Intestinal flora and human health

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There is a growing interest in intestinal flora and human health and disease. The intestines of humans contain 100 trillion viable bacteria. These live bacteria, which make up 30% of the faecal mass, are known as the intestinal flora. There are two kinds of bacteria in the intestinal flora, beneficial and harmful. In healthy subjects, they are well balanced and beneficial bacteria dominate. Beneficial bacteria play useful roles in the aspects of nutrition and prevention of disease. They produce essential nutrients such as vitamins and organic acids, which are absorbed from the intestines and utilised by the gut epithelium and by vital organs such as the liver. Organic acids also suppress the growth of pathogens in the intestines.

Other intestinal bacteria produce substances that are harmful to the host, such as putrefactive products, toxins and carcinogenic substances. When harmful bacteria dominate in the intestines, essential nutrients are not produced and the level of harmful substances rises. These substances may not have an immediate detrimental effect on the host but they are thought to be contributing factors to ageing, promoting cancer, liver and kidney disease, hypertension and arteriosclerosis, and reduced immunity. Little is known regarding which intestinal bacteria are responsible for these effects. A number of factors can change the balance of intestinal flora in favour of harmful bacteria. These include peristalsis disorders, surgical operations of stomach or small intestine, liver or kidney diseases, pernicious anaemia, cancer, radiation or antibiotic therapies, immune disorders, emotional stress, poor diet and ageing.

However, more importantly, the normal balance of intestinal flora may be maintained, or restored to a normal from an unbalanced state, by oral bacterio-therapy or by a well balanced diet. Oral bacterio-therapy using intestinal strains of lactic acid bacteria, such as lactobacillus and bifidobacteria, can restore normal intestinal balance and produce beneficial effects. Benefits include suppression of intestinal putrification so as to reduce constipation and other geriatric diseases; prevention and treatment of diarrhoea including antibiotic-associated diarrhoea; stimulation of the immune system; and increased resistance to infection.

Ecological significance of intestinal flora

A single individual harbours in the intestine 100 trillion viable bacteria and some 100 different bacterial species, which constitute the intestinal flora. In mutual symbiotic or antagonistic relationships, these organisms grow on ingested food components and those secreted into the alimentary tract by the host, and excreted. In the past, most of these organisms have been considered to be dead, but marked advances in culturing techniques for anaerobic bacteria enable cultivation of over 70% of the microscopic count of bacteria in human faeces, and often more than 90%.

Major bacterial groups composing the intestinal flora

The major bacterial groups detected in the intestinal flora are roughly divided into the following three groups:

1) the lactic acid bacteria group (LAB), including *Bifidobacterium, Lactobacillus* and *Streptococcus* including *Enterococcus*;
2) the anaerobic group, including *Bacteroidaceae*, anaerobic curved rods, *Eubacterium, Peptococcaceae, Veillonella, Megasphaera, Gemmiger, Clostridium*, and *Treponema*; and
3) the aerobic group, including *Enterobacteriaceae, Staphylococcus, Bacillus, Corynebacterium, Pseudomonas*, and yeasts (Table 1)[1].

Development of the intestinal flora of infants

The fetus exists in a sterile environment until birth. After birth it rapidly becomes colonised by bacteria. On the 1st to 2nd days of life, the large intestine of neonates fed with breast milk and supplementary cow's milk is colonised by enterobacteriaceae, streptococci including enterococci, and clostridia. On the 3rd day, bacteroides, bifidobacteria and clostridia occur in 40% of infants. Between days 4 and 7, bifidobacteria become predominant accounting to 10^{10} to 10^{11} organisms per gram faeces, and clostridia, bacteroides, enterobacteriaceae, streptococci, and staphylococci decrease. Thus, nearly 100% of all bacteria cultured from stools of breast-fed infants were bifidobacteria (Fig.1)[1].

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Table 1. Differentiation of major intestinal bacterial groups

Bacterial group	Gram-staining	Morphology	Aerobic growth	Spore	Major fermentation products
LAB group					
Lactobacillus	+		+	--	Lactic acid
Bifidobacterium	+		--	--	Acetic acid + lactic acid
Streptococcus	+		+	--	Lactic acid
Anaerobic group					
Bacteroidaceae	--		--	--	Various products
Anaerobic curved rods	--		--	--	Succinic acid, butyric acid
Eubacterium	+		--	--	Various products
Peptococcaceae	+		--	--	Various products
Veillonella	--		--	--	Acetic acid + propionic acid
Megasphaera	--		--	--	Caproic acid + butyric acid
Gemmiger	--		--	--	
Clostridium	+/--		--	+	Various products
Treponema	--		--	--	
Aerobic group					
Enterobacteriaceae	--		+	--	
Staphylococcus	+		+	--	
Bacillus	+		+	+	
Corynebacterium	+		+	--	
Pseudomonas	--		+	--	
Yeasts	+		+	--	

