Received: November 11, 2025
Revised: June 6, 2026
Accepted: June 14, 2026
Published: June 30, 2026

Elicit Journal of Medical Science and Discovery
ISSN:3093-0480

https://elicitpublisher.com

REVIEW PAPER

Harnessing the Gut Microbiome for Chronic Disease Management and Public Health: A Systematic Literature Review

Kayode Omowunmi Ahmed[1*], Tolulope Ayokunle Esan[2]

Affiliations

[1]Department of Animal Science, Faculty of Agriculture, University of Ibadan, Nigeria
[2]Department of Nursing, Faculty of Medicine and Health Sciences, Keele University, United Kingdom

ORCID Identifiers

Kayode Omowunmi Ahmed
0009-0005-0018-3139

Tolulope Ayokunle Esan
0009-0004-0996-5543

DOI

10.65820/ejmsd-1vol2-issue1-2026

Abstract

Purpose: The human gut microbiome has become a crucial regulator of metabolic, cardiovascular, and gastrointestinal health, presenting novel avenues for chronic disease prevention and tailored nutrition. This systematic literature review synthesised evidence regarding the effectiveness of microbiome-targeted interventions in chronic disease management and evaluated their implications for public health.

Methodology: A thorough examination of peer-reviewed studies was performed utilising terminology associated with the gut microbiome, chronic diseases, and therapeutic interventions. Thirty-three studies were included, encompassing a range of interventions including dietary modification, probiotic and prebiotic supplementation, synbiotics, faecal microbiota transplantation (FMT), and microbiome-guided nutrition.

Results: The results demonstrated that high-fibre and plant-based diets, probiotic and prebiotic supplements, and FMT significantly improved metabolic and inflammatory by increasing microbial diversity, increasing short-chain fatty acid production, and enhancing intestinal barrier integrity. These results were most noticeable in people with type 2 diabetes, obesity, inflammatory bowel disease, and heart problems.

Novelty and Contribution: This review contributes to the existing literature by integrating microbiome-targeted nutrition with chronic disease prevention frameworks, thereby bridging clinical microbiology and population health perspectives. It adds to the growing field of precision nutrition, highlighting the gut microbiome as a promising therapeutic and preventive target.

Social and Practical Implications: The study emphasises the necessity of integrating microbiome considerations into dietary guidelines, chronic disease policies, and public health strategies, especially in advocating for equitable access to microbiome-based interventions globally.

Keywords: Gut Microbiome; Chronic Disease; Public Health; Faecal Microbiota Transplantation; Systematic Literature Review

*Corresponding author
E-mail address: Kayodeahmed22@gmail.com

How to cite this article:

Ahmed, K.O., & Esan, T.A. (2026). Harnessing the Gut Microbiome for Chronic Disease Management and Public Health: A Systematic Literature Review. *Elicit Journal of Medical Science and Discovery*, 2(1), 1-23. https://doi.org/10.65820/ejmsd-1vol2-issue1-2026

1 Introduction

The human body hosts trillions of dynamic and diverse microbial communities that may influence the host's physiology, commonly referred to as the "microbiome" (Malard et al., 2021). The human microbiome executes essential biological activities, including immune system homeostasis, regulation of host metabolism, inhibition of pathogen invasion, and enhancement of epithelial barrier performance (Malard et al., 2021; Siddiqui et al., 2021). The greatest concentration of bacteria is found in the human gastrointestinal system, referred to as the "Gut microbiome" (Dwivedi et al., 2021). Numerous studies have been conducted on the human microbiome. The human body contains trillions of microbial cells whose collective genome greatly exceeds the human genome in genetic diversity (Siddiqui et al., 2021). Research indicates that the microbiome protects against various conditions, including inflammatory bowel disease, systemic metabolic diseases (such as type 2 diabetes and obesity), atopic eczema, and allergy diseases (Facchin et al., 2020; Li et al., 2024; Srivastava et al., 2024).

In recent times, research has connected the gut microbiota as a crucial modulator of chronic diseases, notably in situations such as diabetes, autoimmune disorders, and cancer (Qin et al., 2021; Kostic et al., 2012). These disorders were formerly considered to be predominantly affected by hereditary and environmental factors. They are currently believed to be influenced by the makeup and function of the gut microbiome. Microbes are vital in preserving gut homeostasis and affecting numerous pathways. These include fermentation of dietary fibre, preserving the integrity of the intestinal barrier, inflammatory pathway regulation, and short-chain fatty acids (SCFAs) synthesis (Inayat et al., 2025). Dysbiosis is an imbalance in the composition and function of the microbiota. It is implicated in the aetiology of various chronic illnesses. For instance, in type 2 diabetes mellitus (T2DM), modifications in the microbial composition and reduction in beneficial bacteria have been connected with systemic inflammation and insulin resistance (Tilg & Moschen, 2014).

Likewise, in autoimmune disorders such as rheumatoid arthritis (RA), inflammatory bowel disease (IBD), and multiple sclerosis (MS), disturbances in gut microbial balance can generate abnormal immune responses. This can lead to constant inflammation and tissue damage (Inayat et al., 2025). Consequently, the gut microbiome has emerged as a novel therapeutic target, with therapies such as probiotics, prebiotics, synbiotics, dietary modification, and faecal microbiota transplantation (FMT) being studied for disease prevention and management (Biazzo & Deidda, 2022). These efforts try to restore microbial balance, boost beneficial metabolites, and alter host immunological and metabolic pathways.

Outside individualised clinical interventions, the gut microbiome carries profound implications for public health. The interaction between host and microorganisms has a vital role in both health and illness management (Afzaal et al., 2020). Human microbiome has promising potential in modifying appetite, boosting nutritional harvest, and expending energy from various meal components. Microbes play also a crucial part in xenobiotic metabolism. In xenobiotic metabolism, diverse gut bacteria affect the chemical structures of numerous diet components, medications, contaminants, and many insecticides (Nakov and Velikova, 2020). Several population-based research has proven the significantly beneficial impact of human gut microbiota in healthy persons (Afzaal et al., 2020). In healthy settings, the gut microbiota demonstrates stability, resilience, and symbiotic contact with the host (Hou et al., 2022).

High-throughput sequencing has transformed microbiome research over the last ten years, resulting in an unprecedented increase in research on the relationships between human diseases and gut microbiota. These microbiome research have associated alterations in the human gut microbiome with several illness outcomes, including obesity, type 2 diabetes, liver diseases, many forms of cancer, allergies, and neurodegenerative diseases (Wu et al., 2021). Despite a significant development of research on the gut microbiota, evidence remains fragmented among clinical, nutritional, and epidemiology fields (Kim et al., 2024). Many research vary in methodology, population characteristics, and microbiome profiling methodologies, limiting the capacity to derive consistent results. While various reviews have explored the microbiome’s function in individual diseases, few have consolidated findings across multiple chronic ailments and related them directly to public health concerns.

A comprehensive and systematic synthesis is therefore warranted to consolidate current knowledge, identify mechanistic and intervention-based insights, and highlight pathways for integrating microbiome science into chronic disease management and public health practice. This systematic review fills these gaps by carefully looking at the current literature and looking at both individual and population-level points of view. This systematic literature review seeks to consolidate existing evidence regarding the gut microbiome's role in chronic disease management and to

investigate its public health implications. The review aims to investigate the mechanistic relationships between gut microbiome composition and chronic diseases, assess the efficacy of microbiome-targeted interventions such as dietary modifications, probiotics, prebiotics, and faecal microbiota transplantation (FMT) in disease prevention and management, and evaluate the potential incorporation of microbiome insights into public health strategies, including nutrition policy, preventive health initiatives, and community-level interventions. The review seeks to answer the following research questions,

1. Which microbiome-targeted interventions improve chronic disease outcomes?
2. What are the key public health implications of harnessing the gut microbiome for chronic disease prevention?

2 Methodology

2.1 Study Design and Reporting Standards

This review was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines (Page et al., 2021) to ensure transparency, accuracy, and reproducibility. The review protocol was prospectively registered with the International Prospective Register of Systematic Reviews (PROSPERO) with registration ID CRD420251161566. All methods adhered to the PRISMA framework, encompassing systematic identification, selection, appraisal, and synthesis of relevant studies.

Database

A thorough literature search was conducted in PubMed and Scopus, chosen for their extensive coverage of biomedical and interdisciplinary research. PubMed was included because it has a lot of high-quality, peer-reviewed biomedical literature, and it combines MEDLINE, PubMed Central, and the Bookshelf to make sure that microbiome science studies in clinical, translational, and epidemiological fields are available (Lee et al., 2023). Scopus was chosen because it covers a wide range of disciplines and has a large citation database. It is known as one of the best places to find academic information in health, biological, and environmental sciences. Using Google Scholar to look at grey literature helped reduce publication bias and find reports, theses, or policy documents that weren't in traditional databases.

2.2 Search Strategy

A structured and reproducible search strategy was designed using a combination of Medical Subject Headings (MeSH) and free-text terms to identify studies examining the role of the gut microbiome in chronic disease management and public health. Boolean operators "AND" and "OR" were used to combine key concepts. The search string on Scopus includes "gut microbiome" OR "gastrointestinal microbiome" AND "chronic disease" OR obesity OR "Type 2 Diabetes" OR T2DM OR "cardiovascular disease" AND probiotics OR prebiotics OR synbiotic OR "faecal microbial transplant" OR FMT OR "dietary fibre" AND "public health" OR "population health". While the search string on PubMed are

("Gastrointestinal Microbiome"[MeSH] OR "Microbiota"[MeSH] OR gut microbiome OR intestinal microbiota OR gut flora OR human microbiome)

AND

("Chronic Disease"[MeSH] OR "Metabolic Syndrome"[MeSH] OR "Obesity"[MeSH] OR "Diabetes Mellitus, Type 2"[MeSH] OR "Cardiovascular Diseases"[MeSH] OR "Neoplasms"[MeSH] OR "Inflammatory Bowel Diseases"[MeSH] OR chronic disease OR noncommunicable disease OR metabolic disease)

AND

("Therapeutics"[MeSH] OR "Diet Therapy"[MeSH] OR "Probiotics"[MeSH] OR "Prebiotics"[MeSH] OR "Faecal Microbiota Transplantation"[MeSH] OR management OR prevention OR intervention OR therapy OR treatment OR probiotics OR prebiotics OR diet OR dietary fibre OR synbiotics OR faecal microbiota transplantation OR FMT)

AND

("Public Health"[MeSH] OR "Population Health"[MeSH] OR public health OR population health OR preventive health OR community health).

