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# The Link between Gut Microbiome, Nutraceuticals, Diet, and Diabetes Mellitus: A Bibliometric and Visual Analysis of Research and Emerging Trends from 2012 to 2022

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**Abstract:** The increasing prevalence of diabetes mellitus (DM) worldwide is a cause for global concern. Recent evidence suggests that the interaction between one's diet and the gut microbiome are key modifiers of diabetes, highlighting the potential role of microbiome-modulating nutraceuticals. This bibliometric analysis examines literature published between 2012 and 2022 to explore trends in the latest research, with additional discussion on major takeaways and future directions. We selected and analyzed 640 articles from an initial pool of 4,099 from the Web of Science using Microsoft Excel 2016 and VOSviewer software (version 1.6.19). Our exploration covered the most common journals, countries, study designs, experimental subjects, types of DM, organisms and nutraceuticals studied, and the most cited articles. We also evaluated the most cited publications in terms of journals, organizations, and countries, along with the collaborative networks among authors, organizations and countries, and the co-occurrence of author keywords from the selection. It is evident from the increasing number of publications each year that this field has attracted growing attention over the last decade. Nonetheless, continued research is essential to sustain this trend. Our overarching study of diabetes research marks steady progress in understanding the role of—and potentially discovering applications of—microbiome modulation to enhance metabolic pathways and health outcomes. Advancements in this field may lead to potential therapeutic applications for specific diets and nutraceuticals that modulate the gut microbiota in DM.

**Keywords:** T2DM; gut microbiota; diet; probiotics; prebiotics; bibliometrics

## 1. Introduction

The escalating global prevalence and profound health implications of Diabetes Mellitus (DM) demand a strategic approach to combat its impact. DM, is a group of metabolic and endocrine diseases that is characterized by poor glycemic control. Globally, the prevalence of DM was estimated to be 10.5% in 2021, and expected to increase to 12.2% by 2045 (1). The Centers for Diseases Control and Prevention (CDC) identifies DM as the eighth leading cause of mortality in the United States, highlighting its association with substantial morbidity (2). This condition notably increases the risk of developing multisystem complications such as diabetic ketoacidosis (DKA), cardiovascular disease (CVD), end-stage renal disease (ESRD), retinopathy, neuropathy, cancer, and pregnancy and neonatal complications (3). The economic impact of DM is substantial. It is estimated to cost about $327 billion in terms of medical expenses and lost work hours. Additionally, patients with DM are estimated to incur costs twice the average in medical expenses when compared to individuals without DM (2). Therefore, early diagnosis and effective management is critical in preventing the onset of debilitating complications and improving health outcomes in persons living with DM.

DM comprises of at least four clinically distinct forms: Type 1 diabetes (T1DM), Type 2 diabetes (T2DM), prediabetes, and gestational diabetes mellitus (GDM). T1DM is a result of the autoimmune destruction of the β-cells within the pancreatic islet cells, ultimately leading to insulin deficiency. Genetic factors play a major role in its development and incidence. Polymorphisms in the major histocompatibility complex (MHC) and human leukocyte antigen (HLA) genes are known to influence the risk of developing T1DM (3). Environmental factors and certain viral infections such as rubella, cytomegalovirus, mumps, Coxsackie and enterovirus, have also been found to contribute to the onset of T1DM (4). On the other hand, the more prevalent T2DM is a multifactorial disease which involves both genetic and environmental factors such as diet, lifestyle and aging (3). Some gene mutations associated with T2DM include the transcription factor 7-like 2 (TCF7L2) gene, which affects the expression of the insulin gene and insulin secretion, and the ATP binding cassette subfamily C member 8 (ABCC8) gene, which helps insulin regulation (5,6). The major mechanism in T2DM is insulin resistance and insensitivity. Patients with both T1DM and T2DM have fasting plasma glucose (FPG) levels greater than 126 mg/dL, 2-hour postprandial glucose levels greater than 200 mg/dL, and/or glycated hemoglobin (HbA1c) levels higher than 6.5% (3). Prediabetes is characterized by plasma glucose levels just below the DM threshold. The mechanism of action for prediabetes also revolves around impaired insulin resistance and impaired glucose tolerance. Prediabetic patients have FPG levels between 100-125 mg/dL, postprandial glucose levels between 140-199 mg/dL, and/or HbA1c levels between 5.7 and 6.4% (7). GDM is DM that occurs during pregnancy. It is of unknown etiology; however, some suggestions include HLA antigens such as HLA DR2, 3 and 4, β-cell stress due to excess proinsulin, and excess hormonal concentrations during pregnancy. Patients are diagnosed with GDM if they have a positive 3 hours oral glucose tolerance tests (OGTT) with at least one abnormal reading of the plasma glucose concentration (3).

