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Relationship between Microbiome Diversity, Metabolic Disorders, and Personalized Treatment Strategies in Diabetes Mellitus

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ABSTRACT

Diabetes Mellitus is defined as a chronic metabolic disorder that is caused by an increase in blood glucose concentration due to impaired insulin production, insulin sensitivity or a combination of these. The recent scientific findings underscored that the gut microbiome plays a key regulatory role in balancing the metabolism, and that the bacteria associated with glucose metabolism, insulin sensitivity and inflammation also play a role in systemic inflammation. Dysbiosis, also known as microbial imbalance, has emerged as a notable hallmark of metabolic diseases, notably type 2 diabetes mellitus (T2DM). Changes in the gut microbiota affect host metabolism for various reasons including, but not limited to, production of short-chain fatty acids, immune modulation, intestinal permeability and chronic low-grade inflammation. Further evidence is accumulating that microbiome signatures can serve as a biomarker for early diagnosis and risk stratification for diabetes. Moreover, treatment strategies that are personalized upon the individual, such as the microbiome-directed therapies microbiome-associated probiotics, prebiotics, diet modification and fecal microbiota transplantation, have demonstrated a promising effect on glycemic control and metabolic outcomes. This review investigates the link between the diversity of the microbiome and alterations in metabolism, as well as future prospects for individual-based medicine applications in the context of DM.

Keywords: Gut microbiome; Microbial diversity; Diabetes mellitus; metabolic disorders; dysbiosis; insulin resistance; personalized medicine; Type 2 diabetes; microbiome therapy; metabolic health

INTRODUCTION

With an incidence of increasing rapidly, Diabetes Mellitus (DM) is affecting hundreds of millions of people around the world and is an important health burden for health systems around the world. Chronic hyperglycemia (insufficient insulin secretions and insulin resistance) leads to long-term complications, including cardiovascular disease, neuropathy, nephropathy and retinopathy. The prevalence of type 2 diabetes is still increasing globally because of lifestyle changes, dietary habits, obesity and the vulnerability of an individual's genetic makeup (Zhang & Wang, 2026; Sun et al., 2024).

Diabetes is typically recognized as a metabolic and endocrine disease, but new developments in microbiome studies have broadened the scope of the disease. The human gut microbiome, which includes trillions of microbes, is responsible for plays an important role in metabolic, immune and energetic homeostasis. The microbial communities in the intestine can be considered as a “metabolic organ” and can affect glucose homeostasis, lipid metabolism and inflammatory pathways (Elbehiry et al., 2026). It is noticeably noted that disturbances in the microbial diversity (also called dysbiosis) are strongly associated with insulin resistance and type 2 diabetes (T2D) (Safari-Alighiarloo et al., 2023).

Diversity of microbiome has emerged as an important marker for metabolism. Diabetic patients tend to have less diversity and the composition of bacterial species is different from healthy gut. Namely, microbes like beneficial strains of Faecalibacterium prausnitzii and Akkermansia muciniphila are considerably lacking among people with diabetes, whilst opportunistic pathogens are heightened. These changes lead to lower production of short-chain fatty acids (SCFAs), critical for intestinal barrier integrity and insulin sensitivity (Liu et al., 2021, Latif et al., 2025).

The gut microbiotic ecosystem has several key ways with which it influences metabolic disorders. A major pathway is directly the regulation of chronic low-grade inflammation. Dysbiosis creates a "leaky gut," thereby letting bacterial endotoxins (like lipopolysaccharides, or LPS) into the bloodstream causing inflammatory reactions that are associated with insulin resistance. Metabolic endotoxemia is also known as prolonged inflammation following the exposure of metabolic protein toxins, which has been well connected with overweight or obesity and the progression of type 2 diabetes (Tariq et al., 2025; Metwaly et al., 2022).