The search was limited to English-language publications between January 2015 and November 2025 to capture the most recent and relevant developments in the field. The database search was conducted on 12 June, 2025 and updated on 20 August 2025 before final study selection. Reference lists of included studies and related reviews were also screened for additional eligible publications.

2.3 Eligibility Criteria (PICOS Framework)

Study eligibility was defined using the Population–Intervention–Comparator–Outcome–Study Design (PICOS) framework.

Table 1 Eligibility criteria using the PICO framework

Component	Criteria
Population (P)	Adults (≥18 years) with or at risk of chronic diseases (e.g., type 2 diabetes, cardiovascular disease, obesity, inflammatory bowel disease, or cancer).
Intervention (I)	Any microbiome-targeted intervention, including dietary modification, probiotics, prebiotics, synbiotics, postbiotics, or faecal microbiota transplantation (FMT).
Comparator (C)	Placebo, usual care, or other active interventions.
Outcomes (O)	Primary outcomes**:** Gut microbiome composition, structure, and diversity. Secondary outcomes**:** Clinical or metabolic outcomes such as BMI, HbA1c, lipid profile, inflammatory markers, and other indicators of chronic disease management.
Study Design (S)	Eligible studies included randomised controlled trials, crossover trials, placebo-controlled clinical trials, and other prospective intervention studies conducted in human adults. Although cohort and cross-sectional studies were initially considered during protocol development, no observational studies met the final inclusion criteria after screening.

Studies were excluded if they: (1) were conducted in animals or in vitro; (2) were reviews, editorials, or conference abstracts; or (3) did not include an intervention or outcome related to chronic disease management through microbiome modulation.

2.4 Study Selection Process

All search results were imported into EndNote 21 for reference management and duplicate removal. Screening was conducted in two phases:

Title and abstract screening: To identify potentially relevant studies.

Full-text screening: To confirm eligibility based on the PICOS criteria.

Two independent reviewers performed the screening, and any disagreements were resolved through discussion or consultation with a third reviewer to ensure consistency and objectivity.

2.5 Quality Assessment

The methodological quality and bias risk of the included studies were independently assessed using standardised instruments, specifically The Cochrane Risk of Bias Tool (RoB 2) for randomised controlled trials and. This tool looks at things like how to choose studies, how to compare groups, how to measure validity, and how to report bias in outcomes. The risk of bias for each study was rated as low, moderate, or high. Consensus was used to settle differences between reviewers.

2.5 Data Extraction

To guarantee reproducibility and transparency, a standardised data extraction form was created. Each included study's author(s), year of publication, country or region, study design and sample size, type of chronic disease, type of

microbiome-targeted intervention (e.g., probiotic, diet modification, FMT), comparator and duration of intervention, and primary and secondary outcomes (microbiome composition/diversity, clinical endpoints) were extracted. Two reviewers independently extracted the data, and disagreements were settled by consensus or by a third reviewer.

3 Results and Discussions

A search of the three databases yielded 1,350 articles, of which 1,220 remained after duplicates were removed, as shown in the PRISMA flow diagram (Figure 1). After screening by title and abstract, 350 articles were left for full-text screening. 317 publications were excluded from full-text screening for a number of reasons, including omission of pertinent information. There were no more publications available for data extraction after the full-text screening of grey literature sources from internet searches.

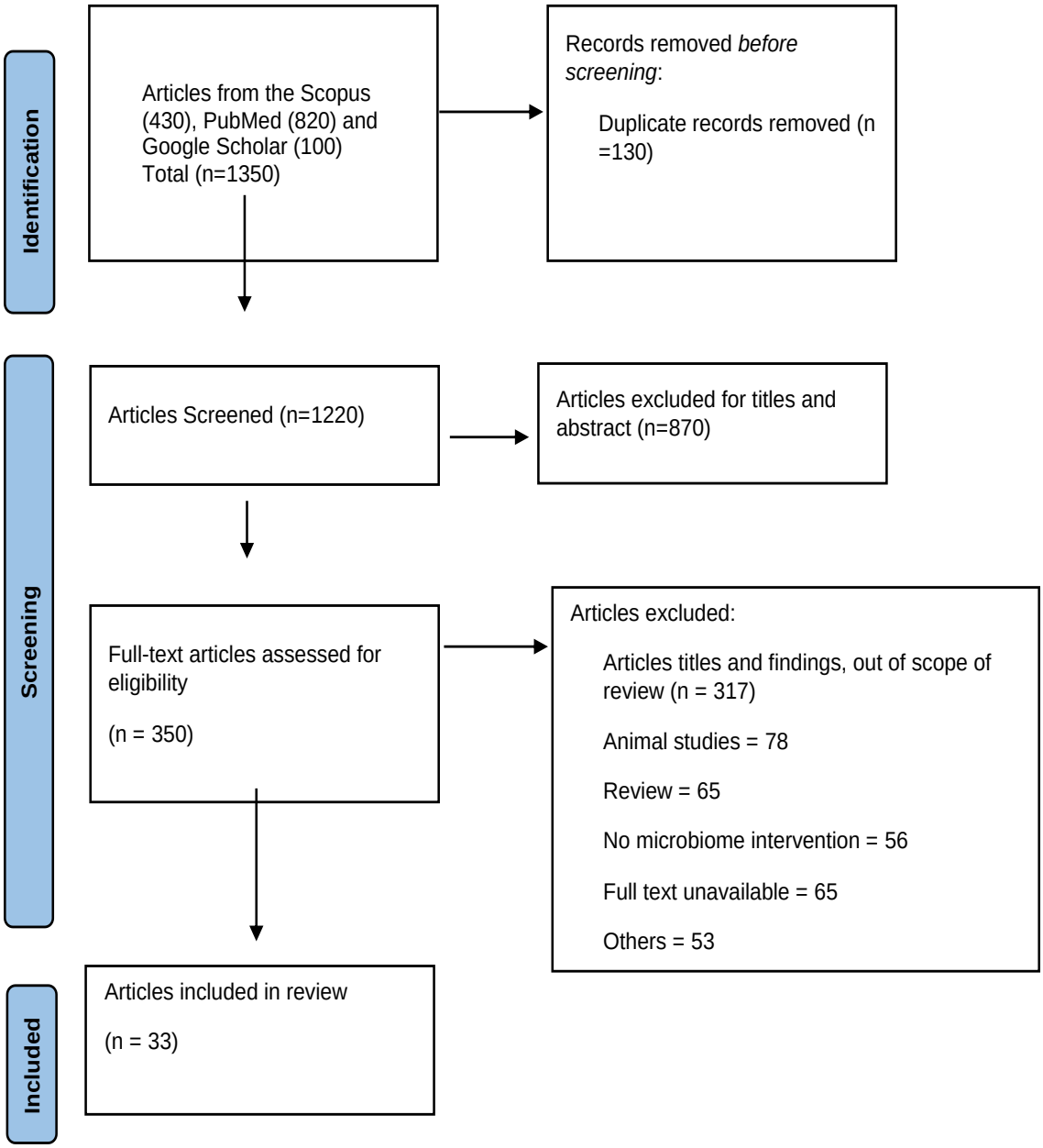

Figure 1 PRISMA flow diagram

3.1 Study selection and overall characteristics

The synthesis included thirty-three (n = 33) clinical studies that satisfied the inclusion criteria. According to the data extraction table (table 2), the included literature (published 2017–2025) (figure 2) was primarily randomised controlled trials (double-blind, placebo-controlled, crossover, and open-label designs) with sample sizes ranging from n = 19 to n = 309. Adult samples (≥18 years) with or at risk for chronic conditions such as type 2 diabetes mellitus (T2DM), obesity/metabolic syndrome, nonalcoholic fatty liver disease (NAFLD), inflammatory bowel disease (IBD; ulcerative colitis, Crohn's), cardiovascular disease (CVD), and chronic kidney disease (CKD) comprised the study populations. Results consistently included microbiome composition/diversity measures (16S or shotgun metagenomics), functional/metabolomic readouts (SCFAs, bile acids, BCAAs), and clinical endpoints (HbA1c, HOMA-IR, BMI, lipid profiles, disease activity indices). The duration of the intervention varied greatly (4 weeks to 12 months). With a number of trials conducted in North America and fewer studies from other regions, the geographic distribution revealed a concentration in East Asia and Europe (figure 3).

