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Effects of High-Fiber Diets on Type 2 Diabetes Mellitus in China

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Abstract:

Amid continued socioeconomic development and improvements in living conditions in China, the population affected by type 2 diabetes mellitus has steadily expanded, thereby imposing a substantial and growing burden on the public health system and the broader economy. At present, lifestyle-based adjunctive interventions for patients with type 2 diabetes mellitus have yielded encouraging results; among these, high-fiber dietary patterns—capable of markedly enhancing intestinal microbiota diversity and improving metabolic profiles—have attracted widespread attention. Drawing on a randomized controlled trial of a high-fiber dietary intervention in 43 adults with type 2 diabetes mellitus, together with corroborating observational data from large population cohorts, the literature outlines a coherent evidence chain indicating that high-fiber dietary interventions can effectively improve clinical metabolic outcomes in this patient population. This review synthesizes and evaluates the modulatory effects of high-fiber diets on the gut microbiota and its metabolites among Chinese patients with type 2 diabetes mellitus, and—based on identified mechanistic and observational evidence as well as their limitations—proposes practice-oriented design recommendations and priority areas for future comprehensive management.

Keywords: High-Fiber Diet; type 2 diabetes; metabolic disorders.

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1. Introduction

Type 2 diabetes mellitus is a prevalent chronic metabolic disorder marked by sustained elevations in blood glucose, inadequate secretion of insulin, and resistance to the actions of insulin. Clinical manifestations include excessive thirst, frequent urination, and weight loss; over time, the condition can lead to severe complications such as heart disease, stroke, nontraumatic blindness, and kidney failure. Recent years have witnessed a marked worsening in the epidemiology of type 2 diabetes mellitus in China, resulting in persistent strain on the national public health system and the broader socioeconomic sphere. Estimates from the International Diabetes Federation indicate that in 2024, 11.9 percent of Chinese adults aged 20 to 79 years are living with diabetes, totaling approximately 148 million individuals, the largest national caseload worldwide. diabetes-related health expenditures are about 16.9 billion U.S. dollars, and the number of patients is projected to rise to approximately 168 million by 2050 [1]. Beyond genetic susceptibility, changes in lifestyle and dietary patterns are regarded as major drivers of the high prevalence of type 2 diabetes mellitus in China, with insufficient dietary fiber intake and gut microbiota dysbiosis drawing particular attention. Multiple investigations have documented that individuals with type 2 diabetes mellitus tend to have diminished microbial diversity, an enrichment of taxa with pathogenic potential, and disturbed microbial homeostasis; these microbiome alterations are tightly linked to impaired regulation of blood glucose and dysfunction of pancreatic islet cells [2]. Dietary fiber predominantly originates from whole grains, legumes, fruits, and vegetables; although it is neither digested nor absorbed by humans, it is fundamental to intestinal health and the regulation of blood glucose. Adherence to a high-fiber dietary pattern selectively enriches gut microorganisms that generate short-chain fatty acids, concurrently expands the abundance of health-promoting taxa, and enhances overall microbial diversity and ecological stability. Within the colon, dietary fiber is fermented by the intestinal microbiota to produce acetate, propionate, and butyrate. These metabolites fuel the intestinal epithelium, improve host glucose and lipid metabolism, and fortify the intestinal mucosal barrier, thereby restricting the translocation of bacterial lipopolysaccharide into the bloodstream. As systemic inflammation is attenuated, insulin resistance declines, leading to downstream improvements in glycemic control and insulin sensitivity in individuals with type 2 diabetes mellitus. Accumulating evidence indicates that adherence to a high-fiber diet improves glycemic control and metabolic parameters in individuals with type 2 diabetes mellitus [3]. This review provides an integrated account of how dietary fiber modulates the gut microbiota and its metabolites, consolidates evidence from clinical trials and observational research, and examines the pertinent limitations in light of the characteristics and practical needs of the Chinese population; it further proposes actionable directions for clinical practice and public health to inform the comprehensive management of type 2 diabetes mellitus.

