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Research article

Gut mucosal microbiota profiles linked to development of positional-specific human colorectal cancer

Chunze Zhang[1,6], Mingqian Ma[2], Zhenying Zhao[1], Zhiqiang Feng[2], Tianhao Chu[2], Yijia Wang[3], Jun Liu[4,*] and Xuehua Wan[5,*]

[1] Department of Colorectal Surgery, Tianjin Union Medical Center, Nankai University, Tianjin, China
[2] School of Integrative Medicine, Tianjin University of Traditional Chinese Medicine, Tianjin, China
[3] Tianjin institute of spinal surgery, Tianjin Union Medical Center, Nankai University, Tianjin, China
[4] Department of Radiology, The Fourth Central Hospital Affiliated to Nankai University, Tianjin, China
[5] TEDA Institute of Biological Sciences and Biotechnology, Nankai University, TEDA, Tianjin, China
[6] Tianjin Institute of Coloproctology, Tianjin, China

* **Correspondence:** Email: junliu_sci@163.com, xuehua.wan@nankai.edu.cn.

Supplementary

Table S1. List of bacterial taxa identified in this work.

Bacterium	Metabolism and pathogenicity	Reference
Acidaminococcus	Increased relative abundance of *Acidaminococcus* is associated with future linear growth deficits.	[1]
Actinomyces	*Actinomyces* is significantly increased in multiple polypoid adenomas and intramucosal carcinomas.	[2]
Aggregatibacter	*Aggregatibacter* is positively correlated with visceral fat, fasting plasma insulin, and HOMA-IR in non-alcoholic fatty liver disease.	[3]
Agrobacterium	Mainly known as plant pathogen. Rarely known to infect human.	[4]
Atopobium	Gram-positive, anaerobic, catalase-negative, fastidious bacteria belonging to the family *Coriobacteriaceae*. Maturation of the biofilm and coaggregation of "secondary colonizers" such as *Atopobium* spp. Five patients (18.5%) had polymicrobial bacteremia, and pathogens associated with concomitant polymicrobial infection included *Atopobium*.	[5]
Bacilli	*Bacillus cereus* human pathogen.	[6]
Beijerinckia	The genus *Beijerinckia* was initially isolated from acidic soils.	[7]
Bifidobacterium	A possible role of *Bifidobacteria* in determining distinct tumor characteristics or as an indicator of dysfunctional mucosal barrier in CRC. *Bifidobacterium longum* suppresses colorectal carcinogenesis.	[8,9]
Butyricimonas	A closely interaction between *Butyricimonas* and *Clostridium* is observed in the microbiome network in CRC samples.	[10]
Campylobacter	*Campylobacter jejuni* produces a genotoxin, cytolethal distending toxin, which has DNAse activity and causes DNA double-strand breaks and promotes colorectal tumorigenesis.	[11]
Capnocytophaga	*Capnocytophaga* causes infection in wound.	[12]
Catenibacterium	Compared to normal samples, *Catenibacterium* is only detected in CRC tumor samples.	[13]
Christensenella	The abundance of longevity related *Christensenella* species in gut microbiota increases after fasting and is inversely correlated with age as well as body mass index.	[14]
Citrobacter	*Citrobacter* is able to induce colitis.	[15]
Desulfovibrio	*Desulfovibrio* is commensal microbe colonising the mucus gel layer of the colon, metabolises the sulfate moiety of sulfated mucins, and has increased affinity to ulcerative colitis mucin.	[16]
Dialister	*Dialister* is Gram-stain-negative in healthy faecal sample, and utilizes succinate and causes repetitive bartholinitis episodes.	[17,18]
Dickeya	*Dickeya* relates to potato infection.	[19]

