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Opinion

Can Changes in Gut Microbiota Predict Progression Toward Diabetes?

Alexander Machado Cardoso*

Laboratory of Environmental Biotechnology, Western Rio Janeiro State University - UEZO, Rio de Janeiro, Brazil

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Abstract

The incidence of diabetes has been increasing dramatically in recent years, and diabetes remains a severe threat to global health. Herein, the updated viewpoint regarding the potential impact of gut microbiota on type 2 diabetes mellitus (T2DM) is discussed, and it is emphasized that standardized methods are essential for future studies.

Type 2 diabetes mellitus (T2DM) is a common metabolic disorder in adults and accounts for approximately 90% of all diabetes cases. T2DM is characterized by hyperglycemia and is associated with obesity, hyperlipidemia, beta cell dysfunction, insulin resistance, and low-grade chronic inflammation. T2DM cases are estimated to exceed 578 million by 2030.[1] The development of T2DM is primarily caused by an individual's genetic susceptibility, a sedentary lifestyle, and excessive weight and/or obesity. Obesity-related insulin resistance and low-grade inflammation during the development of T2DM are associated with specific changes in the composition and abundance of the gut microbiota, which are crucial for the digestion and absorption of nutrient components, detoxification of xenobiotics, production of metabolites, and synthesis of essential amino acids and vitamins. Understanding the changes to the gut microbiota during the pathogenic progression of T2DM has recently been attracting attention due to its potential role in the discovery of novel therapeutic targets and development of potential unique therapies.

The difference in microbial community composition between diabetic and healthy individuals has been suggested to predict the development of T2DM with an accuracy of 80%.[2] Diabetic patients usually display an imbalanced bacterial composition with certain taxa, including *Slackia*, *Mitsuokella*, *Abiotrophia*, and *Parascardovia,* as dominant and exhibit varying levels of *Prevotella*. In contrast, healthy controls have a higher abundance of *Moraxella* species. The abundance and composition of the gut microbiota are affected by multiple factors, including daily diet, living environment, personal hygiene habits, and host genetics. Interestingly, some of the oral microbiota may colonize and persistently live in the gut, which has been suggested to play a role in the emergence of chronic inflammatory diseases.[3]

A moderate dysbiosis in the gut microbial population has the potential to affect disease progression toward diabetes.[4] Despite numerous studies supporting the role of the gut microbiota in the pathophysiology of T2DM, research is still at an early stage and many observations remain controversial. Nevertheless, patients with T2DM have been shown to have a shift in the abundance of gut *Lactobacillus* species and butyrate-producing bacteria.[5] Furthermore, many genera including *Bifidobacterium*, *Bacteroides*, *Faecalibacterium*, *Akkermansia*, and *Roseburia* are negatively associated with the development of T2DM, while *Ruminococcus*, *Fusobacterium*, and *Blautia* are positively associated with diabetes. However, understanding the influence of the gut microbiota and their metabolites on the pathogenesis of diabetes is still limited and the effect of microbial metabolites on host health remains in its infancy.[6]

Changes in microbial metabolites also contribute to the development of insulin resistance, chronic inflammation, and glucose intolerance. These metabolites, such as short-chain fatty acids (acetate, butyrate), trimethylamine-N-oxide, and imidazole propionate, may interact in the gut or enter the systemic circulation to induce several different effects.[7–9]

The relationship between gut microbiota and the triad of obesity, chronic inflammation, and diabetes is still under revision. An elevated body mass index is associated with an increased risk of developing T2DM and associated complications. Low-grade inflammation is one of the most important factors contributing to the progression of diabetes associated with obesity.[10]

However, it is still unclear whether the different animal models and conditions used to study T2DM-associated gut microbiota will generate heterogeneous results, cause inaccurate interpretations, and lead to low reproducibility. Therefore, standardized methods and transparent protocols (including DNA extraction, polymerase chain reaction conditions, and detailed bioinformatic analyses) for

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***Correspondence to**: Alexander Machado Cardoso, Avenida Manuel Caldeira de Alvarenga, 1203 – CEP: 23070-200, Rio de Janeiro, RJ, Brazil. ORCID: http://orcid.org/0000-0003-2974-0232. Tel: +55-21-23327530, E-mail: amcardosopf@yahoo.com.br, alexandercardoso@uezo.edu.br
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evaluation of the gut microbiota are necessary. Assessment of the gut microbiota using stool samples from patients should be more cost-effective, as this procedure is non-invasive for screening, diagnosis, and monitoring of the development and progression of diabetes. Furthermore, given that the balance of gut microbiota is important for human health, the findings from gut microbiome analyses may help to develop novel, precise and personalized medicines. Therefore, anti-diabetic compounds, prebiotics, and probiotics should be selected for patients based on their age, sex, ethnicity, eating habits, lifestyle, and daily physical activities.

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Conflict of interest

There are no conflicts of interest to declare.

Author contributions

AMC is the sole author for this work.

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