Impact of Nutrition on the Microbiome

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NUTRITION AND THE MICROBIOME

Over the past 15 years, the scientific community has recognized the important role of the microbiome as a regulator of human health. The term "microbiome" refers to the trillions of microorganisms that naturally reside throughout the body, particularly the gut. Variations in the diversity of the gut microbiota have been linked to numerous diseases, ranging from obesity to cancer. 1-3 Emerging evidence indicates that diet exerts a powerful influence on the diversity of microbial species in the gut, carrying significant implications for health and disease. Scientific data has elucidated certain healthy eating patterns, such as diets rich in whole foods, plant fibers, and phytonutrients, each of which support a balanced gut microbiota and health maintenance throughout the lifespan.

WHY THE MICROBIOME MATTERS: **GUT HEALTH AND SOCIETY**

Diseases associated with changes in the gut microbiota are some of the most common and costly in developed countries. Many conditions like obesity, diabetes, cardiovascular disease, inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), colorectal cancer, and other diseases have been linked to the typical Western diet, comprising saturated fats and processed foods. ⁴⁻⁶ The prevalence of obesity and diabetes, for example, has reached epidemic proportions; in the US, more than 1 in 3 adults are obese and more than 30 million have diabetes.⁷⁻⁹ Diseases of the gut are also common and costly. Chron's disease, a form of IBD, carries mean annual direct medical costs of \$12,417 per patient. Overall, IBD accounts for nearly 6 million physician visits and more than 160,000 hospitalizations per year in the US.¹⁰ Evidence links each of these conditions to the gut microbiota, suggesting that an unhealthy microbiome can have a broad and deep impact on the health of the US population.

Our growing awareness of the microbiome and its influence on common and costly disease states prompted the National Institutes of Health (NIH) to undertake the Human Microbiome Project. The aim of this program is to characterize microbial

communities in the human body and to look for correlations between changes in the microbiome and human health.¹¹ This project is analogous to the Human Genome Project, which sought to sequence the human genome to facilitate research into genetic causes of disease. In fact, it is estimated that the microbiome as a whole accounts for more genetic information that the entire human genome, with perhaps 1000 more genes.¹¹ Unlike the human genome, the composition of the microbiome varies substantially between individuals and can change within an individual in response to alterations in diet, medication, disease states, and the aging process. 12,13

FRIEND AND FOE: THE MICROBIOME

Our understanding of the microbiome and its role in health and disease has evolved tremendously in the last two decades. We now know that these microorganisms exist in symbiosis with the intestinal mucosa and are essential for gut homeostasis. 14,15 The composition of the microbiome affects the conversion of food into energy and nutrients, mucosal immunity, intestinal permeability, overall gastrointestinal (GI) health, and systemic inflammation.^{1,2} Perturbations in the microbiome have been linked to the development of a variety of disorders, both directly in the GI system and through the development and perpetuation of inflammatory states common to systemic diseases, such as diabetes and arthritis.3

The Healthy Gut

Current evidence describes a healthy microbiome as one characterized by high microbial diversity and the ability to resist change under physiological stress.³ In healthy individuals, the gut microbiome contributes to the digestion of foods and the generation of nutritive compounds. In fact, the microbiome is considered by many to be a metabolic organ, contributing to energy homeostasis and intestinal immunity. Bacteria in the gut

- 1. Furet JP, Kong LC, Tap J, et al. Differential adaptation of human gut microbiota to bariatric surgery-induced weight loss: links with metabolic and low-grade inflammation markers. Diabetes. Dec 2010;59(12):3049-3057
- 2. Ley RE. Obesity and the human microbiome. Curr Opin Gastroenterol. Jan 2010;26(1):5-11.
- 3. Chan YK, Estaki M, Gibson DL. Clinical consequences of diet-induced dysbiosis. Ann Nutr Metab. 2013;63 Suppl 2:28-40.
- Schippa S, Conte MP. Dysbiotic events in gut microbiota: impact on human health. Nutrients. Dec 2014;6(12):5786-5805.
- Lloyd-Price J, Abu-Ali G, Huttenhower C. The healthy human microbiome. Genome Med. Apr 27 2016;8(1):51.
- Vernocchi P, Del Chierico F, Putignani L. Gut Microbiota Profiling: Metabolomics Based Approach to Unravel Compounds Affecting Human Health. Front Microbiol. 2016;7:1144.
- Flegal KM, Carroll MD, Kit BK, Ogden CL. Prevalence of obesity and trends in the distribution of body mass index among US adults, 1999-2010. JAMA. Feb 01 2012;307(5):491-497
- Ogden CL, Carroll MD, Kit BK, Flegal KM. Prevalence of obesity and trends in body mass index among US children and adolescents, 1999-2010. JAMA. Feb 01 2012;307(5):483-490.
- Centers for Disease Control and Prevention. National Diabetes Statistics Report: Estimates

- of Diabetes and Its Burden in the United States, 2014. . Atlanta, GA: US Department of Health and Human Services;2014.
- 10. Butcher L. Digestive diseases: epidemiology, economics, and the pipeline. Biotechnol Healthc. Nov 2008;5(4):12-13.
- 11. National Institutes of Health. NIH human microbiome project. 2017; Available at: http:// hmpdacc.org/. Accessed July 12, 2017
- 12. Tachon S, Zhou J, Keenan M, Martin R, Marco ML. The intestinal microbiota in aged mice is modulated by dietary resistant starch and correlated with improvements in host responses. FEMS Microbiol Ecol. Feb 2013;83(2):299-309.
- 13. Lopez-Legarrea P, Fuller NR, Zulet MA, Martinez JA, Caterson ID. The influence of Mediterranean, carbohydrate and high protein diets on gut microbiota composition in the treatment of obesity and associated inflammatory state. Asia Pac J Clin Nutr. 2014;23(3):360-368.
- 14. Hooper LV, Macpherson AJ. Immune adaptations that maintain homeostasis with the intestinal microbiota. Nat Rev Immunol. Mar 2010;10(3):159-169.
- 15. Hooper LV, Littman DR, Macpherson AJ. Interactions between the microbiota and the immune system. Science. Jun 8 2012;336(6086):1268-1273.

facilitate the digestion of otherwise inaccessible nutrients, such as many starches, oligosaccharides, alcohols, and proteins, and influence ion absorption, vitamin production, and amino acid supply. 16 Finally, beneficial microorganisms compete with potential pathogens for space and nutrition within the gut and influence immune response and the differentiation and proliferation of epithelial cells. 17-20

Here are two specific examples of how gut microbiota can influence health and disease. The first is the generation of shortchain fatty acids (SFCA) from macronutrients like carbohydrates. SFCAs, mainly butyrate, acetate, and propionate, are generated by fermentation of carbohydrates by certain gut bacteria (Figure 1). These SFCAs account for up to 15% of a person's daily energy supply and up to 70% of the energy supply for intestinal colonocytes. 16 An insufficient supply of SFCAs can impact colonocyte function and contribute to deficits in gut health. In several studies, administration of SFCAs to patients with IBD or other intestinal disorders improved GI symptoms, suggesting that components of diet may contribute to these diseases and their treatment. 16, 21-23

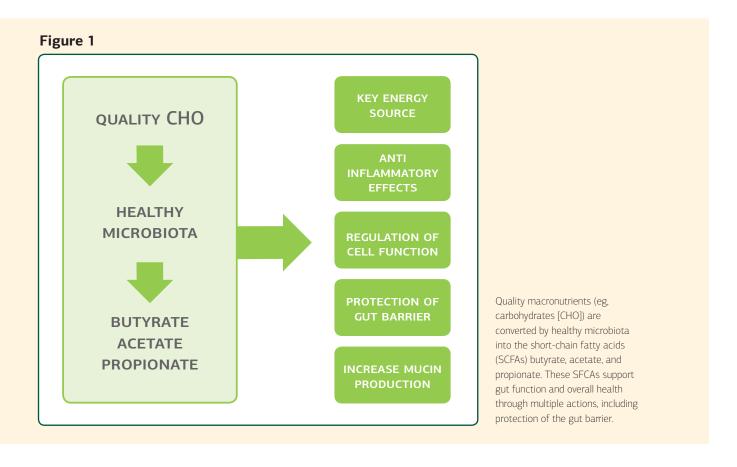
A second example is the bacterium Akkermansia muciniphila, which constitutes 1%-4% of microbiota in healthy adults.²⁴ In human and animal studies, the abundance of A. muciniphila in the gut has been inversely associated with markers of inflammation and fasting glucose levels, as well as several disorders, including obesity, IBD, and diabetes.²⁵⁻²⁹ Specific molecular mechanisms have been identified through which A. muciniphila may influence immune function and gut health.³⁰ Factors that can negatively affect the abundance of this symbiont include increasing age and consumption of a high-fat diet.²⁶ Conversely, administration of fruit polyphenols can increase growth of A. muciniphila, even in mice fed a high-fat diet.31 Together, these studies demonstrate the potential impact of diet and aging on specific bacterial components of the microbiome, with consequences for health maintenance.

