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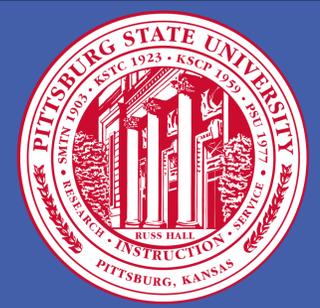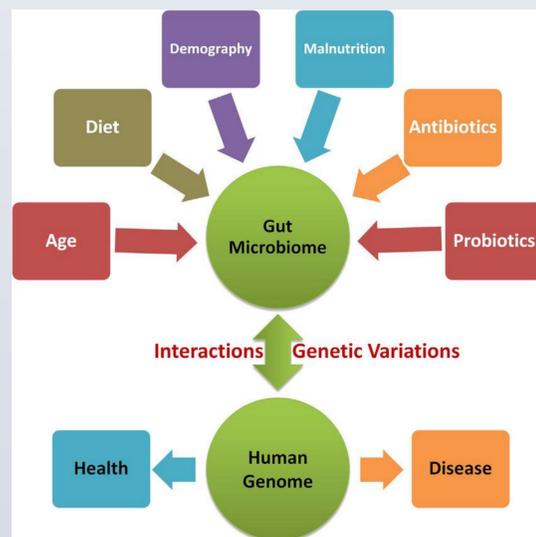# Human Gut Microbiome

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INTRODUCTION

The human body function as an ecosystem for many microbes, which are naturally found in the body, referred as *natural flora*. Some coexist without any significant effect, commensalism, while others may have a mutualistic relationship. The microbial imbalance in the body, known as dysbiosis, can lead to negative effects as it disturbs the vicious cycle the body maintains.

The human gut microbiome role and effects studies have been an area of interest for many as there is a stablished link with human metabolism, nutrition, physiology, and immune function. Disease such as type 2 diabetes and obesity has been link with imbalance in the gut microbiome.

PURPOSE

-Expand knowledge about the topic in a way both people in the field and outside of it can understand its importance.

-Explain why human gut microbiome is a something to be considered when studying metabolism.

-Show data found on an experiment and talk about its significance.

MATERIALS/METHODS

Determination of the composition of the human gut microbiome has been studied with different tools, which lead to a variety of results. More often than not it was accepted that about 80% of the bacterial species found where unculturable. In the recent years an interest for this unculturable species emerged

Two African stools were used, both from healthy young males living in rural Senegal, and a stool from a French obese individual with a body mass index of 48.2 kg/m^2.

212 culture conditions were designed, using physicochemical conditions, pre-incubations in blood cultures bottles, rumen fluid and sterile stool extract to mimic the natural environment.

Antibiotics, both active and passive filtration and bacteriophages were used with the aim of selecting a minority population.

The threshold similarity of >98.7% was chosen to define a new bacterial species.

RESULTS/CONCLUSIONS

For the first African sample, 56 different culture methods were applied, 3000 colonies where isolated. MALDI-TOF MS analysis for rapid identification of microbial species was used.
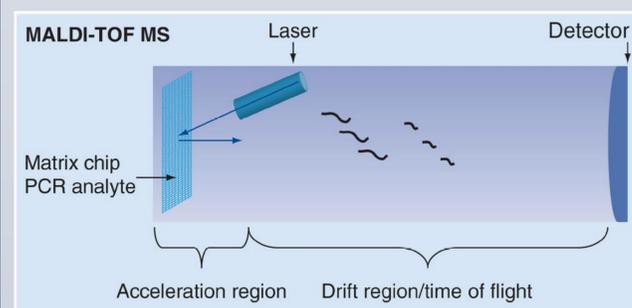

It resulted in 99 bacterial species, 42 of which had never been found in the human gut.

The other two stool samples, only those culture conditions that proved to be efficient with the first sample were used again, and many additional culture conditions were applied to maximize chance of isolation of new species.

It yielded 191 distinct bacteria's isolates, two new genera and six new species from the obese individual`s stool sample, the largest number of bacteria ever identified in a single stool (219 bacteria, 5 fungi, 3 new genera, 18 new bacteria species) were isolated from the second African sample.

Described more known bacterial species by systematically applying a large sample of culture conditions than by pyrosequencing. The paradigm shift became possible thanks to MALDI-TOF-MS. Reducing the time and cost considerably. Both time-effective and cost-effective.
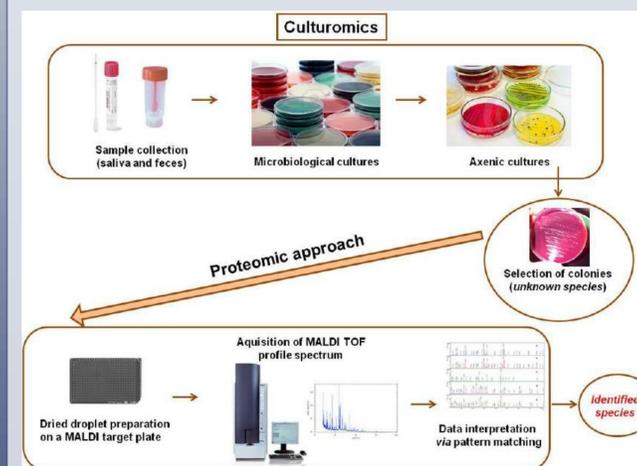
CONCLUSIONS

Results found show that the biodiversity of the microbes in the human gut is far broader than expected. By using different conditions, with microbial culturomics is the best way to capture the functional and viable gut microbiota biodiversity of each human individual through large-scale isolation.

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