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Irritable bowel syndrome and microbiota: Preliminary study on correlations between gut bacteria, Dientamoeba fragilis, Blastocystis and eating habits

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Diagnosing IBS can be challenging for the physician, due to the potential for overlap between the symptoms that sufferers report and those of organic gastrointestinal conditions such as coeliac disease, small intestinal bacterial overgrowth, bile acid diarrhea, exocrine pancreatic insufficiency, inflammatory bowel disease and even colorectal cancer. Several studies have examined the yield of diagnostic testing for these conditions in individuals with symptoms suggestive of IBS, but clear evidence for the routine exclusion of any of these disorders, with the exception of coeliac disease, is lacking. Attempts to identify a biomarker for the condition have, to date, been unsuccessful. Medical treatment for IBS is considered to be unsatisfactory as placebo response rates in treatment trials for IBS are high, perhaps because there is no structural abnormality that can be corrected by successful therapy, and therefore any benefit following treatment is often assessed by an improvement in global symptoms, an endpoint that may be less objective than those used in trials conducted for organic diseases. Because of this huge variation in IBS sampling, meta-analysis has erupted using more and more samples from all over the world. Pooled sensitivity of these individual symptom items ranged from 39 to 74%, and pooled specificity from 45 to 77%. This preliminary research leads us to a topic outside the scope of what we have originally intended. In the beginning, we have several hypothesis related with IBS and parasites. In the end, we have been amused by dynamic nature of microbiome and the roles of microorganism can be addressed misguidedly to terms like “parasitism”, “mutualism”, “commensalism” and opportunistic pathogenicity. Although we do not have enough sample size for addressing valid prediction, we have enough statistical results for carrying on further microbiome research. Starting without preliminary research may misguide researcher to dead end. With the current preliminary work, we have enough results to set up microbiome consortium for gastrointestinal diseases. In the future, we will also include metabolomics and deep NGS sequencing and will validate our new prediction models with qPCR experiments. New prediction models will be created with increased sample size and coupled with metabolomics. We will be pleased to integrate immunological researchers in future microbiome consortium for gastrointestinal diseases.

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