Dysbiosis and Disease

Reduced species diversity, fewer beneficial microbes, and the presence of harmful microbes have been associated with multiple disease states. These types of alterations to the microbiome constitute dysbiosis, which describes a pattern of microbiota associated with disease.4 One mechanism by which dysbiosis can affect health and disease is an increase in intestinal permeability, which results in abnormal function of the epithelial barrier that lines the intestines (sometimes called the "leaky gut"). Increased intestinal permeability has been linked to autoimmune, inflammatory, and atopic diseases, among others. These changes have serious consequences for gut health and function. In IBD, for example, altered epithelial permeability increases the infiltration of inflammatory mediators through the epithelium, leading to stimulation of underlying immune cells and a reinforcing cycle of cytokine release, worsened mucosal barrier dysfunction, and increased inflammation.32,33

- 3. Chan YK, Estaki M, Gibson DL. Clinical consequences of diet-induced dysbiosis. Ann Nutr Metab. 2013;63 Suppl 2:28-40.
- 16. Broussard JL, Devkota S. The changing microbial landscape of Western society: Diet, dwellings and discordance. Mol Metab. Sep 2016;5(9):737-742.
- 17. Kamada N, Chen GY, Inohara N, Nunez G. Control of pathogens and pathobionts by the gut microbiota. Nat Immunol. Jul 2013;14(7):685-690.
- 18. Artis D. Epithelial-cell recognition of commensal bacteria and maintenance of immune homeostasis in the gut. Nat Rev Immunol. Jun 2008;8(6):411-420.
- 19. Compare D, Coccoli P, Rocco A, et al. Gut--liver axis: the impact of gut microbiota on non alcoholic fatty liver disease. Nutr Metab Cardiovasc Dis. Jun 2012;22(6):471-476.
- 20. Laparra JM, Sanz Y. Interactions of gut microbiota with functional food components and nutraceuticals. Pharmacol Res. Mar 2010;61(3):219-225.
- 21. Donohoe DR, Garge N, Zhang X, et al. The microbiome and butyrate regulate energy metabolism and autophagy in the mammalian colon. Cell Metab. May 04 2011;13(5):517-
- 22. Binder HJ. Role of colonic short-chain fatty acid transport in diarrhea. Annu Rev Physiol. 2010;72:297-313.
- 23. Di Sabatino A, Morera R, Ciccocioppo R, et al. Oral butyrate for mildly to moderately active Crohn's disease. Aliment Pharmacol Ther. Nov 01 2005;22(9):789-794.
- 24. Derrien M, Collado MC, Ben-Amor K, Salminen S, de Vos WM. The Mucin degrader Akkermansia muciniphila is an abundant resident of the human intestinal tract. Appl Environ Microbiol. Mar 2008;74(5):1646-1648.

- 25. Dao MC, Everard A, Aron-Wisnewsky J, et al. Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. Gut. Mar 2016;65(3):426-436.
- 26. Schneeberger M, Everard A, Gomez-Valades AG, et al. Akkermansia muciniphila inversely correlates with the onset of inflammation, altered adipose tissue metabolism and $% \left(1\right) =\left(1\right) \left(1\right)$ metabolic disorders during obesity in mice. Sci Rep. Nov 13 2015;5:16643.
- 27. Rajilic-Stojanovic M, Shanahan F, Guarner F, de Vos WM. Phylogenetic analysis of dysbiosis in ulcerative colitis during remission. Inflamm Bowel Dis. Mar 2013;19(3):481-
- 28. Karlsson CL, Onnerfalt J, Xu J, Molin G, Ahrne S, Thorngren-Jerneck K. The microbiota of the gut in preschool children with normal and excessive body weight. Obesity (Silver Spring). Nov 2012;20(11):2257-2261.
- 29. Zhang X, Shen D, Fang Z, et al. Human gut microbiota changes reveal the progression of glucose intolerance. PLoS One. 2013;8(8):e71108.
- 30. Ottman N, Reunanen J, Meijerink M, et al. Pili-like proteins of Akkermansia muciniphila modulate host immune responses and gut barrier function. PLoS One. 2017;12(3):e0173004
- 31. Roopchand DE, Carmody RN, Kuhn P, et al. Dietary Polyphenols Promote Growth of the Gut Bacterium Akkermansia muciniphila and Attenuate High-Fat Diet-Induced Metabolic Syndrome. Diabetes. Aug 2015;64(8):2847-2858.



Factors thought to contribute to dysbiosis include diet, physical activity, host genetics, and medical therapies such as antibiotic use. The typical Western diet, one rich in saturated fats and processed foods, is strongly linked to dysbiosis and disease by a growing body of evidence.34-40

Although the "healthy" microbiome remains to be fully characterized, most bacterial species in normal human gut belong to the phyla Bacteroides and Firmicutes. 41 The relative proportions of these and other bacterial species vary between individuals and

in many disease states. In IBD, for example, studies have described reduced proportions of Bacteroides and Firmicutes species and increased proportions of other phyla, such as Proteobacteria and Actinobacteria. 42-44 Overgrowth of Proteobacteria can lead to a reduction in bacterial species that protect the gut barrier, potentially contributing to leaky gut and increasing exposure to bacterial lipopolysaccharide (LPS), which can be toxic to the host. 45,46 Higher levels of LPS have been associated with a high-fat diet, obesity, and higher levels of proinflammatory mediators.⁴⁶

- Schippa S, Conte MP. Dysbiotic events in gut microbiota: impact on human health. Nutrients. Dec 2014;6(12):5786-5805.
- 32. Bruewer M, Samarin S, Nusrat A. Inflammatory bowel disease and the apical junctional complex. Ann N Y Acad Sci. Aug 2006;1072:242-252.
- 33. Mankertz J, Schulzke JD. Altered permeability in inflammatory bowel disease: pathophysiology and clinical implications. Curr Opin Gastroenterol. Jul 2007;23(4):379-383.
- 34. Martinez-Medina M, Denizot J, Dreux N, et al. Western diet induces dysbiosis with increased E coli in CEABAC10 mice, alters host barrier function favouring AIEC colonisation. Gut. Jan 2014;63(1):116-124.
- 35. Huang EY, Devkota S, Moscoso D, Chang EB, Leone VA. The role of diet in triggering human inflammatory disorders in the modern age. Microbes Infect. Nov 2013;15(12):765-774.
- 36. Pendyala S, Walker JM, Holt PR. A high-fat diet is associated with endotoxemia that originates from the gut. Gastroenterology. May 2012;142(5):1100-1101 e1102. 37. Krogius-Kurikka L, Lyra A, Malinen E, et al. Microbial community analysis reveals high level
- phylogenetic alterations in the overall gastrointestinal microbiota of diarrhoea-predominant irritable bowel syndrome sufferers. BMC Gastroenterol. 2009;9:95.
- 38. Salonen A. de Vos WM. Palva A. Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology. Nov 2010;156(Pt 11):3205-3215.
- 39. De Palma G, Nadal I, Medina M, et al. Intestinal dysbiosis and reduced immunoglobulin-

- coated bacteria associated with coeliac disease in children. BMC Microbiol. 2010;10:63.
- 40. Shen XJ, Rawls JF, Randall T, et al. Molecular characterization of mucosal adherent bacteria and associations with colorectal adenomas. Gut Microbes. May-Jun 2010;1(3):138-147.
- 41. Eckburg PB, Bik EM, Bernstein CN, et al. Diversity of the human intestinal microbial flora. Science. Jun 10 2005;308(5728):1635-1638.
- 42. Frank DN, St Amand AL, Feldman RA, Boedeker EC, Harpaz N, Pace NR. Molecularphylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. Proc Natl Acad Sci U S A. Aug 21 2007;104(34):13780-13785.
- 43. Ott SJ, Musfeldt M, Wenderoth DF, et al. Reduction in diversity of the colonic mucosa associated bacterial microflora in patients with active inflammatory bowel disease. Gut. May 2004;53(5):685-693.
- 44. Manichanh C, Rigottier-Gois L, Bonnaud E, et al. Reduced diversity of faecal microbiota in Crohn's disease revealed by a metagenomic approach. Gut. Feb 2006;55(2:205-211. 45. Cani PD, Bibiloni R, Knauf C, et al. Changes in gut microbiota control metabolic
- endotoxemia-induced inflammation in high-fat diet-induced obesity and diabetes in mice. Diabetes. Jun 2008;57(6):1470-1481.
- 46. Cani PD, Amar J, Iglesias MA, et al. Metabolic endotoxemia initiates obesity and insulin resistance. Diabetes. Jul 2007;56(7):1761-1772

GUT-BRAIN AXIS

Interactions between the gut and brain (the so-called gut-brain axis) have been described in academic literature for some time. Pathways such as the autonomic and enteric nervous systems, the hypothalamic-pituitary-adrenal axis, and neuroendocrine and immune systems mediate this two-way influence. A relatively newly identified influence on this communication is the gut microbiome (Figure 2). Some gut bacteria have receptors for neurotransmitters and can even produce neurochemical substances (like serotonin and acetylcholine) that can modulate the enteric nervous system and vagus nerve, potentially affecting functions in the brain. 47-50 Certain bioactive bacterial metabolites, such as SFCA, can also stimulate the enteric and autonomic nervous systems.

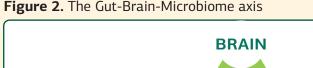
The pathway is bidirectional. Signals from the central nervous system related to stress or emotion can modulate the production of mucus (an energy source for some gut bacteria) and antimicrobial peptides in the gut, as well as intestinal

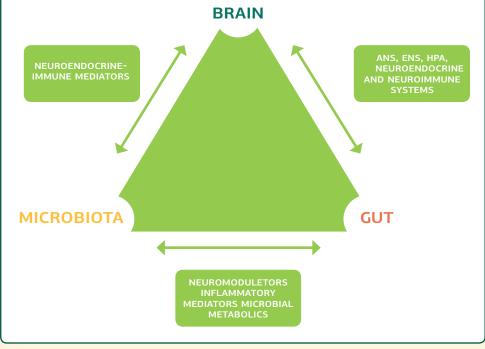
permeability and motility. 47-50 Bacterial gene expression may be affected by neurochemicals, such as norepinephrine. Together, these mechanisms and others may alter the composition and diversity of the gut microbiota.

