



Predicting Individual Responses to Probiotics: The Role of Gut Microbiota and Artificial Intelligence

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Abstract

The disturbance of normal microflora has been associated with susceptibility to diseases e.g., mental as well as metabolic disorders. According to the literatures, refinements of normal microbial balance would be therapeutic effects against diseases. However, microbial-based therapies have several challenges such as lack of sufficient local delivery, short half-life, as well as destruction within the stomach environments. Nowadays, Artificial intelligence has been gain attention through the scientists. AI-based therapies could improve pharmacological characteristics of the microbiota-based therapies that reshape the microbial medicine.

Keywords: Gut microbiota, Probiotics, Disease, Artificial Intelligence.

Introduction

There are numerous studies emphasizing the crucial role of the gut microbiome in human health. The gut microbiota consists of about 1014 microorganisms from more than 200 distinct microbial species such as bacteria, fungi, and viruses that vary between individuals [1]. The clinical importance of gut microbiota in physio-pathological conditions, including gastrointestinal ailments, metabolic syndrome, neurological disorders, and even cancers, is supported by growing evidence [2–3]. For example, new approaches to therapy, such as "microbiome medicines," have emerged to achieve appropriate levels of disease prevention and treatment. Nonetheless, probiotics have major constraints, notably in terms of delivery to specific organs and administration in sufficient amounts [4]. Furthermore, colonization of these bacteria is intermittent and is mostly impacted by severe conditions such as gastric acid and bile salts [5]. In this context, next-generation probiotics are increasingly gaining attention as a potential approach for treating diseases associated with microbial dysbiosis, a condition that can arise if the fragile microbial equilibrium is disrupted. However, controversial evidence has been produced, implying that current technology will not be able to fill the present deficiencies [6-7]. Herein, we discuss about the impact of AI-based techniques on the development of new microbial medicine approach for diseases through the searching relevant documents on PubMed, ISI Web of Sciences, as well as Scopus databases.

Results Discussion

John McCarthy proposed the term "artificial intelligence" in 1955. Artificial intelligence (AI) is an area of computer science that uses learning to deliver high-quality responses. Over the last few decades, there has been an increase in the use of AI in medicine, including ophthalmology, cardiology, radiology, and pharmaceuticals [8]. However, we predict that AI-based technologies may have favorable features in terms of improving microbiome therapeutics in terms of both prevention and treatment of disorders relating to gut dysbiosis.

AI-based food product technology dates back to the 1990s, when Dettmar et al. predicted the origin of fruit from collected orange juice samples [9]. Numerous studies on nutrition and gut microbiota have been conducted in recent years using AI-based approaches. Shima et al., for example, investigated the impact of diet on the gut environment using a combination of machine learning (ML) and network visualization [10]. Besides, Devika et al. showed that genome-scale analysis of bacteria could differentiate Bifidobacteria strains [11]. Furthermore, Mohammed et al. demonstrate the impact of intestinal microbiota on human metabolism by developing a new hierarchical enzyme classification method based on ML [12]. Surprisingly, active ML has the potential to improve healthy microbiome balance in pharmaceutical excipients of probiotics. In this regard, McCoubrey and co-workers utilized an ML technique to expedite the optimal pharmaceutical concentration of *Lactobacillus paracasei* for sufficient amounts with high scale accuracy [13].

Drug metabolism is a key aspect of achieving an appropriate drug concentration that is influenced by the gut microbiota. Drug metabolism or bioaccumulation (also known as microbial drug metabolism) refers to the production of certain enzymes that are influenced by an individual's microbial composition [14–15]. Over 150 drugs are thought to be digested by the intestinal microbiota [16]. For instance, one study found that people who carry cardiac glycoside reductase-encoding bacteria, such as *Eggerthella lenta*, metabolize digoxin more efficiently than control patients [17]. Besides, Guo et al. demonstrated that patients who were gastrointestinally colonized with *Faecalibacterium prausnitzii* had immunosuppressive action that was 15-fold lower than the original drug concentration [18]. Although it is evident that gut microbiota might influence drug metabolization, there is no gold standard method for approving microbial-related drug bioaccumulation. AI-based technologies are being evaluated as a new candidate strategy for predicting drug microbiome depletion. Several studies have emphasized the accuracy of an AI-based technique for the biotransformation of pharmaceuticals by the human gut microbiota [19]. McCoubrey and co-workers demonstrated the application of a new ML technique for assessing drug sensitivity to depletion by gut microbiota, with an AUROC of 75.1% [16].

Conclusions

In conclusion, the gut microbiota is a diverse array of living microorganisms that are beneficial to human health. Otherwise, gut dysbiosis will disrupt normal metabolic processes and increase the risk of disease susceptibility. However, there are several challenges to understanding the nature of gut microbiota and microbial medications. As previously discussed, AI-based techniques are a promising approach for establishing a new branch in microbial medicines, such as distinguishing the nature of gut microbiota in both diseases and health status, probiotic delivery, and the prediction of bioaccumulation of drug molecules.

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