



**What You Need To Know About The 51
Critical Germs Living In Your Gut**

This guide is an easy way for you to get more information regarding the bacteria and fungi in your gut. Importantly, it is not meant as an all-encompassing review of the topic, but meant to give you additional guidance in your personal research of your microbiome.

It was created by Dr. Mahmoud Ghannoum, the scientist who named the mycobiome. He is considered the leading fungal scientist in the world, and has published over 400 scientific papers on his research. He has been funded by the NIH since 1993, and his research has been cited over 18,000 times. He is also founder of BIOHM, the first microbiome company to develop probiotics and microbiome sequencing tests that address both bacteria and fungi in your gut.

The normal makeup of microorganisms found in the gastrointestinal tract is called the “microbiome,” which consists of both bacteria (bacteriome) and fungi (mycobiome). Our intestinal tracts are populated with many different kinds of bacteria soon after birth, which are necessary for the digestion of the food we eat. The gut contains trillions of bacteria that each perform differing roles in keeping us nourished and healthy; however, an imbalance in the bacterial makeup of our gut can adversely impact your gut health.

Critically, this guide should not be construed as medical advice or guidance. No guide can replace the expertise and medical advice of a physician. Please consult your doctor before making any decisions that affect your health, particularly if you suffer from any medical condition or have any symptoms that require treatment.

Gut Bacteria

Phylum Bacteroidetes

Bacteroidetes are frequently found in soil and water and are specialists in degrading organic matter such as proteins and carbohydrates.

High Bacteroides levels have been associated with excessive weight gain in pregnancy and in obesity. Low Bacteroides levels are found in obese children.

Reduced patterns of Bacteroides are reported in Irritable Bowel Syndrome and Ulcerative Colitis.

Bacteroides vulgatus – *Bacteroides vulgatus* has been found to represent part of the core gut microbiota in healthy humans. High levels of *B. vulgatus* is a risk factor for infant celiac disease and have also been associated with Autism. Low levels of *B. vulgatus* have been associated with IBS.

Barnesiella spp. – *Barnesiella* spp. is currently identified as a common but low abundance genus. Higher fecal *Barnesiella* have been associated with protection against Vancomycin Resistant enterococcus (VRE) in transplant patients.

It has also been associated with a negative influence on *C. Difficile*. Antibiotics have been shown to have negative impact on the abundance of *Barnesiella* spp. in the gut.

Prevotella spp. – *Prevotella* spp. is known for its ability to degrade complex plant polysaccharides (carbohydrates) and fiber.

Higher levels of *Prevotella* spp. are found in populations who eat high fiber diets. Higher levels have also been associated with smokers.

Prevotella spp. has also been associated with obesity, new-onset of Rheumatoid arthritis and Irritable Bowel Disease (which differs from

Irritable Bowel Syndrome in that it involves inflammation and/or ulcers in the bowel).

Prevotella corpi – *Prevotella corpi* has been connected to dietary fiber induced improvement in glucose metabolism and has been over-represented in new-onset Rheumatoid arthritis (RA).

Odoribacter spp. – *Odoribacter spp.* has been reported at lower levels in humans with Ileal Crohn's and Pancolonial Ulcerative Colitis.

Phylum Firmicutes

Firmicutes make up a large part of the human gut. Obesity has been specifically associated with a greater abundance of Firmicute when Bacteroides is low.

Anaerotruncus colihominis – A reduction in the levels of *Anaerotruncus colihominis* in the gut is associated with an increase in body mass index (BMI) and levels of triglycerides in the blood.

Butyrivibrio crossotus – Higher levels of *Butyrivibrio crossotus* may help protect against weight gain.

Blautia obeum – An increased abundance of *Blautia obeum* has been associated with a return to a normal adult gut configuration.

Clostridium spp. – *Clostridium spp.* is found in the intestinal tract of humans. Higher *Clostridium* counts and increased number of *Clostridium* species have been reported in people with Autism. Both higher and lower abundance of *Clostridium* has been observed in Irritable Bowel Disease.

The genus *Clostridium* includes two serious human pathogens:

1. *C.botulinum* produces the toxin that causes botulism, which occurs primarily from food poisoning but can also result from wounds or injecting street drugs with infected needles.
2. *C.difficile*, a normal part of the gut bacteriome, can cause severe diarrhea and abdominal pain when the balance of normal bacteria is impacted. *C.*

difficile is disrupted by taking antibiotics. The elderly or those with Irritable Bowel Syndrome or Colorectal cancer are at a greater risk of developing a C. difficile infection.

