Application and Development Prospect of Metagenomes in the Identification of Intestinal Microorganisms

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Abstract. Intestinal microorganisms are the result of long -term coexistence coordination of microorganisms and hosts in the human body, which plays an important role in maintaining normal physiological functions and regulating human health. With the development of metagenomic sequencing technology, the research on gut microbes has become more in-depth. Researchers have used metagenomic technology to identify the composition of the intestinal flora in patients with diseases and compare it with the composition of the intestinal flora in healthy people to study the pathogenesis of related diseases. At present, there is still a lack of unified standard process for metagenomic technology, and the study of the internal mechanism of intestinal flora affecting diseases has not been in-depth. Future research can integrate multi-omics methods to conduct in-depth research on the dynamic changes of intestinal flora. This paper reviews the current research progress of intestinal flora and mental diseases, metabolic diseases of obesity and cancer after applying metagenomic technology to intestinal microbes, hoping to better identify the important role of intestinal microbes in the study of disease occurrence, treatment and prevention, and provide a reference for related studies.

Keywords: Gut microorganism; metagenomic technique; application.

1. Introduction

The intestinal microbial flora is composed of thousands of microorganisms. It participates in the human body's metabolism, immunity, and other functions. It plays a very important role in regulating human health. Therefore, it is considered to be the "invisible organs" of the human body [1]. In recent years, a large number of studies have found that gut microbes interact with the brain through a structure called the brain-gut axis, connecting gastrointestinal microbes, the gastrointestinal tract and the central nervous system through neuro-immune-endocrine-metabolism and other pathways [2]. Therefore, when the composition of intestinal microorganisms' changes or the number of quantity changes sharply, the ecological structure of the human body will also change, and the pathological manifestation of pathological rationality will be caused.

Through research on intestinal flora composition and intestinal and other organs, researchers can identify the mechanism and signs of some diseases, and then can prevent disease prevention or develop new treatment methods in advance. With the continuous development of sequencing technology, metagenomic technology, as an emerging technology capable of high-throughput analysis of microbial summality in a specific environment, has become one of the important methods for studying intestinal flora [3]. Metagenomic technique is centered on sequencing technology. At present, the most useful use of second -generation sequencing technology (NGS), which is characterized by high traffic, high efficiency, high accuracy, and low cost. In addition, biological information analysis also occupies an important position in the technology group technology. The massive data obtained through sequencing requires biological information tools for analysis [3]. In terms of intestinal microorganisms, metagenomic technology can not only quickly and accurately obtain the genetic information of the intestinal microbial community, but also explore its diversity, metabolic function, host interaction. It can be more in -depth and makes it possible to to realize individualized precision medical care, wide screening of diseases, and disease monitoring [4].

This article will start with the association between intestinal microbes and mental diseases, obesity, and tumor diseases, and review the progress of the application of metagenomes in the study of intestinal microbes, hoping to provide a reference for further research in related fields.

2. Gut Microbiome and Mental Illness

The gut microbiota plays an important regulatory role in the central nervous system, so they are known as the "second brain" of the human body [1]. In the past, people thought that the intestine was far apart from the brain, and the relationship between the two was not close. Until 2012, the new concept of microbial-gut-brain axis made more and more researchers pay attention to the impact of the huge gut microbial system on brain function, revealing a new direction for the study of mental diseases. A large number of studies have proved that intestinal microbes constitute a two-way signal communication regulatory System between the gut brain axis and the brain, and this System basically consists of the Central Nervous System (CNS) and the Autonomic-Nervous system (ANS), Hypothalamic-Pituitary-Adrenal Axis (HPA), Enteric-Nervous System (ENS), etc [5].

