

## Introduction

The human gut microbiome and its role in both health and disease has been the subject of extensive research in recent years due to advancing technology. Often referred to as “the forgotten organ”, the human gut microbiota, found in the gastrointestinal tract (GI), is a complex community that provides important metabolic functions to the host. While there are over 50 bacterial phyla on Earth, human-associated bacteria primarily belong to one of four phyla: *Actinobacteria*, *Firmicutes*, *Proteobacteria* and *Bacteroidetes*. Bacteria belonging to these phyla have coevolved to exist with the human gut microbiota in a mutualistic relationship, where a uniquely suited environment is provided in return for physiological benefits (Kelsen and Wu 2012).

While there are multiple factors that contribute to the establishment and health of the human gut microbiota, our research emphasizes the impact that the environment can have on the microbiome. Specifically, research has shown that dietary components, such as fibre, play a crucial role in maintaining and improving the human gut microbiome. Elements such as prebiotics can increase *Bifidobacterium* and *Lactobacillus* abundance in

the human microflora. Maintaining a balance of these bacteria, as well as all the organisms in the microbiome, can help reduce the risk of diseases such as obesity, irritable bowel syndrome, even skin diseases such as psoriasis (Singh *et al.* 2017). Studies have also revealed how the genome of the host and heredity of certain bacterial strains can influence the composition of the microbiome through various experiments involving gut flora of twin subjects (Goodrich *et al.* 2017). In this poster, we will be further analyzing the intertwining correlations between the effects of external and internal influences on the human gut microbiota.

Kelsen, J.R. and Wu. G.D. The gut microbiota, environment and diseases of modern society. *Gut Microbes.* **3**, 374-382 (2012).

Goodrich, J.K., Davenport, E.R., Andrew, C.G., Ruth, L.E. The relationship between the human genome and microbiome comes into view. *Annu. Rev. Genet.* **51**, 413-443 (2017).

Singh, R.K, Chang, H.W., Yan, D., Lee, K.M., Ucmak, D., Wong, K., Abrouk, M., Farahnik, B., Nakamura, M., Zhu, T.H., Bhutani, T., Liao, W. Influence of diet on the gut microbiome and implications for human health. *J Transl Med.* **15**(73), 1-17 (2017).

**How does diet impact the human gut microbiome? How does this affect human health and risk of disease? What are the potential impacts on personalized nutrition?**

Humans are reliant on countless different organisms for survival. Not only do we depend on external organisms, we depend on internal organisms in our GI tract to help us with metabolic processes such as energy extraction, vitamin production and immune defense (Hall *et al.* 2017). The microbiome of the human gut is home to  $10^{14}$  microorganisms including bacteria, viruses and fungi which live in symbiosis with the host (Ercolini and Fogliano 2018). Because these organisms reside in the gastrointestinal tract, they are directly impacted by the diet of the host which can significantly affect the composition of the GI tract microbiome within just 24 hours (Singh *et al.* 2017). Diet can alter population size of many organisms and therefore alter crucial metabolic processes (Singh *et al.* 2017). For example, many irritable bowel diseases (IBDs) are linked to poor species diversity in the microbiome. This is because each species in the gut has its own job to transform energy from ingested substances into new molecules which take part in

metabolic processes such as digestion and communication (Heiman and Greenway 2016). In the case of IBD, patients have been observed to have lower bacterial diversity and lower numbers of Bacteroides and Firmicutes than healthy patients (Singh *et al.* 2017). Bacteroides and Firmicutes are bacteria that contribute to the production and development of butyrate, a short fatty acid chain which has an anti-inflammatory effect on the human gut (Singh *et al.* 2017). When levels of Bacteroides and Firmicutes drop, levels of butyrate drop, resulting in unrestrained inflammation that leads to IBD (Singh *et al.* 2017). There are also multiple species of bacteria in the gut that play a role in the formation of anti-inflammatory T-regulatory cells, proinflammatory Th17 cells and B lymphocytes (mucous producing cells) that, when put out of balance, can cause IBD and other GI diseases (Wu and Lewis 2013). Another example of disease caused by poor gut microbiome composition is obesity. Obese subjects were observed to have a high ratio of Firmicutes to Bacteroidetes. The dominance of Firmicutes results in altered methylation in promoters of genes related to cardiovascular disease and obesity (Singh *et al.* 2017).

