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Case study of the intestinal microbiota using the XGN-MBI metagenomic assay.

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Introduction

The microbiota of the colon and rectum is the most abundant and diverse of the human body, with a density of up to 1-2 kg of weight and a diversity that exceeds a thousand species. The main bacteria of the intestinal microbiota correspond to four phylums: Bacterioidetes, Firmicutes, Actinobacteria and proteobacteria, with the first two accounting for 90% of all intestinal bacteria. The microbiota is considered, today, as a new organ due to the important functions it performs and which are fundamental for health.

Metagenomics can be defined as the application of modern genomic techniques for the direct study of communities of microorganisms in their natural environment, without the need to isolate and cultivate each of the species that make up the community, thus avoiding errors introduced by traditional technologies. In addition, speed, specificity and reliability, one of the advantages of metagenomics with respect to the sequencing of sequences 16s and 18s, is that it allows the identification of viruses. It also allows the identification of parasites.

Objetives

Prove the usefulness of new technologies based on metagenomics, such as the XGN-MBI assay to realize gut microbiota studies.

Material and Method

A study carried out in the Xenogene Laboratories about an anonymous patient, from whom previously informed consent has been obtained to publish his data in this article, has been utilized to demonstrate the usefulness of the XGN-MBI assay.

From a stool sample, collected on a swab in the Cary Blair transport medium, an extraction of nucleic acids and a massive sequencing was made. No crops or PCRs are carried out to avoid introducing artifacts into the results.

The sequencing results in a Fastq file that is analyzed with Ubioma software (owned by Xenogene laboratories), which is compared with various international databases and whose results are visualized with the Krona program and interpreted by an expert.

Results and Conclusions

The dysbiosis found, with a marked decrease in the percentage of firmicutes and a considerable increase in the percentage of bacterioidetes, together with a decrease in diversity is associated with inflammatory disease (IBD) and Chron (CD). Simultaneously, it is observed that the species *B. vulgatus, B. ovatus, B. fragilis, B. dorei*, which are indicative of inflammatory disease (IBD) and Chron (CD) and are associated with overweight and obesity, have been found in very high proportions.

The patient is diagnosed with IBD, which is a risk factor for Chron\'s disease and colorectal cancer. It is possible that it is in a previous stage to the disease, since familiar antecedents are known, although on the other hand it is possible to emphasize the high index of *Faecalibacterium prausnitzii* found, that apparently has a protective role of the intestinal mucosa. It emphasizes the practically absence of lactobacillus.

Among the proteobacteria there is a clear predominance of *E. coli*, which is normal. In the Phylum actinobacteria, more than 50% correspond to the species *Bifidobacterium adolescentes*, but a low diversity is observed.

The few human cells found indicate that there is no excessive desquamation, so the intestinal mucosa should not be very altered.

Based on the study realized, we can conclude that the use of the XGN-MBI assay allows to have a clear vision of the intestinal microbiota as a whole, without incurring the error that supposes for the proportions and composition a selection according to the culture medium and allows to observe in the same test bacteria, fungi, viruses and parasites. Provides rapid identification of pathogens. Depending on the number of human cells detected, it can be inferred if there is excessive desquamation of the mucosa. The direct study of proportions between individuals allows rapid detection of whether or not there is dysbiosis and the enterotype of the patient.

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