2. Mechanisms by Which Dietary Fiber Influences Type 2 Diabetes Mellitus

2.1 Dietary Fiber Intake and Gut Microbiota Dysbiosis

Chinese individuals with type 2 diabetes mellitus harbor gut microbiota that are substantially distinct from those observed in healthy controls. It is characterized by reduced richness and evenness and by an elevated Firmicutes-to-Bacteroidetes relative proportion. A substantial body of research has shown that patients with type 2 diabetes mellitus exhibit lower microbial diversity, diminished populations of beneficial taxa, and increased abundance of bacteria with pathogenic potential. This dysbiotic configuration is strongly associated with metabolic derangements, particularly abnormal glycemic regulation and impaired pancreatic islet function [4]. Changes in dietary patterns are considered an important factor precipitating gut microbiota dysbiosis. Compared with recommended intakes, contemporary Chinese populations exhibit widespread insufficiency of dietary fiber: surveys indicate a mean daily intake of approximately 11.7 g, less than half of the recommended amount, and only about one quarter of individuals achieve 13.5 g or more [5]. In this context, fiber deficiency reduces the substrate available to beneficial, short-chain fatty acid–producing microbial communities, potentially aggravating microecological imbalance and promoting metabolic inflammation, thereby increasing the risk for the development and progression of type 2 diabetes mellitus.

2.2 Clinical Research on High-Fiber Dietary Interventions

In a randomized controlled clinical study, Zhao and colleagues assigned forty-three adults with confirmed type 2 diabetes mellitus to a high-fiber diet group (n = 27; incorporating whole grains, traditional Chinese ingredients, and prebiotics, with standardized concomitant use of acarbose) or to a usual-care control group (n = 16; also receiving acarbose) for a 12-week intervention. The results showed that, relative to baseline, the high-fiber group experienced a significant reduction in glycated hemoglobin, with a greater decline than the control group; concomitantly, body mass and blood lipid parameters improved more markedly. There was a significant rise in overall gut microbial diversity together with an expansion of beneficial lineages, most notably a marked increase in short-chain fatty acid–producing groups such as Bifidobacterium and Prevotella. Following transplantation of post-intervention fecal microbiota from the high-fiber group into germ-free mice, only this microbiota conferred improved glucose tolerance and lower blood glucose levels in recipients, whereas recipients of microbiota from the control group exhibited deteriorated glucose metabolism, further supporting a contributory role of microbial alterations in mediating the therapeutic effect [6]. In addition, a systematic review and meta-analysis that included twenty-nine randomized controlled trials encompassing 1,527 adults with type 2 diabetes mellitus showed that, compared with control diets, supplementation with soluble dietary fiber significantly reduced glycated hemoglobin (mean difference −0.63%, P < 0.00001) and fasting plasma glucose (mean difference −0.89 mmol/L, P < 0.00001), and improved fasting insulin, homeostatic model assessment of insulin resistance, fructosamine, two-hour postprandial glucose, and body mass index; dose–response analysis indicated an appropriate intake range of approximately 7.6–8.3 g per day [7]. The study also noted substantial heterogeneity in the pooled results and generally short follow-up durations; Definitive confirmation of these findings and identification of the most effective intervention protocols will require randomized controlled trials with extended follow-up and greater methodological rigor. Taken together, a high-fiber diet, as a lifestyle intervention, shows considerable promise for application among Chinese populations with type 2 diabetes mellitus.

3. Mechanisms of Action of High-Fiber Diets

3.1 Microbial Community Structure and Short-Chain Fatty Acid Pathways

Adoption of a high-fiber dietary pattern preferentially enriches gut microbial consortia capable of synthesizing short-chain fatty acids, resulting in greater production of metabolites such as acetate, propionate, and butyrate. At the functional level, a high-fiber diet directs the expansion of a set of key short-chain fatty acid–producing strains; this functional consortium stabilizes by day 28 of the intervention, and a composite index of its abundance and evenness is inversely associated with glycated hemoglobin, suggesting that early microbiological changes may predict subsequent improvements in metabolic outcomes. At the level of metabolic pathways, the high-fiber intervention markedly enriched genes encoding key enzymes involved in acetate production. By contrast, a significant upregulation of the butyrate biosynthetic route catalyzed by butyryl–coenzyme A:acetate coenzyme A transferase was observed exclusively in the high-fiber group. This molecular shift coincided with higher fecal butyrate concentrations and a sustained reduction in fecal pH, collectively indicating luminal acidification alongside an overall increase in short-chain fatty acid production. Additionally, the high-fiber group showed selective enrichment of genes encoding adhesion structures and multi-enzyme complexes involved in the degradation of plant cell walls, indicating that the distribution of the carbohydrate-active enzyme profile is more informative of functional enhancement than total gene abundance; this is consistent with an increased capacity of short-chain fatty acid–producing taxa to utilize substrates such as starch, inulin, and arabinoxylan. Analysis of community interactions demonstrated that the fifteen promoted strains were significantly negatively correlated with the suppressed members, suggesting that this functional consortium not only enhances the production of short-chain fatty acids but also maintains low levels of unfavorable taxa through niche competition, thereby linking to metabolic benefits for the host [6]. Short-chain fatty acids provide energy to the intestinal epithelium and, through multiple signaling pathways, improve host glucose and lipid metabolism, thereby helping to maintain glycemic homeostasis.

