

# THE LINKS BETWEEN HUMAN GASTROINTESTINAL MICROBIOME COMPOSITION AND AUTOIMMUNE DISEASE

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## Abstract

The human microbiome has a critical role in human health. Due to their importance, it is expected that drastic changes to the microbiome and its population and composition would translate into equally drastic changes to the hosts' well being. This paper utilizes secondary and systemic data analysis to find a correlation between the composition of the human microbiome and the occurrence of autoimmune systemic lupus erythematosus. It was found that compositions composing less of the phylum Firmicutes and more Bacteroidetes are tied to SLE

## Purpose

The purpose of this project is to identify links between the microbiome of the G.I. tract and the occurrence of SLE

**Research Question:** Is there a link between the G.I. microbiome and SLE?

**Hypothesis:** There is no such link between the G.I. microbiome and SLE

## Introduction

Systemic Lupus Erythematosus is an autoimmune condition which affects an approximate 1.5 million Americans living in the United States - among the highest incidence rates of any singular country in the world (Lupus Foundation of America). It is a systemic condition in which the immune cells mistakenly attack body tissue and is characterized by a hyperactive immune response to antigens. Recent breakthroughs in technology however, have opened up a new field of study which can help in the understanding of the development and treatment of this disease. This has led to now ongoing research focused on the human microbiome.



The human microbiome is the community of prokaryotic and eukaryotic organisms in the human body consisting of mainly bacteria, viruses, and fungi. Having coevolved with vertebrates, it has a symbiotic relationship with the human host in which it assumed a critical role in immune defense and basic human processes (Macia et al., 2011). Due to this connection with the development of the immune system, this project will focus on if the microbial composition has an impact on the development of autoimmunity

## Method

The research was done through systematic literature review. Information on the impact of the human microbiome on autoimmune incidence was collected through peer reviewed papers. This includes data concerning the occurrence of SLE in patients of different microbial composition. Information was retrieved from sources from databases Google Scholar, Ebscohost, JSTOR, and CSUCI College library databases. Detailed research on this topic is from 2000-current.

## Results

Data demonstrates the bacterial composition of the microbiota as arranged by phylum. There is a difference between the Phylum of the healthy control and the Phylum of the SLE patient. Data taken from two sources demonstrate roughly the same trend of a decrease in Firmicutes percentage and increase in Bacteroidetes percentage. The total average of all data taken demonstrates that the percentage of Firmicutes decreases ~14.4% and the percentage of Bacteroidetes increases 21.7%.

Additional data demonstrates the bacterial composition based on family.

Additional data collected on other autoimmune diseases were also considered on Table 4, where studies involving Type 1 Diabetes (T1D) were tied in with studies concerning Systemic Lupus Erythematosus. These studies showed control groups with similar Firmicute/Bacteroidetes ratios and were therefore able to be compared with each other.

be 15.51% and the average increase in Bacteroidetes is 24.95%. These average values were visually represented in Figure 2.

