 (+) IL-1β (−) IL-12 (−) IL-18 (−) TNF-α (+) MDA (−) CAT (+) SOD (-) Th17 cell (−) TLR4 (−)	Acetate (+) Propionate (+) Butyrate Isovalerate (+) *B. fragilis* toxin (−)	[2,3,6,10,15,16,25,33,34,37]
Rikenellaceae (+)	*Alistipes* (+)		Lipid metabolism (+) Colitis (−) Skin aging (−)	IL-1β (−) IL-6 (−)	Acetate (+) Propionate (+) Butyrate (+)	[10,15,17,28,38]

Influenced Gut microbiota			Functions & Therapeutics	Involved Proteins/ Cytokine/Pathway	Changes of Metabolites	Reference
Family	Genus	Species				
			Hypertension (−)	IL-10 (+) TNF-α (−) AMPK (+) NF-κB (−)		
Prevotellaceae (+)	*Prevotella* *Alloprevotella*	*Prevotella_9* (−)	Colitis (−) Inflammation (−) Hypertension (−)	TLR4/MyD88/NF-κB (−) IL-1β (−) IL-6 (−) TNF-α (−)	Acetate (+) Propionate (+) Butyrate (+)	[5,8,15,17,27]
Muribaculaceae (+/-)	*Muribaculum*		Gut barrier function (+) Uric acid excretion (+) Hyperuricemia (−) IBD (−)	ABCG2 (+) GLUT9 (−) SMCT (−) URAT1 (−) IL-10 (+) IL-1β (−) IL-12 (−) IL-18 (−) IL-6 (−) TNF-α (−)	Acetate (+) Propionate (+) Isobutyrate (+) NO (−)	[16,28,34]
Tannerellaceae	*Parabacteroides* (+/−)		Glucose metabolism (+) Lipid metabolism (+) Obesity (−) IBD (−) Gut microenvironment homeostasis (+)	TLR4 (−) IL-10 (+) IL-1β (−) IL-6 (−) TNF-α (−)	SCFAs (+)	[10,25,27,39]
Porphyromonadaceae	*Porphyromonas*		Lipid metabolism (+) Inflammation (−) Colorectal cancer (−)			[40,41]
Odoribacteraceae	*Butyricimonas*		Gut-skin axis homeostasis (+) Skin aging (-)		Butyrate (+)	[17]
Proteobacteria (Pseudomonadota)						
Helicobacteraceae (−)	*Helicobacter* (−)	*H. pylori* (−)	Infection (−) Intestinal inflammation (−) IBD (−) Obesity (−) Immunity (+) Gut microenvironment homeostasis (+) oxidative stress (−) Gut barrier function (+)	TLR4/MyD88/NF-κB AMPK/NF-κB IL-1 β (−) IL-6 (−) TNF-α (−) IL-10 (+) MDA (−) CAT (+) T-SOD (+)	Acetate (+) Propionate (+) Butyrate (+)	[8,25,28,30,33]
Desulfovibrionaceae (−)	*Desulfovibrio* (−)		Gut barrier function (+)	TLR4 (−)	Blood metabolites (+)	[3,11,12,25,27,38,42]

Influenced Gut microbiota			Functions & Therapeutics	Involved Proteins/ Cytokine/Pathway	Changes of Metabolites	Reference
Family	Genus	Species				
			Intestinal inflammation (−) Gut microenvironment homeostasis (+) Lipid metabolism (+) Glucose metabolism (+) Insulin sensitivity (+) Reproductive capacity (+)	TNF-α (−) COX-2 (−) IL-1 β (−) IL-6 (−) TNF-α (−)	Acetate (+) Propionate (+) Butyrate (+)	
Enterobacteriaceae (−)	*Escherichia*	*E. coli*	Gut barrier function (+) Mucosal immunity (+) Colitis (−) Infections (−) Inflammation (−) Neuroprotection (+)	TLR4/MyD88/NF-κB (−) AMPK/NF-κB IL-6 (−) TNF-α (−) IFN-γ (−)	LPS (−) SCFA (+)	[7,28,43]
	Salmonella	*S. enteritidis*		IL-1β (−) *S. enteritidis* specific IgA (+) ROS (−)		[44]
	Shigella					[30]
Pseudomonadaceae	*Pseudomonas* (−)	*P. aeruginosa*	Quorum sensing (−) Biofilm formation (−) Infection (−)			[45,46]
Succinivbrionaceae	*Anaerobiospirillum*		Immune homeostasis (+) Inflammation (−)	TLR4 (−) COX-2 (−) TNF-α (−)		[27]
Burkholderiaceae	*Burkholderia*	*B. cenocepacia*	Infection (−) Lipid metabolism (+) Obesity (−) Intestinal inflammation (−) Neuroprotection (+) Gut microenvironment homeostasis (+) Osteoporosis (−)	TLR4 (−) COX-2 (−) TNF-α (−)	SCFAs (+) BAs (+)	[3,13,25,27,37]
	Ralstonia	*R. mannitolilytica*	Infection (−)			[47]
Comamonadaceae	*Comamonas* (−)		Hyperuricemia (−)	ABCG2 (+) GLUT9 (−) URAT1 (−) IL-10 (+) IL-1β (−) IL-12 (−) IL-18 (−)	Acetate (+) Propionate (+) Isobutyrate (+)	[16]
Actinobacteria						
Bifidobacteriaceae	*Bifidobacterium* (+)	*B. gallinarum*	Intestine immunity (+)	IL-6 (−)	SCFAs (+)	[10,13,29,29,37,48]

Influenced Gut microbiota			Functions & Therapeutics	Involved Proteins/ Cytokine/Pathway	Changes of Metabolites	Reference
Family	Genus	Species				
			Gut barrier function (+) Intestinal inflammation (−) Neuroprotection (+) Oxidation (−) Obesity (−) Osteoporosis (−)	IL-1β (−) TNF-α (−) Th17 cells (−)	BAs (+)	
Eggerthellaceae (+)	*Parvibacter* (+)		Inflammation (−) Gut barrier function (+) Infection (−) Glucose metabolism (+) Diabetes (−)	IL-6 (−) IL-1β (−) TNF-α (−) MPO (−) Blood glucose (−) HOMA-IR (−)	Acetate (+) Propionate (+) Butyrate (+)	[11,29]
Verrucomicrobia						
Akkermansiaceae	*Akkermansia* (+)	*A. muciniphila*	Immunity (+) Intestinal barrier function (+) Glucose metabolism (+) Lipid metabolism (+) Obesity (−) Inflammation (−) Insulin resistance (−) Oxidation (−) Diabetes (−) Hyperuricemia (−) IBD (−) Metabolic disorders (−)	IL-6 (−) IL-1β (−) TNF-α (−) IFN-γ (−) MDA (−) T-SOD (+) LDL-C (−) TG (−)	Propionate (+) Butyrate (+)	[10,16,48]
Verrucomicrobiaceae			Diabetes (−)			[49]
Fusobacteria (Fusobacteriota)						
Fusobacteriaceae	*Cetobacterium (+)*		Intestinal digestion & absorption (+) Glucose metabolism (+) Lipid metabolism (+)	Apoa1 (+) Apoa4 (+) Apoa48 (+) FBP2 (+) DGAT (+)		[50]
	Fusobacterium	*F. nucleatum*	Gut barrier function (+) Inflammation (−) Colorectal cancer (−)	Wnt signaling pathway		[51]

(+) Increasing, upregulating, promoting, accelerating, or maintaining effects of AOS.

(−) Decreasing, downregulating, inhibiting, or suppressing effects of AOS.

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