Figure 1. Development of the faecal flora of neonates

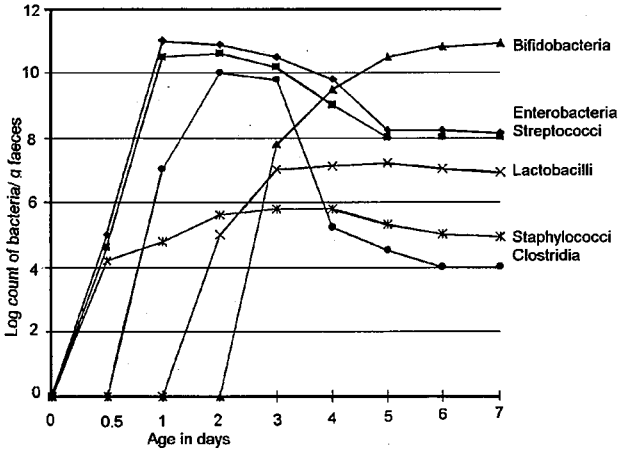
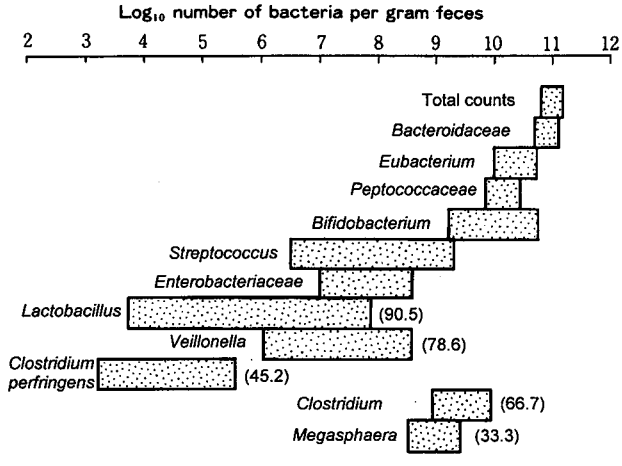


Figure 2. Composition of the faecal flora in adults



The intestinal flora of children and adults

Although bifidobacteria have been considered to be the most important organisms for infants and lactobacilli and *Escherichia coli* are more numerous bacteria for children and adults than bifidobacteria, it has now become clear that bifidobacteria also constitute a member of the major organisms in the colonic flora of healthy children and adults. During weaning, when an adult diet is consumed, the stools of infants shifted to the Gram-negative bacillary flora of adults: bifidobacteria decrease by 1 log, the numbers of bacteroidaceae, eubacteria, peptococcaceae, and usually clostridia outnumber bifidobacteria, which constitute 5 to 10% of the total flora. The counts of enterobacteriaceae, and streptococci decrease to less than 10^8 per gram faeces. Lactobacilli, megasphaerae, and veillonellae are often found in adult faeces, but the counts are usually less than 10^7 per gram faeces. The species and biovars alter from infant-type such as *B. infantis* and *B. breve* to adult-type such as *B. adolescentis* and *B. longum* (Fig.2)[1].

The intestinal flora of elderly persons

In elderly persons bifidobacteria decrease or diminish, clostridia including *C. perfringens* significantly increase, and lactobacilli, streptococci and enterobacteriaceae also increase. This phenomenon is considered to be a result of ageing, but it might accelerate senescence (Fig.3)[1].

