P-175 - CAN THE TREATMENT OF CLASSICAL HOMOCYSTINURIA PATIENTS BE ASSOCIATED WITH THE DIVERSITY OF GUT MICROBIOTA?

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INTRODUCTION: Classical homocystinuria (HCU) is an inborn error of metabolism (IEM) with a combination of different treatments (formula, vitamins and diet) which varies according to the needs of each patient. Diet and treatment are known to modulate the gut microbiota, which is currently associated with the host’s health.

OBJECTIVES: To characterize the gut microbiota of a sample of HCU patients on treatment, by next-generation sequencing, and compare it with healthy individuals.

MATERIALS AND METHODS: Observational, cross-sectional, controlled study with convenience sampling. Stool samples were collected from 7 HCU patients on treatment from IEM Clinics of Hospital de Clínicas de Porto Alegre, Rio Grande do Sul (RS), Brazil and compared with 7 sex and age matched unrelated healthy controls, recruited among RS population. Clinical information was obtained from patients’ medical records. Nutritional assessment was performed from 3-day food record and 24-hour food recall through the Nutribase™ Software. Bacterial DNA was extracted and evaluated through partial V4-16S rRNA gene sequencing (PGM Ion Torrent™ System) according to the recommendations of the Brazilian Microbiome Project. Microbiota structure was analyzed through MicrobiomeAnalyst online software. Statistical analysis between groups was performed through IBM SPSS Statistics software. The study was approved by the ethics committee of HCPA (n. 15-0218).

RESULTS: Among patients, there were different treatments: methionine-restricted diet (n=6/7); metabolic formula (n=4/7); pyridoxine (n=6/7); vitamin B12 (n=3/7); folic acid (n=6/7) and betaine (n=4/7). The daily intake of total fat (p=0.015), saturated fat (p=0.002), monounsaturated fat (p=0.008), cholesterol (p=0.004) and vitamin D (p=0.002) was lower in patients. HCU patients had higher Alpha-diversity, presenting increased richness of communities to Observed (p=0.017) and Chao1 (p=0.017) indexes. Shannon index displayed no difference (p>0.999). HCU patients and controls also differed in bacterial communities for Beta-diversity based on Principal Coordinates Analysis (PCoA) for PERMANOVA (r²=0.202. p<0.026) and ANOSIM (r=0.464. p<0.026) measures.

DISCUSSION: HCU treatment is related to diet and vitamin supplementation, mainly B-complex, which plays an important role in bacterial and host metabolism. Despite the small sample size, the results revealed...
a potential relationship between treatment and bacterial diversity. **CONCLUSION:** The HCU patients showed high diversity in bacterial communities than the healthy controls.