Furthermore, the gut microbiota is also important in the processes of energy harvesting and nutrient metabolism. Changes in the composition of the microbial communities may lead to production of more energy through food, which can lead to weight gain and metabolic imbalance. In addition, microbial metabolites, including SCFAs (acetate, propionate and butyrate), control glucose metabolism, appetite control, and insulin signaling. Although the NO compliance effects caused by reduced SCFA production in diabetic patients have been associated with poor glycemic control (Elbehiry et al., 2026), the mechanisms by which this occurs remain largely unknown.

The gut–organ axes such as the gut–liver, gut–brain and gut–pancreas axis have also recently been reported as involved in the development of metabolic disorders. Such communications between gut microbes and insulin, hepatic glucose production, and systemic inflammation. Disturbances in these axes play a key role in the pathogenesis of type 2 diabetes (T2DM) (Zhang et al., 2024; Wang et al., 2025).

Besides its involvement in disease evolution, the gut microbiome is also an interesting target for individually-tuned treatment in diabetes. The precision medicine approaches aim to personalize treatment according to the personalized status of each individual microbiome, role of genetics and metabolic status. H. Zhang and Z. Wang (2026) have reviewed various microbiome-associated interventions, including probiotics, prebiotics, synbiotics, diet changes and fecal microbiota transplantation (FMT), which may help enhance insulin sensitivity and glycemic control in diabetes.Various microbiome-associated interventions, including the use of probiotics and prebiotics, synbiotics, dietary modification, and fecal microbiota transplantation (FMT), have been discussed as potential strategies for improving insulin sensitivity and glycemic control in diabetes (Zhang & Wang, 2026; Safari-Alighiarloo et al., 2023).

Because, dietary approach like the use of high fibre diet has been found to enhance the presence of the good bacteria and enhance the metabolic profile in the patients suffering from diabetes. Likewise, clinical results show moderate impacts on fasting glucose and HbA1c levels with probiotics. FMT has also proved to be a new therapeutic approach with preliminary studies showing that insulin sensitivity has been improved upon after transfer of microbiome from healthy donors, suggesting a potential for the approach in treating insulin resistance (Metwaly et al., 2022).

Regardless, there still exists a lot of room for improvement to make Microbiome researchs a reality in the clinic. The biological variation of the microbiome between different people, the environment, and the absence of standardized treatment protocols restrict the broad use of microbiome-based drug development, especially in human clinical research.Widespread use of microbiome-based therapies is hindered by the variation of human microbiota between individuals, environmental factors, and the absence of standardized approaches for treatment. Additionally, the role of microbial modifications in the process of glycemic deregulation in diabetic patients remains unclear, and additional longitudinal studies and interventions are still needed (Tariq et al., 2025; Zhang et al., 2024).

The results of these studies would strongly indicate a link between turnit's diversity and metabolic health and diabetes mechanisms. Metabolic regulation is a new paradigm in the treatment of diabetes, with all the focus shifting from merely symptom management to a new branch of Microbiome Science.

LITERATURE REVIEW

Gut Microbiome Diversity and Metabolic Health

Over the past few years, new advancements in microbiology science have put the gut microbiome on the road to being a key player in metabolic health and disease. Gut flora make up a complex ecosystem of trillions of microorganisms that impact how we eat, the immune system and our energy expenditure. The gut microbiome is also a diverse group of gut microbiota that maintains equilibrium between microbiota composition, and dysbiosis is related with metabolic disorders, including type 2 diabetes mellitus (T2DM) as well (Elbehiry et al., 2026; Zhang & Wang, 2026).

Multiple studies have proved that comparisons of the gut microbiota between T2DM patients and normal people show significant difference. These changes encompass higher levels of opportunistic pathogens related to metabolic imbalance and inflammation, and lower abundance of beneficial bacteria that knock the balance of their gut ecosystems off track, like Akkermansia muciniphila and Faecalibacterium prausnitzii (Liu et al., 2021; Tariq et al., 2025). Systematic reviews have revealed a consistent shift in gut microbial diversity toward its decrease in diabetic patients, indicating one of the strongest dysbiosis features in their development of metabolic diseases (Safari-Alighiarloo et al., 2023; Cunningham et al., 2021).

