

CORRELATION OF PHYSICAL ACTIVITY LEVELS WITH **GUT MICROBIOTA COMPOSITION**



Jurica Zucko^{*}, Antonio Starcevic, Elena Malešić, Patricia Balorda, Valentina Bačić, Ivana Rumora Samarin

Faculty of Food Technology and Biotechnology, University of Zagreb, Pierottijeva 6, Zagreb, Croatia *jzucko@pbf.hr

Introduction

The gut microbiota is the largest part of the human-microorganisms macrocosm, populated by trillions of microorganisms that influence our health and well-being. The microbiota can influence various physiological processes in the human body, and conversely, it is influenced by almost every actions we take – from diet to lifestyle and exercise. Recently, changes in the microbiota have been observed depending on an individual's level of physical activity. Until now several bacterial taxa have been correlated with increased stamina and endurance, such as Prevotella, which was positively correlated with a number of amino acid metabolism pathways, and Veillonella, which metabolises the conversion of exercise-induced lactate to propionate, thereby enhancing athletic performance [1,2]. We wanted to test whether we can detect differences in microbiota composition based on varying levels of physical activity in a cohort of 40 volunteers from MicroEquilibrium project. Subjects were of different Body Mass Indexes and had different dietary habits and lifestyles. The level of physical activity was measured using Global Physical Activity Questionnaire [3], which allows us to express it numerically and correlate it with the composition of the subject's gut microbiota.

Jnassigned;

d Bacteria;

Materials and methods



Figure 1. Simplified flowchart of the experiment.

Each individual was assessed for health, lifestyle, dietary and physical activity status using respective questionnaires, followed by anthropometric measurements and fecal sample collection. When all fecal samples were collected DNA was isolated, sent for amplicon sequencing of variable regions 3 and 4 of 16S rRNA gene and resulting data processed using QIIME 2 platform.

Results



Subjects were recruited from the Microequilibrium study, that had focus on microbial equilibrium states in obese subjects. In total 40 subjects had participated in the study, 20 females and 20 males, average age was 25,75 years. Subjects had no known chronic ailments and did not take antibiotics in the last 3 months and were subjected to same data collecting procedure – questionnaires to assess health, lifestyle, dietary and physical activity status; anthropometric measurements and a collection of fecal sample. For the assessment of physical activity Global Physical Activity Questionnaire (GPAQ) was used to quantify total weekly energy expenditure expressed as Metabolic Equivalents (MET) [3]. Fecal samples were stored at – 80 °C until DNA was isolated using the QIAmp PowerFecal Pro DNA kit and sent to sequencing to Molecular Research Lab. Sequencing was carried on Illumina MiSeq instrument using the MiSeq Reagent Kit v3 on amplicons of variable regions 3 and 4 of the 16S rRNA gene. Generated raw data was transferred from Illumina's Basespace cloud and was processed in QIIME 2 platform to obtain information about taxonomic composition and diversity measures of the samples.



Figure 2. Taxonomic composition of gut microbiota of subjects at the phylum level. Each subject was assigned a level of physical activity based on its MET score



Figure 4. Scatter plot and the linear regression for absolute abundance of phyla *Firmicutes* and *Bacteroidetes* in relation to habitual physical activity expressed as METs per week

Conclusions

- No significant difference in gut microbiota composition in relation to the level physical activity was determined
- Differences in microbial diversity were observed between groups based on level of physical activity but are not significant
- More balanced group of subjects in regard of level of physical activity should be



Figure 3. Alpha rarefaction curve showing phylogenetic distance metric, subjects grouped according to MET score

Gut microbiota in this study was dominated by two phyla – Firmicutes (54.66±13.55 %) and Bacteroidetes (33.42±14.40 %), which is in concordance with general findings of gut microbiota composition. Level of physical activity did not affect abundance of those phyla in obese and undernourished individuals, while in individuals of adequate body mass index negative correlation of abundance of phyla Firmicutes and Bacteroidetes and level of physical activity was observed. Association of physical activity level and alpha diversity dana did not result in any statistical significance. Although, as can be seen in figure 3 phylogenetic diversity metric resulted in higher phylogenetic diversity observed in group with low physical activity but considering number of subject in this group (2) this result can be ignored. In this data set we have not observed higher abundance of *Prevotella* and *Veillonella* in individuals with higher physical activity level.

References



functions via lactate metabolism. Nat Med. 25(7):1104-1109.

[3] Bull FC. et al. (2009) Global physical activity questionnarie (GPAQ): nine country reliability and validity study. J

Phys Act Health. 6, 790-804.

[4] Bolyen E. et al. (2019) Reproducible, interactive, scalable and extensible microbiome data science using QIIME

2. Nature Biotechnology 37: 852–857.

^[1] Shahar RT. et al. (2020) Attributes of Physical Activity and Gut Microbiome in Adults: A Systematic Review. Int J Sports Med. 41(12):801-814.

^[2] Scheiman J. et al. (2019) Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that