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REVIEW

# Targeting the gut microbiota by Asian and Western dietary constituents: a new avenue for diabetes

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## Abstract

Increasing numerous diabetes annually is a great concern in public health globally. Gut microbiota recently has been suggested to be an emerging organ acting as a critical regulator in diabetes. Notably, gut microbiota is closely affected through an individual's nutrient intake and dietary pattern. Moreover, the metabolites of diets through gut microbiota are closely associated with the development of diabetes. Increasing evidence has established the association of different dietary pattern with alterations of the gut microbiota profile, in particular, the Asian diet and Western diet are typically as essential components linked to the interactions between gut microbiota and induction of obesity which is a significant risk factor for diabetes. In addition, some bacteria-related therapeutic methods including probiotics, dietary short-chain fatty acids immunotherapy, and gut microbiome transfer would be applied in the clinical prevention and control diabetes. Taken together, based on current published observations, the gut microbiota may serve as regulator or targets by the Asian diet and Western diet, contributing to the prevention or induction of diabetes eventually. In general, in the upcoming future, one of the emerging strategies for the prevention and control of diabetes may modulate gut microbiota through precise dietary strategies.

**Main finding of the work:** Dietary strategies that modulate the gut microbiota or their metabolic activities are emerging as efficacious tools for reducing diabetes risk and indicate that indeed, the way to a healthy gut microbiota may be through a dietary pattern.

**Key words:** Asian food; Western food; gut microbiota; diabetes

## Introduction

The rising amount of diabetes gradually is a major concern in public health worldwide. People with diabetes would have decreased life quality, increased risk of subsequent complications including foot ulcers [1], cancer [2], and leading to significant morbidity and premature mortality [3]. According to the report, in 2017, almost nearly 500 million population were affected by diabetes, which occupies about 7% of the world's population [4]. It is estimated about 6059 diabetes per 100,000 population and approximately >1 million deaths annual are caused by the reason for diabetes [4]. Notably, the burden of this disease is increasing dramatically, especially at an extremely increase rate in most of developed countries. Moreover, the incidence is projected to rise to 7079 individuals per 100,000 by 2030 across the world [4]. However, increasing studies have found the prevalence of diabetes varies widely among racial/ethnic groups [5]. In the USA in 2013, the incidence of diabetes was an average of 856.4/100,000 [6]. Notably, a national survey showed that the incidence of diabetes was 22.1% for Hispanic White, and 19.1% for

non-Hispanic Asian adults [7]. In China, which is the largest number of population of 1.38 billion, the prevalence of diabetes in 2013 was reported to be 10.9% [8], which was lower than the prevalence of total diabetes incidence of 12–14% among the US population in 2011 and 2012, respectively [8]. Japan is another Asian country with an incidence of 7.9% of the total population in 2010 [9]. Some reports suggested that global estimates of diabetes incidence are discrepancies in different regions may partly be attributed to the diversity of methods and data used to produce them [10, 11]. For instance, the International Expert Committee recommended the use of glycated hemoglobin (HbA1c) with a threshold of ≥6.5% (48 mmol/mol) to diagnose diabetes [12], whereas The American Diabetes Association, World Health Organization, and Japan Diabetes Society used other different criteria, respectively [13, 14]. However, although the diversity of identification methods and different data used for analysis, it has been confirmed that dietary behavior is typically associated with diabetes. In a recent review written by Nathanael et al. [15], it was pointed out that a high-fat diet (HFD) is linked to triggering diabetes. Animal experiments have indicated that the withdrawal of high-carbohydrate and HFD contributed to ameliorate the symptoms in rats with diabetes [16]. Indeed, there exists an extremely different dietary pattern between people in Western countries such as American and Asian countries such as China. And the different incidence of diabetes may be attributed to the different dietary patterns. Hence, in this review, we would compare the Western food pattern and Asian food patterns serving as regulators in diabetes.

