

Bacterial Taxonomy

In this section you will find each major bacterial phyla and their associated members that are relevant to the human gut.

Nomenclature & Terminology

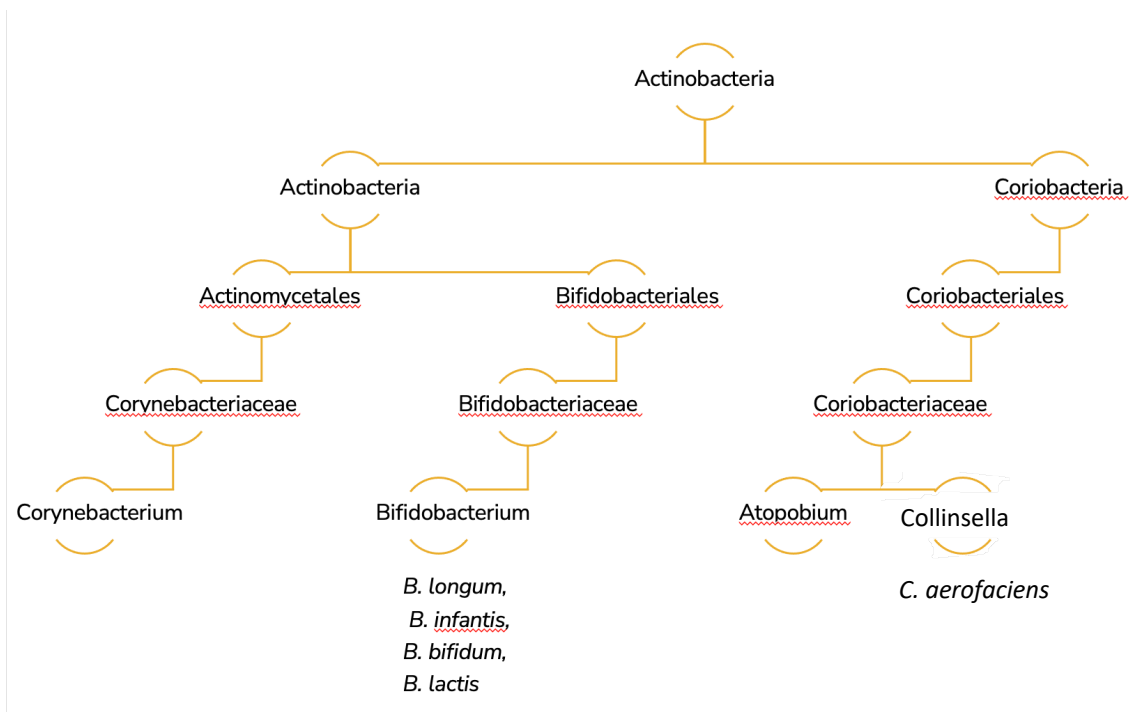
Bacterial Taxonomy is the term used to describe the classification of bacteria. All bacteria are related to each other and share general features that are not shared with any other organism, so all bacteria fall within the Kingdom of Bacteria. From there bacteria are grouped by features, such as what other bacteria they are closely related to, morphology, metabolism and environments in which they live. As you move down the ladder from Kingdom to Phylum, Class, Order, Family, Genus and Species the bacteria within each level share more and more characteristics. Appendix 1 lists the bacterial taxonomy with a focus on those frequently found within the gut microbiome.

The colors of bacteria are consistent throughout this report. For example, any species or family in red corresponds to the Actinobacteria Phylum.

Phylum: Actinobacteria

Actinobacteria constitute one of the largest bacterial phyla, yet account for only 0.05-0.2% of bacteria in a human stool sample. These bacteria have characteristics that are both bacterial and fungal in nature and produce about 2/3 of all naturally derived antibiotics in clinical use. *Corynebacterium* and *Bifidobacterium* are members of Actinobacteria that are often associated with the human microbiome.