A diverse diet is the key to having both a healthy microbiome and host (Ercolini and Fogliano 2018). The microorganisms in the human gut microbiome thrive on food with low bioavailability to humans; in other words, they thrive on whatever the host is unable to digest/absorb (Ercolini and Fogliano 2018). Foods that have low bioavailability include raw nuts, in-tact plant tissues and fiber rich foods (Ercolini and Fogliano 2018). To lower bioavailability in your diet you can eat these foods as well as raw fruits/vegetables and foods that are in-tact (cooking and flouring/juicing foods causes a change in structure that increases bioavailability) (Ercolini and Fogliano 2018). Consuming an appropriate balance of bioavailable and non-bioavailable is the best way to ensure the host and its microbiome are in complete symbiosis.

Ercolini, D., Fogliano, V. Food Design to Feed the Human Gut Microbiota. *J Agric Food Chem.* **66**(15), 3754–3758 (2018).

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Heiman, M.L., Greenway, F.L. A healthy gastrointestinal microbiome is dependent on dietary diversity. *Mol Metab.* **5**(5), 317-320 (2016).

Singh, R.K, Chang, H.W., Yan, D., Lee, K.M., Ucmak, D., Wong, K., Abrouk, M., Farahnik, B., Nakamura, M., Zhu, T.H., Bhutani, T., Liao, W. Influence of diet on the gut microbiome and implications for human health. *J Transl Med.* **15**(73), 1-17 (2017).

Wu, G.D., Lewis, J.D. Analysis of the Human Gut Microbiome and Association With Disease. *Clin Gastroenterol Hepatol.* **11**(7), 774-777 (2014).

## Conclusion

Through our combined research, we now have a clearer understanding of the importance of the human gut microbiome to human health as well as the varying environmental components that can have an effect on this “forgotten organ”. It is important to note that while diet and consumption of dietary fibre can help increase the abundance of healthy bacteria in the human microbiome, abiotic environmental factors, such as temperature, can have an immense effect on the number of bacteria that can survive within the host as well (Kelsen and Wu 2012).

Bringing our individual investigations together has allowed us to see that there is still significant amounts of research that needs to be completed in order to understand the complexity of the human microbiome. For example, one study conducted using multiple pairs of twins attempted to discover a connection between host genes and microbiome composition (Goodrich *et al.* 2017). This test led to biased results due to twins having such similar genomes (Goodrich *et al.* 2017). Additionally, while research advancements have been made regarding the positive effects of *Bifidobacterium* and *Lactobacillus* on

the gut microbiome, much still needs to be done in terms of analyzing the specific molecular reactions that take place (Kelsen and Wu 2012). Studies that looked at changes in abiotic factors for *Bifidobacterium* have been taking place to see why they are very prevalent in many areas of the intestinal tract (Ruiz *et al.* 2011). Seeing that some of these bacterial strands can resist significant changes such as pH levels, it is clear there is still much more research to conduct in order to understand why this occurs (Ruiz *et al.* 2011).

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Ruiz, L., Ruas-Madiedo, P., Gueimonde, M., de Los Reyes-Gavilán, C.G., Margolles, A., and Sánchez, B. How do bifidobacteria counteract environmental challenges? Mechanisms involved and physiological consequences. *Genes. Nutr.* **6**(3), 307-318 (2011).

## **Team Integration Question**

Based on our team concept map, the concept that is most relevant in addressing how the environment plays a role in affecting the microbiome is abiotic factors from the internal and external environment. When looking at our concept map, a majority of branches stem from the abiotic factors found in the environment. This includes factors such as radiation, pH levels, and temperature of both the host and the environment. Due to these factors, we may see changes in gut microbiota diversity levels, genetic variation, and damage to the host and therefore the microbiome. When abiotic factors alter the environment of the microbiome, the composition of the resident population changes and affects crucial metabolic processes in the host.

In this poster, we will be evaluating the interconnectedness and close relationships between the harmful and beneficial effects of the internal and external components of the environment. In particular, natural selection, mutations, and diet all play a significant role in the health and maintenance of the human gut microbiome.