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Bacterium	Metabolism and pathogenicity	Reference
Dysgonomonas	*Dysgonomonas* is Gram-stain negative cocci. It grows optimally at 37 °C and is catalase positive but oxidase negative.	[20]
Eikenella	*Eikenella* produces lysine decarboxylase.	[21]
Eubacterium	Compared to healthy samples, abundance of *Eubacterium* decreases in patients with IBD and CRC.	[22,23]
Faecalibacterium	*Faecalibacterium* plays a major role in the regulation of gut barrier, inflammation and metabolic functions.	[24]
Finegoldia	*Finegoldia magna* is an anaerobic opportunistic pathogen.	[25,26]
Fusobacterium	*Fusobacterium* has high abundance in intestine in CRC patients, and low abundance in health intestine.	[27]
Gemella	*Gemella* is associated with CRC. The risk of CRC is increased in patients with bacteremia from *Gemella*.	[28]
Granulicatella	*Granulicatella* causes infective endocarditis and endophthalmitis.	[29,30]
Haemophilus	*Haemophilus* was depleted in the transition from stage 0 to early-stage CRC.	[31]
Klebsiella	*Klebsiella* induces pneumosepsis, produces cytotoxin, and is associated with necrotizing enterocolitis.	[32,33]
Labrys	Budding bacteria isolated from rhizosphere habitats in environments.	[34]
Lactobacillus	As a probiotic, *Lactobacillus* prevents dimethylhydrazine-induced colorectal cancers.	[35]
Leptotrichia	*Leptotrichia* is significant co-occurrence within individual tumors.	[36]
Megasphaera	A butyrate-producing bacterium.	[37]
Morganella	*Morganella* produces extended-spectrum β-lactamase, and causes wound infections after colorectal surgery.	[38]
Moryella	*Moryella* is weakly saccharolytic and produces indole, acetate, butyrate and lactate as major metabolic end products.	[39]
Neisseria	Anti-inflammatory microenvironment causes decreased *Neisseria* abundance.	[40]
Oscillospira	High *Oscillospira* abundance indicates constipation and low BMI.	[41]
Parvimonas	Bacterial biomarker of colorectal cancer.	[42]
Peptococcus	*Peptococcus magnus* human pathogen. *Peptococcus niger* is a Gram-positive, non-motile, obligatory anaerobic cocci that is a constituent of the normal human intestinal mucous membranes and umbilicus flora.	[43]
Peptoniphilus	*Peptoniphilus* is a Gram-positive anaerobic coccus mainly involved in polymicrobial infections, and is reported in a case of peritoneal infection in a patient with intestinal occlusion.	[44]
Peptostreptococcus	Bacterial biomarker of colorectal cancer.	[42]
Plesiomonas	*Plesiomonas* has several virulence factors, such as lysophospholipase, a twin-arginine translocation system and the type VI secretion effector Phospholipase A1, which relate to diarrhoeal disease.	[45]

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Bacterium	Metabolism and pathogenicity	Reference
Porphyromonas	*Porphyromonas gingivalis* is a keystone pathogen in periodontitis and promotes the proliferation of colorectal cancer cells by activating the MAPK/ERK signaling pathway.	[46]
Prevotella	Intestinal *Prevotella* colonization results in metabolic changes in the microbiota, which reduce IL-18 production and consequently exacerbate intestinal inflammation and potential systemic autoimmunity.	[47]
Prevotella	*Prevotella* produces butyrate and reduces abundance in CRC patients.	[48]
Pseudomonas	*Pseudomonas* produces exopolysaccharides and infection.	[49,50]
Pseudonocardia	The genus *Pseudonocardia* belongs to a group of *Actinomycetes*, and is a member of the family *Pseudonocardiacea*. The members of this genus are aerobic, Gram-positive, non-motile bacteria that are commonly found in soil, plant and environment. *Pseudonocardia carboxydivorans* may be human pathogen.	[51]
Pyramidobacter	*Pyramidobacter* produces acetic and isovaleric acids.	[52]
Rickettsia	The genus contains many human pathogens.	
Rothia	The genus *Rothia* are emerging as opportunistic pathogens associated with various infections in immunocompromised and immunocompetent individuals.	[53]
Selenomonas	*Selenomonas* is closely associated with CRC patients with hyperlipoidaemia.	[54]
Shewanella	*Shewanella* is found in water environment and in patients, and can act as theoriginator of oxacillinase in Gram-negative bacteria.	[55]
Slackia	*Slackia* is gut-associated bacteria that play roles in host lipid and xenobiotic metabolism. *Slackia* may be free living in the lumen because it has low adhesion to cells.	[56]
Sneathia	*Sneathia amnii* produces a cytotoxin, named CptA for cytopathogenic toxin, component A, which is capable of permeabilizing chorionic trophoblasts and lysing human red blood cells.	[57]
Streptococcus	*Streptococcus bovis* contributes to the development of CRC via recruiting CD11b TLR-4 cells, and should be investigated for early detection of colorectal pathology. *Streptococcus gallolyticus* subsp. *gallolyticus* (Sgg) infection has gained considerable attention for its strong association with CRC.	[58–60]
Turicibacter	*Turicibacter* is an anaerobic, Gram-positive bacterium, isolated from human feces.	[61]
Treponema	A genus of commonly found oral bacteria that are closely related to periodontitis and the etiology of implant periarthritis.The genus *Treponema* contains both pathogenic and nonpathogenic species. Human pathogens cause four treponematoses: syphilis (*T pallidum* subsp *pallidum*), yaws (*T pallidum* subsp *pertenue*), endemic syphilis (*T pallidum* subsp *endemicum*), and pinta (*T carateum*). Nonpathogenic treponemes may be part of the normal flora of the intestinal tract, the oral cavity, or the genital tract. Some of the oral treponemes have been associated with gingivitis and periodontal disease.	[62]
Vagococcus	The *Vagococcus* is a relatively recently recognized genus of Gram-positive, catalase-negative cocci.	[63]
Veillonella	A causative pathogen of bloodstream and decubitus ulcer infection.	[64]

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