3.2 Inflammation and Intestinal Barrier Regulation

Short-chain fatty acids produced in the context of a high-fiber diet, exemplified by butyrate, fortify the intestinal mucosal barrier, restrict the passage of bacterial lipopolysaccharide from the lumen into the bloodstream, and, as a result, diminish systemic inflammatory activity. At the molecular level, butyrate upregulates the expression and distribution of tight junction proteins, evidenced by enhanced transcription of claudin-1 and concordant localization changes of zonula occludens-1 and occludin, thereby strengthening the epithelial barrier. Restoration of barrier integrity reduces transmembrane permeability to lipopolysaccharide, thereby indirectly lowering the systemic inflammatory burden and the risk of insulin resistance. Within this pathway, bacterial lipopolysaccharide engages Toll-like receptor 4, initiating downstream signaling that elevates proinflammatory cytokines—tumor necrosis factor, interleukin 6, interleukin 8, and interleukin 12—thereby establishing a state of low-grade chronic inflammation that both worsens and is reciprocally reinforced by metabolic dysfunction [8]. Augmenting the availability of short-chain fatty acids through a high-fiber diet, together with reinforcing epithelial barrier integrity, limits lipopolysaccharide translocation into the circulation at its origin and thereby attenuates downstream inflammatory signaling. The alleviation of inflammation can mitigate insulin resistance and is of substantial importance for improving the metabolic status of patients with type 2 diabetes mellitus.

3.3 Enteroendocrine Hormones and Glucose Homeostasis

Short-chain fatty acids bind and activate free fatty acid receptor 2 and free fatty acid receptor 3 on colonic L cells, leading to an increase in intracellular calcium and the consequent secretion of glucagon-like peptide 1 and peptide YY. this enteroendocrine response enhances insulin secretion after meals, suppresses glucagon, and ultimately improves control of postprandial blood glucose. In receptor-deficient models, these effects are markedly attenuated, accompanied by decreased oral glucose tolerance and impaired insulin secretion, indicating that this receptor-mediated signaling axis makes a substantive contribution to glucose homeostasis. Evidence from human intervention studies shows that adherence to a high-fiber diet is accompanied by a higher postprandial glucagon-like peptide 1 exposure, as reflected by an increased area under the curve, and a tendency toward elevated fasting peptide YY. These hormonal changes occur in parallel with rises in acetate and butyrate, supporting the interpretation that short-chain fatty acids potentiate enteroendocrine signaling and thereby contribute to improved regulation of blood glucose. Taken together, by enriching functional taxa that produce short-chain fatty acids and increasing their metabolic flux, a high-fiber diet exerts coordinated effects across three domains—microbial metabolism, mucosal barrier integrity with anti-inflammatory activity, and enteroendocrine secretion—thereby optimizing glucose homeostasis [9].

