Irritable Bowel Syndrome and Microbiota: Preliminary Study on Correlations between Gut Bacteria, Dientamoeba fragilis, Blastoctyisis, and Eating Habits

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Abstract

Turkey is situated on the crossroads between Asia, Africa and Europe. Its geographic location with rich cultural background has a great influence on Turkish cuisine and eating habits of its citizens. The local cuisine has a great diversity in Anatolian regions, which probably influences the gut microbiota.

Irritable Bowel Syndrome (IBS) is a functional bowel disorder with no known organic etiology. Despite studies indicating a correlation between IBS and gut microbiota, the etiology is yet to be clarified.

Here, we assessed the roles of gut microbiota (including Dientamoeba fragilis and Blastoctyisis) and eating habits in IBS patients and controls to identify an organic cause for IBS.

The bacterial component of gut microbiota at species level as well as Blastocytisis and D. fragilis were analyzed for the first time in a Turkish cohort in this pilot study, together with eating habits of participants.

METHODS: The Study Group (SG) consisted of 14 IBS patients diagnosed according to Rome III Criteria, and the control Group (CG) was selected from 14 age and sex-matched individuals who had undergone colonoscopy.

DNA was isolated from stool samples obtained during colonoscopy. Microbiota profiles were determined by amplification of ribosomal genes (16S/18S), and PCR products were sequenced using illumina technology.

A questionnaire on eating habits was completed by all participants. The presence of D. fragilis was determined by Real-Time PCR.

RESULTS:

Bacteriods nordii, Phascolarctobacterium faecium, Escherichia/Shigella spp., and Erysiplorichaeceae were significantly more common in IBS patients (p<0.05).

IBS patients having Bacteriods nordii and Escherichia/Shigella spp. were also positive for Blastocytisis (p<0.05).

Erysiplorichaeceae were common in individuals reporting high fat consumption, while a significant correlation was found between IBS, Bacteriods nordii and consumption of simple carbohydrates (p<0.05).

D. fragilis was identified equally in both groups and showed association with constipation.

CONCLUSION: Despite the small sample size being a limiting factor of this preliminary study, the outcomes appear promising and may unveil some significant relationships between the eating habits of individuals, their gut bacteria and resident eukaryotes.

A relationship between P. faecium, B. nordii and IBS was identified, which may indicate an organic etiology of IBS. Current results for Blastocytisis and D. fragilis warrant further investigations in microbiota studies with more samples in both groups.

The role of D. fragilis as well as Blastocytisis in gut health or diseases deserves further studies as well. Addition of metabolomics may also present novel data about the complicated relationships within the gut.

Materials and Methods

- Individuals in both groups were enrolled according to their colonoscopy results in Acibadem Hospital in Kocaeli province in Turkey. (n=28)*.
- IBS Diagnosis => According to Rome III Standard Criteria for the diagnosis of IBS.
- All participants filled in the survey about their eating habits after enrollment.

- DNA isolation => Qiagene® Stool Mini Kit according to manual instructions.
- Real Time PCR & Sequencing => Real Time PCR was done only for D. fragilis as described (Verweij et al., 2007), while sequencing was done on illumina ®.
- Taxonomy &Bioinformatic analyses: OTUs were clustered according to QIMIE 2. A Decision Tree was developed for the analyses of data.
- Data could not be pooled by other countries’ IBS data, as Manhattan clustering has previously demonstrated that pooled data could not be analysed with meta analysis. Microbiota content are too divergent from each other, and thus Personalized medicine concept should be preferred, even for the analyses of IBS.

- Despite insufficient data for cross validation, overall prediction success of the Decision Tree was found to be 82% (ch-square: 11.6; p=0.006).
- Presence of Escherichia/Shigella unclassified, Bacteriodes nordii and Blastocytisis were related to IBS in our series.
- D. fragilis was found in 2 IBS patients and 4 healthy controls => pathogen or resident of healthy gut.
- Both D. fragilis (+) IBS patients had predominant constipation. They also have a histin-producing bacteria, Allisnella histiniformans. It is known that bowel movement is decelerated to obtain more histidin, which may also cause constipation.

Conclusions

- This is the first report of a Turkish cohort for the comparison of gut microbiota of IBS patients and healthy controls, and eating habits.
- Experimental validations two strains that are listed in our model are available in literature. That means our model has two new species for their possible role on IBS. Microbiome data is consistent with the food intake. Another words, fatty meal consuming samples have microorganisms having strong lipid metabolism, simple sugar consuming samples have altered firmicutes:bacteroides adiposity ratios and also bowel movement altering microorganisms (such as Allisnella.histiniformans) detected in IBS patients.
- Stool samples were collected during colonoscopy in the study. This method increased the bacterial diversity in our analysis. In a previous analysis, Spanish researchers reported 63 different taxonomic families whereas we identified a total of 118 and managed to analyses in species level.

- Stool samples of all participants were collected during colonoscopy in Acibadem Hospital in Kocaeli-Turkey. They were immediately transferred to Acibadem University Research Lab for DNA isolation and PCR. Bioinformatic analyses were done in Statens Serum Institute in Copenhagen. Interpretation of the outcomes was done in Acibadem University School of Medicine Department of Bioinformatics and Bioinformatics.

References


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