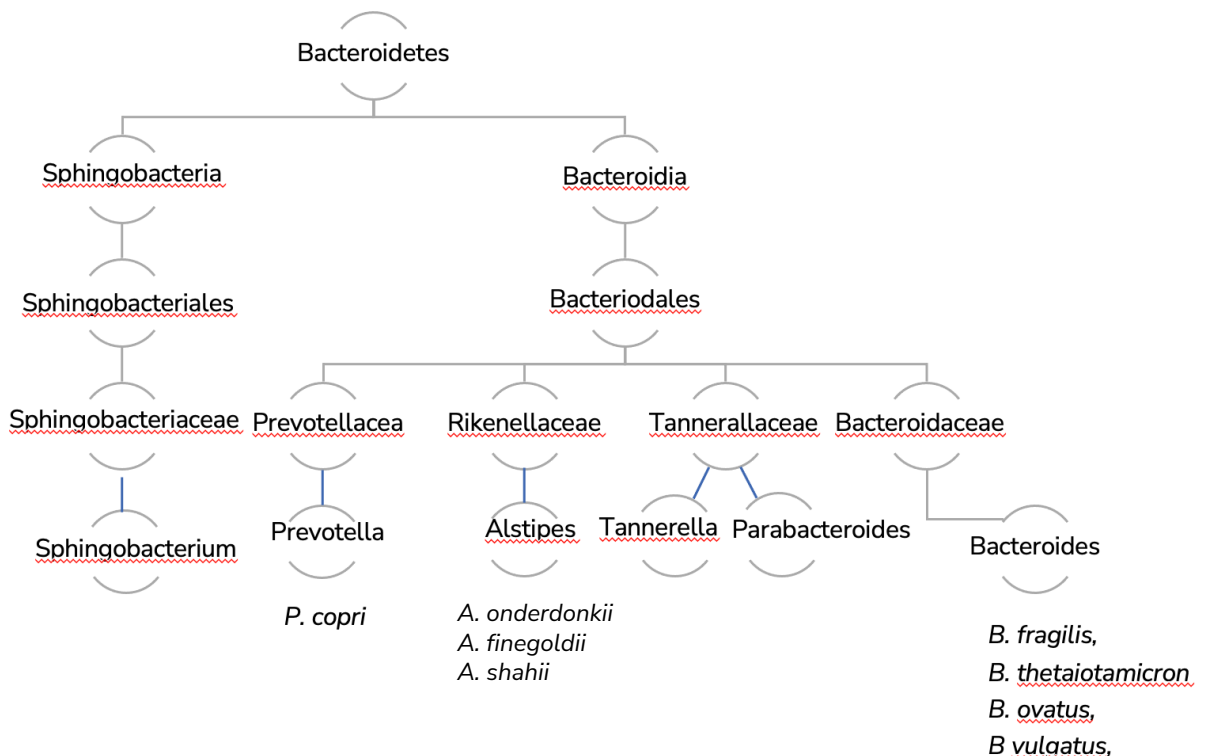
Bifidobacterium have probiotic qualities that promote health. These bacteria kill harmful bacteria, play a role in bile acid metabolism, folic acid production, dampen inflammation, and can adhere to the mucus and intestinal epithelium³⁴. Foods that help your *Bifidobacteria* thrive are fruits and vegetables rich in fiber and that contain prebiotic oligosaccharides. These include foods such as apples, artichokes, almonds, onions, pistachios, cabbage, chicory, wheat, bananas, garlic and leeks.



Phylum: Bacteroidetes

Bacteroidetes is a very diverse phylum that represent 7000 different species of bacteria. A common feature amongst all bacteria within this phyla are that they are excellent at degrading polymeric organic matter, such as dietary polysaccharides. Bacteroidetes account for roughly 50% of the bacteria within the gut microbiota of humans. The most prominent groups of Bacteroidetes found in the gut are members of the genus *Bacteroides* and *Prevotella*.

The main role of Bacteroidetes in our gut is to digest polysaccharides, which cannot be broken down by our own human cells. They can also break down large proteins made by our own bodies such as mucus. The breakdown of these complex molecules leads to the release of short chain fatty acids (propionate, butyrate and acetate) which have important benefits for human health.

