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# *Effects of Common Chemotherapy Drugs on the Human Gut Microbiome*

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## Abstract

The environment within the human gut contains many types of microorganisms, called human gastrointestinal microbiota. Throughout recent years, many studies have found a strong correlation between the strengths and types of bacteria within the human gut microbiome and the overall health of a person. More specifically, studies have shown that the bacterial composition of an individual's gut microbiome has an impact on their physiological response to chemotherapy. This year we have completed the first two phases of our project. We have tested the effect of various concentrations of various chemotherapy drugs on the growth of human gut microbiota samples and identified and preserved samples of interest exhibiting moderate growth and samples without treatment. The next phase of the project is to perform DNA extraction upon the preserved samples, and DNA sequence the samples to determine which specific bacterial species were killed by each specific chemotherapy drug. Further examination of these relationships could be utilized to increase the efficacy and decrease the toxicity of common chemotherapy drugs.

## Hypothesis

When compared to the control group which consists of microbial communities with no treatments, we expect that communities exposed to chemotherapy drugs will have an alteration of the composition of the bacterial species. Specifically, we expect that in high doses of chemotherapy drugs certain bacterial species will be exterminated resulting in a gradient of microbial growth. We expect that wells with moderate microbial growth will have certain species of bacteria that are affected by the different kinds of chemotherapy medication. The aim of this project is to develop a relationship between specific chemotherapy drugs and the specific bacterial species it targets.

## Methodology

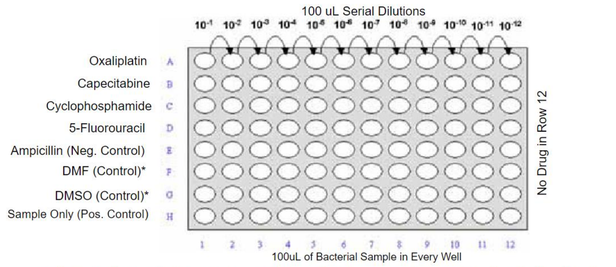



***Figure 1***. 96-Well Plates Set Up

***Figure 2.*** Anaerobic Hood Chamber

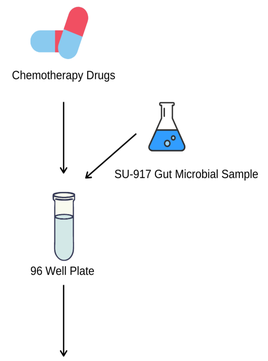



***Figure 3.*** Experimental Design

## Conclusion

- From the results of our trials, the higher concentrations (60-80 microliters) of the chemotherapy drugs had clear effects on the growth of human gut microbial communities and most likely affected different bacterial species.
- We also have concluded that there may be a maximum chemotherapy drug concentration level at which a difference in bacterial composition is seen, as there was not a significant difference in the results seen between the 80 and 100 microliter plates.

## Future Experimentation

•Send the preserved samples of interest for 16S rRNA sequencing

•Use the results to determine which bacterial species are present in each moderate growth well sample and compare it to the bacterial species present in the untreated sample

•Examine which specific bacterial species were affected by each chemotherapy drug

•Repeat the entire research study using a different donor's gut microbiota sample to ensure replicability and results

•Repeat the entire research study with the addition of probiotics to determine if they modulate the effect of the chemotherapy drugs upon the gut microbiota sample

## Introduction

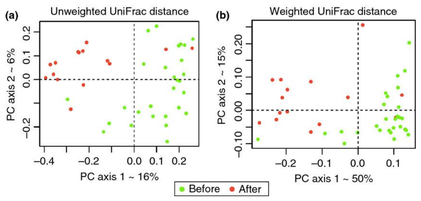



***Figure 1*** Beta-diversity comparisons of the gut microbiomes of the fecal samples collected before chemotherapy and after chemotherapy.

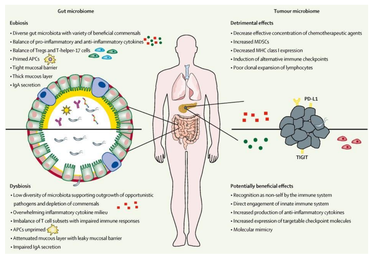



***Figure 2***. Complex interplay of the gut and tumor microbiome and the host immune system

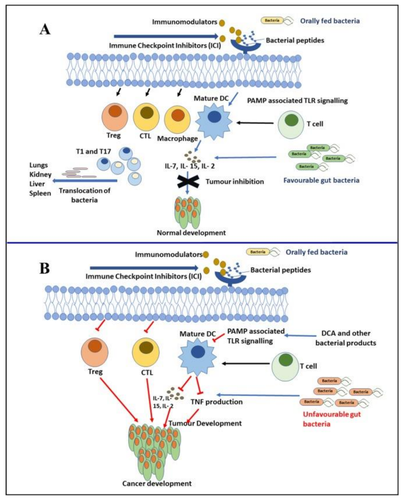
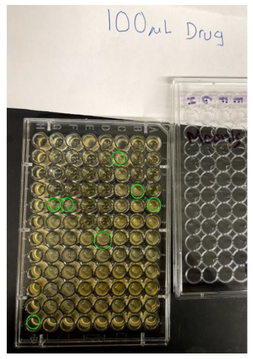
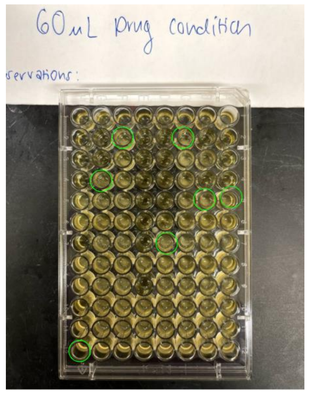
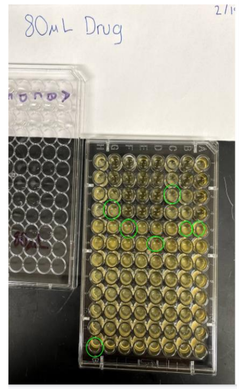



***Figure 3.*** Microbiome and immune response: Diagrammatic representation of immunomodulators and bacterial peptides regulating different proteins of the cancer cascade

## Results


**green circles represent where intermediate bacterial growth began**

## References

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