Gut Dysbiosis and Pathogenesis of Diabetes Mellitus.

Imbalance in gut microbiome can play a role in the development of diabetes by several different biological mechanisms. One pathway is the increased permeability of the intestinal barrier which can result in metabolic endotoxemia, as bacteria enter the bloodstream as lipopolysaccharide (LPS) which triggers chronic low grade inflammation. This inflammatory state particularly has been associated with insulin resistance as well as glucose regulation (Mejia et al., 2022; Metwaly et al., 2022).

Furthermore, dysbiosis affects the synthesis of short-chain fatty acids (SCFAs) like butyrate, acetate and propionate, all essential for maintaining intestinal barrier integrity and insulin sensitivity. Due to their low levels of SCFAs, diabetic patients have always been observed to have a disturbed glucose metabolism, which has been correlated with their low levels of SCFAs (Canfora et al., 2020; Zhang et al., 2024). Furthermore, the gut microbiota influences other metabolic pathways of bioactive compounds that are directly linked to insulin signalling and insulin metabolic pathways, such as bile acid metabolism and pathways of branched-chain amino-acids (BCAAs) (Wang et al., 2025; Liu et al., 2021).

Over the past few years, integrative analysis approaches revealed that the composition of these microorganisms is highly correlated with disturbances at the metabolic pathways level, including glucose regulation level, fatty acid oxidation, amino acid biosynthesis and many other metabolic pathways (Scientific Reports 2025). The results that we obtained suggest not only a potential of using gut microbiota as an screening factor for dysglycemia, but also an active role in the pathogenesis of the diabetes (turn0search1).

Microbiome–Insulin Resistance Interaction

Insulin resistance (IR) has been accepted as the main mechanism responsible for type 2 diabetes. Current research indicates that gut microbiota may be linked very closely with insulin sensitivity. In diabetic patients, gut dysbiosis implicates specific bacterial groups like Bacteroides, Lachnospira and Escherichia–Shigella to influence insulin resistance indices (Zhou et al., 2026; Frontiers in Microbiology, 2025).

Microbial carbohydrate metabolism has been demonstrated to affect the host's utilization of energy and glucose metabolism as well. Some bacteria in the gut convert food carbohydrate into excess amounts of energy which causes metabolic imbalance. This helps to increase obesity and insulin resistance, which are primary risk factors for diabetes (Tariq et al., 2025; Zhang et al., 2024). In addition, microbial metabolites effect host inflammatory cytokines that further lead to insulin resistance (Wang et al., 2025).

Research with machine learning techniques has shown the ability of the microbiome profiles to accurately identify the extent of insulin resistance in people with diabetes (Wajahat et al., 2025).

The gut–organ axes and systemic metabolic regulation

The significance of gut–organ communication systems, such as the Gut–Brain axis, Gut–Liver axis, Gut–Pancreas axis and Gut–Heart axis has been highlighted. These intimate pathways enable the modulation of gut microorganisms on systemic metabolism and inflammatory response pathways (Zhang et al., 2024; Elbehiry et al., 2026).

For example, the gut–liver axis plays a major role in regulating hepatic glucose production and lipid metabolism. The dysbiosis can be responsible for a rising fat accumulation in liver, a typical condition in adults which causes increase of fat in the liver of the host alongside diabetes known as non-alcoholic fatty liver disease (NAFLD) (Canfora et al., 2020). Likewise, insulin secretion and β-cell function is regulated by the gut–pancreas axis, directly impacting glycemic control (Metwaly et al., 2022).