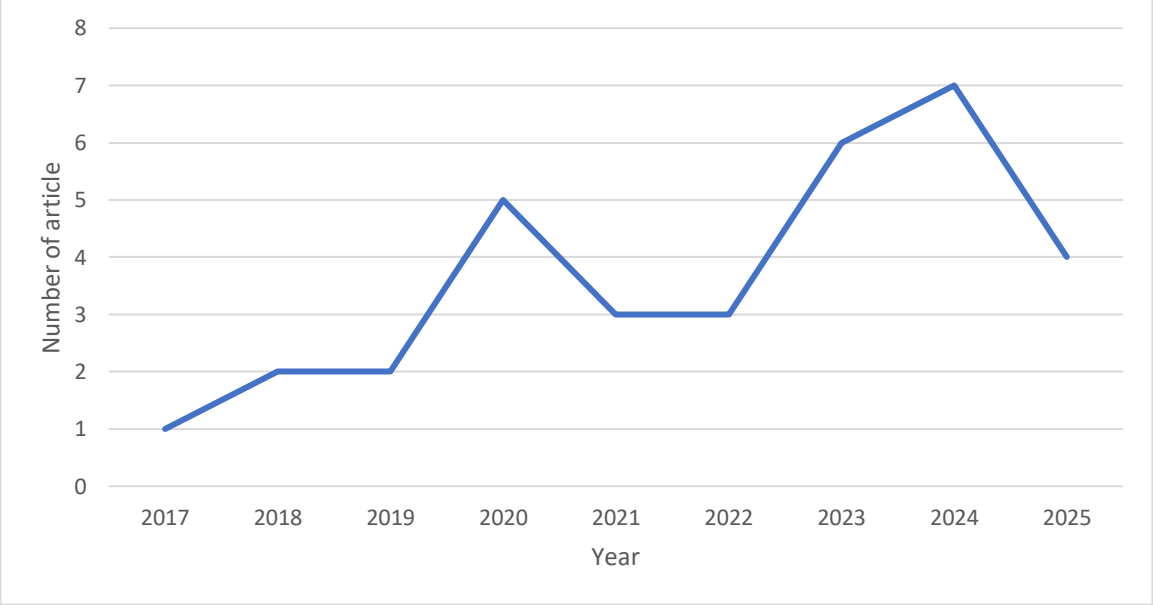

Figure 2 Distribution of included studies by year

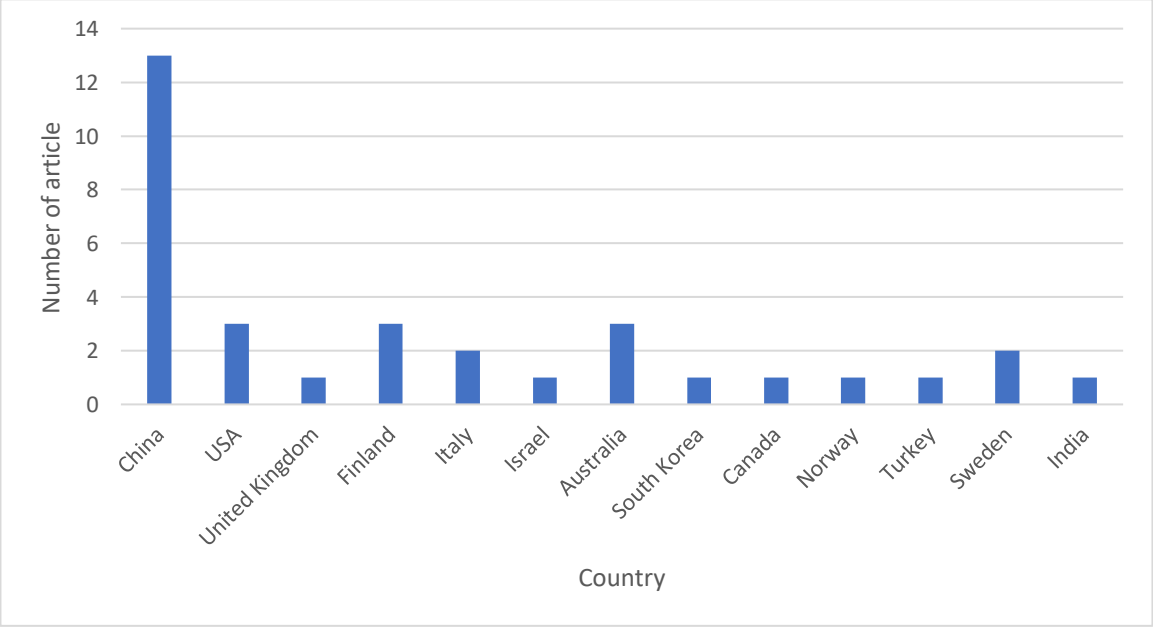

Figure 3 Distribution of studies by country of research

Table 2 Data extraction table

Author (Year)	Country	Study Design	Population (Sample Size, Characteristics)	Intervention / Exposure	Comparator	Chronic Disease type	Intervention and Microbiome Outcome
Zhao et al. (2018)	China	Randomised, open-label, parallel-group clinical trial (RCT)	43 patients with clinically diagnosed T2DM	High-fibre WTP diet: whole grains, traditional Chinese medicinal foods, and prebiotics (isoenergetic, diverse fibre structures)	Usual (U) care per 2013 Chinese Diabetes Society guidelines (patient education + dietary recommendations)	Type 2 Diabetes Mellitus (T2DM)	Clinical metabolic outcomes ↑ diversity & abundance of fibre-promoted SCFA producers
Ni et al. (2023)	China	Randomised, double-blind, placebo-controlled clinical trial	200 adults with NAFLD	Resistant starch (type 2 from high-amylose maize, 40 g/day, 4 months)	Control starch (equal energy supply)	Non-alcoholic fatty liver disease (NAFLD)	↓ Intrahepatic triglyceride content and ↓ serum branched-chain amino acids (BCAAs), gut microbiota restructuring
Li et al. (2024)	China	Randomised, placebo-controlled crossover clinical trial	37 adults with overweight/obesity	Resistant starch (40 g/day from high-amylose maize starch, HAM-RS2)	Control starch (amylopectin, 0 g resistant starch, isoenergetic diet)	Obesity & Metabolic Syndrome (insulin resistance)	↓ Body weight, improved insulin resistance, improved glucose metabolism and ↑ Bifidobacterium adolescentis; altered bile acid profile
Allegretti et al. (2020)	USA	Randomised, double-blind, placebo-controlled pilot RCT	22 obese adults	Faecal Microbiota Transplantation (FMT) capsules from single lean donor	Placebo capsules	Obesity (without metabolic complications)	Safety, microbiome modulation, metabolic markers and Sustained microbiome shifts toward donor profile
Li et al. (2024)	China	RCT	96 overweight/obese adults	Healthy low-carbohydrate diet (HLCD) and 10-h time-restricted eating (TRE), alone or combined, with isocaloric restriction	Isocaloric-restricted feeding alone	Obesity/Overweight	↓ Body weight, ↓ BMI, ↓ fat mass (HLCD), ↓ lean mass (TRE). HLCD ↓ faecal branched-chain amino acids; TRE ↑ probiotic species involved in SCFA synthesis
Guo et al. (2021)	China	RCT	39 adults with metabolic syndrome	8-week "2-day" modified intermittent fasting regimen (69% caloric reduction on fasting days)	Control group (no intermittent fasting)	Metabolic Syndrome / Cardiometabolic disease risk	↓ Fat mass, ↓ oxidative stress, ↓ inflammatory cytokines, ↑ endothelial function. ↑ Diversity, distinct compositional shifts

Cox et al. (2020)	United Kingdom	RCT	52 adults with quiescent Crohn's disease or ulcerative colitis and persistent gut symptoms	Low FODMAP diet (4 weeks)	Control diet with standard dietary advice	Inflammatory Bowel Disease (IBD)	Gut symptom management and microbiome modulation and ↓ Bifidobacterium adolescentis, ↓ Bifidobacterium longum, ↓ Faecalibacterium prausnitzi
Srivastava et al. (2024)	Finland	Randomised, double-blind, placebo-controlled trial	200 adults with diarrhea-predominant irritable bowel syndrome (IBS-D).	Daily oral intake of probiotic Bifidobacterium longum CECT 7347 (ES1) or postbiotic heat-treated B. longum CECT 7347 (HT-ES1) for 12 weeks	Placebo	Irritable Bowel Syndrome (IBS-D)	Symptom improvement, gut function regulation. potential modulation of gut microbiota activity
Wu et al. (2023)	China	RCT	31 patients with Type 2 Diabetes Mellitus (T2DM)	FMT alone and FMT plus metformin	Metformin alone	Type 2 Diabetes Mellitus (T2DM)	↓ HOMA-IR (improved insulin resistance), ↓ BMI, ↓ fasting and postprandial glucose, ↓ HbA1c. ↑ Microbial diversity; successful colonisation of donor microbiota
Tettamanzi et al. (2021)	Italy	Randomised Controlled Crossover Feeding Trial	20 insulin-resistant obese women	High-protein isocaloric diet for 21 days	Mediterranean isocaloric diet	Type 2 Diabetes risk	↓ Insulin resistance, ↓ HOMA-IR, ↓ Glycemic variability. ↑ Lachnoclostridium, shifts in Lachnospiraceae, Ruminococcaceae, Peptostreptococcaceae, Acidaminococcaceae, Clostridiaceae, Coriobacteriaceae, Desulfovibrionaceae
Rinott et al. (2022)	Israel	RCT	294 adults with abdominal obesity and/or dyslipidemia	Green-Mediterranean diet enriched with walnuts (28g/day), green tea, and Mankai aquatic plant	Healthy dietary guidelines (standard counseling) and traditional Mediterranean	Cardiometabolic disorders (obesity, dyslipidemia)	↓ Body weight, ↓ cardiometabolic biomarkers (cholesterol, triglycerides), improved metabolic health. ↑ microbial enzymatic functions in branched-chain amino acid degradation, ↓ Bifidobacterium, ↓

							functions in branched-chain amino acid biosynthesis
Facchin et al. (2020)	Finland	Double-blind, placebo-controlled pilot RCT	49 IBD patients (19 Crohn's disease, 30 ulcerative colitis) + 18 healthy volunteers as reference group	Oral microencapsulated sodium-butyrate supplementation (colonic delivery) for 2 months alongside conventional therapy	Placebo + conventional therapy	Inflammatory Bowel Disease (Crohn's disease, Ulcerative colitis)	Clinical and microbiome outcomes. ↑ SCFA-producing bacteria in ulcerative colitis patients (Lachnospiraceae spp.); ↑ Butyricicoccus in Crohn's disease patients
Ng et al. (2022)	China	Double-blind, Randomised, Placebo-Controlled Trial	61 obese adults with Type 2 Diabetes Mellitus (T2DM)	FMT combined with lifestyle Intervention, every 4 weeks up to 12 weeks	FMT alone, and Sham Transplantation plus lifestyle Intervention	Type 2 Diabetes Mellitus	Improved lipid metabolism and liver function (↓ LDL, ↓ total cholesterol, ↓ liver stiffness). ↑ Engraftment of lean-associated microbiota. ↑ Butyrate-producing bacteria, ↑ Bifidobacterium, ↑ Lactobacillus
Hibberd et al. (2019)	Finland	Randomised, double-blind, placebo-controlled trial	134 overweight or obese adults	(1) Bifidobacterium animalis subsp. lactis 420™ (B420) 10^{10} cfu/d; (2) Litesse® Ultra™ polydextrose (LU) 12 g/d; (3) LU + B420 combination for 6 months	Placebo (12 g/d microcrystalline cellulose)	Obesity-related metabolic disorder	↓ Waist-hip ratio, ↓ body fat mass, improved gut barrier function. ↑ Lactobacillus and Akkermansia with B420; ↑ Akkermansia, Christensenellaceae, Methanobrevibacter; ↓ Paraprevotella
Paramsothy et al. (2019)	Australia	Randomised Controlled Trial (Double-blind)	81 patients with active ulcerative colitis (UC); adults; randomised to FMT or placebo	Intensive multidonor faecal microbiota transplantation via colonoscopy and enemas, 5 days/week for 8 weeks	Placebo enemas (with option for open-label FMT post-trial)	Ulcerative Colitis (Inflammatory Bowel Disease)	↓ Disease activity, induction of remission. ↑ Microbial diversity
De Mauri et al. (2022)	Italy	Randomised, double-blind, placebo-controlled clinical trial	57 adults with advanced chronic kidney disease (CKD) on a low-protein diet	Low-protein diet + probiotics (Bifidobacterium longum and Lactobacillus reuteri)	Low-protein diet + placebo	Chronic Kidney Disease (CKD)	↓ Microbiota-derived uremic toxins, improved microbiota modulation
Palacios et al. (2020)	China	Randomised Controlled Pilot Study	60 adults (with prediabetes or early T2DM	Multi-strain probiotic for 12 weeks	Placebo	Type 2 Diabetes Mellitus / Prediabetes	Adjunctive probiotic intervention with metformin. ↑ Butyrate-producing pathways, ↑ Plasma butyrate, no overall