Figure 3. Changes in the faecal flora with increased age

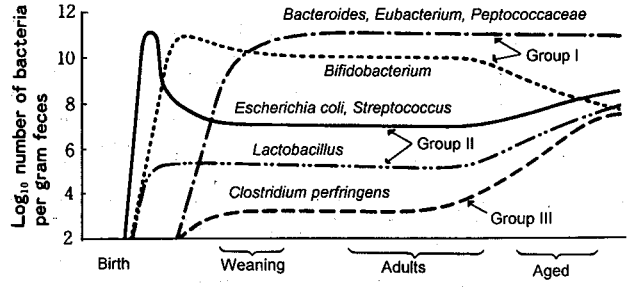


Figure 4. Enzymatic activities of intestinal bacteria

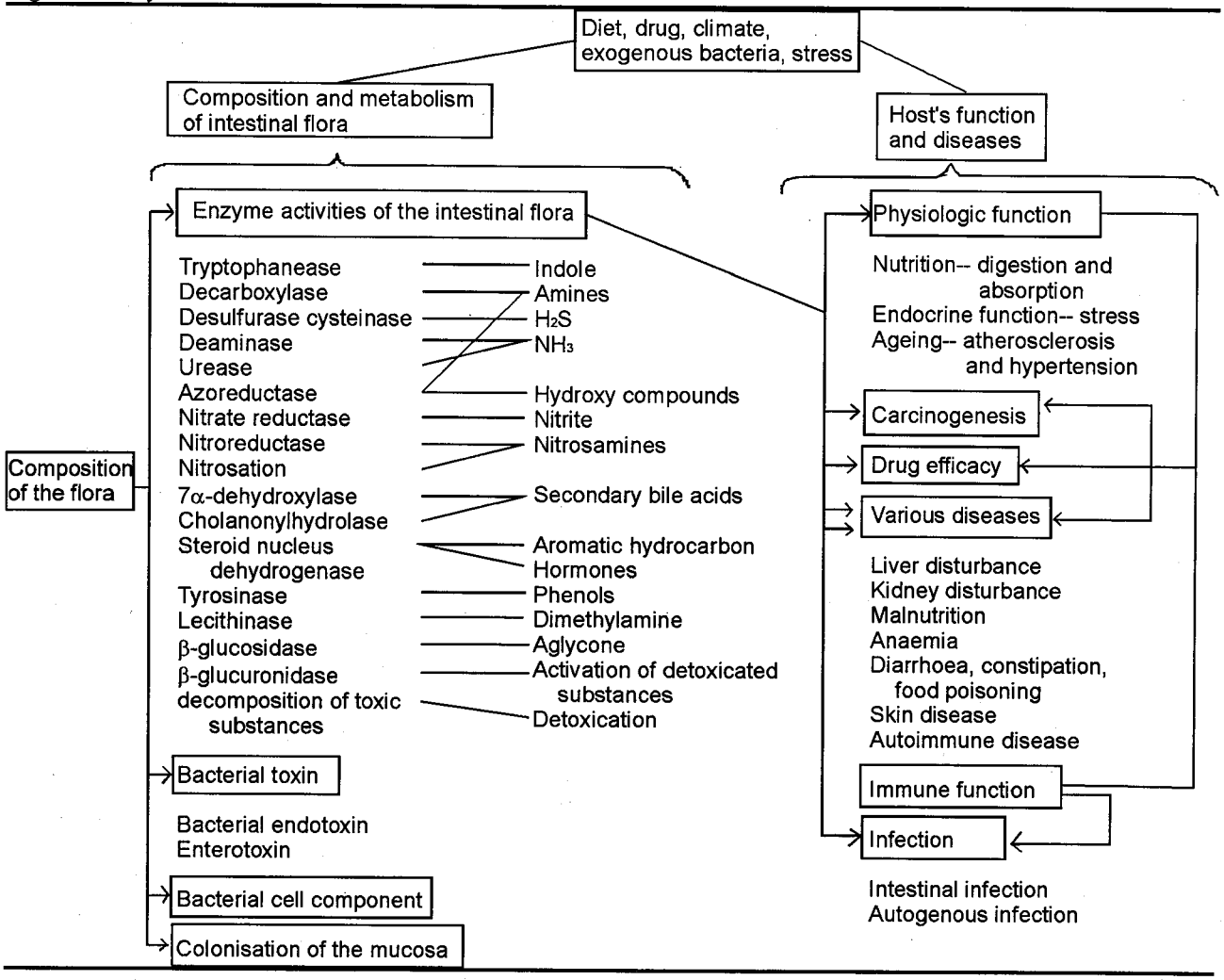
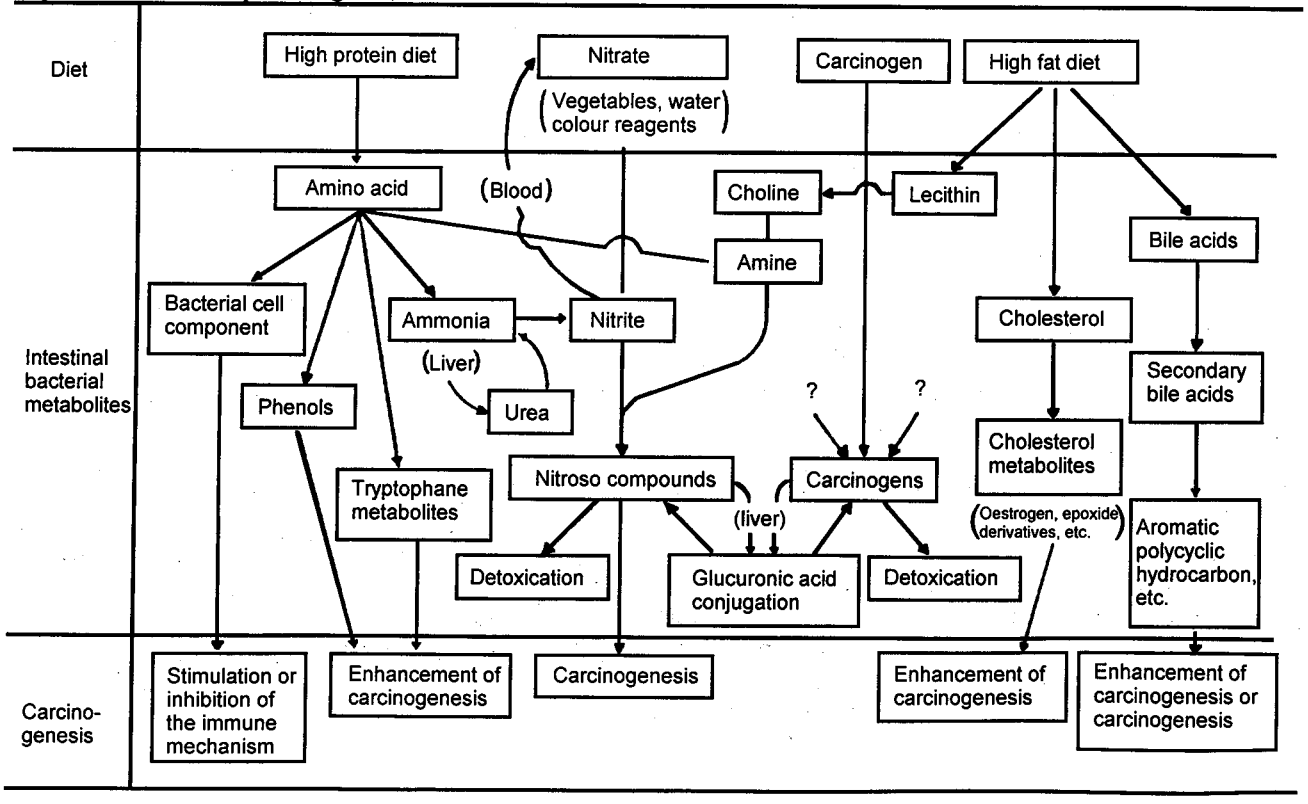


