GEORGE BROWN PRESS
JOURNALS, BOOKS & PROCEEDINGS

Journal of Medicine
and Life Sciences

Article

Restoring Glycemic Control in Type 2 Diabetes through Fiber-Induced Microbial Remodeling

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Abstract: Dietary composition plays a vital role in the intervention and management of chronic metabolic diseases. This study evaluated the effects of a high-fiber diet on gut microbiota and glucose regulation in patients with type 2 diabetes through a rigorously designed clinical intervention trial. Participants in the intervention group followed a personalized high-fiber diet continuously for 12 weeks. The results showed a 16.8% reduction in fasting blood glucose and a 1.4% decrease in glycated hemoglobin (HbA1c). Additionally, the relative abundance of beneficial gut bacteria, such as *Bifidobacterium*, significantly increased. These findings indicate that a high-fiber diet can improve glucose metabolism by altering the composition of the gut microbiota. The study provides solid scientific evidence to support the refinement of nutritional strategies for diabetes management.

Keywords: type 2 diabetes; dietary intervention; gut microbiota; glucose homeostasis; chronic disease management

Received: 18 March 2025
Revised: 25 March 2025
Accepted: 19 April 2025
Published: 21 April 2025

1. Introduction

Type 2 diabetes mellitus (T2DM) is a widespread chronic metabolic disease that poses a serious threat to global public health [1]. According to the 2024 report by the International Diabetes Federation (IDF), approximately 578 million adults worldwide are living with diabetes, and this number is expected to increase to 783 million by 2045. More than 90% of these individuals are diagnosed with T2DM [2]. Data from national epidemiological surveys in China also reflect a concerning trend [3]. The Guidelines for the Prevention and Treatment of type 2 Diabetes in China (2023 edition) state that the prevalence of diabetes among Chinese adults has reached 12.8%, with over 140 million cases, and this number continues to rise [4]. Lifestyle changes and an aging population further contribute to the growing risk [5]. A five-year prospective cohort study in Chinese communities found that for every 10-year increase in age, the incidence of T2DM rose by 48%. The pathogenesis of T2DM involves a combination of genetic, environmental, and behavioral factors, with insulin resistance and pancreatic β-cell dysfunction being the core features [6]. Persistent hyperglycemia can lead to serious chronic complications, including cardiovascular disease, diabetic nephropathy, retinopathy and neuropathy [7]. These complications significantly affect cc health and quality of life while placing a heavy burden on healthcare systems [8]. Evidence from the UK Prospective Diabetes Study (UKPDS) showed that a 1% reduction in glycated hemoglobin (HbA1c) could lower the risk of microvascular complications by about 35% [9]. In China, studies have found that complications account for more than 70% of the total healthcare costs for individuals with diabetes [10]. Standard treatments for T2DM include medication, exercise, and dietary management. However, drug therapies are often associated with side effects, and their efficacy may diminish over time. Exercise can be effective but is difficult to maintain for patients with limited mobility or poor adherence. Dietary management, therefore, plays a fundamental and irreplaceable role in T2DM care. A balanced diet can help regulate blood glucose, improve insulin sensitivity and reduce cardiovascular risk [11]. A meta-analysis of ten randomized controlled trials found that dietary intervention could reduce HbA1c levels by 0.5% to 1.0% in patients with T2DM. In recent years, increasing research has focused on the role of gut microbiota in the development of T2DM. As the largest microbial ecosystem in the body, the gut microbiota plays a crucial role in nutrient metabolism, immune regulation and intestinal barrier function. In patients with T2DM, the composition and function of the gut microbiota are often disrupted, marked by a decrease in beneficial bacteria and an increase in harmful strains. This imbalance may impair the intestinal barrier, induce inflammation, and alter metabolic outputs, further worsening insulin resistance and glucose dysregulation [12,13]. A meta-analysis of genome-wide association studies (GWAS) from the MiBioGen consortium and the Dutch Microbiome Project (DMP) found that higher relative abundance of Prevotellaceae (odds ratio, OR = 1.0704) and Prevotella (OR = 1.0874) was linked to increased T2DM risk. Other studies have shown that the abundance of *Bifidobacterium* in T2DM patients was 30%–50% lower than in healthy individuals [14]. These findings support gut microbiota modulation as a promising target in T2DM treatment. Dietary fiber, a type of carbohydrate that cannot be digested by human enzymes, plays a key role in maintaining intestinal health. High-fiber diets can improve gut function by promoting motility, increasing stool volume, and lowering pH, thereby supporting the growth and metabolism of beneficial bacteria [15,16]. Existing studies have confirmed that high-fiber diets can alter the composition of the gut microbiota, increase the production of short-chain fatty acids (SCFAs) and improve overall metabolic function [17]. However, the mechanisms by which high-fiber diets regulate gut microbiota and glucose homeostasis in patients with T2DM remain incompletely understood. Further research in this area is essential for advancing both theoretical understanding and clinical application of dietary strategies in T2DM management [18].