The health of the microbiome, therefore, may not only influence common systemic diseases, but brain function and health as well. Stress or other psychological factors may in turn affect the health of the microbiome.

AGE AND THE MICROBIOME

The composition of the microbiome changes with age. The initial colonization of the gut and other sites begins at the time of birth, when neonates are exposed to the mother's urogenital microbiota.⁵² Influences of early microbiome development include the method of delivery (C-section vs. vaginal), hygiene, breast milk, and environmental factors.





Evidence suggests that bacterial products can modulate nervous system function, which in turn can affect gut function and microbiota through neuromodulatory compounds and changes in mucus production and intestinal permeability. ANS: autonomic nervous system; ENS: enteric nervous system; HPA: hypothalamic-pituitary-adrenal axis. Adapted from Sirisinha et al.51

^{47.} Mayer EA, Knight R, Mazmanian SK, Cryan JF, Tillisch K. Gut microbes and the brain: paradigm shift in neuroscience. J Neurosci. Nov 12 2014;34(46):15490-15496.

^{48.} Collins SM, Surette M, Bercik P. The interplay between the intestinal microbiota and the brain. Nat Rev Microbiol. Nov 2012;10(11):735-742.

^{49.} Hughes DT, Sperandio V. Inter-kingdom signalling: communication between bacteria and their hosts. Nat Rev Microbiol. Feb 2008;6(2):111-120.

^{50.} Sandrini S, Aldriwesh M, Alruways M, Freestone P. Microbial endocrinology: host-bacteria communication within the gut microbiome. Endocrinol. May 2015;225(2):R21-34.

^{51.} Sirisinha S. The potential impact of gut microbiota on your health: Current status and future challenges. Asian Pac J Allergy Immunol. Dec 2016;34(4):249-264.

^{52.} Haque SZ, Haque M. The ecological community of commensal, symbiotic, and pathogenic gastrointestinal microorganisms - an appraisal. Clin Exp Gastroenterol. 2017;10:91-103.

With aging, the microbiome evolves considerably. The microbiome reaches its full diversity sometime during adolescence. However, the greatest alterations in the microbiome have been documented in older adults.⁵² Studies in older adults have correlated diet and gut microbiota with inflammation and a variety of common age-related conditions, including frailty, Clostridium difficile colitis, and atherosclerotic and metabolic diseases.53

DIET AND THE MICROBIOME

The increasing prevalence of obesity, diabetes, cardiovascular disease, and other conditions corresponds to changes in the Western diet that include higher proportions of fat and refined carbohydrates and lower amounts of fiber and other plant-based nutrients. Until recently, research focused on the direct links

between specific nutrients and excess calories on disease states. Current research defines a role for the microbiome in mediating the interaction between genetics, diet, and health.

The impact of a typical Western diet on the microbiome is illustrated by studies that demonstrated greatly reduced diversity of gut microbiota in people from the US compared to rural native populations in South America and Africa. 54,55 Similar disparities were found between hunter-gatherer and agrarian-based people within the same region, suggesting that a Western-style diet may be responsible for the loss of microbial diversity in the gut.⁵⁵ Differences in diet (and possibly in the microbiome) likely contribute to the very low incidence of Western diseases like diabetes and obesity among native populations, as compared to epidemic proportions in developed countries.¹⁶

Table 1. The effects of specific diets on the microbiome 13,19,56-60

Diet	Microbiota affected	Effects
High fat	Reduced: Bacteroides Firmicutes	Decreased microbial diversity, increased bowel permeability, increased bile acid secretion
Reduced carbohydrate	Reduced: Bifidobacteria, Clostridium Bacteroides, Akkermansia	Decreased SFCA production and fiber-derived phenolic acids
High protein	Increased: Bacteroides, Lactobacillus Bifidobacteria	Beneficial compounds from proteolytic fermentation but toxic products from putrefaction
FODMAP	Reduced: Bifidobacteria Increased: Actinobacteria	Improves IBS symptoms in some patients

^{13.} Lopez-Legarrea P, Fuller NR, Zulet MA, Martinez JA, Caterson ID. The influence of Mediterranean, carbohydrate and high protein diets on gut microbiota composition in the treatment of obesity and associated inflammatory state. Asia Pac J Clin Nutr. 2014:23(3):360-368.

^{16.} Broussard JL, Devkota S. The changing microbial landscape of Western society: Diet, dwellings and discordance. Mol Metab. Sep 2016;5(9):737-742.

^{19.} Compare D, Coccoli P, Rocco A, et al. Gut--liver axis: the impact of gut microbiota on non alcoholic fatty liver disease. Nutr Metab Cardiovasc Dis. Jun 2012;22(6):471-476. 52. Haque SZ, Haque M. The ecological community of commensal, symbiotic, and pathogenic

gastrointestinal microorganisms - an appraisal. Clin Exp Gastroenterol. 2017;10:91-103 53. Salazar N, Arboleya S, Valdes L, et al. The human intestinal microbiome at extreme ages of

life. Dietary intervention as a way to counteract alterations. Front Genet. 2014;5:406. 54. Yatsunenko T, Rey FE, Manary MJ, et al. Human gut microbiome viewed across age and

geography. Nature. May 09 2012;486(7402):222-227. 55. Gomez A, Petrzelkova KJ, Burns MB, et al. Gut Microbiome of Coexisting BaAka Pygmies

and Bantu Reflects Gradients of Traditional Subsistence Patterns. Cell Rep. Mar 08

^{2016;14(9):2142-2153.}

^{56.} Zhang M, Yang XJ. Effects of a high fat diet on intestinal microbiota and gastrointestinal diseases. World J Gastroenterol. Oct 28 2016;22(40):8905-8909.

^{57.} Islam KB, Fukiya S, Hagio M, et al. Bile acid is a host factor that regulates the composition of the cecal microbiota in rats. Gastroenterology. Nov 2011;141(5):1773-1781.

^{58.} Mu C, Yang Y, Luo Z, Guan L, Zhu W. The Colonic Microbiome and Epithelial Transcriptome Are Altered in Rats Fed a High-Protein Diet Compared with a Normal-Protein Diet. J Nutr. Mar 2016;146(3):474-483.

^{59.} Russell WR, Gratz SW, Duncan SH, et al. High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. Am J Clin Nutr. May 2011;93(5):1062-1072

^{60.} Duncan SH, Belenguer A, Holtrop G, Johnstone AM, Flint HJ, Lobley GE. Reduced dietary intake of carbohydrates by obese subjects results in decreased concentrations of butyrate and butyrate-producing bacteria in feces. Appl Environ Microbiol. Feb 2007;73(4):1073-

Macronutrient Diets and the Microbiome

Depending on the proportion of macronutrients (fat, protein, carbohydrate) in a diet, the microbiome may differ as well (Table 1). High-fat diets, for example, are associated with reduced proportions of Bacteroides and increased Firmicutes, with overall reduced microbial diversity.⁵⁶ High-fat diets also may foster increased bowel permeability through changes in the gut microbiota. Dietary fat may indirectly modulate gut microbiota through changes in bile acid secretion; bile acids have selective antimicrobial activity and may mediate some of the changes in microbiota associated with a high-fat diet.57

Although there are few studies on the effects of high protein levels on the gut microbiota, some changes in the microbiota have been noted in association with a high protein diet. High protein diets, such as those commonly used for weight loss, have been associated with lower abundance of Bifidobacteria, Akkermansia, and other beneficial bacteria, as well as reduced production of the important SFCA butyrate. 58-60 Dietary protein content may influence the means by which proteins are broken down in the gut. For example, when consumed in moderate amounts, the digestion of proteins through proteolytic fermentation can generate polyphenols with anti-inflammatory and antioxidant effects. Conversely, putrefaction of proteins by anaerobic bacteria can produce potentially toxic substances, such as ammonia, amines, phenols, thiols, and indols.¹⁹

The findings of studies of diets with differing macronutrient contents must be considered with caution. A change in the proportion of one macronutrient has a corresponding effect on other macronutrients – in other words, a high-fat or high-protein diet is likely to be low in carbohydrates. Therefore, the specific effects of a high-protein diet on the microbiome, for example, may be difficult to discern from the accompanying impact of reduced carbohydrate content.

Therapeutic Diets: FODMAP

Some specific diets have gained popularity for the management of GI disorders, such as IBS. One example is the low FODMAP diet, which restricts intake of certain short-chain fermentable carbohydrates (oligosaccharides, disaccharides, monosaccharides, and polyols). Some studies have shown this diet to improve IBS symptoms and it may also affect the microbiome. In patients with IBS, studies have reported reduced abundance Bifidobacteria and increased Actinobacteria associated with low FODMAP diets. 61-63 Although it is hypothesized that the efficacy of this diet may relate to reduced microbial fermentation in the gut, the clinical significance of documented changes to the microbiome remain unclear.

USING NUTRITION TO FOSTER A HEALTHY MICROBIOME

The consumption of certain specific nutrients can help to minimize inflammation, normalize intestinal microbiota, and restore epithelial integrity. Diets rich in vegetable fibers and phytonutrients, for example, can foster bacterial species that ferment dietary fiber, leading to higher concentrations of SFCAs, which can protect against bowel inflammation.⁶⁴⁻⁶⁶ Indeed, research has identified multiple dietary components that can improve the diversity and health of the microbiome. These components include prebiotics (such as plant fibers), probiotics, and phytonutrients, which are typically underrepresented in Western diets.