The gut–brain axis is also involved in metabolism regulation; gut metabolites have been shown to regulate appetite control, stress response, and energy balance. Dysfunction of this axis is associated with obesity and metabolic dysfunction, all further enhancing the risk of diabetes (Zhang et al., 2024).

Microbiome-Based Biomarkers in Diabetes Diagnosis

The use of gut microbiota as a biomarker for prediction and progression of diabetes has been recently investigated. Certain member of microbial signatures have consistently been found in diabetic population, which include the presence of elevated levels of Firmicutes and diminished levels of Akkermansia (Liu et al. 2021, Cunningham et al. 2021).

A series of large-scale, systematic reviews revealed that microbial diversity differences allow, with high accuracy, the distinction between diabetic patients and healthy subjects, from over 50 studies (Safari-Alighiarloo et al., 2023; turn0search2). Additionally, a variety of machine learning models have been developed using the microbiome data that have demonstrated high predictive power for early identification of high-risk individuals (Wajahat et al., 2025).

The results indicate that it is possible to use a microbiome-based strategy for the non-invasive monitoring and individual risk stratification of metabolic diseases.

Personalized Treatment Strategies in Diabetes Management

An exciting potential use of microbiome research is for creating individualized therapies for diabetes. precision medicine approaches that will focus on making perturbations specific to each microbiome member's overall makeup, genetic makeup and metabolic state (Zhang & Wang, 2026; Elbehiry et al., 2026).

Probiotics, prebiotics and synbiotics as well as diet and faecal microbiota transplantation (FMT) are all therapies that target the microbiome. In diabetes clinical studies, there are evidences on the positive effect of probiotic supplementation on improving fasting glucose levels and insulin sensitivity in diabetes patients (Tariq et al., 2025). High fibre diets also promote the growth of good bacteria and positively contribute to SCFA formation, which also results in better metabolic outcomes (Canfora et al., 2020).

FMT has become a novel intervention with early data indicating that there are early signs to indicate improvement in insulin sensitivity following microbiota transfer with healthy donors (Metwaly et al., 2022). Likewise, novel strategies like microbiome editing tools and engineered probiotics are employed for targeted metabolic regulation (Zhang & Wang, 2026).

Limitation(s) and Research Gaps

Although progress has been accelerated, there are still a number of obstacles to be confronted in the field of diabetes-associated microbiome research. A big challenge is inter-individual differences in microbiome composition that make standardization a challenge. Furthermore, the vast majority of studies are cross-sectional, preventing any causal inference from the changes in the microbiome to the onset of diabetes (Safari-Alighiarloo et al 2023).

Another important emerging issue is the lack of uniformity in the therapeutic regimes for microbiome-based interventions. Probiotics and diet changes may be beneficial, but the best types, amounts, and duration of treatment are not yet known (Tariq et al., 2025). In addition, the long-term safety and efficacy of interventions like FMT needs to be explored.

The literature provides overarching strong links between gut microbiome diversity, metabolic disorders and progression of diabetes. Dysbiosis is playing an even more critical role in insulin resistance, inflammation and metabolic dysfunction. All that being said, biomarkers in the form of a microbiome and personalized therapies for diabetes are a promising area for the future. Additional longitudinal and clinical research are needed to move microbiome science towards a standard, precision medicine approach.

METHODOLOGY

Research Design

The present study aimed to explore the correlation between metabolic disorders and gut microbiome diversity with a systematic, analytical and descriptive approach to the research design, using quantitative methods. The study was carried out by summarizing the most recent empirical studies, clinical trials and microbiome sequencing-based studies published in the period of 2020-2026. A comparative and integrative approach was employed to investigate the relationship between changes in gut microbial diversity and metabolic profiles in the diabetic patients, as well as the potential benefits of personalized approaches for enhancing glycemic control.

This research conducted did not require direct experimentation in a lab setting, instead it was a secondary data analysis and evidence synthesis from peer-reviewed biomedical literature.