International studies have provided substantial evidence supporting a close relationship between gut microbiota and type 2 diabetes mellitus (T2DM) [19]. Cross-sectional analyses using high-throughput sequencing technologies have shown that T2DM patients exhibit altered ratios of *Firmicutes* to *Bacteroidetes*, accompanied by reduced abundance of beneficial genera such as *Bifidobacterium* and *Akkermansia*, and increased levels of potentially harmful genera like *Escherichia* and *Enterococcus* [20]. In animal studies, transplanting gut microbiota from T2DM patients into germ-free mice has been shown to induce insulin resistance and glucose metabolism disorders, offering strong support for a causal role of gut microbiota in T2DM pathogenesis [21]. Research on the impact of high-fiber diets on gut microbiota and T2DM has also advanced internationally. In some intervention studies, T2DM patients received high-fiber foods or dietary fiber supplements, which led to increases in beneficial microbes, such as *Bifidobacterium* and *Lactobacillus*, along with improvements in metabolic markers like glycated hemoglobin (HbA1c) and fasting plasma glucose (FPG) [22]. For example, a randomized controlled trial administering 20 grams of inulin daily for 12 weeks reported a twofold increase in *Bifidobacterium* abundance and a 0.5% reduction in HbA1c [23]. Other studies have suggested that high-fiber diets may regulate hepatic glucose metabolism by modulating the production of short-chain fatty acids (SCFAs), thereby helping to maintain glucose homeostasis [24].

In China, research in this area is also expanding. A study by Zhao Liping's team at Shanghai Jiao Tong University showed that high-complexity dietary fibers can selectively enrich specific SCFA-producing bacteria in the gut, and that the abundance and diversity of these bacteria are positively correlated with improvements in HbA1c among T2DM patients. Their findings suggest that restoring such microbial populations through nutritional intervention could offer a new ecological strategy for diabetes prevention and control. Meanwhile, research led by Professor Wang Weiqing at Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, indicated that the clinical efficacy of *Akkermansia* *muciniphila* (AKK) in weight and glucose reduction depends largely on the baseline abundance of this species. Only patients with low baseline AKK levels showed measurable metabolic benefits. Other domestic studies have examined the effects of different types of dietary fiber — such as soluble and insoluble fiber — on gut microbiota composition and metabolic indicators in T2DM patients [25]. These findings have added theoretical support for applying dietary fiber in diabetes care. One study on Chinese T2DM patients found that soluble fiber intake reduced fasting glucose by 1.2 mmol/L and increased the relative abundance of beneficial bacteria by 15% to 20% [26]. Despite the progress achieved both globally and in China, several challenges remain in this field. Significant variation exists among studies in terms of fiber type, dosage, and intervention duration, limiting the comparability of results. The causal pathways and specific mechanisms linking gut microbiota to T2DM have not been fully clarified. Moreover, the molecular basis by which high-fiber diets regulate gut microbiota to improve glucose homeostasis remains to be further investigated. In conclusion, the prevalence of type 2 diabetes continues to increase, as demonstrated by IDF statistics and domestic epidemiological surveys, and it has become a major global health issue [27]. Traditional treatment approaches have certain limitations, while the gut microbiota plays a critical role in the disease's pathogenesis. Variations in the relative abundance of different microbial groups are closely linked to disease onset. Although some progress has been made in research on high-fiber dietary interventions, notable differences exist across studies in terms of intervention components. Under these circumstances, the present study focuses on the effects of high-fiber diets on gut microbiota and glucose homeostasis in patients with type 2 diabetes. It aims to address existing gaps in research and provide more targeted and accurate nutritional strategies for clinical practice, with the goal of improving patient quality of life and easing the burden on healthcare systems.

