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Article

The Effects of Soluble Dietary Fiber Intervention on Gut Microbiota Diversity and Short-Chain Fatty Acid Production in Diabetic Patients

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Abstract: This study explored how soluble fiber affects gut bacteria and blood sugar in adults with type 2 diabetes. Eighty participants were randomly divided into an inulin group (15 g/day) and a control group for 12 weeks. Gut bacterial diversity and short-chain fatty acids (SCFAs) were tested using 16S rRNA sequencing and gas chromatography. The inulin group showed a 28% rise in Shannon index and higher levels of Bifidobacterium and Faecalibacterium compared with the start of the study. Fecal butyrate and propionate increased by 49% and 35%, while HbA1c fell by 1.2 ± 0.3%. Blood C-reactive protein dropped by about 22%. These findings show that inulin may help lower blood sugar by increasing helpful gut bacteria and their fermentation products. The study supports the use of soluble fiber as a simple and safe way to aid blood sugar control in type 2 diabetes.

Keywords: inulin; soluble fiber; gut bacteria; short-chain fatty acids; HbA1c; inflammation; type 2 diabetes

1. Introduction

Type 2 diabetes mellitus (T2DM) is a multifactorial metabolic disorder characterized by chronic low-grade inflammation, insulin resistance, and gut microbiota dysbiosis [1,2]. Individuals with T2DM commonly exhibit reduced microbial diversity and lower production of short-chain fatty acids (SCFAs), both of which are associated with impaired glucose regulation and weakened intestinal barrier integrity [3]. Growing evidence highlights the gut-metabolism axis as a key pathway influencing systemic insulin sensitivity and inflammation [4]. Dietary interventions that modify microbial composition-such as fiber supplementation or low-carbohydrate diets-have shown potential to restore metabolic balance, reduce inflammation, and improve glycemic outcomes [5]. Recent nutritional reviews suggest that such interventions, including ketogenic diets and high-fiber regimens, may complement pharmacological approaches by promoting beneficial microbial fermentation and enhancing glucose homeostasis [6].

Among dietary fibers, inulin-type fructans are particularly effective in modulating intestinal fermentation. As a soluble prebiotic fiber, inulin resists digestion in the upper gastrointestinal tract and undergoes fermentation in the colon to produce acetate, propionate, and butyrate [7]. These SCFAs act as signaling molecules through G-protein-coupled receptors (GPR41 and GPR43), stimulating the secretion of incretin hormones such as GLP-1 and PYY, thereby improving both insulin sensitivity and gut barrier function [8]. Butyrate, in particular, serves as a primary energy source for colonocytes and

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enhances tight-junction integrity by upregulating ZO-1 and occludin [9,10]. Clinical trials have reported reductions in HbA1c and fasting glucose following inulin supplementation, though the magnitude of improvement varies depending on fiber type, dosage, and baseline microbiota composition [11]. Furthermore, several studies observed increases in Bifidobacterium and Faecalibacterium abundance and greater Shannon diversity after inulin intake, yet findings remain inconsistent due to small sample sizes, limited intervention duration, and lack of dietary standardization [12]. Despite these advances, several methodological challenges remain. Many clinical studies rely solely on 16S rRNA sequencing, which provides relative abundance rather than absolute bacterial counts or strain-level resolution [13]. SCFA quantification is often performed at single time points, neglecting circadian and dietary variability that affect metabolite levels [14]. Inadequate adherence tracking and missing dietary background records further reduce data reliability [15]. Moreover, most existing studies analyze microbial composition or glycemic markers separately, rather than investigating how fermentation-derived metabolites mediate glucose regulation [16]. Thus, the causal link between microbial metabolism, SCFA production, and glycemic improvement remains only partially understood [17].

The study conducted a 12-week randomized intervention in adults with T2DM using a fixed daily dose of inulin under standardized sampling and dietary control. We evaluated changes in gut microbiota diversity, SCFA concentrations, and glycemic indicators (HbA1c, fasting glucose). Particular focus was placed on Bifidobacterium, Faecalibacterium, and Clostridium-key butyrate-producing genera-and on the relationship between microbial activity and systemic glucose metabolism. By integrating microbial, metabolic, and clinical data, this work aims to determine whether inulin supplementation enhances beneficial bacterial growth and SCFA-mediated glucose regulation. The study contributes new mechanistic insight into how soluble dietary fiber modulates host metabolism through microbial fermentation, advancing the development of precision nutrition strategies for T2DM management.

2. Materials and Methods

2.1. Participants and Study Area

Eighty adults with type 2 diabetes mellitus (T2DM) were recruited from Zhejiang University Affiliated Hospital between March and June 2024. Participants were 40-70 years old and had HbA1c levels between 7.0% and 10.0%. All had stable medication use for at least three months before the study. Exclusion criteria included antibiotic use, intestinal surgery, chronic liver or kidney disease, or probiotic intake during the last month. The study followed the Declaration of Helsinki and was approved by the hospital ethics board (Approval No. ZJU-2024-T2DM015). Each participant gave written consent before enrollment.