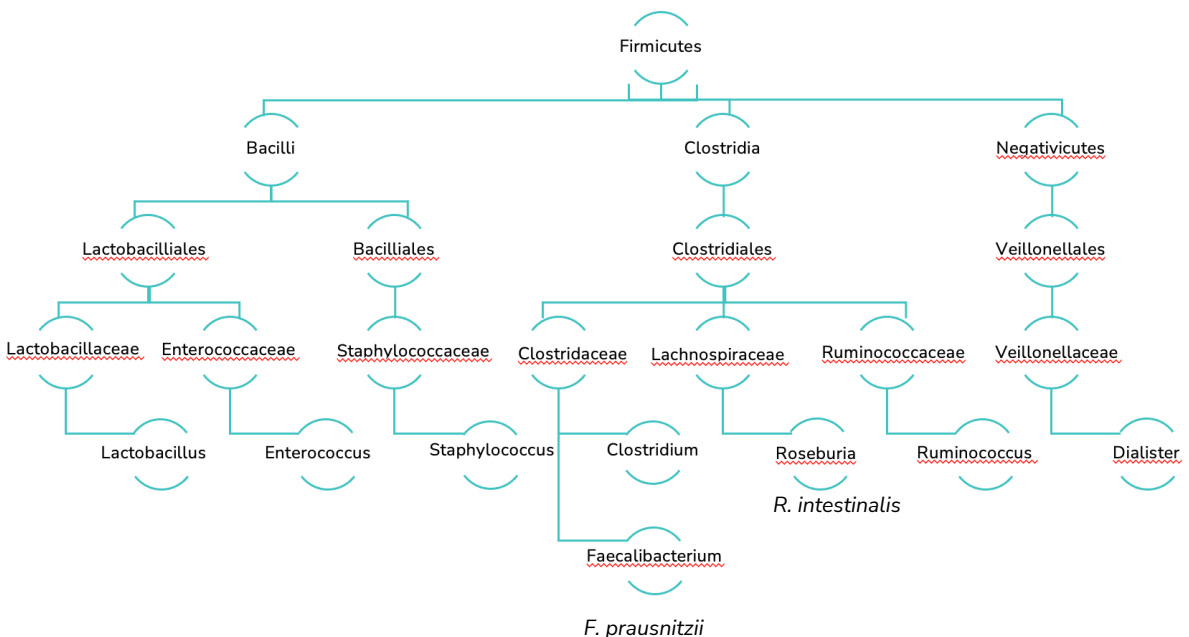


Phylum: Firmicutes

The Firmicutes phylum is made up of more than 250 genera of bacteria that belong mostly to 3 classes; Clostridia, Bacilli and Negativicutes. Overall, Firmicutes comprise 40-60% of the bacteria found in the human gut.

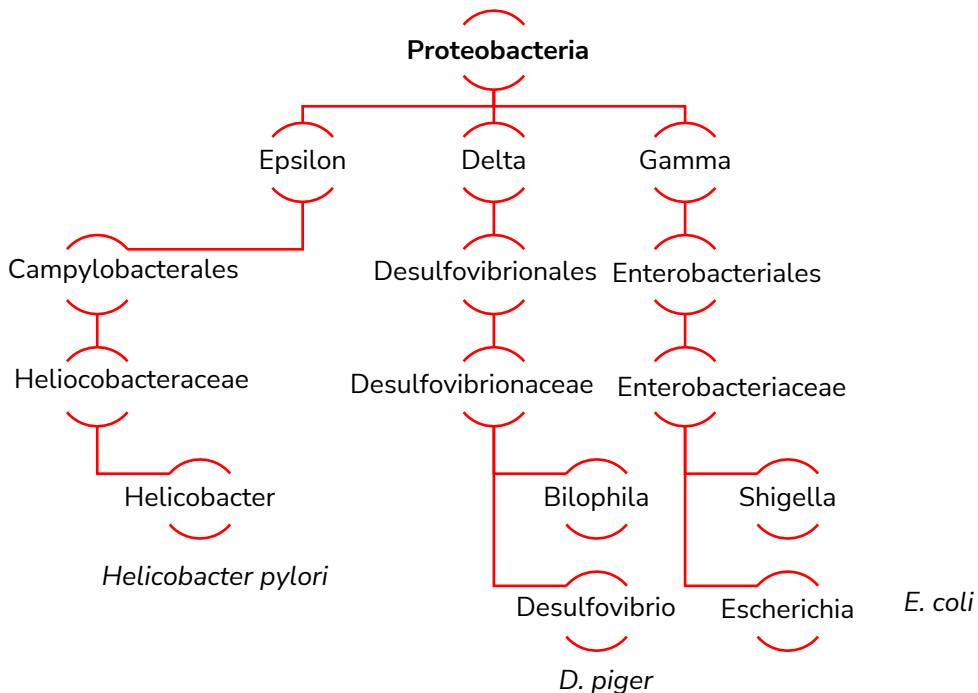
Clostridia are spore-forming bacteria that germinate upon favorable conditions and include bacteria such as Ruminococcus, Faecalibacterium, and Roseburia. Clostridia are able to digest plant polysaccharides which lead to the production of short chain fatty acids, specifically butyrate. While many Clostridia are beneficial for our health, a few can become pathogenic, such as Clostridium difficile.

Bacilli includes two groups: the Bacillales and Lactobacillales. Lactobacillales are mostly lactic acid bacteria that obtain energy by metabolizing sugars into lactic acid via fermentation. Lactobacillales can be found in many different habitats such as dairy products (Lactobacillus, Lactococcus, Leuconostoc, Streptococcus, Pediococcus), soil (Enterococcus, Lactobacillus, Pediococcus and Streptococcus), plants and animals.

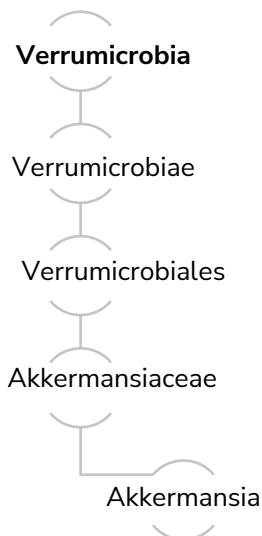


Phylum: Proteobacteria

Proteobacteria is a large phylum associated with disease-causing bacteria. Most bacteria within this phylum have a cell membrane composed of lipopolysaccharide (LPS), a molecule that is associated with inflammation and leaky gut. Members of this phylum are normally at a low abundance in the human gut.



Phylum: Verrucomicrobia



A. mucinophila

Verrucomicrobia is a phylum with only a few described species of bacteria. The species most associated with the human gut is *Akkermansia mucinophila*. This is a bacteria that resides in the mucus layer of the large intestine. It breaks down the mucus for energy and produces short chain fatty acids, particularly acetate. Acetate is then used by the intestinal epithelium to promote barrier integrity and decrease permeability and can be used by other bacteria such as *Faecalibacterium prausnitzii*.