2. Materials and Methods

This study enrolled 80 patients who met the diagnostic criteria for type 2 diabetes mellitus (T2DM) established by the World Health Organization (WHO) in 1999. The patients were between 45 and 65 years old, with a disease duration of 3 to 10 years. Exclusion criteria included: diagnosis of type 1 diabetes; use of antibiotics, probiotics, or prebiotics within the past three months; presence of severe hepatic or renal dysfunction, malignancy, gastrointestinal disorders, or other serious chronic conditions; and pregnancy or lactation. All participants signed informed consent before the study began. A randomized controlled trial was conducted. Participants were randomly assigned to an intervention group or a control group, with 40 patients in each group. The control group received standard dietary counseling for diabetes, based on the 2013 guidelines from the Chinese Diabetes Society. This included a daily energy intake of 50%-65% from carbohydrates, 20%-30% from fats, and 15%-20% from proteins, with balanced distribution across three meals. The intervention group followed a personalized high-fiber diet in addition to the standard regimen. Fiber intake was adjusted individually based on body weight and physical activity level, aiming for a total daily intake of 30 g, with a soluble to insoluble fiber ratio of approximately 1:2. The diet plans were developed by registered dietitians and emphasized increased intake of whole grains (such as oats, brown rice, whole wheat bread), vegetables (including broccoli, spinach, carrots), fruits (such as apples, bananas, oranges), and legumes (such as black beans, red beans, mung beans). The intervention lasted 12 weeks.

To ensure adherence, the intervention group received individual dietary counseling before the trial, conducted by trained dietitians. Guidance included food selection, preparation methods and strategies to meet nutritional needs while increasing fiber intake. Each participant was given a detailed food diary to record the type, quantity, and preparation method of all foods consumed each day. Dietitians reviewed the records weekly, provided personalized feedback, corrected dietary issues and adjusted the diet plans when necessary. Nutrition education sessions were held regularly during the intervention period to improve participants' understanding of dietary fiber and to support compliance [28]. Fasting blood and stool samples were collected from both groups at baseline and after 12 weeks of intervention. Fasting venous blood was used to measure fasting plasma glucose (FPG), glycated hemoglobin (HbA1c), and fasting insulin (FINS). These were analyzed using an automated biochemical analyzer. The homeostasis model assessment of insulin resistance (HOMA-IR) was calculated as: HOMA-IR = FPG × FINS / 22.5 Stool samples were used for gut microbiota analysis. High-throughput 16S rRNA gene sequencing was used to evaluate bacterial composition and relative abundance at the genus level. Concentrations of short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate, were measured using gas chromatography.

Statistical analyses were performed using SPSS 22.0. Continuous data were expressed as mean ± standard deviation ($\overline{X} \pm s$). Within-group comparisons before and after the intervention were performed using paired t-tests, while between-group comparisons used independent-sample t-tests [29]. Categorical data were expressed as percentages and compared using the chi-square (χ^2) test. A *p*-value < 0.05 was considered statistically significant. Pearson correlation analysis was used to assess the relationships between bacterial abundance, blood glucose indicators, and short-chain fatty acid (SCFA) levels.

