

# Reinforce Microbial Changes:

## A First-In-Class Precision Prebiotic™

Tom Bayne, DC



The gut microbiome is currently one of the hottest topics in the health industry, as scientists continue to unearth surprising interconnections between gut microbiota and human health. In fact, many researchers suggest that the gut microbiome should be considered a completely separate organ in the body since it contains a vast ecosystem of bacteria, viruses, fungi, and protozoa. When this vast but delicate ecosystem is thrown out of balance, it can become a breeding ground for many chronic diseases, including obesity, heart disease, diabetes, autoimmunity, mood disorders, and more.<sup>1</sup> Studies have shown that a more diverse gut microbiome results in a more robust and adaptable immune system.<sup>2</sup> Furthermore, low microbial diversity has been linked to autism, insulin resistance, colorectal cancer, Crohn's disease, ulcerative colitis, celiac disease, multiple sclerosis, polycystic ovary syndrome (PCOS), and more.<sup>1-3</sup>

Studies investigating microbial diversity have identified a handful of species as next-generation beneficial bacteria that appear to protect and preserve human health. These bacterial species include *Akkermansia muciniphila*, *Faecalibacterium prausnitzii*, and *Bifidobacterium spp.*

*A. muciniphila* is a mucin-degrading bacterium that plays an important role in the regulation of the gut barrier and metabolism.<sup>4</sup> In humans, *A. muciniphila* is associated with healthier metabolic status, particularly improved insulin sensitivity and glucose homeostasis, and better outcomes after weight loss.<sup>5</sup> Low abundance of *A. muciniphila* has been linked to obesity, diabetes, liver disease, cardiometabolic diseases, and low-grade inflammation.<sup>6</sup> *F. prausnitzii* is a butyrate-producing bacterium that is one of the most abundant and important commensal organisms in the human gut. By producing butyrate, *F. prausnitzii* plays a significant role in providing energy for intestinal cells and reducing intestinal inflammation. Low levels of *F. prausnitzii* are common signatures of inflammatory intestinal disorders like IBS, Crohn's disease, ulcerative colitis, colorectal cancer, obesity, and celiac disease.<sup>7</sup> The genus *Bifidobacterium* also plays an important role in maintaining barrier function and stimulating the immune system.<sup>8</sup> Because *Bifidobacteria* are also butyrate-producers, they can help reduce intestinal inflammation and also appear to help with weight management.<sup>9</sup> Low levels of *Bifidobacteria* have been associated with obesity, diabetes, celiac disease, allergic asthma, dermatitis, IBD, chronic fatigue syndrome, and psoriasis.<sup>10-12</sup>

Given the health benefits of these commensal gut organisms, the natural inclination is to attempt to reseed the gut with these bacteria by taking them orally as probiotics. However, these anaerobic bacteria require oxygen-free environments in order to thrive and are not designed by nature to be reintroduced to the gut orally. Additionally, the aerobic environments in manufacturing plants

make it extremely difficult to produce truly anaerobic probiotics. The good news is that these commensal strains are already present in the gut microbiome. In fact, these protective bacteria are keystone strains that have been passed from mother to child at birth. Antibiotics, diet, stress, and other factors may reduce their abundance, but these commensal bacteria are never completely eradicated – they just need to be revitalized. Reconditioning the gut is very much

unable to produce these significant shifts due to poor survivability and weak colonization. *Bacillus* spores, on the other hand, can effectively **RECONDITION** the gut and encourage the growth of beneficial, keystone bacteria like *A. muciniphila*, *F. prausnitzii*, and *Bifidobacterium* species in as little as 30 days – but the gut restoration doesn't stop there.<sup>13</sup> Just like a growing garden needs continuous care and proper fertilization, it is important to nurture and **REINFORCE** a healthy gut microbiome with a Precision Prebiotic™.