							significant microbiome change in full sample
Zhang et al. (2023)	USA	Randomised controlled dietary intervention trial (crossover design)	55 obese surveillance patients with a history of colourectal neoplasia	Daily consumption of one cup of study beans added to usual diet	Usual diet without beans	Metabolic obesity, colourectal neoplasia risk	Dietary (prebiotic food-based) intervention. ↑ Microbial diversity. ↑ Faecal ibacterium, Eubacterium, Bifidobacterium; Parallel shifts in circulating metabolites
Lauw et al. (2023)	China	Randomised Controlled Trial	55 overweight or obese adults; Hong Kong Chinese individuals	8-week dietary intervention: increased fruit & vegetable intake and/or synbiotic supplementation (L. acidophilus NCFM + B. lactis HN019 + polydextrose)	Dietary intervention only; synbiotic only; baseline	Obesity / Metabolic Syndrome	Clinical outcomes (metabolic and microbiome changes). ↓ Megamonas abundance
Paramsothy et al. (2017)	Australia	Multicentre, double-blind, randomised, placebo-controlled trial	85 adults with active ulcerative colitis (Mayo score 4–10)	Intensive-dosing, multidonor faecal microbiota transplantation via colonoscopic infusion + enemas (5 days/week for 8 weeks)	Placebo colonoscopic infusion and enemas	Ulcerative colitis	Clinical remission and endoscopic response. ↑ Microbial diversity
Haifer et al. (2022)	Australia	Double-blind RCT	35 adults with active ulcerative colitis	Oral lyophilised faecal microbiota transplantation (FMT) following antibiotic pre-treatment	Placebo capsules	Ulcerative Colitis (Inflammatory Bowel Disease)	Clinical and endoscopic remission, histological response. Improved gut microbial diversity and restoration of healthy microbiota composition
Mocanu et al. (2021)	Canada	Double-blind Randomised Controlled Trial (RCT)	70 adults with severe obesity and metabolic syndrome	Oral FMT (from lean donors) + daily low-fermentable (LF) or high-fermentable (HF) fibre supplementation	FMT-HF, HF, and LF groups	Metabolic Syndrome / Type 2 Diabetes risk	↑ Phascolarctobacterium, ↑ Bacteroides stercoris, ↑ Bacteroides caccae associated with improved insulin sensitivity
Mo et al. (2022)	South Korea	Randomised, double-blind, placebo-controlled trial	72 overweight adults	Probiotic supplementation with Lactobacillus curvatus HY7601 and Lactobacillus plantarum KY1032 (1×10^{10} CFU for 12 weeks)	Placebo (same product without probiotics)	Obesity / Overweight	↓ Body weight, ↓ visceral fat mass, ↓ waist circumference, ↑ adiponectin. ↑ Bifidobacteriaceae, ↑ Akkermansiaceae, ↓

							Prevotellaceae, ↓ Selenomonadaceae, improved beta diversity
Ren et al. (2020)	China	RCT	45 adults with Type 2 Diabetes	Almond-based low-carbohydrate diet	Low-fat diet	Type 2 Diabetes (T2DM)	↓ HbA1c, ↓ depression symptoms. ↑ SCFA-producing bacteria
Birkeland et al. (2020)	Norway	Placebo-controlled crossover study	25 patients with type 2 diabetes	16 g/day inulin-type fructans (mixture of oligofructose and inulin) for 6 weeks	16 g/day maltodextrin (placebo), 6 weeks, with 4-week washout	Type 2 Diabetes	↑ Bifidobacterium adolescentis and Bacteroides, ↑ total SCFA, acetic acid, and propionic acid; no change in butyric acid or overall diversity
Yılmaz et al (2018)	Turkey	Prospective, open-label RCT	45 patients with Inflammatory Bowel Disease (25 treatment, 20 control)	400 mL/day kefir for 4 weeks	Control group (no kefir)	Inflammatory Bowel Disease (Ulcerative Colitis, Crohn's Disease)	↑ Lactobacillus spp., ↑ Lactobacillus kefiri , significant microbiome modulation.
Djekic et al. (2020)	Sweden	Randomised crossover trial	27 patients with ischemic heart disease.	Vegetarian diet for 4 weeks	Meat diet for 4 weeks, with 4-week washout between phases	Cardiovascular disease (Ischemic heart disease)	↑ Ruminococcaceae, Lachnospiraceae, Akkermansiaceae; differences in plasma metabolites (↓ L-carnitine, acylcarnitine metabolites)
Lu et al. (2025)	China	Randomised, double-blind, placebo-controlled trial	309 adults with type 2 diabetes and hypertriglyceridemia	4 g/day fish oil (omega-3 fatty acids: DHA + EPA) for 12 weeks	Corn oil (placebo)	Type 2 Diabetes	Minor alterations in gut microbiota
Dwibedi et al. (2025)	Sweden	Randomised, double-blind, placebo-controlled trial (RCT)	74 drug-naive individuals with prediabetes	Broccoli sprout extract containing sulforaphane, once daily for 12 weeks	Placebo	Prediabetes / Type 2 Diabetes risk	Responders exhibited distinct gut microbiota composition; higher abundance of Bacteroides-encoded transcriptional regulator linked to sulforaphane bioactivation
Li et al. (2025)	China	Randomised, double-blind controlled trial	131 adults overweight/obese and healthy adults	Inulin and Fructooligosaccharides supplementation for 4 weeks	Placebo	Metabolic diseases (Type 2 Diabetes risk, hyperhomocysteinemia)	↓ Ruminococcus abundance, ↓ Propionate, ↑ microbial folate & glutathione metabolism (inulin), ↑ purine

							metabolism (Fructooligosaccharides
Wang et al. (2023)	USA	Randomised Controlled Crossover Trial	19 healthy young adults	Healthy U.S.-Style Dietary Pattern : 1) lacto-ovo vegetarian diet 2) lacto-ovo vegetarian diet + 3 oz/day unprocessed lean red meat (URM), 3) lacto-ovo vegetarian diet + 3 oz/day processed lean red meat	Within-subject comparison of 3 diet phases	Cardiovascular Disease	Healthy U.S.-Style Dietary Pattern induced shifts in 23 bacterial taxa; no significant differences in taxonomic composition between meat vs. vegetarian diets; no change in faecal SCFA
Kallapura et al. (2024)	India	Prospective Clinical Trial	30 adults with Type 2 diabetes and hyperlipidaemia	Microbiome-based personalised nutrition guided by BugSpeaks® profiling (whole genome shotgun metagenomics)	Standard diabetic nutritional guidance	Type 2 Diabetes, Hyperlipidaemia	↑ Alpha diversity, ↑ Phascolarctobacterium succinatutens, Bifidobacterium angulatum, Levilactobacillus brevis; ↓ Alistipes finegoldii, Sutterella faecalis
Bai et al. (2024)	China	Randomised, double-blind, placebo-controlled trial	75 overweight or obese young adults	Bifidobacterium breve BBr60 (1×10^{10} CFU/day) for 12 weeks + diet guidance	Placebo + diet guidance	Obesity	↓ BMI, ↓ body weight, ↓ fasting blood glucose, improved lipid and liver function

BCAA = Branched-Chain Amino Acid; BMI = Body Mass Index; CFU = Colony-Forming Unit; CKD = Chronic Kidney Disease; DHA = Docosahexaenoic Acid; EPA = Eicosapentaenoic Acid; ES1 = Bifidobacterium longum CECT 7347; FMT = Faecal Microbiota Transplantation; FODMAP = Fermentable Oligosaccharides, Disaccharides, Monosaccharides and Polyols; HAM-RS2 = High-Amylose Maize Resistant Starch Type 2; HbA1c = Glycated Haemoglobin; HF = High-Fermentable Fibre; HLCD = Healthy Low-Carbohydrate Diet; HOMA-IR = Homeostatic Model Assessment of Insulin Resistance; HT-ES1 = Heat-Treated Bifidobacterium longum CECT 7347; IBD = Inflammatory Bowel Disease; IBS = Irritable Bowel Syndrome; IBS-D = Diarrhoea-Predominant Irritable Bowel Syndrome; LDL = Low-Density Lipoprotein; LF = Low-Fermentable Fibre; LU = Litesse® Ultra™ Polydextrose; NAFLD = Non-Alcoholic Fatty Liver Disease; RCT = Randomised Controlled Trial; SCFA = Short-Chain Fatty Acid; T2DM = Type 2 Diabetes Mellitus; TRE = Time-Restricted Eating; U = Usual Care; UC = Ulcerative Colitis; URM = Unprocessed Lean Red Meat; WTP = Whole Grains, Traditional Chinese Medicinal Foods, and Prebioti

3.2 Risk of bias assessment

The Cochrane Risk of Bias Tool (RoB 2) was used to assess the methodological quality of the included randomised controlled trials (RCTs) in five different domains. The majority of trials showed a low overall risk of bias, as shown in Figure 4, especially in the areas of reporting, outcome measurement, and randomisation. However, adherence and blinding issues, which are frequent problems in nutritional and lifestyle trials, were present in a number of diet- and behaviour-based interventions. Due primarily to open-label designs or inadequate allocation concealment, only a small number of studies were deemed to have a high risk of bias. About 55% of studies were low risk overall, 33% had some concerns, and 6% were high risk. This suggests that while the evidence base is generally strong, participant blinding and intervention fidelity should be interpreted with some caution. No non-randomised study was included in the final review, hence no assessment of non-randomised study.

