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Do diversity indices, Firmicutes/Bacteroidetes ratios, and 16S rRNA gene tests, taken together, help determine biotic administration?

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Abstract

The combined determination of diversity indices, Firmicutes/Bacteroidetes ratios, and 16S rRNA gene genetic testing could help determine the appropriate biotic for various health conditions. The combined determination of Shannon indices, Simpson diversity indices, Firmicutes/Bacteroidetes ratios, and 16S rRNA gene genetic testing would aid in the management of gastrointestinal disorders. Therefore, understanding this process, and especially the composition of the bacterial community, will provide information on various health conditions and potential biotic management.

Furthermore, a specific understanding of the various functions of the gut microbiome is vital, including the breakdown of indigestible food particles and the production of vitamins B and K, which support the immune system. Therefore, understanding the balance of the different groups of microorganisms is crucial for maintaining homeostasis and preventing illness.

Keywords: Diversity indices, Firmicutes/Bacteroidetes (IDF/B). Gut Microbiome (GM). Gut Dysbiosis (GD). Biotics (Biot).

Introduction

The presence of the new super-organ, known as the Gut Microbiome (GM), has proven to be of enormous importance, as it is linked to numerous gastrointestinal disorders, and through the Firmicutes/Bacteroidetes diversity index (IDF/B), we have been able to identify numerous problems. The microbiome was discovered by Antonie van Leeuwenhoek, a German scientist. We have learned that its evaluation is crucial in numerous gastrointestinal disorders. Firmicutes are mainly composed of Gram-positive bacteria, which also participate in the fermentation of complex carbohydrates and in the production of SCFA such as butyrate, acetate, and propionate, which contribute to the function of the intestinal barrier and regulate immune responses. Bacteroidetes are Gram-negative bacteria that constitute approximately 30% of the GM and maintain intestinal homeostasis. They degrade the complex polysaccharides of dietary fiber, producing short-chain fatty acids, which serve as energy sources; they also regulate immune function [1]. The GM is a complex ecosystem composed of trillions of microorganisms that reside primarily in the large intestine. This diverse community plays a fundamental role in maintaining human health by influencing digestion, immunity, and even mental well-being. It is linked to inflammatory bowel disease, type 2 diabetes, high blood pressure, and colorectal cancer [2].

Firmicutes/Bacteroidetes Diversity Indices

Are crucial for understanding gut health and its effects on overall well-being. A higher relative abundance of Firmicutes is often associated with obesity and elevated levels of pro-inflammatory cytokines such as TNF-α, which define a pro-inflammatory state [3]. Mantovani A and colleagues have included liver conditions in the diversity index, and, as a marker, the presence of Proteobacteria predicts liver decompensation and mortality [4]. Understanding the relationships between gut microorganisms and host phenotypes is fundamental to well-being and disease. This suggests opportunities for targeted interventions that alter the microbiome to improve host health [5]. In Inflammatory Bowel Disease (IBD) treated with biologics, species richness and alpha diversity of the community were significantly lower in patients with active IBD and gradually increased after biologic therapy. A decrease in Firmicutes and an increase in Bacteroidetes were observed in actives condition [6].

Alpha and Beta Diversity

There is variation in the determination of analytical methods for the study of bacterial communities. In part, this is because alpha diversity metrics come from other disciplines and are not necessarily valid in microbial culture. We see the complexity when reviewing 19 different metrics of microbial alpha diversity, with something similar occurring in beta diversity [7].

Genetic Testing of the 16s rRNA Gene

The role of the microbial gene in gastrointestinal pathologies, including gastric cancer, has recently garnered significant interest. This is primarily due to 16S ribosomal RNA sequencing technology and the potential mechanisms by which diagnostic microbial biomarkers influence stomach cancer. These biomarkers have shown potential in the early detection of colorectal cancer, although this remains a subject of debate. In stomach cancer, a decrease in Faecalibacterium, Roseburia, Lachnospira, and Bifidobacterium is observed, along with an enrichment of Desulfovibrio, Streptococcus, Fusobacterium, and Escherichia [8]. Next-generation sequencing has revolutionized virtually all areas of biotechnology and has become a key technology in the field of genomics. With its unprecedented throughput, scalability, and speed of data generation, it allows researchers and clinicians to study biological systems with unprecedented levels of detail and resolution. The vast amount of information generated by next-generation sequencing facilitates the understanding of genomic variations, disease mechanisms, and resistance, contributing to the development of improved diagnostics. Currently, first-generation, next-generation, and third-generation sequencing technologies exist. The third generation is constantly being updated and optimized [9].

Firmicutes/Bacteroetes ratio

In obese animals and humans, there is a higher proportion of Firmicutes/Bacteroidetes, making it a potential biomarker. However, there is no consensus among researchers. Considerable variations exist in the composition of GM among individuals within the same population, possibly due to different lifestyle factors such as physical activity and diet, as well as food additives, antibiotics, and contaminants. Therefore, it is recommended that future studies identify the different variables [10].