- 19. Compare D, Coccoli P, Rocco A, et al. Gut--liver axis: the impact of gut microbiota on non alcoholic fatty liver disease. Nutr Metab Cardiovasc Dis. Jun 2012;22(6):471-476.
- 52. Haque SZ, Haque M. The ecological community of commensal, symbiotic, and pathogenic gastrointestinal microorganisms - an appraisal. Clin Exp Gastroenterol. 2017;10:91-103.
- 53. Salazar N, Arboleya S, Valdes L, et al. The human intestinal microbiome at extreme ages of life. Dietary intervention as a way to counteract alterations. Front Genet. 2014;5:406.
- 54. Yatsunenko T, Rey FE, Manary MJ, et al. Human gut microbiome viewed across age and geography. Nature. May 09 2012;486(7402):222-227.
- 55. Gomez A, Petrzelkova KJ, Burns MB, et al. Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. Cell Rep. Mar 08 2016:14(9):2142-2153.
- 56. Zhang M, Yang XJ. Effects of a high fat diet on intestinal microbiota and gastrointestinal diseases. World J Gastroenterol. Oct 28 2016;22(40):8905-8909.
- 57. Islam KB, Fukiya S, Hagio M, et al. Bile acid is a host factor that regulates the composition of the cecal microbiota in rats. Gastroenterology. Nov 2011;141(5):1773-1781.
- 58. Mu C, Yang Y, Luo Z, Guan L, Zhu W. The Colonic Microbiome and Epithelial Transcriptome Are Altered in Rats Fed a High-Protein Diet Compared with a Normal-Protein Diet. J Nutr. Mar 2016;146(3):474-483.
- 59. Russell WR, Gratz SW, Duncan SH, et al. High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. Am J Clin Nutr. May 2011;93(5):1062-1072.

- 60. Duncan SH, Belenguer A, Holtrop G, Johnstone AM, Flint HJ, Lobley GE. Reduced dietary intake of carbohydrates by obese subjects results in decreased concentrations of butyrate and butyrate-producing bacteria in feces. Appl Environ Microbiol. Feb 2007;73(4):1073-
- 61. Staudacher HM, Whelan K. Altered gastrointestinal microbiota in irritable bowel syndrome and its modification by diet: probiotics, prebiotics and the low FODMAP diet. Proc Nutr Soc. Aug 2016;75(3):306-318.
- 62. McIntosh K, Reed DE, Schneider T, et al. FODMAPs alter symptoms and the metabolome of patients with IBS: a randomised controlled trial. Gut. Jul 2017;66(7):1241-1251
- 63. Chumpitazi BP, Cope JL, Hollister EB, et al. Randomised clinical trial: gut microbiome biomarkers are associated with clinical response to a low FODMAP diet in children with the irritable bowel syndrome. Aliment Pharmacol Ther. Aug 2015;42(4):418-427.
- 64. Flint HJ, Bayer EA, Rincon MT, Lamed R, White BA. Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. Nat Rev Microbiol. Feb 2008;6(2):121-131.
- Scheppach W, Weiler F. The butyrate story: old wine in new bottles? Curr Opin Clin Nutr Metab Care. Sep 2004;7(5):563-567.
- 66. Cani PD, Possemiers S, Van de Wiele T, et al. Changes in gut microbiota control inflammation in obese mice through a mechanism involving GLP-2-driven improvement of gut permeability. Gut. Aug 2009;58(8):1091-1103.

Probiotics

Probiotics consist of live bacterial and/or yeast cultures that are consumed in foods. These microbes compete with pathogenic microbes for resources and may alter the composition of the microbiome. They can also modulate immune response, reverse intestinal permeability, reduce cholesterol levels, and improve lactose digestion in lactose-intolerant people, among other benefits. 67-69 To be effective, probiotic bacteria must be resistant to acid and bile in the upper GI tract. However, even resilient bacterial strains do not durably alter the gut microbiota and therefore must be taken regularly to maintain clinical benefits.

The fermented dairy products yogurt and kefir are examples of probiotic-containing foods. In animal models, consumption of kefir leads to an increase in the beneficial bacteria Lactobacillus and Bifidobacteria and decreases in Clostridium species. 70 Changes in the growth rate and gene expression of Bifidobacteria have also been documented, which may facilitate immunomodulation and adherence to the gut.⁷¹

Probiotics are commonly used to treat post-antibiotic diarrhea and may have utility for some patients with IBS or other GI conditions.⁶⁹ Probiotics may also play a role in the management of small-intestinal bacterial overgrowth (SIBO), which is a common form of dysbiosis. 72 This condition can result from the failure of mechanisms that regulate microbiota in the small intestine and is associated with flatulence, bloating, diarrhea, and abdominal pain. Overlap with IBS is common. Antibiotics are typically used to treat SIBO, but some evidence suggests that probiotics can improve symptoms and may enhance the effectiveness of antibiotics. 72,73

Prebiotics

Prebiotics are commonly defined as food ingredients that are not digestible by the human gut but confer health benefits to the host through modulation of specific gut microbes.74 In general, these compounds encourage the growth of Bifidobacteria and Lactobacilli, both of which are anaerobic bacteria that break down carbohydrates in the gut.⁷⁵ Foods that stimulate bacterial fermentation lead to an increase in bacterial mass in the colon and therefore an in increase stool bulk.⁷⁶ Examples of prebiotics include non-digestible oligosaccharides and dietary fibers composed of fermentable carbohydrates.⁷⁷ Common foods that contain oligosaccharides include leeks, onions, garlic, wheat, and oats. Consumption of oat-based foods has been linked to reduced cholesterol levels and reduced gut inflammation, among other actions. 78,79 Both oat bran and buckwheat foster the growth of beneficial gut bacteria, such as Lactobacillus.80

Evidence suggests several major benefits with prebiotics, including increased production of SFCAs, improved gut barrier function and immunity, reduced inflammation, and reduced pathogenic bacteria.⁷⁶ Clinical studies have reported changes in gut microbiota, reductions in cholesterol and peak postprandial glucose levels, and immunological improvements associated with the consumption of whole-grain (ie, prebiotic-containing) foods.81,82 Although the amount of prebiotics in many foods may be too low to significantly affect gut microbiota, the extraction of prebiotics from plant sources allows for fortification of foods to provide sufficient amounts to modulate the gut microbiome.83,84

Phytonutrients

Plants develop bioactive compounds called phytonutrients (or phytochemicals) to protect themselves from various threats, such as fungi and insects. These phytonutrients are plentiful in fruits, vegetables, legumes, and grains and have multiple health benefits for humans.85 Many thousands of phytonutrients have been described; the broad classes relevant to human nutrition include carotenoids, phytosterols, and phenolics.

- 67. Vyas U, Ranganathan N. Probiotics, prebiotics, and synbiotics: gut and beyond. Gastroenterol Res Pract. 2012;2012:872716.
- 68. Ishimwe N, Daliri EB, Lee BH, Fang F, Du G. The perspective on cholesterol-lowering mechanisms of probiotics. Mol Nutr Food Res. Jan 2015;59(1):94-105.
- 69. Kligler B, Cohrssen A. Probiotics. Am Fam Physician. Nov 01 2008;78(9):1073-1078. 70. Hamet MF, Medrano M, Perez PF, Abraham AG. Oral administration of kefiran exerts a bifidogenic effect on BALB/c mice intestinal microbiota. Benef Microbes. 2016;7(2):237-246.
- 71. Serafini F, Turroni F, Ruas-Madiedo P, et al. Kefir fermented milk and kefiran promote growth of Bifidobacterium bifidum PRL2010 and modulate its gene expression. Int J Food Microbiol. May 16 2014;178:50-59.
- 72. Ghoshal UC, Shukla R, Ghoshal U. Small Intestinal Bacterial Overgrowth and Irritable Bowel Syndrome: A Bridge between Functional Organic Dichotomy. Gut Liver. Mar 15 2017:11(2):196-208.
- 73. Khalighi AR, Khalighi MR, Behdani R, et al. Evaluating the efficacy of probiotic on treatment in patients with small intestinal bacterial overgrowth (SIBO)--a pilot study. Indian J Med Res. Nov 2014;140(5):604-608.
- 74. Gibson GR, Probert HM, Loo JV, Rastall RA, Roberfroid MB. Dietary modulation of the human colonic microbiota: updating the concept of prebiotics. Nutr Res Rev. Dec 2004;17(2):259-275.
- 75. Yu ZT, Chen C, Newburg DS. Utilization of major fucosylated and sialylated human milk oligosaccharides by isolated human gut microbes. Glycobiology. Nov 2013;23(11):1281-
- 76. Slavin J. Fiber and prebiotics: mechanisms and health benefits. Nutrients. Apr 22 2013;5(4):1417-1435.