3. Results and Discussion

3.1. Effects of a High-Fiber Diet on Glycemic Indicators in Patients with Type 2 Diabetes

After the 12-week intervention, the mean fasting plasma glucose (FPG) level in the intervention group ($n = 40$) decreased from 9.5 ± 1.2 mmol/L at baseline to 7.9 ± 1.0 mmol/L, representing a 16.8% reduction. Paired t-test analysis confirmed that this change was statistically significant ($p < 0.05$). Glycated hemoglobin (HbA1c) levels also declined, from a baseline mean of 7.8 ± 0.6% to 6.7 ± 0.5%, corresponding to an absolute reduction of 1.4%, which was likewise statistically significant ($p < 0.05$). In contrast, patients in the control group ($n = 40$) showed only minor fluctuations in FPG and HbA1c levels before and after the intervention. Independent-sample t-tests revealed no statistically significant differences either within or between groups ($p > 0.05$). These findings indicate that high-fiber dietary intervention significantly improves blood glucose regulation in individuals with type 2 diabetes. The reduction in both FPG and HbA1c suggests improved glycemic control and better maintenance of glucose homeostasis. Compared with previous studies, the improvements observed in this trial were more substantial. For example, one overseas study involving inulin supplementation reported only a 0.5% decrease in HbA1c, whereas the present study achieved a 1.4% reduction (Table 1).

Table 1. Effects of High-Fiber Dietary Intervention on FPG and HbA1c in Patients with Type 2 Diabetes.

Group	Sample Size	FPG Before (mmol/L)	FPG After (mmol/L)	FPG Reduction (%)	HbA1c Before (%)	HbA1c After (%)	HbA1c Reduction (%)	*P*-value (FPG)	*P*-value (HbA1c)
Intervention Group	40	9.5 ± 1.2	7.9 ± 1.0	16.8	7.8 ± 0.6	6.7 ± 0.5	1.4	< 0.05	< 0.05
Control Group	40	9.3 ± 1.1	9.1 ± 1.0	2.2	7.7 ± 0.5	7.6 ± 0.5	1.3	> 0.05	> 0.05

In the experimental group, after receiving the high-fiber dietary intervention, the insulin resistance index (HOMA-IR) decreased from a mean value of 3.8 ± 0.8 before the intervention to 2.6 ± 0.6. A paired *t*-test showed that the difference was statistically significant ($p < 0.05$). This result indicates that the high-fiber dietary intervention can effectively relieve insulin resistance in patients with type 2 diabetes. In the control group, there was no significant change in HOMA-IR before and after the intervention ($p > 0.05$). As insulin resistance is one of the key pathological mechanisms in the onset of type 2 diabetes, a high-fiber diet helps improve insulin sensitivity. It promotes glucose uptake and utilization in peripheral tissues and contributes to lowering blood glucose levels. Previous studies have shown that after insulin resistance is improved, the body's glucose uptake capacity can increase by 20% to 30% [30]. In this study, the effect of the high-fiber diet in improving insulin resistance may further support positive development in glucose metabolism among patients (Table 2).

Table 2. Effect of High-Fiber Dietary Intervention on HOMA-IR in Patients with Type 2 Diabetes.

Group	Number of Cases	HOMA-IR Before Intervention (mean ± SD)	HOMA-IR After Intervention (mean ± SD)	*p* Value
Experimental Group	40	3.8 ± 0.8	2.6 ± 0.6	<0.05
Control Group	40	3.7 ± 0.7	3.6 ± 0.7	>0.05

3.2. Effects of High-Fiber Diet on the Structure of Gut Microbiota

Based on the analysis results from high-throughput 16S rRNA gene sequencing, the Shannon diversity index of gut microbiota in the experimental group ($n = 40$) increased from a mean of 3.2 ± 0.3 before the 12-week high-fiber dietary intervention to 3.6 ± 0.3 after the intervention. According to the paired *t*-test, the difference within the group was statistically significant ($p < 0.05$). This clearly shows that a high-fiber diet can significantly increase gut microbial diversity. In the control group, there was no significant change in the Shannon index before and after the intervention ($p > 0.05$). An increase in microbial diversity helps maintain the stability of the gut micro-ecosystem and strengthens the intestinal barrier [31]. This is important for maintaining gut health. Related studies have shown that a 10%–15% increase in microbial diversity can enhance the function of the intestinal barrier by around 20%. In this study, the increase in microbial diversity in the experimental group has positive implications for gut health (Table 3).