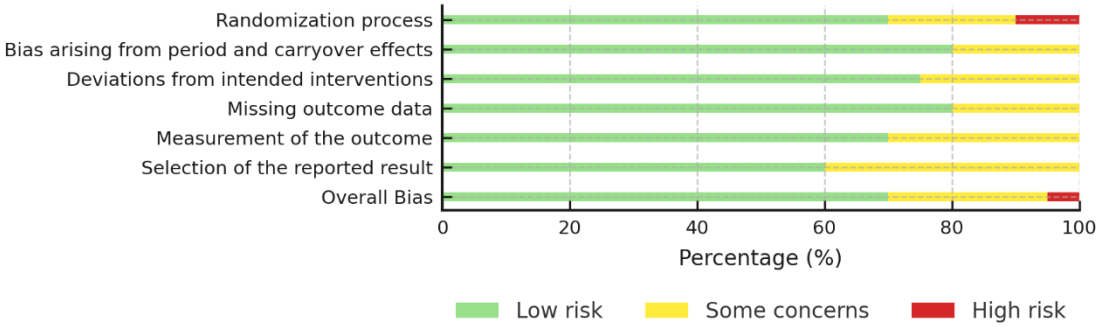

Figure 4 Risk of bias graph as a percentage (per protocol). The six domains of bias, including overall bias, are presented.

3.3 Intervention categories

The results are presented by major intervention class: dietary interventions, probiotics/prebiotics/synbiotics, faecal microbiota transplantation (FMT), and personalised/functional nutrition and combined approaches.

3.3.1 Dietary interventions

Among the included trials (n = 12), dietary modulation of the gut microbiome which includes high-fibre diets, resistant starch supplementation, Mediterranean-style patterns, vegetarian diets, and fasting-based regimens was the most often researched approach. When taken as a whole, these treatments consistently improved metabolic results and microbial diversity.

In comparison to standard diabetic care, Zhao et al. (2018) showed that a varied, high-fibre diet full of whole grains and traditional Chinese medicinal foods significantly improved glycaemic control in people with type 2 diabetes mellitus (T2DM). In addition to enriching Faecalibacterium and Roseburia, taxa linked to the synthesis of short-chain fatty acids (SCFAs), participants who received the high-fibre intervention saw a greater decrease in HbA1c (89 percent achieving < 7% vs. 50% in controls). In a similar vein, Ni et al. (2023) found that supplementing with resistant starch (RS) in patients with non-alcoholic fatty liver disease (NAFLD) reduced serum branched-chain amino acids and increased Bacteroides stercoris, which changed the gut microbiome and resulted in a 9% absolute decrease in hepatic triglyceride content. By enriching Bifidobacterium adolescentis and changing bile-acid profiles, Li et al. (2024) demonstrated that resistant starch from high-amylose maize improved insulin sensitivity and decreased body weight by an average of 2.8 kg in overweight adults.

Positive changes in the microbiome were also brought about by Mediterranean-style diets. In comparison to both the traditional Mediterranean and control diets, the Green-Mediterranean diet supplemented with walnuts, green tea, and the aquatic plant Mankai produced higher cardiometabolic improvements and an increase in Prevotella (Rinott et al., 2022). Similarly, Djekic et al. (2020) found that a vegetarian diet increased Ruminococcaceae and Akkermansiaceae while decreasing body weight and oxidised LDL cholesterol.

Other feeding strategies, like intermittent fasting and time-restricted eating, provided additional evidence for the metabolic advantages mediated by the microbiome. According to Guo et al. (2021), an eight-week modified IF regimen in patients with metabolic syndrome increased microbial diversity and SCFA production while also improving endothelial function and lowering inflammatory cytokines. Beyond calorie restriction alone, Li et al. (2024) discovered that TRE increased probiotic species and SCFA synthesis when combined with a nutritious low-carb diet. When dietary interventions were combined, they consistently improved glycaemic, lipid, and inflammatory profiles by increasing microbial diversity and SCFA-producing taxa. Diet is the most scalable microbiome-modifying strategy for preventing chronic diseases, according to these findings.

3.3.2 Probiotics, Prebiotics, and Synbiotics

The therapeutic potential of probiotics, prebiotics, or synbiotics in regulating the gut microbiome and metabolic health was evaluated in ten studies (n = 10). Overweight adults who took a probiotic supplement containing Bifidobacterium breve BBr60 for 12 weeks saw significant decreases in their BMI, fasting glucose, and liver enzymes. Dialister and Klebsiella species were also regulated (Bai et al., 2024). Similarly, Mo et al. (2022) showed that supplementing with Lactobacillus curvatus HY7601 and L. plantarum KY1032 decreased visceral fat mass and waist circumference while increasing Bifidobacteriaceae and Akkermansiaceae.

The effects of prebiotic fibres were complementary. While Li et al. (2025) reported that inulin and fructooligosaccharides differentially improved glycaemic and homocysteine parameters in overweight adults, Birkeland et al. (2020) found that 16 g/day of inulin-type fructans increased Bifidobacterium adolescentis and total SCFA levels in T2DM patients. This pattern was further supported by the fact that the resistant starch interventions mentioned above worked similarly to prebiotics.

Synergistic improvements were achieved through the use of synbiotic approaches. Combining Bifidobacterium animalis subsp. lactis B420 with polydextrose dramatically decreased body fat and the waist-hip ratio while increasing Akkermansia and Christensenellaceae, according to Hibberd et al. (2019). Lauw et al. (2023) demonstrated in a complementary design that combining increased fruit and vegetable intake with synbiotic supplementation resulted in better lipid profiles and more weight loss than either intervention alone.

3.3.3 Faecal Microbiota Transplantation (FMT)

FMT was assessed as a microbiome-restoration treatment for inflammatory and metabolic disorders in seven trials (n = 7). Because of donor-microbiota engraftment and the enrichment of Bifidobacterium adolescentis and Synechococcus species, Wu et al. (2023) found that FMT, either by itself or in conjunction with metformin, improved insulin sensitivity and decreased BMI and HbA1c in type 2 diabetes. Ng et al. (2022) also demonstrated that, in obese diabetic adults, FMT plus lifestyle modification improved lipid and liver profiles and butyrate-producing bacteria in comparison to either treatment alone. Numerous multicentre trials provided compelling evidence of FMT's effectiveness in treating inflammatory bowel disease. Together, Paramsothy et al. (2017, 2019) and Haifer et al. (2022) showed that corticosteroid-free remission was achieved in as many as 53% of ulcerative colitis patients through intensive multidonor or encapsulated FMT protocols, accompanied by long-lasting improvements in microbial diversity and increases in Roseburia inulivorans and Eubacterium hallii. Similar to the microbial restoration brought about by FMT, Facchin et al. (2020) observed that oral butyrate supplementation acting as a postbiotic increased SCFA-producing Lachnospiraceae and Butyricicoccus. All things considered, FMT interventions were well-tolerated and safe, resulting in significant improvements in inflammation or metabolism as well as the quick restoration of robust microbial ecosystems. However, the need for standardised procedures prior to widespread implementation is highlighted by the variation in recipient response, donor composition, and delivery method.

3.3.4 Personalised and Functional Nutrition Approaches

As precision microbiome interventions, functional bioactive compounds and personalised nutrition were investigated in recent studies. By using microbiome profiling to guide a personalised nutrition trial, HbA1c (from 8.3 to 6.7%), systolic blood pressure (−5%), and C-reactive protein (−19%) were significantly reduced (Kallapura et al., 2024). Additionally, there was an increase in microbial diversity and enrichment of Bifidobacterium and Phascolarctobacterium. Similar

microbiome-dependent responses were shown by functional bioactives: Lu et al. (2025) discovered that omega-3 supplementation changed gut microbial predictors of lipid responsiveness, while Dwibedi et al. (2025) demonstrated that sulforaphane derived from broccoli sprouts decreased fasting glucose by up to 0.4 mmol/L in responders with particular Bacteroides signatures.

3.4 Microbiome–Disease Mechanistic Links

The studies included in this review consistently identified several mechanistic pathways linking gut microbiome modulation to chronic disease prevention and management. Across dietary, probiotic, prebiotic, synbiotic, and faecal microbiota transplantation (FMT) interventions, convergent biological processes were observed, including the regulation of short-chain fatty acid (SCFA) metabolism, bile-acid transformation, gut barrier integrity, and systemic inflammation (table 3). These mechanisms collectively underpin the microbiome's role in modulating metabolic, cardiovascular, and inflammatory diseases.

3.4.1 Short-Chain Fatty Acid (SCFA) Production and Metabolic Regulation

Increased faecal concentrations of acetate, propionate, and butyrate metabolites essential for preserving intestinal and systemic metabolic homeostasis were consistently linked to dietary fibre and prebiotic interventions. A varied, high-fibre diet, for instance, dramatically increased the abundance of SCFA-producing genera like Faecalibacterium prausnitzii and Roseburia intestinalis in patients with type 2 diabetes mellitus (T2DM), according to Zhao et al. (2018). In a similar vein, Birkeland et al. (2020) found that supplementing diabetic adults with inulin-type fructan increased their faecal acetate and butyrate levels, which resulted in quantifiable improvements in gut barrier function and fasting glucose.

Intermittent fasting raised plasma butyrate concentrations and SCFA-producing taxa (Bacteroides, Lachnospiraceae) in metabolic syndrome, which were linked to decreased systemic inflammation and enhanced endothelial function, according to Guo et al. (2021). By restoring SCFA pathways and increasing Bacteroides stercoris activity, Ni et al. (2023) further demonstrated that resistant starch supplementation in nonalcoholic fatty liver disease (NAFLD) decreased circulating branched-chain amino acids and hepatic triglyceride content. Collectively, these investigations highlight the function of SCFA metabolism as a crucial mediator that connects enhanced glucose, lipid, and inflammatory homeostasis with gut microbial activity.

3.4.2 Modulation of Bile Acid Metabolism

Another mechanistic pathway that was consistent across interventions was altered bile acid signalling. A diet high in fibre and polyphenols altered the composition of the gut microbiota to promote the production of secondary bile acids, improving lipid profiles and cardiometabolic risk factors, according to the Green-Mediterranean diet trial by Rinott et al. (2022). In a similar vein, Li et al. (2024) found that Bifidobacterium adolescentis and Bacteroides vulgatus mediated resistant starch intervention, which changed bile acid profiles and enhanced insulin sensitivity. Significant improvements in glycaemic control and lipid regulation in patients with type 2 diabetes were found to be correlated with an increase in beneficial bile acid-metabolizing bacteria, such as Bifidobacterium and Eubacterium hallii, in a metabolic FMT study conducted by Wu et al. (2023).