- 77. Vieira AT, Teixeira MM, Martins FS. The role of probiotics and prebiotics in inducing gut immunity, Front Immunol, 2013:4:445.
- 78. Sotnikova R, Nosalova V, Navarova J. Efficacy of quercetin derivatives in prevention of ulcerative colitis in rats. Interdiscip Toxicol. Mar 2013;6(1):9-12.
- 79. Wilczak J, Blaszczyk K, Kamola D, et al. The effect of low or high molecular weight oat beta-glucans on the inflammatory and oxidative stress status in the colon of rats with LPS-induced enteritis. Food Funct. Feb 2015;6(2):590-603.
- 80. Coman MM, Verdenelli MC, Cecchini C, et al. Effect of buckwheat flour and oat bran on growth and cell viability of the probiotic strains Lactobacillus rhamnosus IMC 501(R), Lactobacillus paracasei IMC 502(R) and their combination SYNBIO(R), in synbiotic fermented milk. Int J Food Microbiol. Oct 15 2013;167(2):261-268.
- 81. Connolly ML, Tzounis X, Tuohy KM, Lovegrove JA. Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population. Front Microbiol. 2016;7:1675.
- 82. Martinez I, Lattimer JM, Hubach KL, et al. Gut microbiome composition is linked to whole grain-induced immunological improvements. ISME J. Feb 2013;7(2):269-280.
- 83. Macfarlane S, Macfarlane GT, Cummings JH. Review article: prebiotics in the gastrointestinal tract. Aliment Pharmacol Ther. Sep 01 2006;24(5):701-714.
- 84. Manning TS, Gibson GR. Microbial-gut interactions in health and disease. Prebiotics. Best Pract Res Clin Gastroenterol. Apr 2004;18(2):287-298.
- 85. Liu RH. Health-promoting components of fruits and vegetables in the diet. Adv Nutr. May 01 2013;4(3):3845-3925

Current evidence suggests that gut bacteria are integral to the metabolism and absorption of phytonutrients and their metabolites.86 Furthermore, phytonutrients can modulate the microbiome. For example, the consumption of certain berries that are rich in polyphenols, such as cranberries, blueberries, and grapes, can increase the abundance of Bifidobactertia and Akkermansia. Studies in mice found that administration of a polyphenol-rich cranberry extract over 8 weeks led to a large increase in the abundance of beneficial Akkermansia.87 Consumption of polyphenols such as quercetin and those found in pomegranate can also increase the abundance of Akkermansia.^{88,89} Separate studies have linked consumption of blueberries and red wine to increases in Bifidobacteria. 90,91 Quercetin, one of the most common polyphenols in fruits and vegetables, has been shown to alter gene expression in important gut bacteria, such as Bifidobactera, Enterococcus, and Ruminococcus 92

Recent research links certain phytonutrients, those associated with bitter taste, to alterations in glucose absorption and utilization. Receptors that sense bitter taste are present throughout the gut, and activation of certain bitter receptors in the gut have been shown to delay glucose absorption and increase the utilization of glucose. 93 This evidence suggests yet another mechanism by which phytonutrients may influence metabolic control and overall health.

Soil Microbiome and Plant Nutrients

One final important point regarding the benefits of plant nutrients has to do with how plants are grown and the impact of the soil microbiome. Differing farming techniques – for example, organic versus conventional farming – have been shown to alter the microbiome of the soil itself. Studies of organic farming systems demonstrate a more heterogeneous soil microbiome and greater nutrient availability to plants, in addition to other benefits. 94,95 And organic farming has also been linked to improve phytonutrient composition in plants – which as discussed can improve the health of the gut microbiome. 96 For example, a meta-analysis of 343

studies found that a range of phytonutrients, including quercetin and other flavonoids, were present in higher concentrations in crops grown organically, compared to conventionally-grown crops.⁹⁶ Investigation into the influence of the soil microbiome on plant and human health is just beginning. Current findings suggest that organic farming practices can alter the soil microbiome, which affects plant health and phytonutrient content, with implications for the human microbiome and health.

CLINICAL ROLE OF THE MICROBIOME

Taken together, current evidence suggests some approaches to the management of common conditions through modulation of the microbiome. Evidence clearly supports the benefits of diets that are rich in whole foods – whole grains, vegetables, and fruit – for overall health. These foods contain multiple important nutrients, including prebiotics and phytonutrients, that support the growth and maintenance of a healthy and diverse microbiome. A healthy microbiome in turn supports the production and absorption of nutrients such as SFCAs, vitamins, and antioxidant and antiinflammatory compounds that can reduce systemic inflammation, improve glucose homeostasis, and limit intestinal permeability.

Other clear avenues for therapy include the use of probiotics to improve post-antibiotic diarrhea.⁶⁹ Evidence supporting the use of probiotics for other conditions is more limited. However, probiotics are a useful adjunct to diet that can support immune function and ameliorate symptoms of IBS in some patients. 69,97 Some data suggest benefits to the use of probiotics such as Lactobacillus preparations in fostering weight loss⁹⁸ and improving anxiety, stress, and depression, 99 although most studies have had small sample sizes or other methodological limitations. Doses found to be most effective in clinical studies are often >5 billion CFU (colon-forming units) in children and >10 billion CFU in adults. However, the type of probiotic is more important than the quantity. Examples of beneficial probiotic strains include Lactobacillus sp., Bifidobacteria, and Saccharomyces (Table 2).

- 69. Kligler B, Cohrssen A. Probiotics. Am Fam Physician. Nov 01 2008;78(9):1073-1078.
- 86. Moco S, Martin FP, Rezzi S. Metabolomics view on gut microbiome modulation by polyphenol-rich foods. J Proteome Res. Oct 05 2012;11(10):4781-4790.
- 87. Anhe FF, Roy D, Pilon G, et al. A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation in association with increased Akkermansia spp. population in the gut microbiota of mice. Gut. Jun 2015:64(6):872-883
- $88.\ Etxeberria\ U,$ Arias N, Boque N, et al. Reshaping faecal gut microbiota composition by the intake of trans-resveratrol and quercetin in high-fat sucrose diet-fed rats. J Nutr Biochem. Jun 2015:26(6):651-660.
- 89. Li Z, Henning SM, Lee RP, et al. Pomegranate extract induces ellagitannin metabolite formation and changes stool microbiota in healthy volunteers. Food Funct. Aug 2015;6(8):2487-2495.
- 90. Guglielmetti S, Fracassetti D, Taverniti V, et al. Differential modulation of human intestinal bifidobacterium populations after consumption of a wild blueberry (Vaccinium angustifolium) drink. J Agric Food Chem. Aug 28 2013;61(34):8134-8140.
- 91. Queipo-Ortuno MI, Boto-Ordonez M, Murri M, et al. Influence of red wine polyphenols and ethanol on the gut microbiota ecology and biochemical biomarkers. Am J Clin Nutr. Jun 2012;95(6):1323-1334.
- 92. Firman J, Liu L, Zhang L, et al. The effect of quercetin on genetic expression of the commensal gut microbes Bifidobacterium catenulatum, Enterococcus caccae and

- Ruminococcus gauvreauii. Anaerobe. Dec 2016;42:130-141.
- 93. jackson KMP, Rathinasabapathy T, Bonney SA, Esposito D, Komarnytsky S. Bitter Receptors Control Glucose Absorption in the Gut by Modifying the G-protein Coupled Receptor Signaling Cascade. FASEB J. 2017;31(1)
- 94. Lupatini M, Korthals GW, de Hollander M, Janssens TK, Kuramae EE. Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. Front Microbiol. 2016:7:2064
- 95. Hartmann M, Frey B, Mayer J, Mader P, Widmer F. Distinct soil microbial diversity under long-term organic and conventional farming. ISME J. May 2015;9(5):1177-1194.
- 96. Baranski M, Srednicka-Tober D, Volakakis N, et al. Higher antioxidant and lower cadmium concentrations and lower incidence of pesticide residues in organically grown crops: a systematic literature review and meta-analyses. Br J Nutr. Sep 14 2014;112(5):794-811
- 97. Hungin AP, Mulligan C, Pot B, et al. Systematic review: probiotics in the management of lower gastrointestinal symptoms in clinical practice -- an evidence-based international guide. Aliment Pharmacol Ther. Oct 2013;38(8):864-886.
- 98. Kadooka Y, Sato M, Imaizumi K, et al. Regulation of abdominal adiposity by probiotics (Lactobacillus gasseri SBT2055) in adults with obese tendencies in a randomized controlled trial. Eur J Clin Nutr. Jun 2010;64(6):636-643
- 99. Roberfroid M. Prebiotics: the concept revisited. J Nutr. Mar 2007;137(3 Suppl 2):830S-837S.

Table 2. Specific probiotic strains and their demonstrated health benefits.

Probiotic strain	Health benefits	
Lactobacillus rhamnosus GR-1	Prevents growth of harmful microbes ^{100,101}	
Lactobacillus acidophilus	Prevents growth of harmful microbes Improves constipation, lactose intolerance, symptoms of IBS ¹⁰²⁻¹⁰⁴	
Lactobacillus paracasei ssp paracasei	Improves immune function, adheres to host gut and inhibits harmful microbes ^{105,106}	
Lactobacillus salivarius ssp. salivarius	Anti-inflammatory effects, inhibits harmful microbes ^{107,108}	
Bifidobacterium lactis	Improves immune function, improves constipation and GI symptoms 102,106,109	
Saccharomyces cerevisiae var. boulardii	Fosters normal gut function, anti-inflammatory effects ^{110,111}	

Synbiotics

The combination of both probiotics and prebiotics is called a synbiotic. The prebiotic improves the survival of the probiotic bacteria and stimulates the activity of host bacteria. In studies, administration of synbiotics to patients following surgery for liver conditions or multiple-trauma led to a reduction in the incidence of infectious complications. 112,113 In patients with non-alcoholic fatty liver disease, symbiotic treatment led to a reduction in liver fat. 114

Although preliminary, these data suggest a role for probiotics, prebiotics, and both together (synbiotics) in the maintenance of overall health, the prevention of infection, and the treatment of certain disease states.