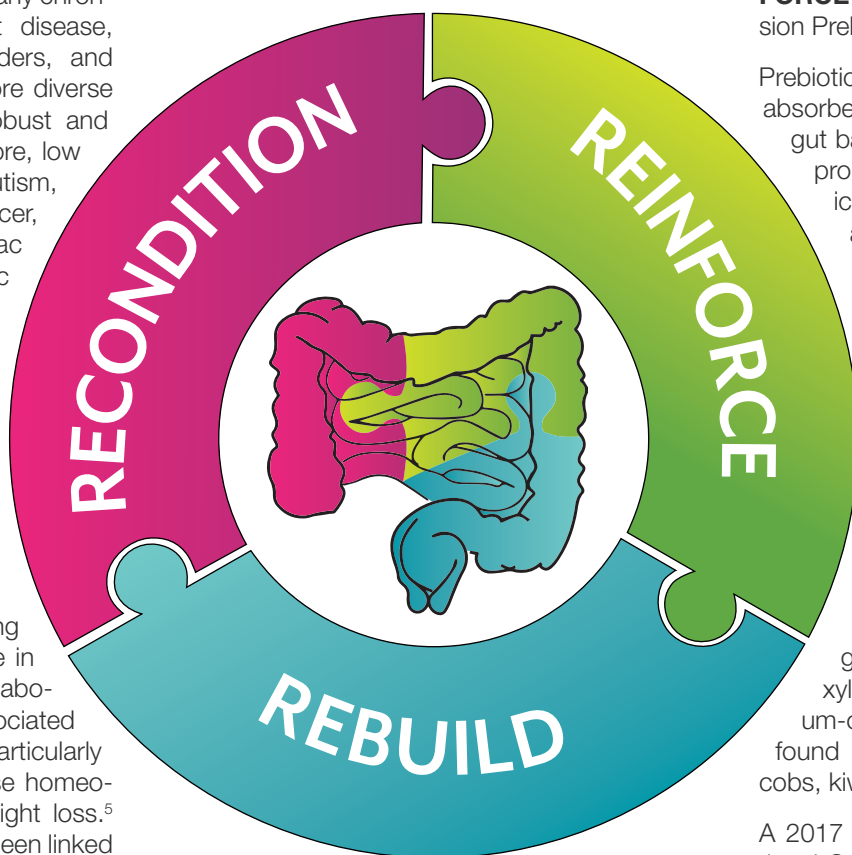
Prebiotics are fibers that cannot be digested or absorbed by humans but can be fermented by gut bacteria. In this sense, prebiotics feed the probiotics in the gut. However, most prebiotics on the market can feed both harmful and beneficial gut bacteria, which can be problematic for people with digestive symptoms. For decades, practitioners had to weigh the benefits of prebiotics with the unwanted side effects of bloating, gas, and abdominal cramping – until now.

In the last few years, scientists have discovered functional fibers that can selectively feed beneficial, keystone bacteria without feeding harmful bacteria. These novel functional fibers include fructo-oligosaccharides (FOS), galacto-oligosaccharides (GOS), and xylo-oligosaccharides (XOS) – medium-chain, non-digestible carbohydrates found in lentils, peas, bamboo shoots, corn cobs, kiwifruit, cow's milk, and honey.

A 2017 study published in the Journal of Nutritional Sciences found that oral supplementation of FOS derived from kiwifruit increased the abundance of *F. prausnitzii* by 100% in 4 weeks.<sup>14</sup> Another study published in Diabetes found that FOS supplementation was correlated with an 8,000% increase in *A. muciniphila* in only 5 weeks.<sup>15</sup>

A study conducted at the University of California Los Angeles in 2014 found that XOS derived from corn cobs increased the abundance of *Bifidobacteria* by 21% in as little as 4 weeks.<sup>16</sup>

Lastly, a randomized, double-blind, and placebo-controlled crossover study published in the American Journal of Clinical Nutrition found that GOS derived from lactose increased the abundance of *Bifidobacteria* by 66% in just 7 days.<sup>17</sup> Increasing populations of these protective bacteria is an integral part of reinforcing a healthy gut microbiome. Once the gut has been reconditioned and reinforced, the final step is to **REBUILD** the intestinal mucosa with the necessary building blocks in order to completely restore the health of the gut microbiome. Stay tuned to hear about the final step of this Total Gut Restoration system.



like revitalizing a withering garden. The existing environment undergoes a complete overhaul which includes removing the weeds, tilling the soil, and fertilizing the plants. A true probiotic should be able to recondition the gut in a measurable way, but many “probiotics” on the market are

Dr. Tom Bayne is a Chiropractic Physician and public speaker dedicated to understanding and improving the gut microbiome. As the President of Microbiome Labs, Dr. Bayne travels around the world to educate other healthcare practitioners on the connection between the gut microbiome and many chronic diseases.