3.4.3 Immune Modulation and Anti-Inflammatory Effects

Numerous studies have demonstrated how immune modulation and inflammation reduction, particularly in chronic inflammatory and metabolic diseases, are facilitated by microbiome remodelling. According to Paramsothy et al. (2019), intensive multidonor FMT reduced Proteobacteria abundance and restored microbial diversity in patients with inflammatory bowel disease (IBD), resulting in steroid-free remission for ulcerative colitis patients. Alongside these alterations, butyrate-producing taxa that are known to block NF-κB-mediated inflammatory cascades, like Roseburia inulivorans and Eubacterium hallii, were enriched. Facchin et al. (2020) observed similar effects using oral sodium butyrate supplementation, which increased Lachnospiraceae and Butyricicoccus abundance and reduced inflammatory biomarkers.

Probiotic supplementation with Lactobacillus curvatus and Bifidobacterium breve decreased systemic inflammatory cytokines (IL-6, TNF-α) in metabolic disorders, which was linked to decreases in visceral adiposity, according to Mo et al. (2022) and Bai et al. (2024). Similarly, Ni et al. (2023) showed that resistant starch decreased oxidative stress and hepatic inflammation in NAFLD.

3.4.4 Gut Barrier Integrity and Endotoxemia Reduction

Synbiotic supplementation (B420 + polydextrose) enhanced Akkermansia abundance, improving intestinal barrier function and lowering plasma lipopolysaccharide (LPS) levels, according to Hibberd et al. (2019). Similarly, probiotic treatment improved insulin sensitivity and decreased intestinal permeability markers (zonulin and LPS), according to Mo et al. (2022). High-fibre and Mediterranean-style diets improved mucosal health in dietary trials, according to Rinott et al. (2022) and Zhao et al. (2018). This demonstrated the functional connection between dietary fermentation, SCFA production, and barrier protection.

3.4.5 Modulation of Host Metabolites and Signalling Pathways

Additionally, host metabolite pools and hormonal pathways implicated in glucose homeostasis and energy balance were affected by microbiome-targeted interventions. For instance, FMT combined with dietary modification improved hepatic lipid metabolism and raised GLP-1 levels, indicating improved enteroendocrine signalling, according to Ng et al. (2022). Ni et al. (2023) demonstrated in another study that increased insulin sensitivity was associated with the suppression of branched-chain amino acids (BCAAs) through resistant starch intervention.

3.4.6 Reduction of Pathogenic and Pro-Inflammatory Taxa

Following multidonor FMT, Paramsothy et al. (2019) observed a significant decrease in Fusobacterium and Escherichia/Shigella, which coincided with ulcerative colitis's clinical remission. In a similar vein, Zhang et al. (2023) and Li et al. (2024) showed that probiotic or RS interventions improved inflammatory and metabolic markers by selectively suppressing Sutterella wadsworthensis and Clostridium bolteae. The decline in these pro-inflammatory taxa emphasises the detoxifying function of the microbiome in preventing chronic illnesses.

Table 3 Mechanistic model linking gut microbiome modulation to chronic disease management.

Mechanistic Pathway	Description / Biological Function	Representative Interventions & Study Examples	Key Microbial Taxa Affected	Associated Clinical Outcomes
Enhanced SCFA Production and Energy Metabolism	Fermentation of dietary fibres and resistant starch produces SCFAs (acetate, propionate, butyrate), which improve insulin sensitivity, regulate lipid metabolism, and reduce systemic inflammation.	High-fibre diet in T2DM (Zhao et al., 2018); Resistant starch in NAFLD (Ni et al., 2023; Li et al., 2024); Inulin-type fructans (Birkeland et al., 2020)	↑ *Faecalibacterium prausnitzii*, *Roseburia*, *Bifidobacterium*, *Akkermansia muciniphila*	↓ HbA1c, ↓ fasting glucose, ↓ hepatic triglycerides, ↑ insulin sensitivity
Modulation of Bile Acid Metabolism	Gut microbes deconjugate bile acids, influencing FXR/TGR5 pathways that regulate	Green-Mediterranean diet (Rinott et al., 2022); Resistant starch (Li et al., 2024); FMT in T2DM (Wu et al., 2023)	↑ *Bacteroides*, *Eubacterium hallii*, *Bifidobacterium adolescentis*	↓ Total cholesterol, ↓ triglycerides, improved lipid metabolism,

	lipid and glucose metabolism.			enhanced GLP-1 signaling
Immune Modulation and Anti-inflammatory Effects	Restoration of eubiosis increases anti-inflammatory metabolites and reduces pro-inflammatory cytokines (IL-6, TNF-α).	Multidonor FMT in ulcerative colitis (Paramsothy et al., 2019; Haifer et al., 2022); Butyrate supplementation (Facchin et al., 2020); Probiotic therapy (Bai et al., 2024)	↑ *Eubacterium hallii*, *Roseburia*, *Lachnospiraceae*, ↓ *Proteobacteria*	↓ CRP, ↓ IL-6, ↓ TNF-α, clinical remission in IBD, ↓ visceral adiposity
Restoration of Gut Barrier Integrity	SCFAs strengthen tight junctions and mucin production, reducing intestinal permeability and endotoxemia.	Synbiotic (B420 + polydextrose) (Hibberd et al., 2019); *L. curvatus* & *L. plantarum* (Mo et al., 2022); High-fibre diet (Zhao et al., 2018)	↑ *Akkermansia muciniphila*, *Faecalibacterium*, *Bifidobacterium*	↓ Plasma LPS, ↓ gut permeability (zonulin), improved inflammation and metabolic control
Reduction of Pathogenic / Pro-inflammatory Taxa	Microbiome modulation suppresses harmful bacteria producing endotoxins and pro-inflammatory metabolites.	FMT in UC (Paramsothy et al., 2019); RS and probiotic interventions (Li et al., 2024; Zhang et al., 2023)	↓ *Fusobacterium nucleatum*, *Escherichia coli*, *Sutterella wadsworthensis*	↓ Inflammatory biomarkers, ↓ oxidative stress, improved IBD remission and metabolic health
Alteration of Host Metabolites and Hormonal Pathways	Gut microbial metabolites modulate GLP-1 secretion, bile acid signaling, and amino acid metabolism, influencing energy balance.	FMT + lifestyle intervention (Ng et al., 2022); RS in NAFLD (Ni et al., 2023); Broccoli sprout extract (Dwibedi et al., 2025); Omega-3 supplementation (Lu et al., 2025)	↑ *Bacteroides*, *Eubacterium*, ↓ *Clostridium bolteae*	↑ GLP-1, ↓ BCAAs, ↓ fasting glucose, improved lipid and inflammatory profiles
Personalised and Precision Nutrition Effects	Microbiome-guided diet personalisation tailors nutrient intake to individual microbial profiles, optimizing response.	Microbiome-based personalised diet (Kallapura et al., 2024)	Individual-specific enrichment (↑ *Phascolarctobacterium*, *Bifidobacterium*)	↓ HbA1c, ↓ CRP, ↓ blood pressure, personalised metabolic improvements

3.5 Integration into Public Health Frameworks

A strong epidemiological basis supports the incorporation of microbiome science into public health frameworks: dysbiosis is both common and treatable with scalable, reasonably priced dietary interventions. Fibre promotion is essentially reframed by microbiome research as a precision intervention that targets particular microbial taxa and metabolic pathways rather than as a general recommendation for digestive health. According to Melby et al. (2025), the public health microbiome curriculum for public health professionals specifically acknowledges that "fibre serves as a primary energy source for beneficial gut bacteria, which, in turn, produce short-chain fatty acids that regulate metabolism, immune function, and gut barrier integrity." This curriculum gives educators evidence-based, mechanistic language to improve the efficacy of dietary counselling.

The viability of population-level fibre-based interventions is supported by empirical data from the included studies. Testing in 55 obese surveillance patients with a history of colourectal neoplasia, bean consumption (Zhang et al., 2023) was associated with favourable changes in circulating metabolites such as pipecolic acid and indole reduction, as well as enhanced microbial diversity and enriched protective taxa (Faecalibacterium, Eubacterium, and Bifidobacterium). Crucially, beans are an inexpensive, culturally acceptable, and shelf-stable food that doesn't need refrigeration or special processing qualities qualities necessary for implementation at the equitable population level. Campaigns to promote whole grains can also use microbiome-informed messaging; the Chinese population's high-fibre, whole-grain dietary intervention (Zhao et al. 2018) shows effectiveness in non-Western settings, confirming the universality of the microbiome-driven health benefits across various food systems and dietary customs.

Formally incorporating fibre promotion into policies aimed at preventing chronic diseases should make use of the public health infrastructure already in place while honing messaging based on microbiome mechanisms. However, insoluble fibre (found in bran and leafy greens) offers mechanistic benefits through reduced colonic transit time and increased stool bulk, while fermentable, soluble fibres (found in whole grains, legumes, and some fruits and vegetables) preferentially enrich SCFA-producing bacteria (Zhang et al. 2023; Zhao et al. 2018). The population impact is quantified by research from the University of Florida (Alahmari, 2024), which shows that every 5 g of dietary fibre consumed daily lowers the incidence of chronic kidney disease by over 10% and every 10 g daily lowers the mortality rate from all causes by 10%. A significant decrease in the burden of disease would result from scaling these reductions across populations. Plant biodiversity should be highlighted in public health campaigns that promote foods high in fibre. People who eat a variety of plant foods have more diverse gut microbiotas and favourable metabolic signatures than people who eat a limited number of plant species, even when they consume the same amounts of fibre.

Since they simultaneously supply probiotic microorganisms and prebiotic substrates that support microbial establishment, fermented foods constitute a special category of public health interventions. In the included study, Ylmaz et al. (2018) showed that 400 mL of kefir per day for four weeks resulted in a significant modulation of the microbiota in patients with inflammatory bowel disease, as evidenced by improvements in haemoglobin, C-reactive protein, erythrocyte sedimentation rate, and symptom scores. Since kefir and other fermented dairy products are part of many cultures' ingrained culinary customs, they may be adopted by the general public.

However, critical misconceptions limit fermented food campaigns' effectiveness. Vinderola et al. (2023) found that 52% of Americans believe fermented foods are inherently probiotic, yet most fermented foods lack live microorganisms meeting the definitional criteria for probiotics (minimum 10^6 CFU/mL at point of consumption). Public health messaging must distinguish between fermented foods providing sensory/cultural benefits, fermented foods with viable probiotics, and standalone probiotic supplementation. Effective campaigns should: (1) specify probiotic viability requirements at point of sale and consumption; (2) promote traditionally fermented products (yogurt, kefir, kimchi, sauerkraut, tempeh) with documented microbial populations; and (3) integrate fermented foods into dietary pattern recommendations rather than positioning them as stand-alone interventions.