Figure 5. Relationships among diet, intestinal bacteria and cancer



Disturbances in the intestinal flora

Although the composition of the intestinal flora is rather stable in healthy individuals, it can be altered by many endogenous and exogenous factors such as peristalsic disorders, cancer, surgical operations of stomach or small intestine, liver or kidney diseases, pernicious anaemia, blind loop syndrome, radiation therapy, emotional stress, disorders of immune systems, administration of antibiotics, and ageing.

Disturbances in the intestinal flora are non-specific: the small intestine harbours large numbers of bacteria, particularly anaerobes, enterobacteriaceae and streptococci; bifidobacteria disappear or considerably decrease in the large intestine, while enterobacteriaceae and streptococci remarkably increase and, some times, *Clostridium perfringens* also increase.

These ecological evidences would suggest that bifidobacteria should exist in the large intestine for maintenance of health and are far more important than *Lactobacillus acidophilus* as the beneficial intestinal bacteria throughout human life. In other words, the reduction or disappearance of bifidobacteria in human intestine would indicate an "unhealthy" state.

Role of the intestinal flora in human health

Metabolic profile of the intestinal flora

The intestinal flora is composed of different bacterial species, and thus, contains a variety of enzymes that perform the extremely varied types of metabolism in the intestine, and influence the host's health and resistance to disease (Fig. 4). This includes such factors as: nutrition, physiological function, drug efficacy, carcinogenesis, ageing, immunological response and resistance to infection, endotoxins, and various other stresses. Within the intestine, the bacteria are implicated in the conversion of various substances that produce both beneficial and detrimental products to the host. In addition, bacterial toxins and cell components produced by some bacterial species modify the host's immune responses, enhancing or inhibiting immune function. The beneficial intestinal flora protect the intestinal tract from proliferation or infection of harmful bacteria, while the detrimental bacteria manifest pathogenicity when the host's resistance is decreased.

The intestinal flora may play an important role in the causation of cancer and ageing

Dietary factors are considered important environmental risk determinants for colorectal cancer development. From epidemiological observations, a high fat intake is associated positively and a high fibre intake negatively with colorectal cancer. This is thought to occur by the following mechanisms. From food components in the gastrointestinal tract, organisms produce various carcinogens from the dietary components and endogenous substances, detoxify carcinogens, or enhance the host's immune function, which results in changes in the incidence of cancers. The ingestion of large amounts of animal fat enhances bile secretion, causing an increase in bile acid and cholesterol in the intestine. These increased substances are converted by intestinal bacteria into secondary bile acids, their derivatives, aromatic polycyclic hydrocarbons, oestrogen and epoxides derivatives that are related to carcinogenesis. Various tryptophan metabolites (indole, skatole, 3-hydroxykinurenine, 3-hydroxyanthranilic acid, etc.) phenols, amines, and nitroso compounds produced by intestinal bacteria from protein also participate in carcinogenesis (Fig. 5). However, some intestinal bacteria reportedly inactivate noxious substances in the intestine.

Recent epidemiological studies have revealed that insufficient intake of dietary fibre is associated with high incidences of Western diseases such as colorectal cancer, obesity, heart disease, diabetes, and hypertension. Ingested dietary fibre causes increased volume of faeces, dilution of noxious substances, and shortening of the transit time of intestinal contents, resulting in early excretion of noxious substances such as carcinogens produced by intestinal bacteria.

The cell components of intestinal bacteria modify the host's immune function; some enhance immune response and others suppress it, involving them indirectly in the suppression or enhancement of carcinogenesis.

It is completely unknown at present which of these mechanisms plays the key role in carcinogenesis.

