REVIEW ARTICLE

Multi-Omics Approaches for Exploring Health Implications: A Review

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Abstract

The concept of metabolic regulations deals with the varied and innumerable metabolic pathways that are present in the human body. A combination of such metabolic reactions paves the way to the proper functioning of different physiological and biological processes. Dealing with the adversities of a disease, the engineering of novel metabolic pathways showcases the potential of metabolic engineering and its application in the therapeutic treatment of diseases. A proper and deeper understanding of the metabolic functions in the human body can be known from simulated yeast models. The current review gives a brief understanding of the interactions between the molecular set of metabolomes and their complexity.

Key words: Metabolic, metabolome, metagenomics, microbe, microbiome, microbiota

INTRODUCTION

As a central hub or an area concentrated with the majority of metabolic reactions, it can be understood from the studies of the gut that systemic metabolism in humans is not just regulated by their genes and their dietary habits but also by gut microbes.[1] If the gut microbiota present in the body is in a state of intestinal dysbiosis, certain microorganisms like *Escherichia coli* can be engineered and modeled metabolically to improve the functioning and growth of the indigenous microbiome.[2] The role of microorganisms has been widely known and explored in recent years due to their exploitable advantages and disadvantages that are meant to be kept in check.[3] Apart from the different cohorts and divisions of microbiota present, a decent understanding and knowledge about the gut microbiota present in the human digestive system are required to evaluate, explore, and treat the different diseases related to the human intestine tract.[4] A proper balance in the growth and bioactivity of different intestinal flora is required for the homeostasis of the human biological system.[5] A metabolic pathway is basic for every disease or any biological function that takes place in the body.[6] Hence, studying these metabolic pathways and identifying the metabolites involved in them as markers helps in the easy diagnosis and treatment of different diseases[7] like non-small cell lung cancer and anaplastic large cell lymphoma, alpha-fetoprotein-liver cancer and germ cell tumors, beta-2-microglobulin multiple myeloma, chronic lymphocytic leukemia, and some lymphomas and problems faced by the organism.[8]

ROLE OF METABOLITES IN PRECISION MEDICINE

It is known from statistics that out of the many people who are being treated with a disease, only a few of them are responding to the treatment, and some are not. As an example, when it comes to radiotherapy and immunotherapy for the treatment of different cancers, only a handful of people are being cured. This is because not every individual's body responds in the same way. Hence, this is where the concept of precision medicine comes into picture.[9] With the required biomarkers and companion (diagnostic tests used as a companion to a therapeutic drug to determine its applicability to a specific patient), researchers, based on the patient's disease progression and other key factors, can stratify patients into subsets.[10]

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This facilitates the better prediction of disease outcomes so that appropriate treatment regimens can be formulated for the different subgroups identified. In turn, stratified medicine can give rise to precision medicine, where treatment is tailored for each patient according to their medical history, results from other tests, their response to medication, and other clinical features.[11] In this respect, there are a set of plant-derived secondary metabolites such as vinblastine,[12] capsaicin,[13] curcumin[14] which are of medicinal impotence. These metabolites can be harnessed by modifying their respective metabolic pathways so that they are produced in large amounts. As a result, they can be commercially produced in large amounts and aid in the treatment of different diseases.[15]

GUT MICROBIOTA-IMPACTING FLORA IN HUMAN BODY

The fluctuation seen in the growth of different gut microbiota can be due to host genotypes, physiological status, diet, drugs, and living conditions. The system formed as a combination of both the gut microbiota and the human system is called a "Superorganism".[16] Based on the effects they induce, the gut microbiota can be divided into three groups: (1) beneficial bacteria; (2) conditional pathogenic bacteria; and (3) pathogenic bacteria. As per the growth and functioning of the different classes of gut microbiota listed above, it results in different diseases and ill effects of the gut and organs concerned with it, like the liver and gall bladder.

SMALL CHAIN FATTY ACIDS (SCFA) AND GUT MICROBIOTA

In general, the food that enters the digestive system is partly digested by the digestive enzymes and partly by the gut microbiota. The complex carbohydrates that enter the human gut are fermented into SCFA via the gut microbiota, which further promotes the process of intestinal gluconeogenesis and the formation of lipids.[17] This SCFA produced is known to play a certain significant role in host organisms by improving intestinal functioning, increases the resistance against pathogenic microorganisms, fighting tumors, maintaining the electrolyte balance of the host, and also provide energy to the host epithelial cells.[18] Another intriguing factor about the gut microbiota is found through a study that the peroxisome proliferation receptor-ɣ (PPAR-ɣ) signal induced by them is the one responsible for maintaining homeostasis. The compound that is responsible for the transduction of PPAR-ɣ is butyrate, which is mainly produced by the metabolism of Clostridia. Butyrate also decreases the production of TGF-β1 and interleukin-6, increases the activity of cytokines (anti-inflammatory), and, by inducing the T-cells, enhances body immunity through anti-inflammatory effects.[19]

It was further known that the *Bifidobacteriaceae* in the intestines of the mice started to increase in number after the treatment with oligofructose weakened weight gain, fat accumulation, and ameliorated metabolic disorders induced by a high-fat diet in mice.[20] *Akkermansia muciniphila* is a microbe whose abundance in the gut is closely related to the health of the host. It majorly survives on the intestinal mucin as the only carbon and nitrogen source, with its main metabolite being propionate (SCFA), and its intestinal abundance is around 1–3%. These bacteria and their metabolites are seen to have an effect on the inflammatory responses of obese and diabetic patients and improve adverse symptoms such as insulin resistance and glucose tolerance.[21]

GUT MICROBIOTA: A REGULATIVE BIOME FOR MANY DISEASES

A comprehensive study of the gut microbiota can give us an idea of the different diseases on which the gut microbiota can have their effect.[22] If seen, every disease has its specific microbial markers for the targeted treatment of diverse diseases. In this point of view, Louis et al. found out that, in a weight loss problem conducted, the *Firmicutes/Bacteroidetes* were high in obese patients,[23] and in *Akkermansia,* an intestinal microbiota abundance was found in successful weight loss patients.[24] In addition, it was also found that the *Lactobacillus* additives maintain homeostasis and reduce body weight considerably.[25] Similarly, when it comes to liver diseases and liver cirrhosis, compared to healthy individuals, a significant increase in the number of *Enterobacteriaceae*, *Enterococcus* species, and *Proteus* species was found in patients with liver cirrhosis.[26] Seen in the pathogenesis of gastrointestinal diseases, microorganisms like Enteritoxigenic *Bacteroides fragilis* induced inflammatory responses in colorectal cancer mouse models.[27] In this disease model, it was also found that colon epithelial regeneration was hindered to an extent due to the low availability or absence of *Bifidobacterium*.[28]

CONCLUSIONS

From the above-mentioned strategies, metagenomics has become a powerful technology for analyzing the gut microbiota and understanding its relationship with the host. However, there are some limitations. It is not an easy task to know the expression of microbial systems, and it also requires higher sequence coverage. The time and cost are also considerable constraints for limitations. Among all the limitations mentioned above, getting highly purified and high-quality DNA samples is important because there may be 50% human contaminants in the DNA sample selected.

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