Clostridium difficile – Commonly known as “C. diff”. A pathogen found when Firmicute and Bacteroides are challenged with antibiotics.

Coprococcus eutactus – Found in a reduced abundance in people who suffer from Irritable Bowel Syndrome.

Coprococcus catus – Coprococcus catus has been associated with the metabolism of lactate that produces propionate and butyrate. Both propionate and butyrate have been linked to exerting a range of health-promoting functions.

Streptococcus agalactiae – Commonly populates the human gut and urogenital tract, and is a major cause of infection-based mortality in neonatal infants and in elderly or immunocompromised adults.

Faecalibacterium prausnitzii – In a normal gut, Faecalibacterium prausnitzii represents more than 5% of the total bacterial population. It has also been associated with controlling inflammation. Lower counts have been reported in Irritable Bowel Disease, Crohn’s Disease and Ulcerative Colitis.

Lactobacillus spp. – Lactobacilli have been recognized as flora that function to inhibit pathogenic bacteria by producing antimicrobial substances such as lactic acid, hydrogen peroxide, and bacteriocins (proteins). Found as normal flora in the oral cavity, gastrointestinal tract, and female urogenital tracts.

Lactobacillus spp. is an established ingredient found in probiotics as a reducer of intestinal inflammation.

Lactobacillus acipophylis – An established probiotic associated with reduction of inflammation.

Lactobacillus rhamnosus – Associated with alleviating penicillin related changes and reduces antibiotic use.

Pseudoflavonifractor spp. – Pseudoflavonifractor spp. has been positively associated with weight loss.

Roseburia spp. – A lower abundance of Roseburia spp. has been associated with Ulcerative Colitis.

Ruminococcus spp. – Ruminococcus spp. is known for its ability to degrade a wide range of plant polysaccharides (carbohydrates) including cellulose.

Ruminococcus albus – Ruminococcus is found in significant numbers in the intestines of humans and are associated with digesting plant material.

Veillonella spp. – Veillonella have been found in atherosclerotic (cardiovascular) plaques, fecal samples, and oral washing from subjects with known cardiac events. These observations suggest an association between Veillonella and cholesterol. Lower levels of Veillonella have been found in people who fall on the severe end of the autistic spectrum.

Phylum Actinobacteria

Included in this group is Bifidobacterium spp., which are among the first colonizers of newborn infants. Since they are considered one of the most beneficial bacteria in the gut, they are often added to probiotics. Lower numbers of this bacteria are associated with more severe symptoms of Ulcerative Colitis. Other Bifidobacterium spp. levels have been shown to be associated with obesity and normal weight.

Collinsella aerofaciens – Collinsella aerofaciens have been measured at a lower level when overweight men were on a weight-loss diet. This bacterium has also been associated with altering gut permeability and Rheumatoid arthritis.

Bifidobacterium spp. – A common component of the microbiota of the human gastrointestinal tract and in particular are amongst the first bacterial colonizers of the intestine. The amount of Bifidobacterium has also been measured at lower levels after weight-loss and gastric bypass surgery. A lower abundance has been associated with Irritable Bowel Syndrome.

Bifidocaterium breve – Associated with a reduction of constipation in children and the clinical improvement of patients with Ulcerative Colitis.

Bifidobacterium adolescentis – Appears to specifically colonize the gut of adult individuals. Bifidobacterium adolescentis has been associated with the ability to metabolize glycans in starch.

Bifidobacterium animalis – Associated with normal weight and has been found at greater levels in non-obese people.

Bifidobacterium pseudolongum – This bacterium helps maintain a normal digestive tract and inhibit the growth of harmful bacteria.

Bifidobacterium longum – Has been associated with weight-loss and found at increased levels in obese subjects.

Phylum Proteobacteria

Phylum Proteobacteria has been found in higher levels in overweight pregnant woman than in normal weight pregnant women. An imbalance in the numbers of these bacteria may lead to an increase in inflammation of the bowel or other mucous membranes, or may be associated with other disorders.

Desulfovibrio piger – Has been reported at higher levels in people with Irritable Bowel Disease and Autism.