- 100. Anukam KC, Osazuwa E, Osemene GI, Ehigiagbe F, Bruce AW, Reid G. Clinical study comparing probiotic Lactobacillus GR-1 and RC-14 with metronidazole vaginal gel to treat symptomatic bacterial vaginosis. Microbes Infect. Oct 2006;8(12-13):2772-2776.
- 101. Martinez RC, Seney SL, Summers KL, Nomizo A, De Martinis EC, Reid G. Effect of Lactobacillus rhamnosus GR-1 and Lactobacillus reuteri RC-14 on the ability of Candida albicans to infect cells and induce inflammation. Microbiol Immunol. Sep 2009;53(9):487-495.
- 102. Magro DO, de Oliveira LM, Bernasconi I, et al. Effect of yogurt containing polydextrose, Lactobacillus acidophilus NCFM and Bifidobacterium lactis HN019: a randomized, doubleblind, controlled study in chronic constipation. Nutr J. Jul 24 2014;13:75
- 103. Ringel-Kulka T. Palsson OS. Majer D. et al. Probiotic bacteria Lactobacillus acidophilus NCFM and Bifidobacterium lactis Bi-07 versus placebo for the symptoms of bloating in patients with functional bowel disorders: a double-blind study. J Clin Gastroenterol. Jul 2011:45(6):518-525
- 104. Pakdaman MN, Udani JK, Molina JP, Shahani M. The effects of the DDS-1 strain of lactobacillus on symptomatic relief for lactose intolerance - a randomized, double-blind, placebo-controlled, crossover clinical trial. Nutr J. May 20 2016;15(1):56.
- 105. do Carmo MS, Noronha FM, Arruda MO, et al. Lactobacillus fermentum ATCC 23271 Displays In vitro Inhibitory Activities against Candida spp. Front Microbiol. 2016;7:1722.
- 106. Lee A, Lee YJ, Yoo HJ, et al. Consumption of Dairy Yogurt Containing Lactobacillus paracasei ssp. paracasei, Bifidobacterium animalis ssp. lactis and Heat-Treated Lactobacillus plantarum Improves Immune Function Including Natural Killer Cell Activity. Nutrients. May 31 2017;9(6).

- 107. Arribas B, Garrido-Mesa N, Peran L, et al. The immunomodulatory properties of viable Lactobacillus salivarius ssp. salivarius CECT5713 are not restricted to the large intestine. Eur J Nutr. Apr 2012;51(3):365-374.
- 108. Neville BA, O'Toole PW. Probiotic properties of Lactobacillus salivarius and closely related Lactobacillus species. Future Microbiol. May 2010;5(5):759-774.
- 109. Eales J, Gibson P, Whorwell P, et al. Systematic review and meta-analysis: the effects of fermented milk with Bifidobacterium lactis CNCM I-2494 and lactic acid bacteria on gastrointestinal discomfort in the general adult population. Therap Adv Gastroenterol. Jan 2017:10(1):74-88
- 110. Jawhara S, Habib K, Maggiotto F, et al. Modulation of intestinal inflammation by yeasts and cell wall extracts: strain dependence and unexpected anti-inflammatory role of glucan fractions. PLoS One. 2012;7(7):e40648.
- 111. Sheele J, Cartowski J, Dart A, et al. Saccharomyces boulardii and bismuth subsalicylate as low-cost interventions to reduce the duration and severity of cholera. Pathog Glob Health. Sep 2015;109(6):275-282.
- 112. Rastall RA, Maitin V. Prebiotics and synbiotics: towards the next generation. Curr Opin Biotechnol. Oct 2002;13(5):490-496.
- 113. Kotzampassi K, Giamarellos-Bourboulis EJ, Voudouris A, Kazamias P, Eleftheriadis E. Benefits of a synbiotic formula (Synbiotic 2000Forte) in critically III trauma patients: early results of a randomized controlled trial. World J Surg. Oct 2006;30(10):1848-1855.
- 114. Wong VW, Won GL, Chim AM, et al. Treatment of nonalcoholic steatohepatitis with probiotics. A proof-of-concept study. Ann Hepatol. Mar-Apr 2013;12(2):256-262.

REFERENCES

- 1. Furet JP, Kong LC, Tap J, et al. Differential adaptation of human gut microbiota to bariatric surgery-induced weight loss: links with metabolic and low-grade inflammation markers. Diabetes. Dec 2010;59(12):3049-3057.
- Ley RE. Obesity and the human microbiome. Curr Opin Gastroenterol. Jan 2010;26(1):5-11.
- Chan YK, Estaki M, Gibson DL. Clinical consequences of diet-induced dysbiosis. Ann Nutr Metab. 2013;63 Suppl 2:28-40.
- 4. Schippa S, Conte MP. Dysbiotic events in gut microbiota: impact on human health. Nutrients. Dec 2014;6(12):5786-5805.
- 5. Lloyd-Price J, Abu-Ali G, Huttenhower C. The healthy human microbiome. Genome Med. Apr 27 2016;8(1):51.
- 6. Vernocchi P, Del Chierico F, Putignani L. Gut Microbiota Profiling: Metabolomics Based Approach to Unravel Compounds Affecting Human Health. Front Microbiol. 2016;7:1144.
- 7. Flegal KM, Carroll MD, Kit BK, Ogden CL. Prevalence of obesity and trends in the distribution of body mass index among US adults, 1999-2010. JAMA. Feb 01 2012;307(5):491-497.
- 8. Ogden CL, Carroll MD, Kit BK, Flegal KM. Prevalence of obesity and trends in body mass index among US children and adolescents, 1999-2010. JAMA. Feb 01 2012;307(5):483-490.
- 9. Centers for Disease Control and Prevention. National Diabetes Statistics Report: Estimates of Diabetes and Its Burden in the United States, 2014. . Atlanta, GA: US Department of Health and Human Services;2014.
- 10. Butcher L. Digestive diseases: epidemiology, economics, and the pipeline. Biotechnol Healthc. Nov 2008;5(4):12-13.
- 11. National Institutes of Health. NIH human microbiome project. 2017; Available at: http://hmpdacc.org/. Accessed July 12, 2017.
- 12. Tachon S, Zhou J, Keenan M, Martin R, Marco ML. The intestinal microbiota in aged mice is modulated by dietary resistant starch and correlated with improvements in host responses. FEMS Microbiol Ecol. Feb 2013;83(2):299-309.
- 13. Lopez-Legarrea P, Fuller NR, Zulet MA, Martinez JA, Caterson ID. The influence of Mediterranean, carbohydrate and high protein diets on gut microbiota composition in the treatment of obesity and associated inflammatory state. Asia Pac J Clin Nutr. 2014;23(3):360-368.
- 14. Hooper LV, Macpherson AJ. Immune adaptations that maintain homeostasis with the intestinal microbiota. Nat Rev Immunol. Mar 2010;10(3):159-169.
- 15. Hooper LV, Littman DR, Macpherson AJ. Interactions between the microbiota and the immune system. Science. Jun 8 2012;336(6086):1268-1273.
- 16. Broussard JL, Devkota S. The changing microbial landscape of Western society: Diet, dwellings and discordance. Mol Metab. Sep 2016;5(9):737-742.
- 17. Kamada N, Chen GY, Inohara N, Nunez G. Control of pathogens and pathobionts by the gut microbiota. Nat Immunol. Jul 2013;14(7):685-690.
- 18. Artis D. Epithelial-cell recognition of commensal bacteria and maintenance of immune homeostasis in the gut. Nat Rev Immunol. Jun 2008;8(6):411-420.
- 19. Compare D, Coccoli P, Rocco A, et al. Gut--liver axis: the impact of gut microbiota on non alcoholic fatty liver disease. Nutr Metab Cardiovasc Dis. Jun 2012;22(6):471-476.
- 20. Laparra JM, Sanz Y. Interactions of gut microbiota with functional food components and nutraceuticals. Pharmacol Res. Mar 2010;61(3):219-225.
- 21. Donohoe DR, Garge N, Zhang X, et al. The microbiome and butyrate regulate energy metabolism and autophagy in the mammalian colon. Cell Metab. May 04 2011;13(5):517-526.
- 22. Binder HJ. Role of colonic short-chain fatty acid transport in diarrhea. Annu Rev Physiol. 2010;72:297-313.
- 23. Di Sabatino A, Morera R, Ciccocioppo R, et al. Oral butyrate for mildly to moderately active Crohn's disease. Aliment Pharmacol Ther. Nov 01 2005;22(9):789-794.
- 24. Derrien M, Collado MC, Ben-Amor K, Salminen S, de Vos WM. The Mucin degrader Akkermansia muciniphila is an abundant resident of the human intestinal tract. Appl Environ Microbiol. Mar 2008;74(5):1646-1648.
- 25. Dao MC, Everard A, Aron-Wisnewsky J, et al. Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. Gut. Mar 2016;65(3):426-436.
- 26. Schneeberger M, Everard A, Gomez-Valades AG, et al. Akkermansia muciniphila inversely correlates with the onset of inflammation, altered adipose tissue metabolism and metabolic disorders during obesity in mice. Sci Rep. Nov 13 2015;5:16643.
- 27. Rajilic-Stojanovic M, Shanahan F, Guarner F, de Vos WM. Phylogenetic analysis of dysbiosis in ulcerative colitis during remission. Inflamm Bowel Dis. Mar 2013;19(3):481-488.
- 28. Karlsson CL, Onnerfalt J, Xu J, Molin G, Ahrne S, Thorngren-Jerneck K. The microbiota of the gut in preschool children with normal and excessive body weight. Obesity (Silver Spring). Nov 2012;20(11):2257-2261.
- 29. Zhang X, Shen D, Fang Z, et al. Human gut microbiota changes reveal the progression of glucose intolerance. PLoS One. 2013;8(8):e71108.
- 30. Ottman N, Reunanen J, Meijerink M, et al. Pili-like proteins of Akkermansia muciniphila modulate host immune responses and gut barrier function. PLoS One. 2017;12(3):e0173004.
- 31. Roopchand DE, Carmody RN, Kuhn P, et al. Dietary Polyphenols Promote Growth of the Gut Bacterium Akkermansia muciniphila and Attenuate High-Fat Diet-Induced Metabolic Syndrome. Diabetes. Aug 2015;64(8):2847-2858.