2.2. Intervention Design and Group Setting

Subjects were randomly divided into two equal groups. The intervention group received 15 g/day of inulin powder, divided into two doses after meals, for 12 weeks. The control group received the same amount of maltodextrin. Participants were advised to keep their usual diet and physical activity. They were asked not to take other fiber or probiotic supplements during the study. Compliance was checked every two weeks through phone follow-ups and by counting unused sachets. Stool and blood samples were collected at baseline and at week 12 after an overnight fast.

2.3. Measurement Methods and Quality Control

Fasting blood glucose and HbA1c were measured on an automatic analyzer (Hitachi 7600, Japan). Stool samples were collected in sterile tubes, frozen immediately at −80 °C, and later tested for microbiota and short-chain fatty acids (SCFAs). Bacterial DNA was extracted using a stool DNA kit (Qiagen, Germany). The V3-V4 region of the 16S rRNA gene was amplified and sequenced on an Illumina MiSeq platform. Clean reads were

classified by QIIME2 software to identify bacterial taxa and calculate the Shannon index. SCFAs (acetate, propionate, and butyrate) were measured by gas chromatography (Agilent 7890B, USA). For quality control, all samples were tested twice, and only results with less than 10% difference were accepted. Blank and standard samples were included in each batch to check consistency.

2.4. Data Processing and Statistical Formulas

All statistical tests were performed in SPSS version 26.0 (IBM, USA). Continuous variables were shown as mean ± standard deviation (SD). Within-group changes were tested by paired t-test, and group differences were tested by independent t-test. A simple regression model was used to describe the relation between SCFA level and HbA1c change:

$$HbA1c_{post} = \alpha + \beta \times SCFA_{change} + \varepsilon$$

where $HbA1c_{post}$ is the HbA1c value after 12 weeks, $SCFA_{change}$ is the change in total SCFAs, and ε is the random error term [18].

The evenness of gut microbial species (E) was estimated as:

$$E = \frac{H'}{\ln(S)}$$

where H' is the Shannon index, and SSS is the total number of observed species. A P-value below 0.05 was considered statistically significant.

2.5. Ethical Standards and Data Reliability

The research protocol was reviewed and approved by the ethics committee of Zhejiang University Affiliated Hospital. All participants gave written consent before participation. Data were entered and checked by two independent researchers. Missing data were replaced using the mean substitution method to avoid bias. All laboratory steps followed standard procedures. Raw sequence data were uploaded to the NCBI Sequence Read Archive (Accession No. PRJNA1056213). The study was carried out under controlled conditions to ensure reliable and repeatable results.

3. Results and Discussion

3.1. Gut Microbial Diversity and Taxonomic Changes

After 12 weeks, participants in the inulin group showed a clear increase in microbial diversity (Figure 1). The Shannon index rose by about 28%, while no major change appeared in the control group. Bifidobacterium and Faecalibacterium levels increased, and Ruminococcus slightly decreased. These patterns suggest that inulin favored acid-producing bacteria and improved microbial balance. Similar effects were found in clinical trials reporting that inulin raised Bifidobacterium abundance and reduced gut inflammation in adults with metabolic disorders [19]. This trend matches the gut community response to fermentable fibers seen in controlled studies.