Without specifically mentioning microbiome mechanisms, the American Heart Association, American Diabetes Association, and American Cancer Society's current nutritional guidelines place a strong emphasis on plant-based dietary patterns, whole grain consumption, and legume inclusion. First, with recommendations for fermentable fibre sources, dietary guidelines should specifically focus on fibre diversity rather than total quantity. In the included studies, the microbiome metrics and health outcomes are consistently better for the Mediterranean and plant-based dietary patterns. When comparing three different dietary patterns in 294 adults with abdominal obesity and/or dyslipidaemia, Rinott et al. (2022) found that the Green-Mediterranean diet which was enhanced with walnuts, green tea, and the aquatic plant Mankai produced better cardiometabolic improvements than the standard Mediterranean and control diets. Additionally, the microbiota shifted towards increased Bifidobacterium, which supports biosynthesis pathways, and Prevotella abundance, which is linked to the breakdown of branched-chain amino acids.

Second, using new technologies for microbiome assessment, guidelines should advocate for customised fibre implementation as opposed to universal fixed targets. Dietary intervention response is predicted by baseline microbiome composition; Mocanu et al. (2021) demonstrated that in certain patient subgroups, combining FMT with low-fermentable fibre improved insulin sensitivity more than high-fermentable fibre or fibre-only approaches. Personalised nutrition based on baseline microbiota assessment is more effective than population-level recommendations as microbiome testing becomes more widely available (Kallapura et al., 2024). In order to facilitate precision prevention strategies and preserve population-level dietary pattern guidance for unscreened populations,

policy should encourage the development of easily accessible microbiome assessment tools that allow clinicians to customise fibre recommendations to individual microbial profiles.

Third, in addition to standard clinical outcomes (glucose, lipids, weight), guidelines should specifically include metabolite endpoints (SCFAs, secondary bile acids). The included studies provide mechanistic biomarkers for the effectiveness of interventions and show that microbiota-driven metabolite changes frequently occur before clinical improvements. By including SCFA measurement in nutrition evaluations, it may be possible to identify dietary patterns more quickly and optimise interventions.

4 Conclusions and Recommendations

As a key connector between immunity, metabolism, nutrition, and general health, this systematic review shows how important the gut microbiota is to the prevention and treatment of chronic diseases. Interventions like dietary modification, probiotic and prebiotic supplementation, synbiotics, and faecal microbiota transplantation have been shown in randomised and controlled trials to improve intestinal barrier function, promote short-chain fatty acid production, restore microbial diversity, and control inflammation. All of these effects work together to improve gastrointestinal, cardiovascular, and metabolic health outcomes.

The results confirm that focussing on the gut microbiota presents a viable avenue for holistic disease management and precision nutrition. Thus, it is advised that microbiome assessment be incorporated into frameworks for the prevention and treatment of chronic diseases in future studies and clinical practice. Dietary patterns that support a healthy microbiome should be promoted by public health policies, especially those high in fibre, fermented foods, and plant-based nutrients. Additionally, the creation of individualised nutrition plans and dietary recommendations based on microbiome information may strengthen efforts to prevent disease, lower medical expenses, and enhance population health outcomes.

Implication For Practice

The implications of this review extend to clinical, community, and policy settings. Clinicians and nutritionists should consider the gut microbiome as a modifiable therapeutic target when designing individualised interventions for patients with obesity, diabetes, cardiovascular diseases, or inflammatory bowel disorders. Promoting microbiome-supportive diets can serve as an effective and sustainable preventive measure within primary healthcare frameworks. On a broader level, integrating microbiome science into national nutrition and chronic disease strategies could help shape evidence-based policies that prioritise dietary diversity and gut health. Policymakers should also ensure equitable access to microbiome-related innovations, especially in low-resource settings, where dietary transitions and chronic disease burdens are rapidly increasing.

Limitations and Recommendation for Future Studies

This review recognises a number of limitations despite the strength of the new evidence. The generalisability and comparability of the results are limited by the comparatively small sample sizes and inconsistent methodologies of many of the included studies. It is also challenging to establish clear causal relationships due to the variability in dietary interventions, measured outcomes, and microbiome sequencing techniques. Additionally, because the majority of research was done in high-income nations, populations from low- and middle-income areas, where dietary practices and microbiome profiles may vary significantly, were under-represented. These elements emphasise the need for more standardised, internationally inclusive research designs as well as for careful interpretation of recent findings.

Future investigations should focus on large-scale, multicentre, and longitudinal randomised controlled trials to confirm the efficacy of microbiome-targeted interventions across diverse populations. Standardisation of protocols for microbiome analysis and outcome measurement will be essential to enhance the reliability of evidence synthesis. Furthermore, there is a pressing need for studies that explore the cost-effectiveness, accessibility, and cultural adaptability of microbiome-based nutritional and therapeutic strategies in low- and middle-income countries. Such research will not only advance scientific understanding but also inform equitable, sustainable public health interventions.

Acknowledgements

The authors would like to sincerely thank the editorial team and the reviewer for their insightful criticism and helpful recommendations, which have greatly improved the calibre and readability of this work.

Conflict Of Interest

The authors certify that they do not have any competing interests to declare.

Declaration Of Use of Generative Ai

The authors affirm that generative AI tools were utilised exclusively for language refinement and formatting purposes, in accordance with Elicit Publishing Limited's publication ethics guidelines. All research content, analyses, and interpretations are entirely the responsibility of the authors.

Funding

This research received no funding.

References

Afzaal, M., Saeed, F., Shah, Y. A., Hussain, M., Rabail, R., Socol, C. T., ... & Aadil, R. M. (2022). Human gut microbiota in health and disease: Unveiling the relationship. *Frontiers in microbiology*, *13*, 999001.

Alahmari, L. A. (2024). Dietary fibre influence on overall health, with an emphasis on CVD, diabetes, obesity, colon cancer, and inflammation. *Frontiers in Nutrition*, *11*, 1510564.

Allegretti, J. R., Kassam, Z., Mullish, B. H., Chiang, A., Carrellas, M., Hurtado, J., ... & Thompson, C. (2020). Effects of faecal microbiota transplantation with oral capsules in obese patients. *Clinical Gastroenterology and Hepatology*, *18*(4), 855-863.

Bai, Z., Wu, Y., Gao, D., Dong, Y., Pan, Y., & Gu, S. (2024). Gut microbiome and metabolome alterations in overweight or obese adult population after weight-loss bifidobacterium breve BBr60 intervention: a randomized controlled trial. *International journal of molecular sciences*, *25*(20), 10871.

Biazzo, M., & Deidda, G. (2022). Faecal microbiota transplantation as new therapeutic avenue for human diseases. *Journal of clinical medicine*, *11*(14), 4119.

Birkeland, E., Gharagozlian, S., Birkeland, K. I., Valeur, J., Måge, I., Rud, I., & Aas, A. M. (2020). Prebiotic effect of inulin-type fructans on faecal microbiota and short-chain fatty acids in type 2 diabetes: a randomised controlled trial. *European journal of nutrition*, *59*(7), 3325-3338.

Cox, S. R., Lindsay, J. O., Fromentin, S., Stagg, A. J., McCarthy, N. E., Galleron, N., ... & Whelan, K. (2020). Effects of low FODMAP diet on symptoms, faecal microbiome, and markers of inflammation in patients with quiescent inflammatory bowel disease in a randomized trial. *Gastroenterology*, *158*(1), 176-188.

De Mauri, A., Carrera, D., Bagnati, M., Rolla, R., Vidali, M., Chiarinotti, D., ... & Del Piano, M. (2022). Probiotics-supplemented low-protein diet for microbiota modulation in patients with advanced chronic kidney disease (ProLowCKD): results from a placebo-controlled randomized trial. *Nutrients*, *14*(8), 1637.

Djekic, D., Shi, L., Brolin, H., Carlsson, F., Särnqvist, C., Savolainen, O., ... & Frøbert, O. (2020). Effects of a vegetarian diet on cardiometabolic risk factors, gut microbiota, and plasma metabolome in subjects with ischemic heart disease: a randomized, crossover study. *Journal of the American Heart Association*, *9*(18), e016518.

Dwibedi, C., Axelsson, A. S., Abrahamsson, B., Fahey, J. W., Asplund, O., Hansson, O., ... & Rosengren, A. H. (2025). Effect of broccoli sprout extract and baseline gut microbiota on fasting blood glucose in prediabetes: a randomized, placebo-controlled trial. *Nature Microbiology*, *10*(3), 681-693.

Dwivedi, M., Powali, S., Rastogi, S., Singh, A., & Gupta, D. (2021). Microbial community in human gut: a therapeutic prospect and implication in health and diseases. *Lett. Appl. Microbiol* 73, 553–568.

Facchin, S., Vitulo, N., Calgaro, M., Buda, A., Romualdi, C., Pohl, D., ... & Savarino, E. V. (2020). Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. *Neurogastroenterology & Motility*, *32*(10), e13914.

Guo, Y., Luo, S., Ye, Y., Yin, S., Fan, J., & Xia, M. (2021). Intermittent fasting improves cardiometabolic risk factors and alters gut microbiota in metabolic syndrome patients. *The Journal of Clinical Endocrinology & Metabolism*, *106*(1), 64-79.

Haifer, C., Paramsothy, S., Kaakoush, N. O., Saikal, A., Ghaly, S., Yang, T., ... & Leong, R. W. (2022). Lyophilised oral faecal microbiota transplantation for ulcerative colitis (LOTUS): a randomised, double-blind, placebo-controlled trial. *The lancet Gastroenterology & hepatology*, *7*(2), 141-151.

Hibberd, A. A., Yde, C. C., Ziegler, M. L., Honoré, A. H., Saarinen, M. T., Lahtinen, S., ... & Stenman, L. K. (2019). Probiotic or synbiotic alters the gut microbiota and metabolism in a randomised controlled trial of weight management in overweight adults. *Beneficial Microbes*, *10*(2), 121-136.

Hou, K., Wu, Z. X., Chen, X. Y., Wang, J. Q., Zhang, D., Xiao, C., ... & Chen, Z. S. (2022). Microbiota in health and diseases. *Signal transduction and targeted therapy*, *7*(1), 135.

Inayat, N., Zahir, A., Hashmat, A. J., Khan, A., Ahmad, A., Sikander, M., ... & Hashmat, A. (2025). Gut Microbiota as a Key Modulator of Chronic Disease: Implications for Diabetes, Autoimmunity, and Cancer. *Cureus*, *17*(5).