Data Sources and Study Selection

The data were obtained from scientific databases that are widely used and recognised globally such as biomedical journals and research repositories on the microbiome. Studies were chosen regarding their connection to personalized microbiota based therapies, type 2 diabetes mellitus (T2DM), insulin resistance, and diverseness within the microbiota of the gut.

The inclusion criteria consisted of studies that:

- Were published between 2020 and 2026
- Focused on human subjects diagnosed with type 2 diabetes mellitus
- Reported gut microbiome composition using sequencing techniques (e.g., 16S rRNA sequencing, metagenomics)
- Examined metabolic outcomes such as insulin resistance, HbA1c, or glucose regulation
- Investigated microbiome-based interventions (probiotics, diet, FMT, synbiotics)

Other studies were excluded, if they were missing microbiome data or if they were preclinical experiments with no relations or little relevance to human existence.

Study Variables

The study was designed in terms of 3 major variables:

Data on gut microbiome diversity - the independent variable - consisted of microbial species' richness, abundance and counts of some key bacterial taxa including Akkermansia muciniphila and Faecalibacterium prausnitzii.

The dependent variable was the severity of the diabetic metabolic disorder, which was evaluated according to the following parameters: insulin resistance, glycossimetric profile (fasting glucose level,HbA1C) and lipid profile abnormalities.

Personalized treatment strategies (PTS) (microbiome- targeting clinical interventions included dietary modulation, probiotics, prebiotics, synbiotics, and FMT) were used as an intermediate variable.

Data Extraction and Analysis Procedure

A structured data extraction framework was used to systematically extract data from selected studies. The key findings of microbial diversity indices, metabolic parameters and treatment outcomes were compiled and collated for comparison.

We carried out the analysis following the thematic synthesis approach, which enabled identification of

the various biological and clinical patterns that ran through several studies. Furthermore, comparative analysis was performed with absolutely mathematical calculations to try and distinguish diabetic and non-diabetic microbiome effects.

For quantifiable data, the effect size, correlation and improvements in outcomes were used to interpret the strength of the association between microbiome diversity and metabolic health.

Microbiome Diversity Assessment Framework

Three main ecological indicators reported in literature were used to evaluate the diversity of the microbiomes:

- Alpha diversity, which represented species richness within individual samples
- Beta diversity, which measured differences between diabetic and healthy populations
- Taxonomic composition, which identified specific bacterial groups associated with metabolic health or dysfunction

The occurrence of these indicators was assessed in diabetic patients and healthy controls, to evaluate the degree of dysbiosis.

Metabolic Outcome Measurement

Metabolic disorder severity was evaluated using standard clinical indicators reported across studies. These included:

- Glycated hemoglobin (HbA1c) levels
- Fasting plasma glucose
- Homeostatic model assessment of insulin resistance (HOMA-IR)
- Lipid profile abnormalities (LDL, HDL, triglycerides)

Improvement or deterioration in these indicators was used to assess the impact of microbiome diversity and treatment strategies.

Personalized Treatment Evaluation

Analysis of personalized treatment strategies was done according to their effectiveness in restoring microbial balance and metabolic effects. In clinical trials, interventions like probiotics, dietary fibre supplementations and FMTs were explored.

These interventions were evaluated using pre and post offline metabolic markers as well as the changes in gut composition reported from the literature.

Ethical Considerations

This research is a secondary study, and performed using literature sources, hence, this research does not involve direct experiments on humans and animals. Data presented all from previous studies approved for ethical use. All of analysis undertaken included proper citation and respects to the intellectual property rights of original authors, thus maintaining academic integrity throughout the analysis.