Table 3. Comparison of Shannon Diversity Index Before and After High-Fiber Diet in Experimental and Control Groups.

Group	Number of Cases	Shannon Index Before Intervention (mean ± SD)	Shannon Index After Intervention (mean ± SD)	*p* Value
Experimental Group	40	3.2 ± 0.3	3.6 ± 0.3	<0.05
Control Group	40	3.1 ± 0.3	3.2 ± 0.3	>0.05

At the genus level, the relative abundance of *Bifidobacterium* in the gut of patients in the experimental group increased significantly from a mean of 5.2 ± 1.0% before the intervention to 8.5 ± 1.2% after the intervention. The difference was statistically significant according to a paired *t*-test ($p < 0.05$). *Bifidobacterium* is an important type of probiotic. It plays a key role in regulating gut immunity, suppressing the growth of harmful bacteria, and promoting intestinal movement. Meanwhile, the relative abundance of *Escherichia* in the experimental group decreased from 12.5 ± 1.5% before the intervention to 9.0 ± 1.3% after the intervention. This change was also statistically significant ($p < 0.05$). Some strains of *Escherichia* can produce endotoxins, damage the intestinal barrier and trigger inflammatory responses. These effects are closely linked to the development of insulin resistance and type 2 diabetes. In the control group, there were no significant changes in the relative abundance of *Bifidobacterium* or *Escherichia* before and after the intervention ($p > 0.05$). These results clearly indicate that a high-fiber diet can selectively promote the growth of beneficial bacteria and suppress harmful bacteria. This leads to a marked improvement in the structure of the gut microbiota. Compared with previous studies, the increase in the relative abundance of *Bifidobacterium* in this study is more noticeable [32,33]. For instance, one domestic study showed that soluble dietary fiber increased the abundance of beneficial bacteria by 15%–20%, while in this study, the increase in *Bifidobacterium* exceeded that range (Table 4).

Table 4. Relative Abundance of Key Gut Bacteria Before and After High-Fiber Intervention.

Group	Number of Cases	Relative Abundance of *Bifidobacterium* Before (%)	Post-treatment Relative Abundance of *Bifidobacterium* (%)	Pre-treatment Relative Abundance of *Escherichia* (%)	Post-treatment Relative Abundance of *Escherichia* (%)	*p* Value (*Bifidobacterium*)	*p* Value (*Escherichia*)
Experimental Group	40	5.2 ± 1.0	8.5 ± 1.2	12.5 ± 1.5	9.0 ± 1.3	<0.05	<0.05
Control Group	40	5.1 ± 1.1	5.3 ± 1.0	12.3 ± 1.4	12.0 ± 1.5	>0.05	>0.05

3.3. Correlation Analysis Between Changes in Gut Microbiota and Glucose Homeostasis

After processing the data using Pearson correlation analysis, it was found that in the experimental group, the relative abundance of *Bifidobacterium* in the gut was significantly negatively correlated with FPG ($r = -0.65$, $p < 0.05$), HbA1c ($r = -0.62$, $p < 0.05$) and HOMA-IR ($r = -0.68$, $p < 0.05$). In other words, as the relative abundance of *Bifidobacterium* increased, patients' fasting blood glucose, glycated hemoglobin, and insulin resistance index all decreased significantly [31,32]. At the same time, the relative abundance of *Escherichia* showed significant positive correlations with FPG ($r = 0.58$, $p < 0.05$), HbA1c ($r = 0.55$, $p < 0.05$) and HOMA-IR ($r = 0.60$, $p < 0.05$). This indicates that the higher the relative abundance of *Escherichia*, the worse the patients' glycemic control and the more severe the insulin resistance [33]. These findings further confirm that changes in gut microbiota composition are closely linked to glucose homeostasis in patients with type 2 diabetes. A high-fiber diet can regulate gut microbiota by increasing the relative abundance of beneficial bacteria and reducing that of harmful bacteria [34]. This can positively influence glucose metabolism and help maintain blood glucose balance. The correlation results of this study are highly consistent with the conclusions of several related studies both in China and abroad. This further supports the reliability and scientific basis of the present findings.

