

The effect of Capsaicin on the abundance of the bacterium *Akkermansia muciniphila* in the human gut

Technical University of Denmark; 27636 Metagenomics & Microbiome Analysis; Anne Frahm (Poster preparation), Harsha Ohri (Poster preparation), Lisbeth Schmidtchen (Poster preparation), Takahiro Shinoda (Programming)

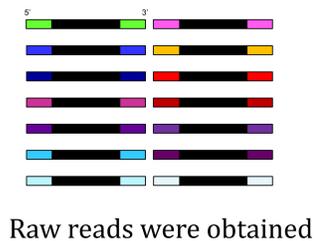
Introduction

This research is centered around a dietary intervention with the purpose to investigate the effect of chili consumption on the human gut microbiome. Previous research showed that the intake of significant amounts of capsaicin, present in chili, affects the mucous membrane in the human gut. Therefore, it was aimed to investigate the effect of capsaicin on the bacteria *Akkermansia muciniphila* which is a human intestinal mucin degrading microbe that resides in the mucus layer. Furthermore, its presence inversely correlates with the body weight in rodents and humans. In fact, researchers showed that the population of *A. muciniphila* increases drastically in High-Fat Diet-Fed mice after an intake of capsaicin. Thus, this research was aimed to show a similar outcome in humans.

Methods

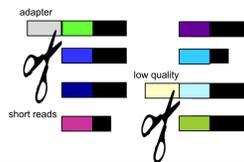
① Intervention, Sample Taking & Sequencing

- 21 participants were divided into a control and a chili intervention group
- 2 stool samples were taken. The intervention group consumed the chili in between
- The DNA of the samples was extracted, purified and sequenced



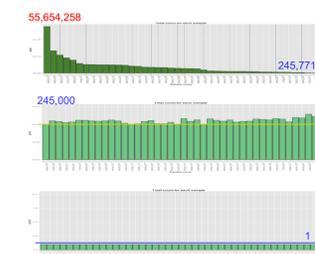
② Pre-processing

- Adapters, low-quality and short reads were removed



③ Quantification of gene abundances

- The reads were mapped to the gene catalogue
- The number of mapped reads were counted
- The counts were resampled to the lowest count size
- Eventually the counts were normalized



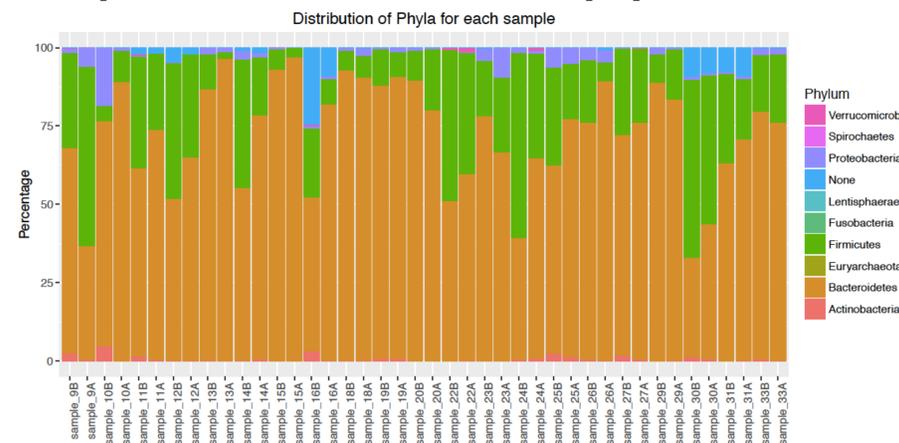
④ Generating the MGS matrix & Determination of *A. muciniphila*

- The abundance of every metagenomic species within the different samples were set into a matrix
- The abundance of *A. muciniphila* was determined for each sample

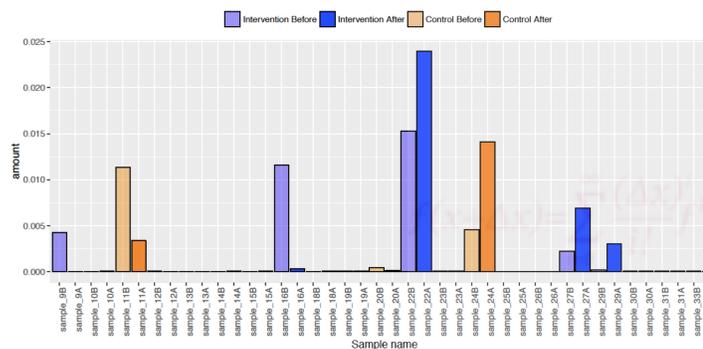
	Sam 9B	Sam 9A	Sam 10B	..
MGS1	691	31	2718	..
MGS2	15187	10502	93155	..
MGS3	133964	64840	197219	..
..

Results

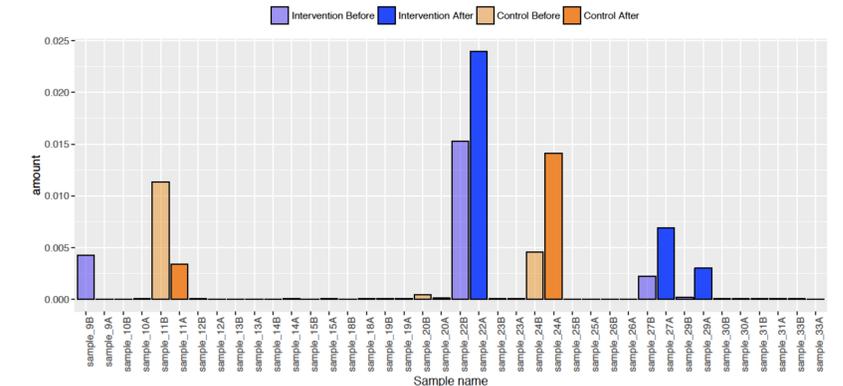
The distribution of all phyla was obtained and showed that Verrucomicrobia (including *A. muciniphila*) is not quite present in the samples. Therefore, the samples were normalized without being resampled to avoid the loss of data of less-proportional microbes.



The bar graphs represent the abundance of MGS 154 (*A. muciniphila*) w.r.t. the samples before and after intervention.



Considering the meta data sample 16 was discarded as the participant consumed lemon drop chili, containing more citric acid than capsaicin. Three samples showed the expected increase significantly.



T-tests were performed to compare the difference in the before and after values of the control and intervention group.

In the first case the p-value depicts that there is no significant difference between the two groups. After omitting Sample 16 the p-value suggests a better rejection of the null-hypothesis. Hence, it shows that the change in abundance of *A. muciniphila* in the intervention group is higher than in the control group.

	All Samples	Without Sam16
Control	90.0	90.0
Intervention	92.1	1245.2
p-value	0.9991	0.4798

Discussion

Checking the metadata revealed that *A. muciniphila* was not found in samples which were not stored in the fridge, which explains why the wanted outcome was only found in the minority of the samples.

In a future repetition of the experiment, a standardization is required to see a potential pattern better. The participants consumed different chili peppers and engaged within the experiment under different conditions. Furthermore, the intervention time needs to be increased to see significant changes within the gut microbiome better.

Literature:

- Baboota et al. - Capsaicin-induced transcriptional changes in hypothalamus and alterations in gut microbial count in high fat diet fed mice, Journal of Nutritional Biochemistry 25 (2014) 893-902
- Dao et al. - Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology, PubMed 2016 Mar;65(3):426-36