Recently, the central role of the gut microbiota in the development and, equally, prevention or control diabetes is becoming abundantly apparent [17]. It is known that our human gut is densely populated by commensal and symbiotic microbes, named gut microbiota [18]. As illustrated in previous studies, gut microbiota can perform multiple functions including diverse and active metabolic activities and exchange metabolites with the host and interacts with host signaling pathways or regulates host gene expression, etc [19–25]. Moreover, gut microbiota can be affected by host diet intake, and in turn, the diet types can also influence the composition and metabolites of gut microbiota [26, 27], leading to the association with disease prevention and control measures selection [28]. Currently, most experts suppose that diet is a major determinant of the gut microbial structure and function [29, 30]. Hence, in this review, we focus on the following content: (i) brief description of Asia food and Western food pattern, (ii) gut microbiota composition may be influenced by Asian food and Western food pattern, (iii) nutrients metabolism is influenced by gut microbiota, (iv) main therapeutic methods on improving diabetes through modification of gut microbiota, (v) challenges and perspectives.

## Brief description of Asia food and Western food pattern

Asian food is generally a blend of several tastes such as Chinese, Japan, Korean, Thai, Vietnamese and Malaysia together. Rice and vegetables are the main compositions of Asian food [31]. The main characteristics of Asian food are sweet, sour, salty, spicy, and bitter [32], meanwhile Asian food is high in fiber, vitamins, minerals, and antioxidants the food is also high in carbohydrate and low in concentrated and total fat [33]. Some experts believe Asian protects us against many chronic diseases such as diabetes and other cardiovascular diseases, but some argue that as of high concentration of carbohydrate, Asian food may be a risk factor for the development of diabetes [34].

Western food or Western cooking is the cooking of Central European, Eastern European, Northern European, Southern European, and Western European Cuisine. Western food is a food with inadequate fruits, vegetables, whole grains, legumes, fish, and low-fat dairy products and excessive amounts of refined and processed foods, alcohol, salt, red meats, sugary beverages, snacks, eggs, and butter [35]. The Western food is also a dietary habit as part of the Western lifestyle chosen by many people in developed countries, and increasingly in developing countries, associated with economic growth [36]. The Western Diet (WD) is enriched in total fat, animal proteins, and refined sugars described by Martinez Medina et al. [37]. The Western food, which is low in potassium, high in sodium, fats, and simple carbohydrates, has been implicated in many diseases, including type II diabetes, hypertension, and obesity [38–40]. In Western cooking, meat is generally the centerpiece of any meal, while sweets are reserved for the end of the meal. This is distinct from Asian cooking, in which rice or noodles are considered necessary to the meal and sugary, sweet sauces are common. Alcohol is often used in Western cooking as well, particularly grape wines; this may be due to the difficulty of spices penetrating those larger cuts of meat [41]. According to the reports, different diet patterns may contribute to the different disease outcomes. As of diabetes, Western lifestyle with a high consumption of high-fat and high-sugar and a low consumption of vegetables has been associated with diabetes [42]. Parackal et al. [43] searched the published literature from 1990 to provide evidence that dietary patterns pave the way to develop diabetes among these South Asians who frequently eating fast foods, Western desserts and snacks, and consumption of large amounts of potatoes, dairy, oil, and meat. In a study by Lovegrove et al. [44], the excessive consumption of high glycaemic index foods is associated with increased risks of a range of chronic diseases including diabetes. In a few prospective studies performed mainly in Western populations, the higher consumption of meat is associated with a higher risk of diabetes [45]. However, although the Asian diet is considered for decreasing the risk of diabetes, it should be noticed that as some kind of Asian food such rice is full of a high level of carbohydrate, then how it influences the risk of diabetes? A study conducted by Kim et al. [46] in adults showed that glycaemic index may be positively associated with the incidence of type II diabetes in women, especially in obese women.

## Gut microbiota composition may be influenced by Asian food and Western food pattern

In terms of gut microbiota, its composition is confirmed tightly associated with human health. Diabetes may be associated with the gut imbalance [47]. The dietary factor is the major factor playing a role in the pathophysiology of diabetes. From the perspective of Moschen [42], although the short-term changes in dietary patterns may not have a major influence in gut microbiota, but long-term diets can substantially influence the gut microbiota. Based on the above description of Asian food and Western food pattern, in this section, we focus on the different effects of Asian food such and Western food on the gut microbiota composition. Although the composition of the gut microbiota depends on intrinsic factors such as sex and extrinsic factors that include diet, hygiene, antibiotic usage, diet is one of the major players in shaping gut microbial communities.