Escherichia coli – Has been associated with Irritable Bowel Syndrome and diarrhea predominant Irritable Bowel Syndrome. It has also been reported in greater abundance with weight-loss after Gastric Bypass.

Escherichia coli-nissle strain – Has been associated with reducing inflammation in people suffering from Ulcerative Colitis.

Oxalobacter formigenes – Associated with its unique ability to metabolize oxalates that can lead to kidney stones.

Phylum Euryarchaeota

Phylum Euryarchaeota includes intestinal bacteria that produce methane. The disorders in which methanogens (methane-producers) are probably involved are Crohn's disease, Irritable Bowel Syndrome, Colorectal cancer, diverticulosis and gas (bloating, stomach pressure and feeling of fullness).

Methanobrevibacter smithii – Methanobrevibacter smithii is highly prevalent in the human gut. Lower counts have been associated with obesity while higher amounts have been associated with anorexia.

Phylum Fusobacteria

Phylum Fusobacteria is part of a normal human gut flora, but species of Fusobacterium are strongly associated with numerous diseases including Colorectal cancer. Fusobacterium are also associated with involvement in mucosal inflammation.

Fusobacterium spp. – Associated with obesity in older subjects with metabolic syndrome.

Phylum Verrucomicrobia

Phylum Verrucomicrobia makes up about 2% of a normal gut. It has been reported at abundant levels in people at a normal weight and also post Gastric Bypass patients, but reported at low levels in obese people.

Akkermansia muciniphila – Associated with a lean phenotype, reduced body weight gain, improvement in metabolic responses and restoration of gut barrier function by modulation of mucus layer thickness.

The normal gut flora is comprised of hundreds of diverse bacterial species, of which only a percentage have been characterized. However, as technology advances, more of the species that make up the bacterial population and their relative abundance will be identified. Importantly, knowing the proportion of each species in the normal GI tract will help to determine the effect that imbalances in the gut flora may have on diverse disease processes such as IBD, IBS, colitis, obesity, rheumatoid arthritis, diabetes, and possibly even cardiac events. Further, the interactions between bacterial and fungal microorganisms in the intestinal tract are being studied. Taken together, this knowledge may serve to identify treatments such as probiotics that would alleviate or prevent symptoms in patients suffering from these often-debilitating diseases.

Gut Fungi

Fungi are found everywhere in the environment, and we are constantly inhaling a multitude of spores and ingesting millions more in the food we eat.

In healthy individuals, these microorganisms are kept in check by our immune system and by the good bacteria that we need to digest our food. However, it is thought that a change in the balance of some fungi within the gut may cause worsening of symptoms in certain diseases such as irritable bowel disease and Crohn's disease. For example, some fungi are useful in food fermentation, though if left unchecked they could overwhelm our system, leading to dysbiosis (imbalance in the microbiome).

There are basically two forms of fungi – yeasts and molds – that are relevant to gut health.

Yeasts are classified into two major groups (called phyla), the first of which are the Ascomycota (Candida and Saccharomyces, for example).

Ascomycota (Yeasts) – Has been positively associated with fasting insulin, meaning that the greater the abundance of these fungi in the gut

— the higher the levels of insulin produced. Ascomycota are also present in higher numbers in obese subjects.

Ascomycota (Molds)

Aspergillus – Fungi of the genus *Aspergillus* are widespread in the environment and in the food we eat.

Some *Aspergillus* species, most commonly *A. fumigatus*, may lead to a variety of allergic reactions and life-threatening systemic infections in humans. Invasive Aspergillosis occurs primarily in patients with severely compromised immune systems, and has dramatically increased in recent years.

Candida – Among the highest concentration of fungal organisms found in the colon, *Candida* is known to colonize in 57% of normal individuals. Inflammatory Bowel Disease has been affiliated with higher abundances of *Candida* along with Cystic Fibrosis. In regard to diet — high sugar consumption over an extended period of time can be traced to *Candida* growth in the intestinal tract.

Candida spp. – Found naturally on the skin and on mucous membranes, but several species are pathogenic.

Candida albicans – The most common isolated derivative of the *Candida* species. It is most prevalent in the gastrointestinal tract, but can be found in other warm, moist areas on your body (mouth, rectum, and vagina). Diets that are high in sugar or beverages fermented with yeast (i.e. alcoholic beverages) have been found to promote the growth of this fungi.