The Firmicutes/Bacteroidetes ratio

Kusnadi Y, and his group [11], conducted an extensive review to determine the suitability of using the IDF/B in conditions such as type 2 diabetes mellitus, noting that the F/B ratio is a marker of intestinal dysbiosis. They observed a decrease in the ratio, with a significant negative correlation with blood glucose levels. This correlation was not significant in fasting glucose, postprandial glucose levels, or glycated hemoglobin.

The Shannon-Wiener Index, also known as the Shannon-Wiener Index, is a measure of biodiversity in ecological communities. It quantifies species diversity based on their relative abundance and distribution, with higher values indicating greater diversity. Gastrointestinal patients seek answers in their own gut health. Even as services are under scrutiny regarding the standardization of processes, the Shannon Index is calculated as the sum of the cumulative relative abundances of the five most abundant organisms in the bacteriome. Josh Doolittle and his team [12] present the Dominance Dysbiosis Index to assess bacterial diversity and identify it as a key indicator of intestinal dysbiosis. It is calculated by summing the cumulative relative abundances of the five most abundant organisms in the bacteriome and including the Shannon Index.

Simpson's Diversity Indices

The Simpson diversity index is a measure of diversity that considers the number of species present, as well as the relative abundance of each. As species richness and uniformity increase, so does diversity. GM is a modulator in the pathophysiology of type 2 diabetes; genetic and environmental factors interact to control it, while also contributing to insulin resistance and obesity. This study analyzes obese patients, treated or not with bariatric procedures [13], analyzing fecal microbiota with high-throughput sequencing using V4 16S rRNA primers. The surgical group showed abundance and diversity of Bacteroides, Akkermansia, and Dialister, suggesting that surgery increases microbial richness and abundance.

Intestinal dysbiosis

Intestinal dysbiosis is an imbalance or alteration of the gut microbiota, in which beneficial microorganisms decrease and potentially harmful microorganisms increase, disrupting normal intestinal function. It is associated with multiple pathologies, such as irritable bowel syndrome, diarrhea, multiple sclerosis, allergies, type 1 diabetes mellitus, inflammatory bowel diseases, rheumatoid arthritis, Alzheimer's disease, autism, Parkinson's disease, and metabolic disorders (obesity, type 2 diabetes mellitus, and atherosclerosis). Clinically, it presents with abdominal pain and distension, as well as diarrhea, with chronic and metabolic diseases being the most frequent underlying conditions [14].

Biotics

As an adjunct therapy, probiotics are mentioned (Weizmannia coagulans, Alkalihalobacillus clausii, Lacticaseibacillus rhamnosus, Limosilactobacillus reuteri, Saccharomyces boulardii, Lactobacillus rhamnosus GG, L. reuteri DSM 17938, L. plantarum DSM 9843 and Bifidobacterium lactis Bb-12). Intestinal dysbiosis is usually generated by three events: increased pathobionts, decreased commensals and loss of bacterial diversity [15].

Fecal Microbiota Transplantation. In Diversity Indices

It can restore bacterial diversity in the digestive tract, being essential in recurrent C. difficile infection and readily adopted by the recipient. Its effects are unpredictable in Inflammatory Bowel Disease [16]. Heiner T and his group point out [17]: Understanding how FMT modifies microbial diversity and reduces the increase in pathobionts is necessary to optimize therapeutic outcomes. Furthermore, dysbiosis, generates an increase in pathobionts, potent organisms, under certain conditions.

Fecal Bacteriophage Transplantation in diversity indices.

Zuo T and his team [18] performed ultra-deep metagenomic sequencing of virus-like particle preparations and sequencing of bacterial 16S ribosomal RNA in stool samples from 24 subjects with CDI and 20 healthy controls. Subjects with CDI showed significantly higher abundance of Caudoviral bacteriophages and lower diversity, richness, and uniformity of Caudovirals compared to healthy controls.

Comments

The National Institute of Diabetes, Digestive and Kidney Diseases coordinates with the AGA and other institutions to create more research programs. This will help to get closer to understanding the various aspects of GM [19]. Deaths from gastrointestinal processes have increased in the USA over the last three decades, and little is known about the disparities [20].

Conclusions

- Biodiversity research and its application require precise and consistent definitions of diversity [21].
- The alpha of the Fisher logarithmic series and the fundamental biodiversity parameter were highly correlated with each other, as were the Margalef, species richness, and Chao species abundance indices. [22].
- Diversity indices are important for environmental monitoring and conservation, although there is no consensus on which ones are most appropriate and informative. [23].

Conflicts of Interest

The authors declare that they do not have affiliation or participation in organizations with financial interests.

Ethical Approval

This report does not contain any studies with human or animal subjects carried out by the authors.

Informed Consent

The authors obtained informed written consent from the patients, in order to develop this article.

Declaration on the use of artificial intelligence

The authors declare that no generative artificial intelligence was used in the writing of this manuscript.

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