- 32. Bruewer M, Samarin S, Nusrat A. Inflammatory bowel disease and the apical junctional complex. Ann N Y Acad Sci. Aug 2006;1072:242-252.
- 33. Mankertz J, Schulzke JD. Altered permeability in inflammatory bowel disease: pathophysiology and clinical implications. Curr Opin Gastroenterol. Jul 2007;23(4):379-383.
- 34. Martinez-Medina M, Denizot J, Dreux N, et al. Western diet induces dysbiosis with increased E coli in CEABAC10 mice, alters host barrier function favouring AIEC colonisation. Gut. Jan 2014;63(1):116-124.
- 35. Huang EY, Devkota S, Moscoso D, Chang EB, Leone VA. The role of diet in triggering human inflammatory disorders in the modern age. Microbes Infect. Nov 2013;15(12):765-774.
- 36. Pendyala S, Walker JM, Holt PR. A high-fat diet is associated with endotoxemia that originates from the gut. Gastroenterology. May 2012;142(5):1100-1101 e1102.
- 37. Krogius-Kurikka L, Lyra A, Malinen E, et al. Microbial community analysis reveals high level phylogenetic alterations in the overall gastrointestinal microbiota of diarrhoea-predominant irritable bowel syndrome sufferers. BMC Gastroenterol. 2009:9:95.
- 38. Salonen A, de Vos WM, Palva A. Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology. Nov 2010;156(Pt 11):3205-3215.
- 39. De Palma G, Nadal I, Medina M, et al. Intestinal dysbiosis and reduced immunoglobulin-coated bacteria associated with coeliac disease in children. BMC Microbiol. 2010;10:63.
- 40. Shen XJ, Rawls JF, Randall T, et al. Molecular characterization of mucosal adherent bacteria and associations with colorectal adenomas. Gut Microbes. May-Jun 2010;1(3):138-147.
- 41. Eckburg PB, Bik EM, Bernstein CN, et al. Diversity of the human intestinal microbial flora. Science. Jun 10 2005;308(5728):1635-1638.
- 42. Frank DN, St Amand AL, Feldman RA, Boedeker EC, Harpaz N, Pace NR. Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. Proc Natl Acad Sci U S A. Aug 21 2007;104(34):13780-13785.
- 43. Ott SJ, Musfeldt M, Wenderoth DF, et al. Reduction in diversity of the colonic mucosa associated bacterial microflora in patients with active inflammatory bowel disease. Gut. May 2004;53(5):685-693.
- 44. Manichanh C, Rigottier-Gois L, Bonnaud E, et al. Reduced diversity of faecal microbiota in Crohn's disease revealed by a metagenomic approach. Gut. Feb 2006;55(2):205-211.
- 45. Cani PD, Bibiloni R, Knauf C, et al. Changes in gut microbiota control metabolic endotoxemia-induced inflammation in highfat diet-induced obesity and diabetes in mice. Diabetes. Jun 2008;57(6):1470-1481.
- 46. Cani PD, Amar J, Iglesias MA, et al. Metabolic endotoxemia initiates obesity and insulin resistance. Diabetes. Jul 2007;56(7):1761-1772.
- 47. Mayer EA, Knight R, Mazmanian SK, Cryan JF, Tillisch K. Gut microbes and the brain: paradigm shift in neuroscience. J Neurosci. Nov 12 2014;34(46):15490-15496.
- 48. Collins SM, Surette M, Bercik P. The interplay between the intestinal microbiota and the brain. Nat Rev Microbiol. Nov 2012;10(11):735-742.
- 49. Hughes DT, Sperandio V. Inter-kingdom signalling: communication between bacteria and their hosts. Nat Rev Microbiol. Feb 2008;6(2):111-120.
- 50. Sandrini S, Aldriwesh M, Alruways M, Freestone P. Microbial endocrinology: host-bacteria communication within the gut microbiome. J Endocrinol. May 2015;225(2):R21-34.
- 51. Sirisinha S. The potential impact of gut microbiota on your health: Current status and future challenges. Asian Pac J Allergy Immunol. Dec 2016;34(4):249-264.
- 52. Haque SZ, Haque M. The ecological community of commensal, symbiotic, and pathogenic gastrointestinal microorganisms - an appraisal. Clin Exp Gastroenterol. 2017;10:91-103.
- 53. Salazar N, Arboleya S, Valdes L, et al. The human intestinal microbiome at extreme ages of life. Dietary intervention as a way to counteract alterations. Front Genet. 2014;5:406.
- 54. Yatsunenko T, Rey FE, Manary MJ, et al. Human gut microbiome viewed across age and geography. Nature. May 09 2012;486(7402):222-227.
- 55. Gomez A, Petrzelkova KJ, Burns MB, et al. Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. Cell Rep. Mar 08 2016;14(9):2142-2153.
- 56. Zhang M, Yang XJ. Effects of a high fat diet on intestinal microbiota and gastrointestinal diseases. World J Gastroenterol. Oct 28 2016;22(40):8905-8909.
- 57. Islam KB, Fukiya S, Hagio M, et al. Bile acid is a host factor that regulates the composition of the cecal microbiota in rats. Gastroenterology. Nov 2011;141(5):1773-1781.
- 58. Mu C, Yang Y, Luo Z, Guan L, Zhu W. The Colonic Microbiome and Epithelial Transcriptome Are Altered in Rats Fed a High-Protein Diet Compared with a Normal-Protein Diet. J Nutr. Mar 2016;146(3):474-483.
- 59. Russell WR, Gratz SW, Duncan SH, et al. High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. Am J Clin Nutr. May 2011;93(5):1062-1072.
- 60. Duncan SH, Belenguer A, Holtrop G, Johnstone AM, Flint HJ, Lobley GE. Reduced dietary intake of carbohydrates by obese subjects results in decreased concentrations of butyrate and butyrate-producing bacteria in feces. Appl Environ Microbiol. Feb 2007;73(4):1073-1078.