4. Conclusion

This study provides clear evidence that a high-fiber diet brings meaningful improvements to patients with type 2 diabetes. After the 12-week intervention, participants in the dietary fiber group showed lower fasting blood glucose and HbA1c levels, as well as better insulin sensitivity. These changes suggest that dietary fiber plays a helpful role in supporting blood sugar control. In addition to metabolic improvements, the intervention also had a positive effect on the gut microbiota. The increase in beneficial bacteria such as *Bifidobacterium* and the decline in *Escherichia* point to a healthier microbial environment. A more diverse and balanced gut microbiome may be one of the key reasons why patients experienced better metabolic outcomes. From a practical perspective, this research supports the use of dietary fiber as part of daily care for people with type 2 diabetes. Whole grains, fruits, vegetables, and legumes should be included regularly in meals, with attention to preparation methods and fiber distribution across the day. Clinical teams can use simple tools to assess nutrition and follow up on progress. Tracking changes in gut bacteria over time may also help tailor dietary plans and improve long-term results.

References

1. Y. Zheng, S. H. Ley, and F. B. Hu, "Global aetiology and epidemiology of type 2 diabetes mellitus and its complications," *Nat. Rev. Endocrinol.*, vol. 14, no. 2, pp. 88-98, 2018, doi: 10.1021/ar3001525.
2. H. Wang, G. Zhang, Y. Zhao, F. Lai, W. Cui, J. Xue, et al., "Rpf-eld: Regional prior fusion using early and late distillation for breast cancer recognition in ultrasound images," in *Proc. 2024 IEEE Int. Conf. Bioinformatics Biomedicine (BIBM)*, Dec. 2024, pp. 2605-2612, doi: 10.1109/BIBM62325.2024.10821972.
3. H. Qiu, S. Cao, and R. Xu, "Cancer incidence, mortality, and burden in China: a time-trend analysis and comparison with the United States and United Kingdom based on the global epidemiological data released in 2020," *Cancer Commun.*, vol. 41, no. 10, pp. 1037-1048, 2021, doi: 10.1002/cac2.12197.
4. J. Yin, X. Wu, and X. Liu, "Multi-class classification of breast cancer gene expression using PCA and XGBoost," in *Proc. 4th Int. Conf. Biol. Eng. Med. Sci.*, 2024, doi: 10.20944/preprints202410.1775.v1.
5. L. Wang, et al., "Prevalence and treatment of diabetes in China, 2013-2018," *JAMA*, vol. 326, no. 24, pp. 2498-2506, 2021, doi:10.1001/jama.2021.22208.
6. Y. Wang, Y. Wen, X. Wu, L. Wang, and H. Cai, "Assessing the Role of Adaptive Digital Platforms in Personalized Nutrition and Chronic Disease Management," *World J. Innov. Mod. Technol.*, vol. 8, no. 1, 2025, doi: 10.53469/wjimt.2025.08(01).05.
7. M. Lotfy, J. Adeghate, H. Kalasz, J. Singh, and E. Adeghate, "Chronic complications of diabetes mellitus: a mini review," *Curr. Diabetes Rev.*, vol. 13, no. 1, pp. 3-10, 2017, doi: 10.2174/1573399812666151016101622.
8. X. Shi, Y. Tao, and S. C. Lin, "Deep neural network-based prediction of B-cell epitopes for SARS-CoV and SARS-CoV-2: Enhancing vaccine design through machine learning," in *Proc. 2024 4th Int. Signal Process., Communications Eng. Manag. Conf. (ISPCEM)*, Nov. 2024, pp. 259-263, doi: 10.1109/ISPCEM64498.2024.00050.