Table 2. Incidence of liver tumour in germfree (GF), conventionalised (CV), and gnotobiotic (GB) C3H/He male mice associated with human intestinal bacteria

Group	Bacteria	NB	Liver tumour (%)*
GF	Germfree	0	30
CV	Conventionalised		75
GB6	*Mitsuokella multiacida* A4052	9.7	75
GB2	*Enterococcus faecalis* M266TA	9.7	67
GB1	*Escherichia coli* M66	10.3	62
GB13	*Bifidobacterium longum* E194b	10.1	47
GB20	*Escherichia coli* M66	10.2	100
	Enterococcus faecalis M266TA	10.2	
	Clostridium paraputrificum VPI1586	9.5	
	Clostridium paraputrificum VP16558		
GB7	*Escherichia coli* M66	9.9	88
	Clostridium perfringens MAC521	9.5	
GB9	*Escherichia coli* M66	9.7	80
	Enterococcus faecalis M266TA	9.9	
	Bacteroides vulgatus M45	10.1	
GB21	*Escherichia coli* M66	9.3	46
	Enterococcus faecalis M266TA	10.2	
	Clostridium paraputrificum VPI1586	9.6	
	Clostridium paraputrificum VP16558		
	Bifidobacterium longum E194b	9.8	

NB= number of bacteria established log/g faeces
*= percentage of animals

Our studies with gnotobiotic mice showed that the presence of bacteria in the intestine can have marked effect on the incidence of liver tumours in C3H/He mice. Mice with conventional microflora had a much higher incidence of hepatic tumours (about 75% after 1 year) than their germfree counterparts (30% incidence after 1 year). Furthermore, when germfree mice were contaminated with specific intestinal bacteria, isolated from humans, the tumour incidence ranged up to 100%; of the mono-

contaminated mice *Mitsuokella multiacida* gave tumours in 75% of the mice, *Enterococcus faecalis* in 67%, *Escherichia coli* in 62%, and *B. longum* in 47%. When mixtures of strains were used, high rates of tumour production were observed with mixtures of *E. coli* + *E. faecalis* + *C. paraputrificum* (100%), *E. coli* + *C. perfringens* (88%), or *E. coli* + *E. faecalis* + *B. vulgatus* (80%). However, this promoting effect was suppressed by 46% by the addition of Bifidobacterium longum to the first promoting combination (Table 2)[3,4].

We also studied the effect of intestinal flora on longevity. Germfree (GF) mice, conventional mice, and gnotobiotic (GB) mice (GB-1) associated with *E. coli, Enterococcus faecalis, Bacteroides vulgatus, Eubacterium aerofaciens, Bifidobacterium longum* and *Clostridium perfringens*, and those associated with the same combination of intestinal bacteria without *B. longum* (GB-2) or *C. perfringens* (GB-3) were produced, and maintained until their natural death (Table 3). Average life spans of GF female were longest, 96.3 weeks, 78.2 weeks in CV, 87.1 weeks in GB-1, 80.7 weeks in GB-2, and 87.1 weeks in GB-3: the average life spans were shorter in GB-2 than in GF. There was also no difference in average life spans between GB-1 and GB-3. These findings suggest that the presence of *B. longum* may be related to longevity in GB animals.

Table 3. Comparison of lifespan of germfree (GF) conventional (CV) female mice and gnotobiotic (GB) CF#1 female mice associated with human intestinal bacteria.

	Animals				
Bacterial strains used	GF	CV	GB-1	GB-2	GB-3
Bifidobacterium longum E194b	–	*	9.8a	–	9.8
Clostridium perfringens MAC521	–	*	8.6	8.6	–
Escherichia coli 123	–	*	9.1	10.0	9.4
Enterococcus faecalis 1-12	–	*	10.1	10.1	10.1
Bacteroides vulgatus M-64	–	*	10.3	10.1	10.3
Eubacterium aerofaciens 151	–	*	10.3	10.3	10.3
Lifespan	96.3	78.2	87.1	80.7	87.1
(Means ± SD of age in weeks)	±14.6	±22.2	±19.9	±21.5	±17.6

*: Conventional rat flora. a: No. of bacteria established (log/ g faeces)

These two studies suggested that intestinal bacteria are related to both promotion and prevention of cancer and ageing. The mechanism of the suppressive effect of bifidobacteria on liver tumours might be related to detoxifying carcinogens by bifidobacteria.

Dietary control of intestinal flora for human health

Evidence that the intestinal flora is closely related to the host's health and disease indicates the importance of the balance of the intestinal flora for health and longevity. In other words, the increase of harmful bacteria in the intestine may ultimately lead to various disorders, such as liver and kidney disorders, atherosclerosis, hypertension, cancer, and ageing. A satisfactory balance of the intestinal flora is possibly achieved by a nutritionally varied diet, and inclusion of dietary fibre and fermented milk which promote useful bacteria or suppress harmful bacteria.