In some animal experiments, the Asian diet was used to investigate whether the gut microbiota would be affected under the Asian diet treatment. Han et al. [48] indicated that rice straw biochar increased the abundance of Firmicutes and Bacteroidetes

ratio and decreased abundances of Prevotella and Bacteroides. The findings from Higuchi *et al.* [49] indicated that mice treated with rice endosperm protein during the juvenile period changed gut microbiota diversity, suppressing the activity of *Escherichia coli*, which is a major producer of lipopolysaccharide. Similarly, a study by Xiao *et al.* [50] also found that rat treated with rice bran phenolic extract ameliorates gut microbiota dysbiosis, suggesting intake of this diet may be an effective way to mitigate alcoholic liver injury. The vegetable is another major component of Asian food, the effects of vegetable on the gut microbiota composition have also been intensively investigated recently. Mice treated with high-fiber diet modified the gut microbiota composition, increasing the ratio of Firmicutes to Bacteroidetes, therefore, played a protective role in the development of cardiovascular disease [51]. Bloodgood *et al.* [52] used a mixed seafood-vegetable diet to fed green turtles and found the increased Firmicutes and decreased Bacteroidetes abundance in gut microbiota. However, when the animal treated with Western food patterns, the gut microbiota composition may be changed in another type. Poutahidis *et al.* used mouse models consuming Western fast food like potato chips to detect the gut microbiota alterations. The results found that restructures the gut microbiota and accelerates obesity in mice [53]. Another study compared the rats treated with a Western diet characterized with 42.5% kcal being derived from fat and high in simple carbohydrates and low fiber, cafeteria diet comprising of a few human snacks such as cheese, cake, cookies, etc., to evaluate which type was more closely to obesity. The results showed that different diet selection leads to different phenotypes. The Western diet was most more likely to induce obesity and obesity-related disease, meanwhile, the Western diet caused gut microbiota dysbiosis and cafeteria diet caused decreased gut microbiota diversity, indicating Western diet may disrupt the gut microbiota composition [54]. Soy protein is another common diet in Asian food and found have beneficial for improving Western-style diet-related phenotypes. Butteiger et al. [55] supplemented soy protein concentrates in a Western-style diet for 3 weeks and observed significant increases in Bifidobacteriaceae, Clostridiales, and Deferribacteraceae and decreases in Bacteroidetes in a Golden Syrian hamster model.

Also, there are existing many studies on Asian food and Western food on the gut microbiota composition in human studies. Shin *et al.* [56] compared the differential effects of typical Korean versus Western food patterns on gut microbiota composition in a randomized crossover trial. The difference between the Korean diet and Western diet is mainly that the Korean diet is 60% carbohydrates and 20–25% fat whereas the Western diet is 50% carbohydrates and higher fat of 35%. The results of this 4-week length trial showed that the Korean diet promoted diversity whereas the Western diet did not to the gut microbiota, furthermore, Korean diet consumption significantly increased Firmicutes and decreased Bacteroidetes abundance [56]. Similarly, as a traditional nut consumption in the Asia area, palm intake was showed to increased Firmicutes and decreased Bacteroidetes abundance as well [57]. Seural *et al.* investigated the effects of Japanse diet on the gut microbiota composition by the cross-sectional study. The outcome showed that a higher consumption of rice was associated with a significantly lower relative abundance of Prevotella [58]. In another study, it supposed that rice consumption for infants for ~8–12 months changed the gut microbiota beta diversity as well as increased Bifidobacterium and Lachnospiriaceae abundance [59]. Indeed, vegetable-based diets have been extensively obtaining acceptance and public because of its health benefits [60]. In a single group-design trial by Hiel *et al.* [61], they found that participants consumed with inulin-rich vegetables increased the proportion of the Bifidobacterium genus and decreased level of Clostridiales and Oxalobacteraceae after 3 weeks intervention. Choi *et al.* [62] demonstrated that daily fruits and vegetable juice intake for 3 weeks increased the $\alpha$ diversity of gut microbiota, accompanied by an increased abundance of Faecalibacterium. Another study using broccoli indicated that human gut microbiota was impacted, Broccoli consumption decreased the relative abundance of Firmicutes [63]. Soybean food is very popular across the world. Recent human studies have identified gut microbiota serving as a critical sensor interacting with soybean, therefore affecting the human development, physiology, and immunity across the entire life. In general, the consumption of soy foods increases the levels of bifidobacteria and lactobacilli and alter the ratio of Firmicutes and Bacteroidetes in human gut microbiota [64].

