

00132 Irritable bowel syndrome and microbiota: first clinical study on correlations between gut bacteria, *Dientamoeba fragilis*, *Blastocystis* and eating habits in Turkey

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Background: Irritable Bowel Syndrome (IBS) is a functional bowel disorder with no proven organic etiology. Next Generation Sequencing (NGS) technology has dramatically improved the identification of microorganisms constituting the gut microbiota. Here, we assessed the relationship between the gut microbiota (including *Dientamoeba fragilis* and *Blastocystis*) and eating habits in Turkish IBS patients and healthy controls using NGS.

Materials/methods: The Study Group (SG) consisted of 41 IBS patients while the Control Group (CG) was selected from age and sex-matched individuals who were found to be negative for cancer and IBS after colonoscopy. A questionnaire on eating habits was completed by all participants. DNA was isolated from colonic wash fluids (CWF) obtained during colonoscopy. Microbiota profiles were determined by amplification of 16S+18S ribosomal genes, and PCR products were sequenced using NGS (Illumina MiSeq Platform). The prevalence of *D. fragilis* was determined by Real-Time PCR. Bioinformatic analyses were conducted by matching the raw data with SG and CG. Statistical significance was determined by chi square analyses.

Results: *Escherichia/Shigella* spp., *Phascolarctobacterium faecium*, *Erysipelotrichaceae* and *Bacterioides nordii* were significantly higher in IBS patients than controls ($p < 0.05$). *Blastocystis* was identified in both IBS patients having *Escherichia/Shigella* spp. and *Bacteroides nordii*. *Erysipelotrichaceae* species was identified in all individuals who reported high fat consumption, while all *B. nordii*-positive individuals with high carbohydrate intake were IBS patients. Outcomes of the initial bioinformatic analyses indicated that 97 of 560 microorganisms were different between SG/CG, while 18 and 41 of them were found only in SG and CG, respectively. *D. fragilis* was identified in 10 (24.4%) individuals in SG and 6 (14.6%) in CG by PCR ($p < 0.05$).

Conclusions: This is a pioneer clinical study on gut microbiota in Turkish population, in which gut microbiota of IBS patients were compared with healthy controls using NGS. *D. fragilis* was identified more in IBS patients than in controls. Evaluation of the outcomes of NGS and preliminary bioinformatic analyses indicated a possible relationship between gut microbiota, *D. fragilis*, eating habits of individuals and IBS, which is currently defined as a functional, not organic, disorder.

