Analysis of Microbiome-Host SNP Associations and the Immune System Profile

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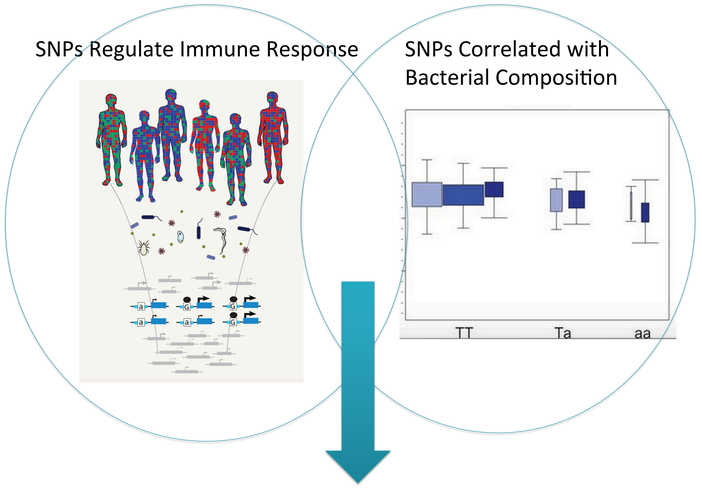
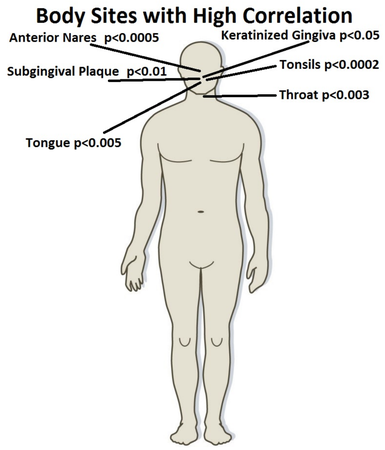
Introduction

By aggregating data from multiple sources I worked to determine if the same SNPs were responsible for both the microbiome-host associations found and the immune system profiles.
This poster shows that there is a statistically significant relationship between the data sets and some of the same SNPs were associated with both the microbiome and human immune profiles, especially those SNPs associated with the mouth and nose body sites. This work is the basis for future studies into host gene regulation and microbiome composition.



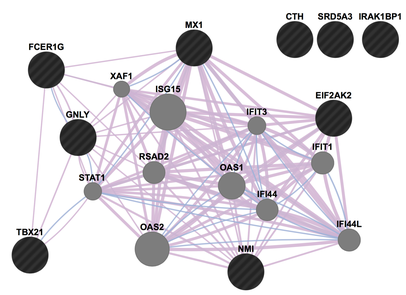
Limiting Factors



The microbiome data came divided into associated body sites. These sites were tested for their relatedness to the immune profiles and those near the mouth and nose were highly correlated.

Significant Gene's Functions

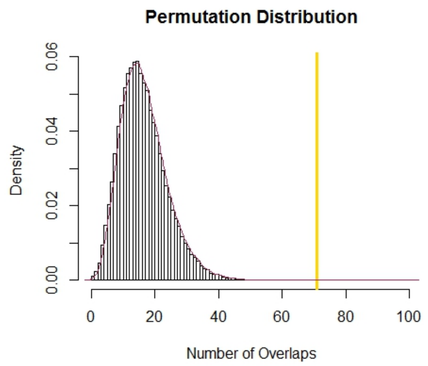
Feature	FDR	Genes in network	Genes in genome
Cellular response to type I interferon	1.24E-11	8	74
Response to virus	1.24E-11	10	205
Type I interferon signaling pathway	1.24E-11	8	74
Response to type I interferon	1.24E-11	8	75
Negative regulation of viral genome replication	3.94E-09	6	38
Regulation of viral genome replication	2.12E-08	6	51
Negative regulation of viral process	7.25E-08	6	65
Viral genome replication	7.25E-08	6	64
Negative regulation of multi-organism process	2.15E-07	6	79
Regulation of viral process	4.84E-06	6	134



Top: Table has the function of the top 10 most significant genes associated with the overlap SNPs

Left: Black genes are those found and gray genes are close associations from the human genome

Overall Significance



There were 71 SNPs that were significantly associated with both data sets.

Permutation testing shows that the overlap is most likely not due to random chance ($p<0.0005$)

Conclusions and Future Direction

- There are SNPs that are associated with both microbiome composition and immune system profiles
- Once the SNPs are deemed significantly associated with microbiome composition, degree of significance is a not a large factor.
- The body sites with the most signficant microbiome associations and immune profiles are those near the mouth and nose, common pathogen entrance points.
- Future work:
  - Determine specific bacteria associated with immune response.
  - Analyze the effect of a changed microbiome on immune profile.
    - Calculate change in immune profile after major changes in the microbiome.

Acknowledgments and References

- Ye, C. J., Feng, T., Kwon, H.-K., Raj, T., Wilson, M. T., Asinovski, N., … Benoist, C. (2014). Intersection of population variation and autoimmunity genetics in human T cell activation. *Science*, *345*(6202), 1254665–1254665. doi: 10.1126/science.1254665
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