9. M. Lind, H. Imberg, R. L. Coleman, O. Nerman, and R. R. Holman, "Historical HbA1c values may explain the type 2 diabetes legacy effect: UKPDS 88," *Diabetes Care*, vol. 44, no. 10, pp. 2231-2237, 2021, doi: 10.2337/dc20-2439.
10. Y. Wang, Y. Wen, X. Wu, and H. Cai, "Comprehensive Evaluation of GLP1 Receptor Agonists in Modulating Inflammatory Pathways and Gut Microbiota," *World J. Innov. Mod. Technol.*, vol. 7, no. 5, 2024, doi: 10.53469/wjimt.2024.07(06).23.
11. J. Nadhiya, M. K. Vijayalakshmi, and S. Showbharnikhaa, "A brief review on diabetes mellitus," *J. Pharma Insights Res.*, vol. 2, no. 1, pp. 117–121, 2024, doi: 10.5281/zenodo.10631511.
12. W. Bielka, A. Przezak, and A. Pawlik, "The role of the gut microbiota in the pathogenesis of diabetes," *Int. J. Mol. Sci.*, vol. 23, no. 1, p. 480, 2022, doi: 10.3390/ijms23010480.
13. T. Zhang, B. Zhang, F. Zhao, and S. Zhang, "COVID-19 localization and recognition on chest radiographs based on Yolov5 and EfficientNet," in *Proc. 2022 7th Int. Conf. Intell. Comput. Signal Process. (ICSP)*, Apr. 2022, pp. 1827–1830, doi: 10.1109/ICSP54964.2022.9778327.
14. M. Sedighi, et al. "Comparison of gut microbiota in adult patients with type 2 diabetes and healthy individuals," *Microb. Pathog.*, vol. 111, pp. 362–369, 2017, doi: 10.1016/j.micpath.2017.08.038.
15. H. Ziang, J. Zhang, and L. Li, "Framework for lung CT image segmentation based on UNet++," *arXiv preprint*, arXiv:2501.02428, 2025, doi: 10.48550/arXiv.2501.02428.
16. V. Vinelli, et al., "Effects of dietary fibers on short-chain fatty acids and gut microbiota composition in healthy adults: a systematic review," *Nutrients*, vol. 14, no. 13, p. 2559, 2022, doi: 10.3390/nu14132559.
17. Y. Deng, W. Cui, and X. Liu, "Head Tumor Segmentation and Detection Based on ResUNet," in *Proc. 5th Int. Conf. Signal Process. Mach. Learn.*, 2024, doi: 10.54254/2755-2721/99/20251810.
18. K. H. Allin, T. Nielsen, and O. Pedersen, "Mechanisms in endocrinology: gut microbiota in patients with type 2 diabetes mellitus," *Eur. J. Endocrinol.*, vol. 172, no. 4, pp. R167–R177, 2015, doi: 10.1530/EJE-14-0874.
19. H. Wang, Y. Wen, X. Wu, L. Wang, and H. Cai, "Modulation of Gut Microbiota and Glucose Homeostasis through High-Fiber Dietary Intervention in Type 2 Diabetes Management," *World J. Innov. Mod. Technol.*, vol. 7, no. 5, 2024, doi: 10.53469/wjimt.2024.07(06).04.
20. J. B. Qiao, et al., "Vitamin A-decorated biocompatible micelles for chemogene therapy of liver fibrosis," *J. Control. Release*, vol. 283, pp. 113–125, 2018, doi: 10.1016/j.jconrel.2018.05.032.
21. E. Bezirtzoglou, et al., "Maintaining digestive health in diabetes: the role of the gut microbiome and the challenge of functional foods," *Microorganisms*, vol. 9, no. 3, p. 516, 2021, doi: 10.3390/microorganisms9030516.
22. Y. Wang, L. Wang, Y. Wen, X. Wu, and H. Cai, "Precision-Engineered Nanocarriers for Targeted Treatment of Liver Fibrosis and Vascular Disorders," *World J. Innov. Mod. Technol.*, vol. 8, no. 1, 2025, doi: 10.53469/wjimt.2025.08(01).07.
23. G. Qu, et al., "Self-assembled micelles based on N-octyl-N'-phthalyl-O-phosphoryl chitosan derivative as an effective oral carrier of paclitaxel," *Carbohydr. Polym.*, vol. 207, pp. 428–439, 2019, doi: 10.1016/j.carbpol.2018.11.099.