<https://bit.ly/2F54Yrr>



RECONDITION



REINFORCE



REBUILD

**REFERENCES:** 1) Mosca A, et al. Gut Microbiota Diversity and Human Diseases: Should We Reintroduce Key Predators in Our Ecosystem? *Front Microbiol.* 2016;7:455. 2) Le Chatelier E, et al. Richness of human gut microbiome correlates with metabolic markers. *Nature.* 2013;500:541-546. 3) Lingheim L, et al. Alterations in Gut Microbiome Composition and Barrier Function Are Associated with Reproductive and Metabolic Defects in Women with Polycystic Ovary Syndrome (PCOS): A Pilot Study. *PLoS One.* 2017;12(1):e0168390. 4) Chelakkot C, et al. *Akkermansia muciniphila*-derived extracellular vesicles influence gut permeability through the regulation of tight junctions. *Exp & Molecular Med.* 2018;50:e450. 5) Dao MC, et al. *Akkermansia muciniphila* and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. *Gut.* 2016;65:426-436. 6) Schneeberger M, et al. *Akkermansia muciniphila* inversely correlates with the onset of inflammation, altered adipose tissue metabolism and metabolic disorders during obesity in mice. *Scientific Reports.* 2015; 5:16643. 7) Martin R, et al. Functional Characterization of Novel *Faecalibacterium prausnitzii* Strains Isolated from Healthy Volunteers: A Step Forward in the Use of *F. prausnitzii* as a Next-Generation Probiotic. *Front Microbiol.* 2017; 8: 1226. 8) Picard C, et al. Review article: bifidobacteria as probiotic agents – physiological effects and clinical benefits. *Aliment Pharmacol Ther.* 2005;22:495-512. 9) Stenman LK, et al. Potential probiotic *Bifidobacterium animalis ssp. lactis* 420 prevents weight gain and glucose intolerance in diet-induced obese mice. *Benef Microbes.* 2014;5(4):437-445. 10) Collado MC, et al. Imbalances in fecal and duodenal *Bifidobacterium* species composition in active and non-active celiac disease. *BMC Microbiol.* 2008;8:232. 11) Gao X, et al. Obesity in school-aged children and its correlation with gut *E. coli* and *Bifidobacteria*: a case-control study. *BMC Pediatr.* 2015;15:64. 12) Akay HK, et al. The relationship between bifidobacterial and allergic asthma and/or allergic dermatitis: a prospective study of 0-3-year-old children in Turkey. *Anaerobe.* 2014;28:98-103. 13) Possemiers S, et al. Evaluation of the *Bacillus subtilis* strain HU-58 in the SHIME technology platform. *ProDigest Final Report.* 2013: 1-40. 14) Blatchford P, et al. Consumption of kiwifruit capsules increases *Faecalibacterium prausnitzii* abundance in functionally constipated individuals: a randomized controlled human trial. *J Nutr Sci.* 2017; 6: e52. 15) Everard A, Lazarevic V, Derrien M, et al. Responses of Gut Microbiota and Glucose and Lipid Metabolism to Prebiotics in Genetic Obese and Diet-Induced Leptin-Resistant Mice. *Diabetes.* 2011 Nov; 60(11): 2775-2786. 16) Finegold SM, et al. Xylooligosaccharide increases bifidobacteria but not lactobacilli in human gut microbiota. *Food Funct.* 2014;5(3):436-45. 17) Depeint F, et al. Prebiotic evaluation of a novel galactooligosaccharide mixture produced by the enzymatic activity of *Bifidobacterium bifidum* NCIMB 41171, in healthy humans: a randomized, double-blind, crossover, placebo-controlled intervention study 1-3. *Am J Clin Nutr.* 2008;87(3):785-91.