Designing a Personalized Probiotic to Prevent/Alleviate Type Two Diabetes and Inflammatory Bowel Disease

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The human microbiome makes up 90% of the cells in our body and that makes us just 10% human. The microbiome has long been associated with several human diseases. Our microbiome in homeostasis with the human body systems helps in several metabolic pathways and is also known to be responsible for the regulation of our immune system. However, during dysbiosis, our microbiome can introduce pathogens to our system causing several diseases depending on the type of disturbance to the microbiome makeup. This project performs metagenomic analysis on individual samples of healthy, IBD and Type-2-Diabetes patients .The results of these experiments are then compared to the published data from metagenomic analysis and taxonomic profiling papers performed on large cohorts of Healthy, IBD and Type-2-Diabetes. The goal is to prove that the microbiota has a differentiated profile when comparing healthy vs disease state and most importantly at the individual level the microbiome profile varies again within the disease profile. The results on individual metagenomic analysis showed the following: The bacteriodes: firmicute ratio was almost 1:1 in healthy and was highly skewed in disease patients. The diversity of the profiles decreased in Type-2D vs Healthy and it was worse in IBD. The butyrate producing bacteria decreased in Type-2D and was worse in IBD. Individual samples within the same disease showed variation. Based on results the design of the probiotic will require to include bacteria specific to the individual and as a final test, the probiotic design is tested in vitro in a gut environment model to see if the probiotic maintains optimal cytokine levels and increased butyrate levels while not skewing the bacteriodes: firmicutes ratio.

Awards Won:

University of North Texas at Dallas: $2,500 scholarship, renewable up to four years