- 61. Staudacher HM, Whelan K. Altered gastrointestinal microbiota in irritable bowel syndrome and its modification by diet: probiotics, prebiotics and the low FODMAP diet. Proc Nutr Soc. Aug 2016;75(3):306-318.
- 62. McIntosh K, Reed DE, Schneider T, et al. FODMAPs alter symptoms and the metabolome of patients with IBS: a randomised controlled trial. Gut. Jul 2017;66(7):1241-1251.
- 63. Chumpitazi BP, Cope JL, Hollister EB, et al. Randomised clinical trial: gut microbiome biomarkers are associated with clinical response to a low FODMAP diet in children with the irritable bowel syndrome. Aliment Pharmacol Ther. Aug 2015;42(4):418-427.
- 64. Flint HJ, Bayer EA, Rincon MT, Lamed R, White BA. Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. Nat Rev Microbiol. Feb 2008;6(2):121-131.
- 65. Scheppach W, Weiler F. The butyrate story: old wine in new bottles? Curr Opin Clin Nutr Metab Care. Sep 2004;7(5):563-
- 66. Cani PD, Possemiers S, Van de Wiele T, et al. Changes in gut microbiota control inflammation in obese mice through a mechanism involving GLP-2-driven improvement of gut permeability. Gut. Aug 2009;58(8):1091-1103.
- 67. Vyas U, Ranganathan N. Probiotics, prebiotics, and synbiotics: gut and beyond. Gastroenterol Res Pract. 2012;2012:872716.
- 68. Ishimwe N, Daliri EB, Lee BH, Fang F, Du G. The perspective on cholesterol-lowering mechanisms of probiotics. Mol Nutr Food Res. Jan 2015;59(1):94-105.
- 69. Kligler B, Cohrssen A. Probiotics. Am Fam Physician. Nov 01 2008;78(9):1073-1078.
- 70. Hamet MF, Medrano M, Perez PF, Abraham AG. Oral administration of kefiran exerts a bifidogenic effect on BALB/c mice intestinal microbiota. Benef Microbes. 2016;7(2):237-246.
- 71. Serafini F, Turroni F, Ruas-Madiedo P, et al. Kefir fermented milk and kefiran promote growth of Bifidobacterium bifidum PRL2010 and modulate its gene expression. Int J Food Microbiol. May 16 2014;178:50-59.
- 72. Ghoshal UC, Shukla R, Ghoshal U. Small Intestinal Bacterial Overgrowth and Irritable Bowel Syndrome: A Bridge between Functional Organic Dichotomy. Gut Liver. Mar 15 2017;11(2):196-208.
- 73. Khalighi AR, Khalighi MR, Behdani R, et al. Evaluating the efficacy of probiotic on treatment in patients with small intestinal bacterial overgrowth (SIBO)--a pilot study. Indian J Med Res. Nov 2014;140(5):604-608.
- 74. Gibson GR, Probert HM, Loo JV, Rastall RA, Roberfroid MB. Dietary modulation of the human colonic microbiota: updating the concept of prebiotics. Nutr Res Rev. Dec 2004;17(2):259-275.
- 75. Yu ZT, Chen C, Newburg DS. Utilization of major fucosylated and sialylated human milk oligosaccharides by isolated human gut microbes. Glycobiology. Nov 2013;23(11):1281-1292.
- 76. Slavin J. Fiber and prebiotics: mechanisms and health benefits. Nutrients. Apr 22 2013;5(4):1417-1435.
- 77. Vieira AT, Teixeira MM, Martins FS. The role of probiotics and prebiotics in inducing gut immunity. Front Immunol. 2013;4:445.
- 78. Sotnikova R, Nosalova V, Navarova J. Efficacy of quercetin derivatives in prevention of ulcerative colitis in rats. Interdiscip Toxicol. Mar 2013;6(1):9-12.
- 79. Wilczak J, Blaszczyk K, Kamola D, et al. The effect of low or high molecular weight oat beta-glucans on the inflammatory and oxidative stress status in the colon of rats with LPS-induced enteritis. Food Funct. Feb 2015;6(2):590-603.
- 80. Coman MM, Verdenelli MC, Cecchini C, et al. Effect of buckwheat flour and oat bran on growth and cell viability of the probiotic strains Lactobacillus rhamnosus IMC 501(R), Lactobacillus paracasei IMC 502(R) and their combination SYNBIO(R), in synbiotic fermented milk. Int J Food Microbiol. Oct 15 2013;167(2):261-268.
- 81. Connolly ML, Tzounis X, Tuohy KM, Lovegrove JA. Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population. Front Microbiol. 2016;7:1675.
- 82. Martinez I, Lattimer JM, Hubach KL, et al. Gut microbiome composition is linked to whole grain-induced immunological improvements. ISME J. Feb 2013:7(2):269-280.
- 83. Macfarlane S, Macfarlane GT, Cummings JH. Review article: prebiotics in the gastrointestinal tract. Aliment Pharmacol Ther. Sep 01 2006;24(5):701-714.
- 84. Manning TS, Gibson GR. Microbial-gut interactions in health and disease. Prebiotics. Best Pract Res Clin Gastroenterol. Apr 2004;18(2):287-298.
- 85. Liu RH. Health-promoting components of fruits and vegetables in the diet. Adv Nutr. May 01 2013;4(3):384S-392S.
- 86. Moco S, Martin FP, Rezzi S. Metabolomics view on gut microbiome modulation by polyphenol-rich foods. J Proteome Res. Oct 05 2012;11(10):4781-4790.
- 87. Anhe FF, Roy D, Pilon G, et al. A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation in association with increased Akkermansia spp. population in the gut microbiota of mice. Gut. Jun 2015;64(6):872-883.
- 88. Etxeberria U, Arias N, Boque N, et al. Reshaping faecal gut microbiota composition by the intake of trans-resveratrol and quercetin in high-fat sucrose diet-fed rats. J Nutr Biochem. Jun 2015;26(6):651-660.
- 89. Li Z, Henning SM, Lee RP, et al. Pomegranate extract induces ellagitannin metabolite formation and changes stool microbiota in healthy volunteers. Food Funct. Aug 2015;6(8):2487-2495.
- 90. Guglielmetti S, Fracassetti D, Taverniti V, et al. Differential modulation of human intestinal bifidobacterium populations after consumption of a wild blueberry (Vaccinium angustifolium) drink. J Agric Food Chem. Aug 28 2013;61(34):8134-8140.
- 91. Queipo-Ortuno MI, Boto-Ordonez M, Murri M, et al. Influence of red wine polyphenols and ethanol on the gut microbiota ecology and biochemical biomarkers. Am J Clin Nutr. Jun 2012;95(6):1323-1334.

- 92. Firrman J, Liu L, Zhang L, et al. The effect of quercetin on genetic expression of the commensal gut microbes Bifidobacterium catenulatum, Enterococcus caccae and Ruminococcus gauvreauii. Anaerobe. Dec 2016;42:130-141.
- 93. jackson KMP, Rathinasabapathy T, Bonney SA, Esposito D, Komarnytsky S. Bitter Receptors Control Glucose Absorption in the Gut by Modifying the G-protein Coupled Receptor Signaling Cascade. FASEB J. 2017;31(1).
- 94. Lupatini M, Korthals GW, de Hollander M, Janssens TK, Kuramae EE. Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. Front Microbiol. 2016;7:2064.
- 95. Hartmann M, Frey B, Mayer J, Mader P, Widmer F. Distinct soil microbial diversity under long-term organic and conventional farming. ISME J. May 2015;9(5):1177-1194.
- 96. Baranski M, Srednicka-Tober D, Volakakis N, et al. Higher antioxidant and lower cadmium concentrations and lower incidence of pesticide residues in organically grown crops: a systematic literature review and meta-analyses. Br J Nutr. Sep 14 2014:112(5):794-811.
- 97. Hungin AP, Mulligan C, Pot B, et al. Systematic review: probiotics in the management of lower gastrointestinal symptoms in clinical practice -- an evidence-based international guide. Aliment Pharmacol Ther. Oct 2013;38(8):864-886.
- 98. Kadooka Y, Sato M, Imaizumi K, et al. Regulation of abdominal adiposity by probiotics (Lactobacillus gasseri SBT2055) in adults with obese tendencies in a randomized controlled trial. Eur J Clin Nutr. Jun 2010;64(6):636-643.
- 99. Roberfroid M. Prebiotics: the concept revisited. J Nutr. Mar 2007;137(3 Suppl 2):830S-837S.
- 100. Anukam KC, Osazuwa E, Osemene GI, Ehigiagbe F, Bruce AW, Reid G. Clinical study comparing probiotic Lactobacillus GR-1 and RC-14 with metronidazole vaginal gel to treat symptomatic bacterial vaginosis. Microbes Infect. Oct 2006;8(12-
- 101. Martinez RC, Seney SL, Summers KL, Nomizo A, De Martinis EC, Reid G. Effect of Lactobacillus rhamnosus GR-1 and Lactobacillus reuteri RC-14 on the ability of Candida albicans to infect cells and induce inflammation. Microbiol Immunol. Sep 2009;53(9):487-495.
- 102. Magro DO, de Oliveira LM, Bernasconi I, et al. Effect of yogurt containing polydextrose, Lactobacillus acidophilus NCFM and Bifidobacterium lactis HN019: a randomized, double-blind, controlled study in chronic constipation. Nutr J. Jul 24
- 103. Ringel-Kulka T, Palsson OS, Maier D, et al. Probiotic bacteria Lactobacillus acidophilus NCFM and Bifidobacterium lactis Bi-07 versus placebo for the symptoms of bloating in patients with functional bowel disorders: a double-blind study. J Clin Gastroenterol. Jul 2011;45(6):518-525.
- 104. Pakdaman MN, Udani JK, Molina JP, Shahani M. The effects of the DDS-1 strain of lactobacillus on symptomatic relief for lactose intolerance - a randomized, double-blind, placebo-controlled, crossover clinical trial. Nutr J. May 20 2016;15(1):56.
- 105. do Carmo MS, Noronha FM, Arruda MO, et al. Lactobacillus fermentum ATCC 23271 Displays In vitro Inhibitory Activities against Candida spp. Front Microbiol. 2016;7:1722.
- 106. Lee A, Lee YJ, Yoo HJ, et al. Consumption of Dairy Yogurt Containing Lactobacillus paracasei ssp. paracasei, Bifidobacterium animalis ssp. lactis and Heat-Treated Lactobacillus plantarum Improves Immune Function Including Natural Killer Cell Activity. Nutrients. May 31 2017;9(6).
- 107. Arribas B, Garrido-Mesa N, Peran L, et al. The immunomodulatory properties of viable Lactobacillus salivarius ssp. salivarius CECT5713 are not restricted to the large intestine. Eur J Nutr. Apr 2012;51(3):365-374.
- 108. Neville BA, O'Toole PW. Probiotic properties of Lactobacillus salivarius and closely related Lactobacillus species. Future Microbiol. May 2010;5(5):759-774.
- 109. Eales J, Gibson P, Whorwell P, et al. Systematic review and meta-analysis: the effects of fermented milk with Bifidobacterium lactis CNCM I-2494 and lactic acid bacteria on gastrointestinal discomfort in the general adult population. Therap Adv Gastroenterol. Jan 2017;10(1):74-88.
- 110. Jawhara S, Habib K, Maggiotto F, et al. Modulation of intestinal inflammation by yeasts and cell wall extracts: strain dependence and unexpected anti-inflammatory role of glucan fractions. PLoS One. 2012;7(7):e40648.
- 111. Sheele J, Cartowski J, Dart A, et al. Saccharomyces boulardii and bismuth subsalicylate as low-cost interventions to reduce the duration and severity of cholera. Pathog Glob Health. Sep 2015;109(6):275-282.
- 112. Rastall RA, Maitin V. Prebiotics and synbiotics: towards the next generation. Curr Opin Biotechnol. Oct 2002;13(5):490-496.
- 113. Kotzampassi K, Giamarellos-Bourboulis EJ, Voudouris A, Kazamias P, Eleftheriadis E. Benefits of a synbiotic formula (Synbiotic 2000Forte) in critically III trauma patients: early results of a randomized controlled trial. World J Surg. Oct 2006;30(10):1848-1855.
- 114. Wong VW, Won GL, Chim AM, et al. Treatment of nonalcoholic steatohepatitis with probiotics. A proof-of-concept study. Ann Hepatol. Mar-Apr 2013;12(2):256-262.