One of typical characteristic of Western food is high-fat component. Recent lines of evidence have indicated that the consumption of a HFD increases gut inflammation by stimulating the production of sulfate-reducing bacteria [36]. A study on the European children's intervened with Western food increased Proteobacteria and decreased *Prevotella* and *Xylanibacter* abundance [65]. Another study showed that compared with the gut microbiota composition of the Venezuela population, the United States American gut microbiota had less microbial diversity [66]. Another study indicated that the Western diet would be a means to counteract the risk of losing the bacterial memory that has accompanied our ancestors throughout human evolutionary history [67]. Okazaki *et al.* investigated the pattern of HFDs including lard, soybean oil, corn oil, or olive oil in rats. The outcomes demonstrated this high-fat food increased the number of Lactobacillus spp. [68]. A randomized crossover intervention trial showed that the red meat diet increased Collinsella aerofaciens and Clostridium sp. abundance [69]. Shankar *et al.* study found that in the US children. The gut microbiota communities were of the *Bacteroides*enterotype, moreover, the gut environment of US children was rich in amino acids and lipid metabolism-associated compounds as well as the abundances of members of *Faecalibacterium* and *Akkermansia* [70].

Together these data suggest that consumption of Asian food or Western food may affect gut microbiota composition. In detail, Asian food is helpful to increase beneficial bacterial abundance such as Firmicutes and inhibit non-beneficial bacterial abundance, such as Bacteroidetes. In contrast, general studies showed that Western food leads to increased non-beneficial bacterial abundance and inhibit beneficial bacterial abundance. Nevertheless, many factors including interior factors, such as gender, gene polymorphisms, and external factors such as environmental pollution, would change the gut microbiota composition, and the microbes themselves also would evolve and intend to adapt to the interior or external changes much more rapidly than humans can, thus, when taking measures to prevent or control diabetes, it should comprehensively consider diet and other factors. However, diet modifications, especially, the diet intake under extremely different food cultures are more likely to be among one of the most efficient methods [71]. The gut microbiota dysbiosis is linked with the increased generation of toxic metabolic products in the intestine and elevates the burden of the endocrine system, as well as leads to the aberrant metabolism of dietary component such as choline, leading to impair the lipid metabolism [72].

## Fiber, fat, and protein are metabolized by gut microbiota

As the main difference of nutrients in Asia food and Western food is the carbohydrates, fats, and proteins, in this section, we mainly focused on these three nutrients metabolized by gut microbiota. In fact, before absorbing into the blood system, these three nutrients, carbohydrates, fats, and proteins, are metabolized by gut microbes in the large intestine. Many kinds of bacteria can metabolize dietary carbohydrates, fats, and proteins, such as *Roseburia*, *E. rectale*, and *R. bromii* [73].