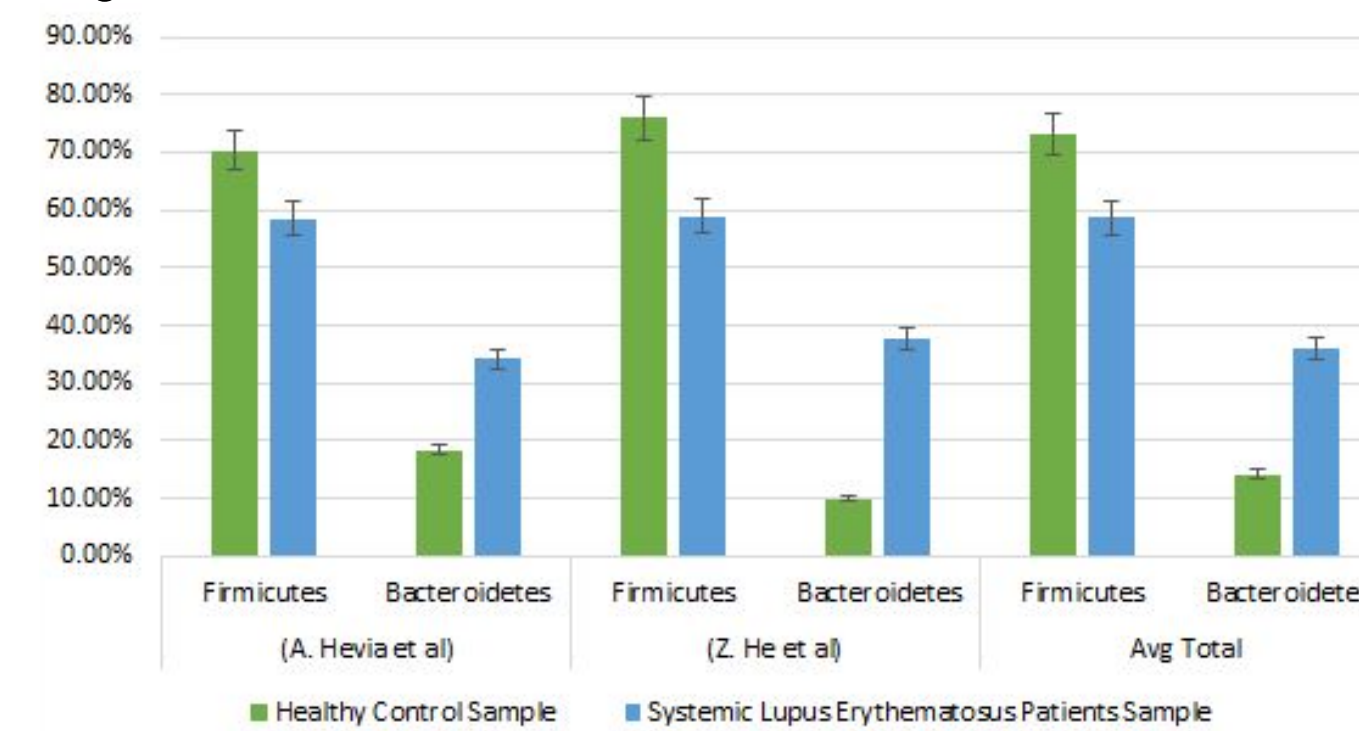


Figure 1. Figure 3: Shows microbial composition of the intestinal microbiome according by Phylum and compares them between a sample of healthy control and a sample of SLE patients.