Table 4. Utilisation of 5 sugars by various intestinal bacteria

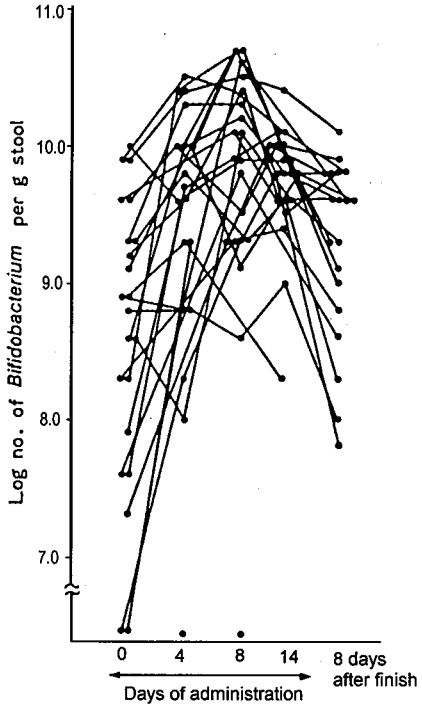
Bacterial species	Number of strains	SOR	RAF	STA	FOS	GLU
Bifidobacterium:						
B. bifidum	6	–	–	±	–	++
B. longum	8	+++	++	+++	++	+++
B. breve	4	+++	+++	+++	+	+++
B. infantis	2	+++	+++	+++	++	+++
B. adolescentis	9	++	++	++	++	+++
Lactobacillus:						
L. casei	2	–	–	–	–	+
L. acidophilus	3	±	±	±	+	++
L. gasseri	1	+	+	–	+	+
L. salivarius	2	++	++	++	+	++
Bacteroides:						
B. vulgatis	9	±	±	+	+	++
B. fragilis	3	+	+	+	+	++
B. distasonis	5	+	±	+	±	+
B. ovatus	4	+	+	+	+	++
B. thetaiotamicron	2	±	±	±	+	+
B. uniformis	1	+	+	+	+	+
B. melaninogenicus	1	+	+	+	+	+
Fusobacterium:						
F. varium	1	–	–	–	–	±
F. necrophorum	1	–	–	–	–	–
***Mitsuokella** multiacida*	4	++	++	++	+	++
***Megamonas** hypermegas*	1	++	++	++	+	+++
Eubacterium:						
E. limosum	3	–	–	–	±	++
E. aerofaciens	2	±	±	±	±	++
E. nitritogenes	1	–	–	–	–	++
E. lentum	1	–	–	–	–	–
Clostridium:						
C. perfringens	6	–	–	–	–	+
C. paraputrificum	4	–	–	–	–	+++
C. difficile	4	–	–	–	–	+
C. butyricum	2	++	++	++	++	+++
C. clostridiforme	2	±	±	±	–	+
C. innocuum	1	–	–	–	±	+++
C. ramosum	1	±	+	±	++	+++
C. sordelli	1	–	–	–	–	±
C. septicum	1	–	–	–	–	+++
C. cadaveris	1	–	–	–	–	±
C. sporogenes	1	–	–	–	–	±
***Propionibacterium** acnes*	1	–	–	–	–	++
Peptostreptococcus:						
P. magnus	1	–	–	–	–	–
P. anaerobius	1	–	–	–	–	±
P. productus	2	±	±	±	+	++
P. asaccharolyticus	1	–	–	–	–	±
P. prevotti	1	±	±	±	–	+
Veillonella:						
V. dispar	1	–	–	–	–	–
V. parvula	2	–	–	–	–	–
***Megashaera** elsdenii*	1	–	–	–	–	±
***Escherichia** coli*	6	–	±	–	–	++
***Klebsiella** pneumoniae*	3	+	+	+	+	++
***Enterobacter** aerogenes*	1	+	±	±	±	±
Enterococcus						
E. faecalis	1	±	±	±	+	+++
E. faecium	1	+	±	+	+	+++
***Streptococcus** pyogenes*	1	–	–	–	±	+
***Staphylococcus** aureus*	1	–	–	–	+	++

SOR, soybean oligosaccharides refine; RAF, raffinose; STA, stachyose; FOS, fructo-oligosaccharide; GLU, glucose. Evaluation of bacterial growth (OD_{630}) (OD carbohydrate - OD control): --, < 0.099; ±, 1.100-0.199; +, 0.200-0.399; ++, 0.400-0.599; +++, > 0.600

Effect of intake of dietary fibre or oligosaccharides

Human digestive enzymes have little or no effect on raw starch and polysaccharides such as cellulose, pectin, hemicellulose, and pentosan; and oligosaccharides such as melibiose, raffinose, stachyose, fructo-oligosaccharides, isomalto-oligosaccharides, and galacto-oligosaccharides. These substances are hydrolysed to varying degrees and digested by colonic bacteria with the production of organic acids, mainly volatile fatty acids (acetate, propionate, and butyrate), and gas (carbon dioxide and hydrogen). Small amounts of lactic, formic and succinic acids are also produced. Methane may be produced in some people.

Figure 6. Changes in faecal bifidobacteria by the administration of FOS. FOS (8g/ day) were administered to aged subjects.



Most *Bifidobacterium* species metabolise a wide rage of indigestible polysaccharides and oligosaccharides to acetic and lactic acids and subsequently act as effective scavengers in the large intestine, when many oligosaccharides are ingested in the diet, while *E. coli* and *C. perfringens* do not.