Short-chain fatty acid (SCFA) metabolites, notably butyrate, propionate, and acetate are the by-products of bacterial fermentation of indigestible carbohydrates, mostly fiber [74]. SCFAs which are metabolites derived from the fermentation of dietary fiber by gut microbiota are important for host metabolic health through the regulation of lipid and glucose metabolism. SCFAs are end-products resulting from the fermentation of dietary fiber by gut microbiota. Bifidobacterium animals subsp. lactic GCL2505 (GCL2505) treatment suppressed body fat accumulation, improved glucose tolerance, and enhanced systemic fatty acid oxidation in a HFD-fed wild-type (WT) mice [75]. Some bacteria such as *Bifidobacterium* and *Subdoligranulum* can produce SCFAs through metabolizing dietary fiber [76]. Species such as *Akkermansia municipally* have been identified as key propionate producing mucin degrading organisms [77]. *Ruminococcus bromii* was proved responsible for the production of butyrate [78]. Also, a surprisingly small number of organisms, dominated by *Faecalibacterium prausnitzii, Eubacterium rectale, Eubacterium hallii, and R. bromii*, appear to be responsible for the major fraction of butyrate production [79]. In a recent diet-switch study, where African Americans were fed a diet and rural Africans a high-fat, low-fiber Western-style diet, a shift toward the butyrate-producing organisms *Roseburia intestinal Eubacterium rectale* and *Clostridium symposium* along with increased butyrogenesis was observed on low-fat, high fiber feeding [80]. SCFA also has potential in metabolism glucose homeostasis. Acetate, propionate, and butyrate appear to regulate hepatic lipid and glucose homeostasis in an adenosine monophosphate-activated protein kinase-dependent manner involving peroxisome proliferator-activated receptor-$\gamma$ regulated effects on gluconeogenesis and lipogenesis [81]. These studies highlight the gut microbiota metabolize the diet and the changes in SCFAs and the association with profound effects on lipid and host metabolism [82]. Increasing numerous studies regarding such as SCFAs following dietary change, but the significance of the microbiota changes to human health, with the possible exception of the stimulation of butyrogenic taxa by fiber-rich foods, is generally implied and not measured. Further studies are needed to determine how these changes in microbiota composition and metabolism can improve our health and be used to prevent and treat diabetes. A study assessed the impact of dietary fat sources of palm oil and the gut microbiota metabolization of dietary fat. The results showed that dietary cholesterol as a candidate ingredient affecting the crosstalk between gut microbiota and host metabolism [83].

Triglycerides represent 95% of total dietary fat, whereas phospholipids, mostly in the form of phosphotidylcholine [84], constitute a minor portion, but are also derived endogenously from bile acids. Microorganisms in the gut are known to possess lipases, which can degrade triglycerides and phospholipids into their polar head groups and free lipids [85]. After comparing the metabolic profile between mice fed a low- and high-fat diet, tryptamine, and indole-3-acetate (I3A) are metabolites that depend on the microbiota, helping to reduce fatty-acid- LPS-stimulated production of pro-inflammatory cytokines [72]. Bo

*et al*. [86] indicated that B. pseudolongum treatment significantly plasma triglycerides markedly recovered the gut microbiota dysbiosis in obese mice. Obese mice administrated with Akkermansia muciniphilalowered serum triglyceride through the gut microbiota regulation [87]. Protein metabolism in the gut is generally catalyzed into amines, phenols, and sulfurous compounds [88, 89]. A microbe can metabolize amino acid via either deamination or decarboxylation reactions and generates SCFAS or amines, respectively [88]. Furthermore, the amino acid continues to metabolize into tricarboxylic acid cycle intermediates, pyruvate, or coenzyme A-linked SCFA precursors via gut microbiota [90]. Additionally, some gut microbial species, mainly from the class Bacilli, also possess a specialized branched-chain keto acid dehydrogenase complex to yield energy from the oxidized forms of the branched-chain amino acids directly, which also leads to BCFA production [91]. Mafra *et al*. [91] showed that red meat intake increased metabolites of trimethylamine n-oxide (TMAO), indoxyl sulfate, and p-cresyl sulfate via gut microbiota, which are linked with increased risk of cardiovascular mortality. TMAO is a low-molecular-weight amine oxide derived by the microbial metabolism of choline-containing compounds [92]. Western foods such as red meat, eggs, saltwater fish serving as potential precursors of TMAO comprise of a rich concentration of choline. Studies in humans and animals suggested that several families of bacteria are engaged in TMAO production, such as Deferribacteraceae, Enterobacteriaceae, Anaeroplasmataceae, and Prevotellaceae [93]. Another study identified the following nine strains of bacteria that have the ability to produce TMAO in the gut, Anaerococcus hydrogenates, Clostridiumasparagiforme, Clostridium Hatheway, Clostridium sporogenes, Escherichia Ferguson, Proteus penner, Providenciarettgeri, and Edwardsiella tarda [94, 95]. As studies have identified that the digestion of animal protein or other constituents of animal products causes the gut microbiota forms TMAO leading to the development of diabetes-related symptoms, such as insulin resistance [95]. Currently, TAMO has been suggested to serve a novel potential therapeutic target for controlling insulin resistance [96, 97].