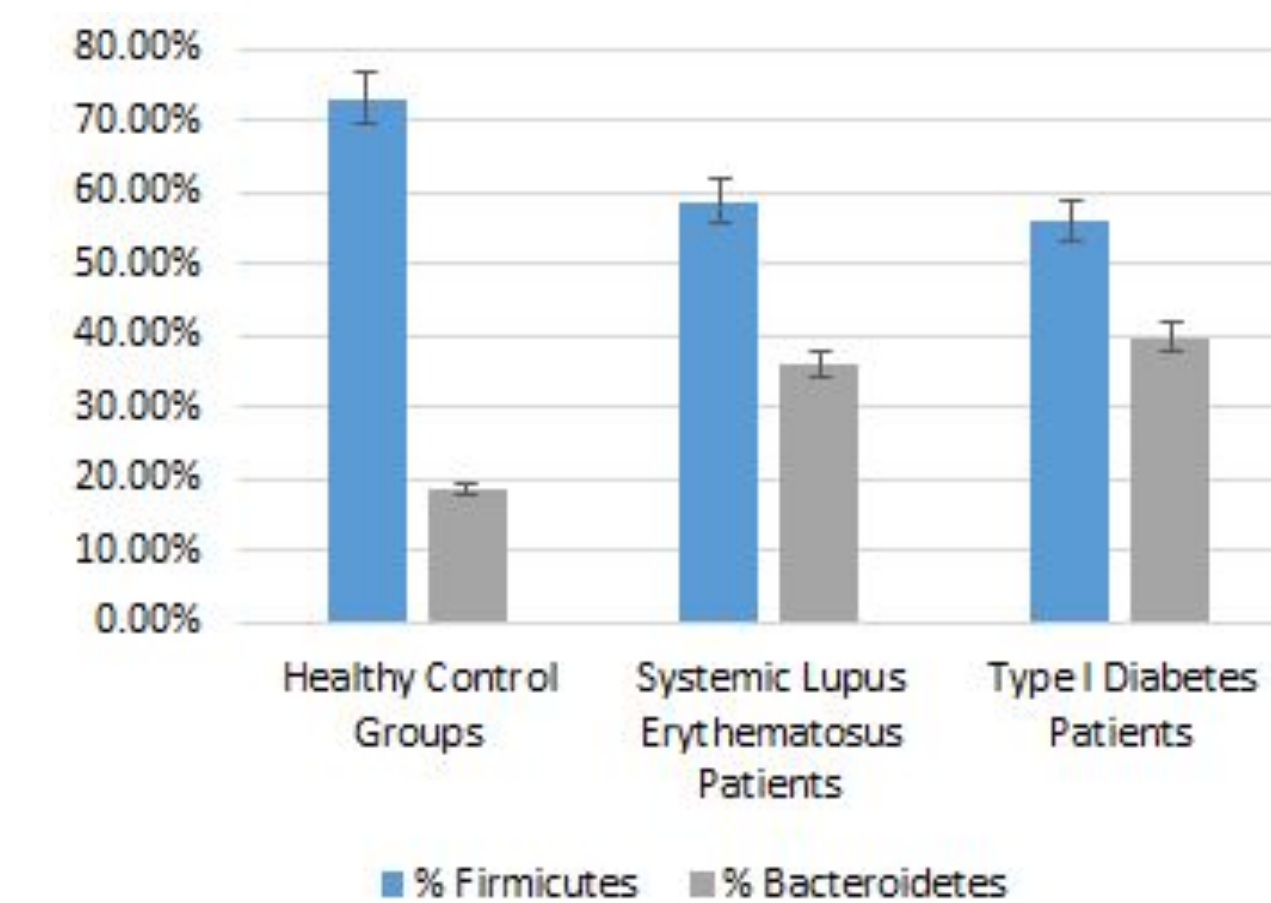


Figure 2. Differences in G.I. Microbiome composition based on percentage of Phylum and compares healthy compositions with SLE and T1D compositions.

## Discussion

What is observed in the data shows firstly that the control samples in the studies are consistent and therefore concerns on weather or not microbial compositions may depend on different regions and geography may be put aside. Additionally, SLE studies show a consistent pattern of microbial composition in which the Firmicutes consist of ~60% while Bacteroidetes ~30%. It is reasonable to assume therefore that around this range that may be associated with Systemic Lupus Erythematosus. However, it cannot be asserted that this is specifically the reason to their development of their disease.

Due to the lack of research on gastrointestinal microbiome composition and systemic lupus erythematosus, research concerning other autoimmune diseases were also tied in. It is reasonable to assume that there would be some parallels between these autoimmune diseases and thus, the trends observed in other autoimmune diseases may help in predicting and understanding the SLE compositions. Indeed, as observed in table 4, data concerning the microbial composition of patients with autoimmune type 1 diabetes showed similarities with the SLE studies. Increases in Bacteroidetes percentages and decreases in Firmicutes percentages were observed in both the T1D and SLE studies. This shows that perhaps these dysbiotic percentages aid in the process of immune dysregulation and eventually autoimmunity.

## Conclusion

The results of this experiment point towards the direction that there is an observable impact made by the composition of the human gastrointestinal microbiota and the incidence of systemic lupus erythematosus.

## Further Works

It is critical that our human microbiome be studied in relation to autoimmunity and inflammation, which pose a serious threat to the health of the general public. In this manner, we can find the methods to solve these connections to autoimmunity. It is also an opportunity to further understand the microbiome, which still has much to offer in terms of research and awareness.

## References

- He, Z., Shao, T., Li, H., Zie, H., Wen, C. (2016). Alterations of the gut microbiome in Chinese patients with systemic lupus erythematosus. *Gut Pathogens*, 8(64). doi: 10.1186/s13099-016-0146-9
- Hevia, A., Milani, C., Lopez, P., Cuervo, A., Margolles, A. (2014). Intestinal dysbiosis associated with systemic lupus erythematosus. *mBio* doi: 10.1128/mBio.01548-14
- Macia, L., Thorburn, A., Binge, L., Marino, E., Rogers, K., Maslowski, K., Vieira, A., Kranich, J., Mackary C. (2012). Microbial influences on epithelial integrity and immune function as a basis for inflammatory diseases. *Immunological Reviews*, 245.
- Turnbaugh, P., Ridaura, V. K., Faith, J. J., Rey, F. E., Knight, R., Gordon, J. (2010) The effect of diet on the human microbiome: a metagenomics analysis in humanized gnotobiotic mice. *Science Translational Medicine* 1(6).
- Mu, Q., Zhang, H., Liao, X., Lin, K., Liu, H., Edwards, S., Ahmed, A., Yuan, R., Li, L., Cecere, D., Kirby, J., Goswami, P., Leeth, C., Read, K., Oestreich, K., Vieson, M., Reilly C., Luo, X. (2017). Control of lupus nephritis by changes of gut microbiota. *Mu et al. Microbiome* 5. doi:10.1186/s40168-017-0300-8