P-009 - HEPATIC GLYCOGEN STORAGE DISEASES ARE ASSOCIATED TO MICROBIAL DYSBIOSIS

Colonetti K², Dos Santos BB¹,², Nalin T⁴,⁵, De Souza CFM⁴, Dobbler PT³, Schwartz IVD¹,²,⁴, Roesch LFW³

(1) Universidade Federal do Rio Grande do Sul, Postgraduate Program in genetics and Molecular Biology. (2) Hospital de Clínicas de Porto Alegre, BRAIN Lab. (3) Universidade Federal do Pampa, CIP-Biotec. (4) Hospital de Clínicas de Porto Alegre-HCPA, Medical Genetics Service. (5) Universidade Federal do Rio Grande do Sul, Postgraduate Program in Medicine: Medical Sciences. Porto Alegre- Brazil. kcolonetti@gmail.com

INTRODUCTION: Glycogenosis (GSD) are diseases with a defective glycogen pathway. Manifestations like obesity, liver and inflammatory bowel diseases (IBD) are present in GSD and associated with dysbiosis. GSD treatment relies in large amounts of uncooked cornstarch (UCCS) and restriction of simple sugars. Host genetics and diet are the two main drivers of the gut microbiome.

OBJECTIVES: To characterize the faecal microbiome of GSD patients compared to healthy controls (HC), and its association with food intake and faecal pH.

METHODS: Cross-sectional, observational, controlled study with convenience sampling approved by local Research Ethics Committee. GSD patients (n=24; Ia=14, Ib=05, III=01, IX=03) on treatment with UCCS were recruited from the HCPA, Rio Grande do Sul (RS), Brazil, and compared with 16 unrelated HC, recruited among the RS population. Patients and HC were paired by sex and age (±1y). All participants must be ≥3 years of age and not on antibiotics. Patients and controls had their faecal microbiota evaluated through V4-16S rRNA gene sequencing. Microbiome diversity and structure were evaluated trough alpha and β diversity/PERMANOVA and LefSe/LDA analysis. Faecal pH, mean daily nutrient intake and relevant clinical data (IBD, obesity and current medications) were correlated with the gut microbiome.

RESULTS: Patients had higher intake of UCCS, prevalence of IBD (n=04/24) and obesity/overweight (n=18/24) compared to controls (n=0 and 06/16, respectively). To patients, the main calorie source was UCCS, and fat, calcium, sodium, and vitamin intake was lower. There were differences (p=0.001) among usage of ACE inhibitors (patients=11, controls=0), multivitamins (patients=22, controls=01), and mean faecal pH (patients=6.23; controls=7.41). Patients had lower diversity (average Shannon index, patients=2.48, controls=3.49) and distinct microbial community structure, which differed by the presence/absence of taxa (r²=0.182; p=0.003) and their relative abundances (r²=0.166; p=0.001). Several genera differed between the groups. The operational taxonomic unit abundance was influenced by faecal pH (r=0.77; p=6.8e-09), total carbohydrate (r=-0.6; p=4.8e-05) and simple sugars (r=0.057; p=0.00013).

CONCLUSION: GSD patients presented intestinal dysbiosis, showing low faecal microbial diversity. Several taxa previously associated with inflammatory bowel disease and obesity were present in cases and may contribute
for phenotypic variation in patients. The main driver of these differences is unknown.