4. Observational Evidence and Regional Differences

Epidemiological research further supports the potential benefits of a high-fiber diet. In a study based on two follow-up waves among Chinese patients with type 2 diabetes mellitus in 2016 and 2017, Fu and colleagues conducted two cross-sectional analyses and one longitudinal analysis, with sample sizes of 356 and 310 and a common follow-up cohort of 293 participants. The study assessed habitual dietary fiber intake using three-day, twenty-four–hour dietary recalls, stratified participants at 7.2 grams per day, and evaluated the fecal microbiota by sequencing of the 16S ribosomal Ribonucleic Acid (RNA) gene. Analyses revealed no statistically significant relationship between dietary fiber intake and glycated hemoglobin levels. Higher fiber intake was associated with lower alpha diversity (Shannon index beta coefficient = −0.06, P = 0.011; Chao1 index beta coefficient = −28.78, P = 0.003). At the second follow-up, between-group differences in beta diversity reached statistical significance (P = 0.014). At the level of community composition, participants with higher fiber intake exhibited lower relative abundances of Firmicutes, Fusobacteria, Adlercreutzia, Prevotella, Ruminococcus, and Desulfovibrio. Mediation analysis identified Desulfovibrio and an unclassified genus within the family Ruminococcaceae as negative mediators of the association between dietary fiber intake and glycated hemoglobin (beta coefficient = −0.019, P ≈ 0.02). Overall, low to moderate levels of habitual fiber intake were associated with favorable microecological alterations [5]. To quantify this association, investigators aggregated data from seventeen prospective cohort studies including 488,293 participants with 19,033 incident cases. Greater consumption of total dietary fiber was associated with a reduced risk of type 2 diabetes mellitus. Comparing the highest with the lowest intake categories yielded a summary relative risk of 0.81 (0.73–0.90). Among specific fiber types, the pooled relative risk for cereal fiber was 0.77 (0.69–0.85), for fruit fiber was 0.94 (0.88–0.99), and for insoluble fiber was 0.75 (0.63–0.89). Dose–response analysis indicated a nonlinear association between total fiber intake and risk; the relative risks at intakes of 15, 20, 25, 30, and 35 grams per day were 0.98, 0.97, 0.89, 0.76, and 0.66, respectively. In a linear model, each additional 10 grams per day of total fiber was associated with an approximately six percent reduction in risk. For cereal fiber, the association was linear; each additional 2 grams per day was associated with an approximately six percent lower risk (pooled relative risk 0.94, 95 percent confidence interval 0.93–0.96). Overall, higher total fiber intake and greater cereal fiber intake are both associated with a lower risk of type 2 diabetes mellitus [10]. In addition, a perspective review proposed that stratifying individuals by enterotype into Prevotella-dominant and Bacteroides-dominant types can be used to predict metabolic responses to diet and pharmacologic therapy. Individuals with a Prevotella-dominant enterotype are more likely to experience reductions in body weight and improvements in metabolic status under a high-fiber diet, whereas individuals with a Bacteroides-dominant enterotype are more likely to obtain metabolic benefits from interventions that increase the abundance of Bifidobacterium, such as the use of alpha-glucosidase inhibitors or bifidogenic prebiotics. These patterns point to differences in preferred substrate use and in the capacity to generate short-chain fatty acids, which may, in turn, modulate energy homeostasis through enteroendocrine signaling pathways mediated by glucagon-like peptide 1 and peptide YY [11]. Accordingly, the individual microbiota background should be fully considered when designing fiber-related interventions to achieve more optimal metabolic outcomes.

5. Conclusion

Taken together, studies in Chinese cohorts support that high-fiber dietary interventions improve clinical metabolic endpoints in individuals with type 2 diabetes mellitus, with a portion of the benefit attributable to the remodeling of the gut microbial community. clinical trials and population-based observations corroborate one another, and mechanistic studies provide a biological explanation, forming a relatively complete chain of evidence. However, most intervention studies to date have relatively small sample sizes and short follow-up durations, which are insufficient to evaluate the effects of a high-fiber diet on the long-term complications of diabetes. Concurrently, dietary fiber spans multiple classes—soluble and insoluble fractions and sources such as whole grains, fruits, and vegetables—and the effects of these distinct sources on the gut microbiota can differ. the optimal combination remains to be elucidated. In addition, interindividual differences in the gut microbiota result in heterogeneous therapeutic responses to the same high-fiber diet across patients, underscoring the urgent need to develop personalized nutritional intervention strategies. In sum, a high-fiber dietary pattern acts through modulation of the gut microbiota and its metabolic products to enhance glucose homeostasis and overall metabolic health via multiple mechanisms in Chinese individuals with type 2 diabetes mellitus. as a safe and effective lifestyle intervention, it has the potential to become an integral component of comprehensive diabetes management and to be further promoted in clinical practice; however, its long-term benefits and optimal regimens require further confirmation; future work should undertake larger-scale studies with extended follow-up in local populations to verify effects on long-term outcomes and to identify the most effective intervention strategies. at the same time, personalized nutrition should be prioritized by integrating gut microbiota testing to deliver targeted dietary guidance and improve patient adherence, thereby fully realizing the therapeutic potential of a high-fiber diet.

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