## Main therapeutic methods on improving diabetes through modification of gut microbiota

For prevention or therapy of diabetes through reshaping the gut microbiota, currently, there are a few main strategies including probiotics supplementary, dietary SCFAs immunotherapy, and gut microbiome transfer.

A meta-analysis conducted by Tao *et al*. [98] revealed that probiotics treatment may reduce insulin resistance levels in type II patients. Probiotics were originally defined as "microorganisms causing the growth of other microorganisms," and later on as "live microorganisms which have a beneficial effect at adequate levels on human health" [99]. Numerous studies have found supplementary probiotics have an anti-diabetes effect through the modification of gut microbiota. Wang *et al*. indicated that probiotics significantly improved blood glucose and blood lipid parameters the gut barrier function in DB/DB mice through increasing the levels of SCFA-producing bacteria [100]. Another animal study also showed that the combination of probiotics and salvia miltiorrhiza polysaccharide reduced he liver total cholesterol and total triglyceride levels and the serum levels of free fatty acid, alanine transaminase, aspartate transaminase, low-density lipoprotein cholesterol through modification of gut microbiota [101]. Similarly, the administration of L. Plantarum and inulin could improve gut dysbiosis and oxidative stress status in

diabetes rats through balanced gut microbiota [102]. After the ingestion of probiotics, an improvement in diabetes symptoms is usually observed, such as improved intestinal integrity, decreased systematic liposaccharide concentrations, decreased endoplasmic reticulum stress, and improved peripheral insulin sensitivity [103]. Bifidobacterium, Lactobacillus, Streptococcus, Pediococcus, and Lactococcus species are the common commercial probiotics product components. These data including meta-analysis based on randomized controlled trials suggested that probiotics may be used as a potential of dietary supplement in reducing the glucose-associated metabolic factors related to diabetes through modification of the gut microbiota [100].

Being aware of the inflammatory condition-related diabetes is related to diet and diet-microbiota, many studies performed on the relevant pr-clinical and clinical studies about the dietary SCFAs technology that naturally targets the gut microbiota as a novel therapy method to prevent and treat diabetes and its complications [104]. Many studies have shown that SCFAs intake can lower blood pressure, provide positive effects on appetite regulation and balance of energy intake via the brain-gut axis. Also, it has the effects on inducing lipid oxidation in adipose tissues and intestine [104]. Furthermore, SCFAs stimulate the release of the gut hormones to improve intestine barrier function and reduce uptake of inflammatory compounds which may trigger the insulin resistance liked with diabetes [105]. In a recent review written by Chambers *et al.* [106], they summarized that in the gut epithelium and adipose tissue, there are available many G-protein-coupled receptors, free fatty acid receptor (FFAR) 2 and FFAR3 which can be stimulated by the SCFAs supplement and cause the cascade of numerous hormonal signals in diabetes molecular signaling pathways.