Candida albicans is a leading cause of bloodstream infections in the United States.

Candida tropicalis – Positive correlation noted between high levels of *Candida tropicalis* and Crohn's disease.

Saccharomyces spp. – Yeasts that can turn sugar into carbon dioxide and alcohol with enzymes. *Saccharomyces* species are the yeasts in baked goods, beers, wines, and other alcoholic beverages.

Saccharomyces boulardii – *S. boulardii* has shown effectiveness in the prevention and treatment of many gastrointestinal diseases. For example, *S. boulardii* has been beneficial in alleviating diarrhea symptoms related to antibiotic use, viral and bacterial infections in children and adults. Because of this, *S. boulardii* has been added to probiotics for over 50 years.

This yeast acts directly on pathogenic organisms by altering their ability to adhere to the intestinal wall and colonize the gut. It also changes the ability of pathogens to produce toxins and lessens the body's inflammatory immune response.

Saccharomyces cerevisiae – Commonly known as baker's or brewer's yeast. Anti-*saccharomyces cerevisiae* antibodies are higher in people with Crohn's and Ulcerative Colitis. This may suggest an intolerance to *Saccharomyces cerevisiae*.

Saccharomyces pastorianus – The yeast found in lager beer. Lager brewing strains of *Saccharomyces pastorianus* have been domesticated to become one of the most important industrial microorganisms over the past 500 years.

Pichia – Another fungal genus found in the human body that has a positive effect on the mycobiome. For instance, in the oral cavity, *Pichia* has been shown to be aggressive against *Candida* strains that cause infections in patients with HIV-AIDS. The administration of *Pichia* may prevent the development of painful *Candida* infections, commonly known as thrush.

Another fungal inter-relationship with *Pichia* involves the gut mycobiome. A study comparing obese and non-obese subjects showed that those who are of normal weight demonstrated a higher percentage of *Pichia* species in their gut than obese subjects and also have a lower

incidence of another family of yeast (dipodascaceae) commonly involved in plant and food spoilage.

Pichia fermentans – A yeast that has been found in kefir grains. They are capable of fermentation, but only do so practically and under anaerobic conditions.

Aspergillus spp. – Fungi of the genus *Aspergillus* are widespread in the environment and the food we eat. Some *Aspergillus* species, most commonly *Aspergillus fumigatus* may lead to a variety of allergic reactions and life- threatening systemic infections in humans.

Invasive Aspergillosis occurs primarily in patients with severe immunodeficiency and has dramatically increased in recent years.

Basidiomycota – Though many different species of Basidiomycota exist, the most common examples are found in mushrooms and yeast. It is common to find small traces of this fungi phylum in your gut. These fungi are also linked to the red dye used to color foods such as salmon. It can also be directly ingested through the consumption of mushrooms.

Agaricus bisporus and some more exotic species which can be found on supermarket shelves, Shitakke mushrooms and a mixture of grey, pink, and yellow forms of oyster fungus contain Basidiomycota. Basidiomycota is associated with a low carbohydrate diet and can be balanced by using probiotics. Basidiomycota make up less than 1% of described fungus. Some may be saprobic (decompose organic matter) or parasitic on plants or animals.

Fusarium solani – *Fusarium* species is a commonly found fungus that causes infections. The most important risk factor for invasive Fusariosis in patients are a compromised immune system. It is not common for this fungi to be prevalent in the normal gut.

Zygomycota – If at all present, Zygomycota generally makes up a very small portion of your gut's fungal balance. It responds most vigorously to simple sugars (such as glucose), and to amino-acids and proteins.

High amounts of Zygomycota have been associated with Zygomycosis (infection).

Many of these molds are opportunistic pathogens causing disease in patients with a compromised immune system. Zygomycota falls into arguably the most ecologically diverse group of fungi and is found in a wide variety of places including spoiled fruits, soil and feces. Evidence suggests high zygomycota levels may be found in people who highly restrict dairy in their diet.

Thus far it is not possible to define with certainty the cause and effect of different fungal strains on health and wellness, though some trends have been suggested. The science is definitive that a more diverse microbiome of bacteria and fungi is associated with better health and wellness.

As knowledge about the gut mycobiome expands, new correlations between fungal species and our health will hopefully be better defined.

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