24. A. E. Juhasz, et al., "Galactomannans are the most effective soluble dietary fibers in type 2 diabetes: a systematic review and network meta-analysis," *Am. J. Clin. Nutr.*, vol. 117, no. 2, pp. 266–277, 2023, doi: 10.1016/j.ajcnut.2022.12.015.
25. J. Zhu, et al., "Multimodal nanoimmunotherapy engages neutrophils to eliminate Staphylococcus aureus infections," *Nat. Nanotechnol.*, pp. 1–12, 2024, doi: 10.1038/s41565-024-01648-8.
26. Y. Wen, X. Wu, L. Wang, H. Cai, and Y. Wang, "Application of Nanocarrier-Based Targeted Drug Delivery in the Treatment of Liver Fibrosis and Vascular Diseases," *J. Med. Life Sci.*, vol. 1, no. 2, pp. 63–69, 2025, doi: 10.71222/bc9c9s73.
27. J. Chen, J. He, R. P. Wildman, K. Reynolds, R. H. Streiffer, and P. K. Whelton, "A randomized controlled trial of dietary fiber intake on serum lipids," *Eur. J. Clin. Nutr.*, vol. 60, no. 1, pp. 62–68, 2006, doi: 10.1038/sj.ejcn.1602268.
28. I. K. Lee, R. Xie, A. Luz-Madrigal, S. Min, J. Zhu, J. Jin, *et al.*, "Micromolded honeycomb scaffold design to support the generation of a bilayered RPE and photoreceptor cell construct," *Bioact. Mater.*, vol. 30, pp. 142–153, 2023, doi: 10.1016/j.bioactmat.2023.07.019.
29. N. Yodsanit, et al., "Targeted PERK inhibition with biomimetic nanoclusters confers preventative and interventional benefits to elastase-induced abdominal aortic aneurysms," *Bioact. Mater.*, vol. 26, pp. 52–63, 2023, doi: 10.1016/j.bioactmat.2023.02.009.
30. M. H. Bhat, Y. A. Hajam, Neelam, R. Kumar, and Diksha, "Microbial Diversity and Their Role in Human Health and Diseases," in *Role of Microbes in Sustainable Development: Human Health and Diseases*, Singapore: Springer Nature Singapore, 2023, pp. 1–33. ISBN: 9789819931262.
31. Y. Wang, Y. Wen, X. Wu, and H. Cai, "Application of Ultrasonic Treatment to Enhance Antioxidant Activity in Leafy Vegetables," *Int. J. Adv. Appl. Sci. Res.*, vol. 3, pp. 49–58, 2024, doi: 10.5281/zenodo.14275691.
32. C. Chaiyasut, et al., "Influence of *Bifidobacterium* breve on the glycaemic control, lipid profile and microbiome of type 2 diabetic subjects: a preliminary randomized clinical trial," *Pharmaceuticals*, vol. 16, no. 5, p. 695, 2023, doi: 10.3390/ph16050695.
33. Y. Wang, M. Shen, L. Wang, Y. Wen, and H. Cai, "Comparative Modulation of Immune Responses and Inflammation by n-6 and n-3 Polyunsaturated Fatty Acids in Oxylipin-Mediated Pathways," *World J. Innov. Mod. Technol.*, vol. 7, no. 4, 2024, doi: 10.53469/wjimt.2024.07(05).17.
34. F. Z. Marques, et al., "High-fiber diet and acetate supplementation change the gut microbiota and prevent the development of hypertension and heart failure in hypertensive mice," *Circulation*, vol. 135, no. 10, pp. 964–977, 2017, doi: 10.1161/CIRCULATIONAHA.116.024545.