During the last few years, fecal microbiota transplantation (FMT), known as donor feces transplantation or fecal bacteriotherapy, has attracted increased attention. The majority of clinical experience with FMT has been gathered from the treatment of *Clostridium difficile* infection [107]. To investigate whether FMT could alleviate the symptoms associated with type 2 diabetes, Wang *et al.* [108] conducted an animal study and revealed that after FMT, insulin resistance and pancreatic islet $\beta$-cells were improved. Another study by Zhang *et al.* [107] also found that DB/DB mice treated with FMT, Desulfovibrio, and Clostridium coccoides levels in the gut were significantly decreased, but the fecal levels of Akkermansia muciniphila and colon histone deacetylase-3 (HDAC3) protein expression were increased. Barcena *et al.* [109] found FMT from WT mice enhanced healthspan and lifespan in both progeroid mouse models, and transplantation with the verrucomicrobia Akkermansia muciniphila was sufficient to exert beneficial effects. A clinical study conducted using oral capsules with fecal microbiota showed that obese patients administrated with FMT capsules led to changes in the intestinal microbiome and bile acid profiles [110]. In a recent review written by Aron-Wisnewsky *et al.* [111], they suppose that FMT is an interesting option to modify gut microbiota and help improve obesity or diabetes clinical outcomes. However, as only limited clinical trials are available using FMT in diabetes background, further studies, in particular, randomized controlled trials aiming at evaluating the FMT intervention outcomes on diabetes should be considered. The association of major dietary component and possible outcomes is listed in the Supplementary Table S1.

## Challenges and perspectives

As diabetes prevalence is gradually increasing across the world over the past 2 decades and is projected to continue to rise in the next few decades, prevention and control diabetes are an urgent need indeed. Accumulating evidence has supposed that Asian food and Western food play a different role in the contribution to the development of diabetes. Also, gut microbiota plays a critical role in the pathogenesis of diabetes [112]. Moreover, the gut microbiota composition could be modified significantly by different diet styles, such as Asian food and Western food. Thus, understanding the role of gut microbiota in the contribution of differential roles in the pathogenesis of diabetes would be helpful for further molecular mechanisms study and discover more effective targets serving as possible preventive and therapy for diabetes. However, as an old saying said before: the hope is ahead, but it is a long way to archive, there are still lots of challenges in this field as follows:

First, although many studies have indicated that in the diabetes patients' gut, the microbiota has changed and present dysbiosis [112], these data still exist controversial. This may be due to the different study context and the relative molecular mechanisms remain incompletely clear. Thus, in the future, future studies should be focused on discovering the gut microbiota-related mechanism of diabetes, specifically, the bacterial species role in the diabetes pathogenesis.

Second, despite this review, we list some diet components of Asian foods and Western foods the dietary culture is very complex. Many factors may influence the human dietary habit or culture, such as migration. When Asian people move to Western countries for residents, their dietary habits may be changed, which may influence the risk of diabetes. Other factors, such as ads or poverty also may influence the selection of food. When there are extreme ads on certain food, people always intend to buy and intake them. People in the status of poverty prone to select cheap food such as potatoes with a high concentration of carbohydrates. In terms of this issue, in the future, more socioeconomic studies should be performed to investigate the effects of culture, economical factors on dietary style selection.

Third, concerning studying diabetes-related nutrient science, we indeed face a lot of roadblock, such as to measure discrimination, unclear causal relationships of diabetes, non-strong effect, analysis sensitivity, etc. Thus, in the future, cohort studies and prospective study to survey the food intake in a long-term and space time series study would help to solve this challenge.

Fourth, although some therapeutic methods have been identified effective in therapy diabetes through targeting gut microbiota, it is still lacking data in detail and difficult to transfer into clinical usage. The next step is to develop the ability of diagnosis and therapy based on the interaction of gut microbiota and host. Typically, we need to transfer our study purpose from description to the microbiome therapy. We need to confirm the targeted bacterial species. We have to figure out whether the certain stain abundance or the gut microbiota abundance lead to diabetes. We need to know the metabolism pathway of certain bacterial and the association of bacterial metabolism pathways with the development of diabetes.

## Ethics approval and consent to participate

Not Applicable.

## Consent for publication

Not Applicable.

## Availability of data and supporting materials section

Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

## Author Contributions

R.H. conceived and designed the study; A.R.C. analyzed the data and performed the statistical analysis. A.R.C. and R.H. drafted the initial manuscript. R.H. critically reviewed and revised the manuscript.

## Conflict of interest statement

None declared.

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