In this way several commercially available oligosaccharides including raffinose, stachyose, fructo-oligosaccharides, isomalto-oligosaccharides, galacto-oligosaccharides are effective for proliferation of resident or implanted bifidobacteria in intestine and cause the reduction of faecal ammonia and pH as well as serum cholesterol and triglyceride level of the host[5-8].

In our studies with volunteers, improvement of intestinal flora as well as intestinal environment were observed by oral administration of various oligosaccharides, including fructo-oligosaccharides, palatinose condensate, raffinose, and soybean oligosaccharides. Table 4 shows utilisation of five oligosaccharides by intestinal bacteria. Most of the oligosaccharides stimulated the growth of bifidobacteria *in vitro* and *in vivo* (Fig.6), and caused reduction of faecal pH, beta-glucuronidase, azoreductase, and indole, serum cholesterol and triglycerides levels as well as the blood pressure of elderly patients with hyperlipidaemia. From the results presented here, it may be concluded that oligosaccharides are considered to enhance the intestinal bifidobacteria, to promote the intestinal flora, the consistency of stool, and lipid metabolism.

We also studied the effect of dietary fibre on the faecal flora and faecal metabolite in eight healthy adult volunteers fed with low cholesterol (LC) diet, high cholesterol (HC) diet and high cholesterol supplemented with polydextrose (15g/day) (HC-P) diet for a 12 day interval. While a decrease (ca. 25%) of the faecal weight was observed during HC diet, HC-P diet led to a ca. 30% increase of the faecal weight. The faecal pH increased (ca. 0.2) during HC diet and decreased (ca. 0.6) during HC-P diet. Faecal putrefactive products including phenol, p-cresol, indole, iso-butyric and iso-valeric acids remarkably decreased by the administration of polydextrose (Fig. 7). In addition, the occurrence of clostridia, including *Clostridium perfringens* was higher during HC diet than during HC-P diet. These results suggested that polydextrose has a beneficial effect on the intestinal environment and human health through changing the balance and metabolic activity of the intestinal flora and physiologic activity of the host and that intestinal clostridia are involved in putrefactive activity in the intestinal content[9].

Effect of yoghurt on human health

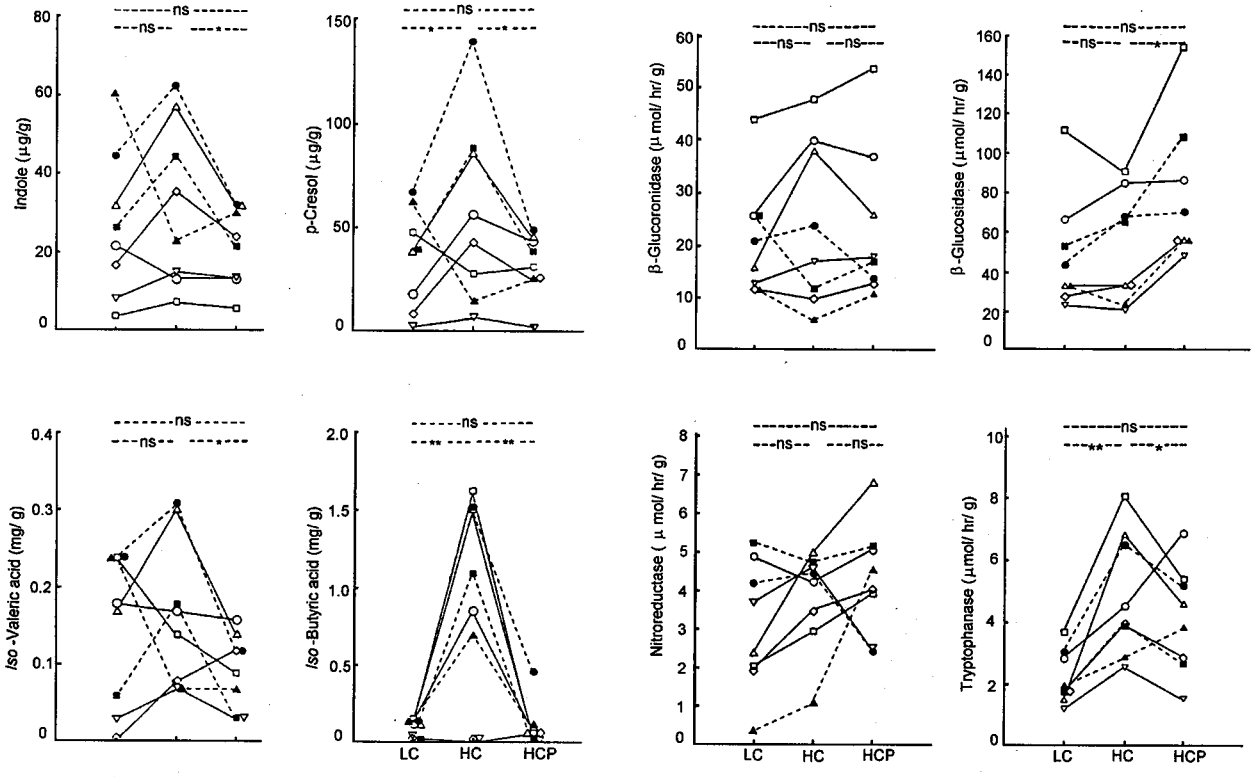
Yoghurt and other fermented milk products may enhance human health by the following mechanisms[10].