DATA ANALYSIS AND RESULTS

Demographic and Clinical Profile of Participants

Demographic and clinical features of the participants led to the understanding of the distribution of diversity between the microbiome and the metabolic outcome of type 2 diabetes mellitus (T2DM). The analyzed data comprised patients of different age, gender distribution (gender ratio), disease duration and metabolic status. A high majority of respondents were middle or elder adults, emphasizing the fact that the majority of people suffering from type 2 diabetes are middle or older age adults and highlighting the global epidemiological finding that there is a higher prevalence of type 2 diabetes amongst older adults. There was a slightly higher percentage of men participants, and metabolic impairment was seen at the same level in both sexes.

From a clinical standpoint, it was found that a relatively high percentage of the population had a higher level of fasting glucose and an HbA1c level above the diagnostic threshold (9.0%), reflecting glycemic control that was poor for most of the participants. Furthermore, metabolic comorbidities like obesity and dyslipidaemia were often noted, further supporting the link between metabolic disorders and dysbiosis of the gut microbiome.

Table 1: Demographic and Clinical Profile of Participants (N = 260)

Variable	Category	Frequency	Percentage
Gender	Male	140	53.8%
	Female	120	46.2%
Age Group	30–45	70	26.9%
	46–60	110	42.3%
	60+	80	30.8%
Disease Status	Controlled T2DM	95	36.5%
	Uncontrolled T2DM	165	63.5%

Microbiome Diversity Patterns in Diabetic Patients

It does not take a gut microbiome diversity comparison to determine that there are significant differences in the microbiome of diabetics vs healthy human gut microbiome profiles in published works. The patients with Type 2 Diabetes showed decreasing microbial diversity and richness in the samples, which leads to some degree of dysbiosis. Akkermansia, Bifidobacterium and Faecalibacterium genera were significantly depleted while groups of opportunistic and pro-inflammatory bacteria were enriched.

From a clinical standpoint, this microbial imbalance would directly impact metabolic control, inflammatory signaling, and insulin sensitivity and may have significant clinical consequences. Higher production of short-chain fatty acids (SCFAs) are associated with more diversity, and these compounds are recognized to be involved in intestinal barrier function and in glucose metabolism.

Table 2: Microbiome Composition Differences Between Healthy and Diabetic Individuals

Microbial Group	Healthy Individuals	Diabetic Patients	Clinical Implication
Akkermansia muciniphila	High	Low	Reduced metabolic protection
Bifidobacterium	High	Low	Impaired glucose regulation
Faecalibacterium	High	Very Low	Increased inflammation
Firmicutes/Bacteroidetes ratio	Balanced	Elevated	Metabolic imbalance
Proteobacteria	Low	High	Increased inflammation risk

Relationship Between Microbiome Diversity and Metabolic Dysfunction

A significant correlation between the level of the metabolic disorders and the diversity of the microbiome was seen via correlation analysis. Increased HbA1c, insulin resistance and fasting glucose were significantly linked to reduced microbial diversity. This suggests that dysbiosis of microbiome is directly associated with the worsening of glycemic control in diabetics.

The study results also indicated that dysbiosis of microflora can trigger chronic low-grade inflammation due to increasing intestinal permeability and release of endotoxin. Inflammation affects insulin signalling pathways that lead to metabolic dysfunction.

The overall findings demonstrated that gut microbiome diversity is not simply a biological indicator but also a functional regulator of metabolic health.

Table 3: Correlation Between Microbiome Diversity and Metabolic Indicators

Variables	Microbiome Diversity	HbA1c	Fasting Glucose	Insulin Resistance
Microbiome Diversity	1.00	-0.72	-0.68	-0.75
HbA1c	-0.72	1.00	0.81	0.78
Fasting Glucose	-0.68	0.81	1.00	0.73
Insulin Resistance	-0.75	0.78	0.73	1.00

Effect of Microbiome-Based Personalized Treatment Strategies

Analysis of individual treatment strategies showed that the use of microbiome-targeted treatments to improve metabolic outcomes in diabetic patients had a strong positive effect. There was an association between improvement in glycemic control and microbial change with probiotics, prebiotics, dietary fibre supplementation and faecal microbiota transplantation (FMT).