Kallapura, G., Prakash, A. S., Sankaran, K., Manjappa, P., Chaudhary, P., Ambhore, S., & Dhar, D. (2024). Microbiota based personalized nutrition improves hyperglycaemia and hypertension parameters and reduces inflammation: a prospective, open label, controlled, randomized, comparative, proof of concept study. *PeerJ*, *12*, e17583.

Kim, B., Song, A., Son, A., & Shin, Y. (2024). Gut microbiota and epigenetic choreography: Implications for human health: A review. *Medicine*, *103*(29), e39051.

Kim, C. S., Jung, S., Hwang, G. S., & Shin, D. M. (2023). Gut microbiota indole-3-propionic acid mediates neuroprotective effect of probiotic consumption in healthy elderly: A randomized, double-blind, placebo-controlled, multicentre trial and in vitro study. *Clinical Nutrition*, *42*(6), 1025-1033.

Kostic, A. D., Gevers, D., Pedamallu, C. S., Michaud, M., Duke, F., Earl, A. M., ... & Meyerson, M. (2012). Genomic analysis identifies association of Fusobacterium with colourectal carcinoma. *Genome research*, *22*(2), 292-298.

Lauw, S., Kei, N., Chan, P. L., Yau, T. K., Ma, K. L., Szeto, C. Y. Y., ... & Kwan, H. S. (2023). Effects of synbiotic supplementation on metabolic syndrome traits and gut microbial profile among overweight and obese Hong Kong Chinese individuals: a randomized trial. *Nutrients*, *15*(19), 4248.

Lee, J. C., Lee, B. J., Park, C., Song, H., Ock, C. Y., Sung, H., ... & Hwang, J. H. (2023). Efficacy improvement in searching MEDLINE database using a novel PubMed visual analytic system: EEEvis. Plos one, 18(2), e0281422.

Li, H., Zhang, L., Li, J., Wu, Q., Qian, L., He, J., ... & Jia, W. (2024). Resistant starch intake facilitates weight loss in humans by reshaping the gut microbiota. *Nature Metabolism*, *6*(3), 578-597.

Li, J., Liu, F., Luo, Y., Wijeyesekera, A., Wang, S., Chen, X., ... & Zhou, H. (2025). Differential effects of inulin and fructooligosaccharides on gut microbiota composition and glycemic metabolism in overweight/obese and healthy individuals: a randomized, double-blind clinical trial. *BMC medicine*, *23*(1), 372.

Li, L., Li, R., Tian, Q., Luo, Y., Li, R., Lin, X., ... & Liu, G. (2024). Effects of healthy low-carbohydrate diet and time-restricted eating on weight and gut microbiome in adults with overweight or obesity: feeding RCT. *Cell Reports Medicine*, *5*(11).

Lu, J., Liu, R., Ren, H., Wang, S., Hu, C., Shi, Z., ... & Wang, W. (2025). Impact of omega-3 fatty acids on hypertriglyceridemia, lipidomics, and gut microbiome in patients with type 2 diabetes. *Med*, *6*(1).

Malard, F., Dore, J., Gaugler, B., and Mohty, M. (2021). Introduction to host microbiome symbiosis in health and disease. *Mucosal Immunol.* 14, 547–554.

Melby, M. K., Mylabathula, S., Azad, M. B., Turner, S., Geva□Zatorsky, N., Tropini, C., ... & Nichter, M. (2025). Public Health Microbiome Curriculum: Looking Below the Tip of the Iceberg for Approaches to Population Health. *Microbial Biotechnology*, *18*(6), e70160.

Mo, S. J., Lee, K., Hong, H. J., Hong, D. K., Jung, S. H., Park, S. D., ... & Lee, J. L. (2022). Effects of Lactobacillus curvatus HY7601 and Lactobacillus plantarum KY1032 on overweight and the gut microbiota in humans: Randomized, double-blinded, placebo-controlled clinical trial. *Nutrients*, *14*(12), 2484.

Mocanu, V., Zhang, Z., Deehan, E. C., Kao, D. H., Hotte, N., Karmali, S., ... & Madsen, K. L. (2021). Faecal microbial transplantation and fibre supplementation in patients with severe obesity and metabolic syndrome: a randomized double-blind, placebo-controlled phase 2 trial. *Nature Medicine*, *27*(7), 1272-1279.

Mokkala, K., Paulin, N., Houttu, N., Koivuniemi, E., Pellonperä, O., Khan, S., ... & Laitinen, K. (2021). Metagenomics analysis of gut microbiota in response to diet intervention and gestational diabetes in overweight and obese women: a randomised, double-blind, placebo-controlled clinical trial. *Gut*, *70*(2), 309-318.

Nakov, R., & Velikova, T. (2020). Chemical metabolism of xenobiotics by gut microbiota. *Current Drug Metabolism*, *21*(4), 260-269.

Ng, S. C., Xu, Z., Mak, J. W. Y., Yang, K., Liu, Q., Zuo, T., ... & Chan, F. K. (2022). Microbiota engraftment after faecal microbiota transplantation in obese subjects with type 2 diabetes: a 24-week, double-blind, randomised controlled trial. *Gut*, *71*(4), 716-723.

Ni, Y., Qian, L., Siliceo, S. L., Long, X., Nychas, E., Liu, Y., ... & Jia, W. (2023). Resistant starch decreases intrahepatic triglycerides in patients with NAFLD via gut microbiome alterations. *Cell metabolism*, *35*(9), 1530-1547.

Page, M. J., McKenzie, J. E., Bossuyt, P. M., Boutron, I., Hoffmann, T. C., Mulrow, C. D., ... & Moher, D. (2021). The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *bmj*, *372*.

Palacios, T., Vitetta, L., Coulson, S., Madigan, C. D., Lam, Y. Y., Manuel, R., ... & Caterson, I. D. (2020). Targeting the intestinal microbiota to prevent type 2 diabetes and enhance the effect of metformin on glycaemia: a randomised controlled pilot study. *Nutrients*, *12*(7), 2041.

Paramsothy, S., Kamm, M. A., Kaakoush, N. O., Walsh, A. J., van den Bogaerde, J., Samuel, D., ... & Borody, T. J. (2017). Multidonor intensive faecal microbiota transplantation for active ulcerative colitis: a randomised placebo-controlled trial. *The Lancet*, *389*(10075), 1218-1228.

Paramsothy, S., Nielsen, S., Kamm, M. A., Deshpande, N. P., Faith, J. J., Clemente, J. C., ... & Kaakoush, N. O. (2019). Specific bacteria and metabolites associated with response to faecal microbiota transplantation in patients with ulcerative colitis. *Gastroenterology*, *156*(5), 1440-1454.

Qin, Q., Yan, S., Yang, Y., Chen, J., Li, T., Gao, X., ... & Ding, S. (2021). A metagenome-wide association study of the gut microbiome and metabolic syndrome. *Frontiers in microbiology*, *12*, 682721.

Ren, M., Zhang, H., Qi, J., Hu, A., Jiang, Q., Hou, Y., ... & Wang, X. (2020). An almond-based low carbohydrate diet improves depression and glycometabolism in patients with type 2 diabetes through modulating gut microbiota and GLP-1: a randomized controlled trial. *Nutrients*, *12*(10), 3036.

Rinott, E., Meir, A. Y., Tsaban, G., Zelicha, H., Kaplan, A., Knights, D., ... & Youngster, I. (2022). The effects of the Green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. *Genome medicine*, *14*(1), 29.

Siddiqui, R., Akbar, N., & Khan, N. A. (2021). Gut microbiome and human health under the space environment. *Journal of Applied Microbiology*, *130*(1), 14-24.

Srivastava, S., Basak, U., Naghibi, M., Vijayakumar, V., Parihar, R., Patel, J., ... & Day, R. (2024). A randomized double-blind, placebo-controlled trial to evaluate the safety and efficacy of live Bifidobacterium longum CECT 7347 (ES1) and heat-treated Bifidobacterium longum CECT 7347 (HT-ES1) in participants with diarrhea-predominant irritable bowel syndrome. *Gut Microbes*, *16*(1), 2338322.

Tettamanzi, F., Bagnardi, V., Louca, P., Nogal, A., Monti, G. S., Mambrini, S. P., ... & Menni, C. (2021). A high protein diet is more effective in improving insulin resistance and glycemic variability compared to a mediterranean diet—a cross-over controlled inpatient dietary study. *Nutrients*, *13*(12), 4380.

Tilg, H., & Moschen, A. R. (2014). Microbiota and diabetes: an evolving relationship. *Gut*, *63*(9), 1513-1521.

Vinderola, G., Cotter, P. D., Freitas, M., Gueimonde, M., Holscher, H. D., Ruas-Madiedo, P., ... & Cifelli, C. J. (2023). Fermented foods: a perspective on their role in delivering biotics. *Frontiers in Microbiology*, *14*, 1196239.

Wang, Y., Lindemann, S. R., Cross, T. W. L., Tang, M., Clark, C. M., & Campbell, W. W. (2023). Effects of adding lean red meat to a US-style healthy vegetarian dietary pattern on gut microbiota and cardiovascular risk factors in young adults: a crossover randomized controlled trial. *The Journal of Nutrition*, *153*(5), 1439-1452.

Wu, G., Zhao, N., Zhang, C., Lam, Y. Y., & Zhao, L. (2021). Guild-based analysis for understanding gut microbiome in human health and diseases. *Genome medicine*, *13*(1), 22.

Wu, Z., Zhang, B., Chen, F., Xia, R., Zhu, D., Chen, B., ... & Hou, K. (2023). Faecal microbiota transplantation reverses insulin resistance in type 2 diabetes: A randomized, controlled, prospective study. *Frontiers in Cellular and Infection Microbiology*, *12*, 1089991.

Yılmaz, İ., Dolar, M. E., & Özpınar, H. (2018). Effect of administering kefir on the changes in faecal microbiota and symptoms of inflammatory bowel disease: A randomized controlled trial. *The Turkish Journal of Gastroenterology*, *30*(3), 242.

Zhang, X., Irajizad, E., Hoffman, K. L., Fahrmann, J. F., Li, F., Seo, Y. D., ... & Daniel, C. R. (2023). Modulating a prebiotic food source influences inflammation and immune-regulating gut microbes and metabolites: insights from the BE GONE trial. *EBioMedicine*, *98*.

Zhao, L., Zhang, F., Ding, X., Wu, G., Lam, Y. Y., Wang, X., ... & Zhang, C. (2018). Gut bacteria selectively promoted by dietary fibres alleviate type 2 diabetes. *Science*, *359*(6380), 1151-1156.