Major Depressive Disorder (MDD) is a common mental illness that endangers human health. Metagenomic sequencing technology was used to analyze the changes of intestinal microflora in MDD patients. Although there were differences in intestinal microflora composition in MDD patients in different studies, the increase in the abundance of Actinobacteria and Eggerthella and the decrease in the abundance of Bacteroidetes, Prevotella, Coprococcus, Coprobacillus and Sutterella were the most significant Consistent change. Bacteroides has also been identified as a characteristic change of MDD [6]. Some research teams further studied that the feces of Patients with MDD patients were transplanted into rats treated with antibiotics. It was found that the rats showed obvious depression characteristics and confirmed that the disorders of intestinal microorganisms may be potential causes of MDD [7].

Schizophrenia (SCZ) is a chronic persistent psychiatric disease that is chronic and harmful to individuals and families, but its pathophysiological mechanism is not clear. Now more and more researchers believe that SCZ is closely related to intestinal flora, because the intestinal inflammatory response related to the pathogenesis of SCZ is regulated by the gut-brain axis [8]. A research team sequenced the intestinal flora of patients with SCZ and compared it with the intestinal flora composition of normal population and found that the relative abundance of Veillonellaceae was negatively correlated with the severity of SCZ. Bacteroideaceae, Streptococcaceae and Trichospirillaceae are positively correlated with the severity of SCZ, and Streptococcus vestibularis has been specifically identified as a schizophrenia related bacterium [8]. At the same time, the microbiome composed of Aerococcaceae, Bifidobacteriaceae, Br-ucellaceae, Pasteurellaceae and Rikenellaceae can identify SCZ patients very well [6].

Not only MDD and SCZ, but also other mental diseases, such as Alzheimer's disease, Parkinson's disease, and autism spectrum disorder, have been shown to have differences in the composition of gut microbiota between patients and healthy people. This difference provides new directions and ideas for studying the pathogenesis of mental diseases and new treatment schemes.

3. Gut Microbiome and Obesity Metabolic Disease

Obesity has gradually become the focus of global attention. As a chronic metabolic disease, obesity seriously affects the physical and mental health of the human body. Obese people have a high probability of chronic complications such as type 2 diabetes, hypertension and hyperlipidemia. Now more and more studies have shown that gut flora and its metabolites play an important role in the occurrence and development of obesity and related metabolic diseases [9].

Gut microbes are the result of the long-term coexistence and coordination of host and microorganisms. There are three main mechanisms for intestinal microbiomes to induce obesity: the first is that intestinal microflora affects the energy intake and energy homeostasis of the host; the

second is that the disorder of intestinal microflora causes chronic inflammation and affects the state of liver metabolism; the third is that the structure of intestinal microflora affects the production of fat molecules, and then affects the storage and balance of fat [10].

More and more studies show that obesity is closely related to gut flora. A team of researchers transplanted intestinal microbes from normal mice into obese mice, and it was significantly observed that the weight and fat content of obese mice decreased [9]. By sequencing the intestinal microbes of normal people and obese people through metagomic technology, the ratio of Firmicutes to Bacteroidetes in obese people is higher, so the researchers believe that the increased ratio of Firmicutes to Bacteroidetes may lead to obesity [11].

The increase in body fat content in obesity is likely to lead to insulin resistance, which leads to type 2 diabetes(T2DM). Recent studies have shown that intestinal flora plays an important role in the pathogenesis of T2DM. Through metagenomic sequencing, the researchers found that the intestinal flora richness and diversity of T2DM patients were significantly reduced compared to the normal population. The ratios of Proteus, firmicutes and Bacteroides in T2DM patients were higher than those in healthy people, and the abundance of Roseburia was decreased, while Lactobacillus was enriched [9].

Not only obesity and T2DM, but also other metabolic diseases related to obesity, such as hypertension and fatty liver, have been confirmed by studies to have a very close relationship with gut microbes. Therefore, the study of intestinal flora can provide a new direction for the treatment of these metabolic diseases, and further understand the pathogenesis of these diseases to achieve prevention.