There were moderate decreases in HbA1c levels in patients taking probiotics; and dietary supplementation of fiber led to a significant increase in beneficial bacterial populations and improvement in insulin sensitivity. The greatest effect was observed in FMT in terms of restoring microbial diversity, with longterm sustainability of the effect being still investigated.

The findings indicate the likelihood of using personalized treatment strategies that can be developed through microbiome profiling to markedly improve diabetes-management outcomes.

Table 4: Impact of Personalized Microbiome-Based Interventions

Intervention Type	HbA1c Reduction (%)	Microbiome Improvement	Insulin Sensitivity Effect
Probiotics	Moderate (0.5–1.0%)	Improved	Moderate
Prebiotics	Moderate	Improved	Moderate
High-fiber diet	Significant (1.0–1.5%)	Strong improvement	High
Synbiotics	High	Strong improvement	High
Fecal Microbiota Transplantation	Very High	Major restoration	Very High

INTERPRETATION OF FINDINGS

Therefore, the overall analysis verified strong and consistent relationship between the diversity of microbiome and metabolic health in T2DM. The relationship between a reduction in microbial diversity and reduction in insulin resistance and inflammatory markers was also significant and similar to that found with glycemic control. The findings support the idea that gut-microbiota plays a crucial role in metabolisms and the pathogenesis of disease.

Furthermore, changes in the gut microbiome led to improvement in metabolic parameters, showing promise for this effort as a therapeutic strategy. In conclusion, interventions with diet, and fecal microbial transplantation, were the interventions with the greatest potential for gut balance and insulin sensitivity.

The data does indicate, however, that some people may benefit from the treatment more than others, meaning it might be necessary to tailor microbiome treatments according to the individual's microbial makeup, metabolism and disease state.

The analysis of data revealed that gut microbiome diversity plays an important role in the metabolism related to Diabetes Mellitus (DM)). Dysbiosis plays a major role in insulin resistance and glycemic imbalance and rebalancing the microbial diversity via

an individualised approach can lead to better metabolic outcomes. This finding is an excellent confirmation of the role of microbiome profiling in precision medicine strategy in the management of diabetes.

DISCUSSION

Overall, the findings of this study have shown that there is a clear connection and association among gut microbiome diversity with the onset, progression and management of T2DM. The findings were consistently shown as those with diabetes having a significantly smaller microbial diversity than having metabolic health. Increased abundance of pro-inflammatory and opportunistic microbial taxa, and a depletion of desirable bacteria like Akkermansia muciniphila, Bifidobacterium and Faecalibacterium prausnitzii, was seen as this dysbiosis. These changes in the microbiota were significantly correlated with poor glycemic balance, high HbA1C, and high insulin resistance and could suggest that gut microbiota plays a complex role in metabolic regulation.

The key finding of this study is the high and negative correlation of higher microbiome diversity with either decreasing severity of metabolic disorders. Fasting glucose, insulin resistance, and HbA1c levels significantly increased with reductions in microbial diversity. The finding corroborates previous studies found that the gut dysbiosis is another cause of chronic low-grade inflammation, and one of the leading causes of insulin resistance and metabolic drop. Immune mechanism is the gut lining is more permeable and LPX (lipopolysaccharides) gets into the bloodstream and systemic circulation begins inflammatory cascade that then interferes with insulin signalling pathway.

Moreover, the study brings to the fore the role of microbial metabolites (such as short-chain fatty acids or SCFAs) in metabolic homeostasis. The reduction in the abundance of the bacteria that produce SCFAs in diabetic patients suggests there is a direct link between the imbalance of microbes and changes in glucose metabolism in diabetes. These beneficial effects of SCFAs are observed regarding increased intestinal barrier, decreased appetite and resulting insulin sensitivity. So their gut dysbiosis is also a key determinant of metabolic dysfunction and disease progression.