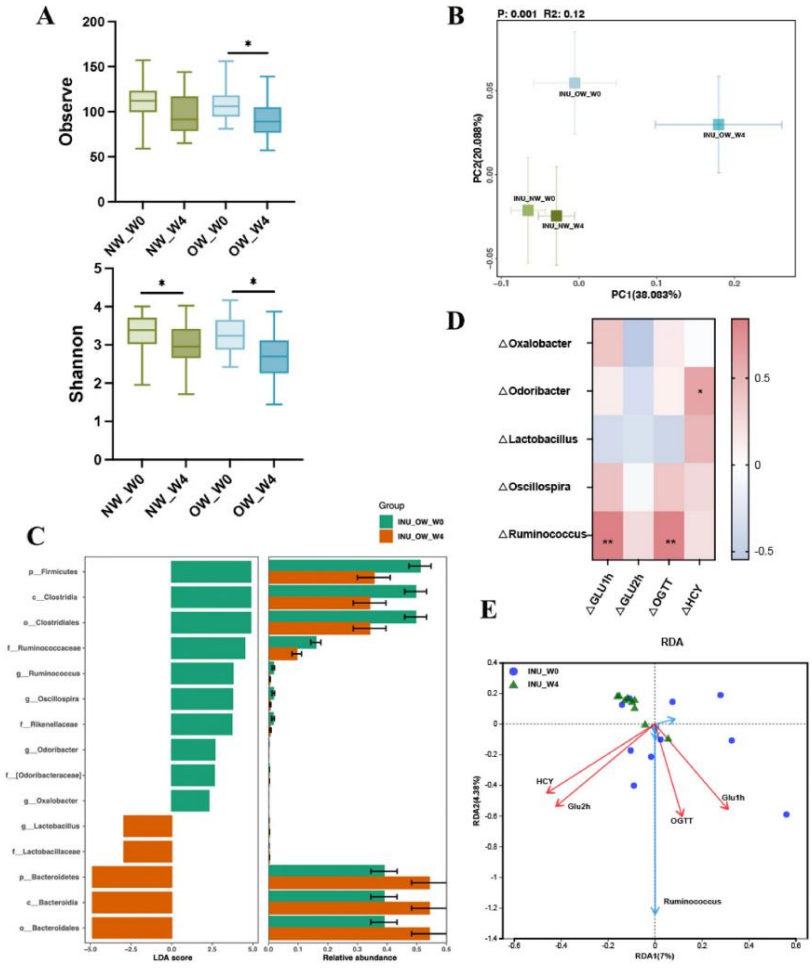

Figure 1. Variation in gut microbial diversity and main bacterial groups after 12 weeks of inulin intake.

3.2. Changes in Short-Chain Fatty Acids and Glucose Control

The inulin group had higher fecal butyrate (+49%) and propionate (+35%) compared to baseline (Figure 2). These increases were linked to a 1.2 ± 0.3% fall in HbA1c. A positive relationship between total SCFA levels and HbA1c reduction was seen ($r = 0.52$, $P < 0.01$). The control group showed no similar pattern. These findings support earlier work showing that SCFAs stimulate GLP-1 and PYY release and improve insulin sensitivity [20]. The results confirm that regular soluble fiber intake may improve glucose regulation by increasing beneficial fermentation products.

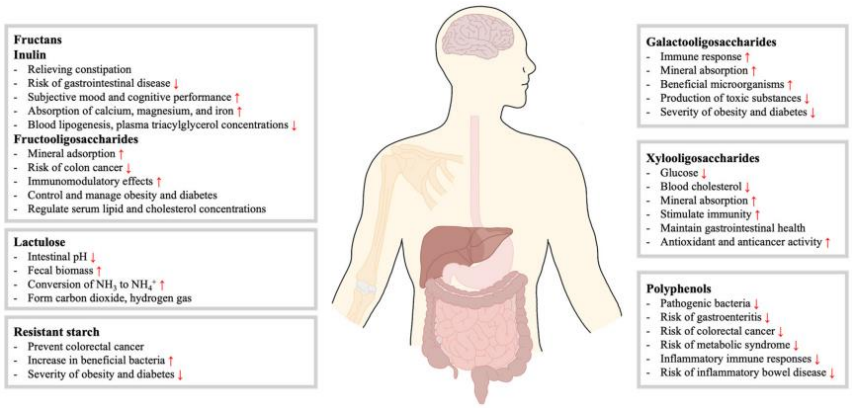

Figure 2. Simplified pathway showing how inulin fermentation increases SCFA levels and supports glucose control in type 2 diabetes.

3.3. Inflammation and Barrier Improvement

C-reactive protein levels fell by about 22% in the inulin group and were correlated with increased butyrate concentration. Participants with greater rises in Faecalibacterium also showed higher expression of tight-junction genes, suggesting improved gut barrier function. These results agree with evidence that butyrate supports mucosal defense and reduces metabolic inflammation [21]. Compared with other dietary fiber studies, the consistent link among bacterial diversity, SCFAs, and inflammation suggests that the chosen dose and duration were sufficient to produce biological effects in T2DM [22].

3.4. Comparison with Previous Findings and Study Limits

This study confirmed that inulin supplementation enhanced gut microbial diversity, raised SCFA production, and improved glycemic outcomes in adults with T2DM [23]. The results are consistent with meta-analyses of dietary fiber trials but add value by analyzing microbial, metabolic, and clinical data together. However, several limits remain. First, 16S rRNA sequencing cannot identify strains or predict functional genes accurately. Second, fecal SCFAs reflect luminal content, not circulating levels [24]. Future work should use metagenomic and metabolomic methods and include plasma SCFA measurements. Even so, these findings strengthen the view that regular soluble fiber intake supports glucose control through changes in the gut microbiota and its metabolites.

4. Conclusion

This study found that a 12-week intake of inulin improved gut microbial balance, increased Bifidobacterium and Faecalibacterium, and raised the levels of short-chain fatty acids in adults with type 2 diabetes. These microbial and metabolic shifts were linked with lower HbA1c values and a drop in blood inflammation markers. The findings suggest that soluble fiber can help control blood sugar by restoring gut balance and increasing helpful fermentation products. The main strength of this study is the combined use of microbiota, metabolite, and clinical data under one controlled design. Still, the study involved a moderate number of participants, and it did not include detailed strain analysis or blood SCFA tracking. Future work should apply metagenomic and metabolomic methods to verify these links and guide fiber-based nutrition plans. In summary, inulin appears to be a safe, affordable, and practical supplement to support diabetes care.

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