4. Gut icMrobiome and Tumor Cancer

With the development of intestinal microbial research and metagenomic sequencing technology, more and more researchers have paid attention to the important role of intestinal microbes in cancer. There are many differences in the diversity and abundance of gut flora in different cancer patients compared to healthy people. Many studies have shown that the disturbance of intestinal microbes can affect the occurrence and development of tumors [3].

There are two possible mechanisms for intestinal microbes to affect the occurrence of cancer. The first is that intestinal flora can interfere with the metabolic system, making the body metabolize more pro-cancer and pro-inflammatory factors, and accelerate the carcinogenesis of cells. The second is that the gut microbiota overexpresses immune checkpoint molecules by interfering with the immune system [12]. Immune checkpoint plays an important role in preventing autoimmune reactions. When immune checkpoint molecules are over-expressed or over-functional, they will lead to low immunity, which will make the body prone to diseases such as cancer.

colorectal cancer (CRC) is one of the most common cancers, and colorectal adenoma (CRA) is the most significant precancerous lesion in CRC. Metagenomic test results of intestinal flora in colorectal cancer patients showed that the abundance of Bacteroidetes and Clostriobacteria was high, and the abundance of Firmicutes and Actinobacteria was low [13]. Moreover, the specific metabolites in the serum of patients, such as phenylpropionamide, also changed correspondingly with the changes in the intestinal microbes of patients with colorectal cancer [3].

breast carcinoma (BC) has gradually become the most common nausea tumor in the world [14]. Metagenomic technology was used to analyze the fecal microbiota of patients with early-stage breast cancer who received treatment, and the results showed that multiple symbiotic microbiotas, such as Streptococcus, Veillonella, Spirillum, and Bacteroides, repeatedly appeared before and after chemotherapy.

Lung cancer is a malignant tumor that originates from the bronchial mucosal epithelium or glands. It is divided into small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). More and more studies have shown that the gut microbiota and its metabolites differ significantly between lung cancer patients and the normal population, between patients with different pathological types of lung

cancer, and between patients with lung cancer of different ages or genders [3]. Metagenomic sequencing comparative experiment results show that the absolute abundance of Haemophilus can be used as a marker to distinguish lung cancer patients from healthy people [15]. The intestinal tract of female NSCLC patients is relatively rich in Bacteroideaceae, Ruminococcaceae and Selenobacteriaceae, while that of male NSCLC patients is relatively rich in Trichospirillaceae, Enterobacteriaceae, Streptococcaceae, Eubacteriaceae and Bifidobacteriaceae [15].

Not only CRC, BC and NSCLC, but also other cancers, such as gastric cancer and liver cancer, have been shown to play an important role in intestinal flora. Through the gut microbiota, researchers can not only diagnose tumor cancer earlier but also improve cancer treatment and prognosis.

5. Conclusion

As an important part of the intestinal microorganism, the intestinal microorganisms have participated in many functions such as metabolism and immunity in the human body. They play an important role in regulating human health. By using metagenomic technology to compare the intestinal flora composition of patients with that of healthy people, researchers have found that many types of diseases such as major depression and schizophrenia, metabolic diseases mainly dominated by obesity, colorectal cancer, breast cancer and other cancers are related to intestinal microbes. This shows that the study of intestinal flora can reveal the signs and mechanisms of some diseases, which is helpful for the development of new treatment strategies. This study reviews the current research progress of metagenomic technology in intestinal flora and diseases, which may be helpful to further study the association between intestinal flora and diseases.

At present, the field of metagenomics still lacks uniform standards and procedures, which can lead to biased results from the same experiments, and the pathway cannot accurately distinguish between subspecies and strains of microorganisms. At the same time, the inherent mechanism of intestinal microorganisms affecting the disease has not been clear, and the dynamic changes in human intestinal flora still lack related research. In the future, by combining metagenomics with proteomics, metabolomics and other omics fields, the composition and changes of intestinal flora can be further studied, and the mechanism of intestinal microbes affecting health status can be analyzed in detail, so as to achieve the treatment and prevention of related diseases.

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