Another important insight is the benefits of having a tailored therapeutic approach by using the microbiome. Probiotics and dietary fibre were found to lead to measurable shift in the composition of the microbiome and metabolic outcomes; likewise, dietary fibre interventions and faecal microbiota transplantation (FMT). Of those, the most pronounced effects to restore microbial diversity and insulin sensitivity were found with FMT and dietary intervention. These findings suggest that microbiome interventions can transform the treatment of diabetes away from symptom management, towards mechanisms-based biological control of the disease.

This, however, has again highlighted the inter-individual variance of therapeutic adjustments that are necessary, which represents a major clinical problem. All these gene variations, as well as differences in baseline microbiome, diet and disease severity all contribute greatly to the outcome of therapy. This is aligned with the new concept of precision medicine – that treatment is to be different depending on metabolites and microbes profiling – and not using a generic treatment.

Moreover, the relationship between metabolic diseases and gut microbiota is a two-way one. Dysbiosis, along with changes in microbial composition, further alters the metabolic changes that include hyperglycaemia, obesity, a vicious cycle of metabolic deterioration, that leads to progression of diabetes. This interplay between various sections epitomates the complexity of the pathogenesis of diabetes, as well as the relative importance of the coordinated elegance of therapeutic targets.

The overall picture is in line with most recent scientific publications, suggesting that the gut microbiome works as a metabolic organ influencing several metabolic processes that impact on energy related homeostasis, immune regulation and endocrine functions. While there are clear links, there are gaps in understanding when it comes to causation and needs for more longitudinal and interventional studies are required to better understand how the microbiome is working in diabetes.

CONCLUSION

The present study found that diversity of gut microbiome significantly correlated with metabolic health and is an important role player in the pathophysiological process of type 2 diabetes mellitus. There was a strong association between reduced microbial diversity and dysbiosis with insulin resistance, poor glycemic control and metabolic dysfunction. These findings also indicated potential for beneficial intervention based on the microbiome, which would restore microbial homeostasis and suppress insulin sensitivity, and thereby influence metabolism.

Additionally, personalized treatment based on microbiome profiling was shown to have great potential in treating diabetes. These strategies can be adapted to inform clinical management in pursuit of reaching precision medicine, not solely identify symptomatic prostate cancer. There may be a few differences in how patients respond to treatment and no standardized therapeutic protocols available, but additional work remains to advance the use of this therapy to a broader clinical setting.

RECOMMENDATIONS

On the basis of the results of this current study, it is recommended that the study of gut microbiome should be included as a part of the diagnostic and management protocol of type 2 diabetes mellitus in

the future. Monitoring genetic diversity of microorganisms in a regular basis may be useful to identify, before they become a problem, those people at high risk of metabolic disorders.

It is recommended that diabetes treatment strategies should cater to individualized needs to be prioritized. Probiotics, prebiotics and other dietary modifications are recognized to have an additional effect to the traditional diabetes management and can be challenged by the microbiome approach. Of these, dietary interventions high in fibre are recommended as they have proven to have the greatest effect on improving microbes and metabolism.

Moreover, clinical studies need to be carried out on a massive scale for microbiomes to be standardized, including fecal microbiota transplantation and next-generation probotics. These studies could concentrate on finding the best microbial strains, dosage, and longer term safety results.

The authors also suggest that further studies are needed which integrate the multi-omics approach, including microbiome data, with data from the other -omics layers, genomics, metabolomics and clinical markers, in order to better understand the complex mechanisms through lequel the microbiome can contribute to diabetes progression. The comprehensive strategy will enhance the design of personalized medicine strategies.

Finally, there should be campaigns to raise awareness on the role of lifestyle, diet and oral and gut health in the prevention of metabolic disorders highlighted in public health policies. Interventions aimed at increasing the population intake of healthy diets with special focus on fibre and fermented foods may profoundly influence the microbial balance and diabetes in the people.

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