1) Effect of milk used for yoghurt production: Milk protein prevents stomach cancer. Lactose increases indigenous bifidobacteria in the intestine. Calcium and iron prevent osteoporosis and anaemia, respectively. Vitamin A may prevent certain cancers.
2) Effect of fermentation products of yoghurt: Lactate prevents constipation and inhibits putrefactive bacteria. Peptone and peptides promote liver function.
3) Effect of lactic acid bacteria (LAB): LAB detoxify carcinogens, stimulate immune response, and lower serum cholesterol.

Several recent studies have focused on bifidobacteria to establish the importance of these bacteria in influencing certain normal functions of the intestinal tract and in exploring its role in human health and diseases. In Japan, bifidobacteria now-a-days have been used as dietary supplements or as starter culture for yoghurt and other cultured milk products with the thought that such products may help the promotion of health. The effects of the daily intake of such products are reported as follows:

1) to suppress the putrefactive bacteria as well as intestinal putrefaction, for the prevention of constipation, geriatric diseases, including cancer,
2) to prevent and treat antibiotic-associated diarrhoea,
3) to stimulate immune response,
4) to contribute to a greater resistance to infection.

Figure 7. Influence of low cholesterol (LC) diet, high cholesterol (HC) diet supplemented with polydextrose. (HCP) on β-glucoronidase, β-glucosidase, nitro-reductase and tryptophanase activity in human faeces.



Results are presented for each volunteer. *, P,0.05; **, P,0.01; ns, not significant. □—□, Subject a; ✧—✧,Subject b; O—O, Subject c; Δ—Δ, Subject d; ▽—▽, Subject e; ■—■, Subject f; ●—●, Subject g; ▲—▲, Subject h.

Effect of oral administration of bifidobacteria on intestinal flora and intestinal metabolites

We observed that oral administration of 10^9 *Bifidobacterium longum* preparation per day for 5 weeks to 5 healthy volunteers from 25 to 35 years old resulted in the increase of the counts of bifidobacteria and the remarkable decrease of the counts and frequencies of occurrence of clostridia in stools. This result also reflected a decrease of ammonia concentration and beta-glucuronidase activity in both faeces and serum[11].

Serum cholesterol in Hartley male rabbits fed with 0.25% cholesterol diet supplemented with 10^{10}/day of *B. longum* for 13 weeks were compared with the control diet group. In 2 of 3 rabbits fed with diet supplemented with *B. longum* there was a remarkably suppressed increase in cholesterol level, but 1 of 3 rabbits showed no effect.

Conclusion

There is a growing consensus that the intestinal flora is closely related to the host's health and proneness to disease. The predominance of harmful bacteria in the intestine may ultimately lead to various disorders, while useful bacteria subsequently act as scavengers and physiological regulation in the large intestine. Maintenance of a satisfactory balance of the intestinal flora is achieved by a diet that includes foods that promote beneficial bacteria or suppress harmful bacteria.

In future, a more effective diet of this type, will be developed. Gene recombination may produce new bacterial strains that colonise firmly in the intestine, have strong aciduric character, and inactivate carcinogens. Ingestion of such bacteria and their substrates and products in the form of food, in viable form, may improve the balance of the intestinal flora, intestinal metabolism, and human health.

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腸道菌群與人體健康

摘要

人們對腸道菌群和人體健康及疾病的關系越來越感興趣。人體的腸道含有 100 千萬不同的細菌，這些活細菌組成 30% 的糞質稱腸道菌群。在腸道菌群中，有有益的和有害的二種不同類型的細菌，在健康者，他們保持平衡並由有益菌群支配。有益細菌在營養和疾病的預防方面起有益的作用。其他腸道細菌產生對宿主有害的物質，例如腐敗產物、毒素、致癌物。這些物質對宿主可能沒有立即的危害作用，但它們可能導致衰老，促進癌症發生，肝臟、腎臟疾病，高血壓和動脈硬化，免疫力低下。似未知道，何種菌群有這些作用。許多因素能改變腸內菌群的平衡而有利於有害細菌，這些包括蠕動紊亂，胃或小腸的外科手術，肝臟或腎臟病，惡性貧血，癌症，放射或抗菌治病，免疫紊亂，情緒壓抑，飲食不良和高齡。然而，更重要的是，腸道菌群的正常平衡可以通過口服細菌治療或較好平衡飲食來保持或修復從非平衡狀態到正常。應用乳酸菌的腸菌株口服細菌治療，例如乳酸杆菌屬（ Lactobacillus ）和勞根式不規則小杆菌（ Bifidobacteria ）可修復正常腸道平衡和產生有益作用，這些有益作用包括腸道腐化抑制而減少便秘和其他老年疾病，腹瀉的預防和治療，包括抗生素相關腹瀉，免疫系統的刺激和增強對感染的抵抗力。

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