Recent studies are increasingly recognizing the potential of the gut microbiota and its pivotal role in regulating glucose metabolism, immunity, inflammation and the onset of DM (8). The dynamic balance in the gut microbiota composition is essential for maintaining metabolic homeostasis; however, a disruption in this balance can lead to insulin resistance, which further increases the risk for T2DM (9). In particular, the composition of the gut microbiota is crucial in determining the body's ability to produce and utilize insulin, thereby playing a decisive role in the onset of T2DM (8,9). Understanding these diverse roles underscores the potential of targeting the gut microbiota in preventing and managing DM. The bacterium *Akkermansia muciniphila*, for instance, is known to improve insulin sensitivity, thus suggesting a protective role against metabolic disorders. Conversely, an increased presence of Firmicutes bacteria correlates with decreased insulin sensitivity, potentially worsening metabolic health (10). A study conducted on Chinese adults with a diagnosis of DM according to the World Health Organization (WHO) criteria, demonstrated that a higher Firmicutes to Bacteroidetes (F:B) ratio increased the risk of developing T2DM (11). The effect of the gut microbiota on DM is mediated by the metabolites resulting from microbial action on the ingested food. Short-chain fatty acids (SCFA), branched-chain amino acids, lipopolysaccharide, imidazole propionate and secondary bile acid are some of the main metabolites associated with T2DM (8). A diet high in fiber, for example, compounding the amount of SCFA-producing microbiota, and thus, increasing the levels of SCFA, which positively impacts T2DM by raising the production of glucagon-like peptide 1 (GLP-1), and reducing the HbA1c levels (12).

DM is frequently characterized as a disease modifiable through lifestyle, mainly where dietary habits play a significant role. The tailored selection of an individual's diet is a crucial factor that can substantially influence both the risk of developing DM and the management of the disease's progression. For instance, a diet rich in carbohydrates and fats can lead to the development of insulin resistance or further worsen the glycemic control in people already living with DM. A study conducted in adult men found that the Western diet, consisting of highly processed red meat, fatty and salty food, refined grains, high-fat dairy products and sweets, was correlated with an approximately 3.5 fold increase in the risk of developing DM, compared to a diet emphasizing fruits, vegetables, fish, poultry and whole grains (13). Another similar diet, now gaining immense popularity, is the Mediterranean diet, which mainly comprises of vegetables, fruits, nuts, legumes, whole grains, seafood, olive oil, and a moderate red wine intake (14). There is recent evidence indicating that stricter adherence to this diet is associated to a lower incidence of DM, highlighting the beneficial effects of the diet against the disease (15).

Analogous to the Mediterranean diet, the vegan diet is a vegetarian diet comprising of plant-based foods such as fruits, vegetables, grains, and legumes. This composition leads to an improved glycemic control and also has lipid-lowering effects, which is imperative to the cardiovascular complications in patients with DM (16,17). Likewise, the plant-based diet includes fruits, vegetables, legumes and cereal, while also containing natural compounds such as polyphenols. These can improve glucose tolerance and metabolism, and further reduce inflammation (18). Building on the foundation of plant-based nutrition, the Dietary Approaches to Stop Hypertension (DASH) diet expands the focus to include heart health alongside diabetes management. It includes fruits, vegetables, and whole grains while limiting sweets, fats, and a daily sodium intake to 2,400 mg. This regimen is beneficial for lipid and glycemic control, along with the systolic and diastolic blood pressure—a common comorbidity in patients with T2DM. (19). Similarly, the macrobiotic Ma-Pi 2 diet takes a holistic approach, integrating legumes, whole grains, fruits, and vegetables, along with unique elements like gomashio (a sesame salt seasoning), fermented products, seaweeds, and Bancha tea. This diet stands out for its positive effects on metabolic health, as evidenced by improved lipid and glycemic control, reduced blood pressure, and increased urine pH in those with T2DM (20).

The ketogenic and low-carbohydrate diets present a different nutritional paradigm, which pivots away from traditional carbohydrate intake. The ketogenic diet is a diet based on very low amounts of carbohydrates, low to moderate amounts of protein and high amounts of fats. This type of diet is often accompanied by fasting to achieve ketosis, and a shift from glucose to fat metabolism. Another diet, the low-carbohydrate diet, is similar to the ketogenic diet, but the key difference lies in the consumption of the amount of carbohydrates. The low-carbohydrate diet employs 50-150 grams of carbohydrates without ketosis, whereas the ketogenic diet uses less than 50 grams of carbohydrates. These diets help patients lose weight, and even reverse or eliminate the need for insulin in patients with T2DM, especially patients with obesity. They also reduce inflammation, improve lipid control and alter the microbiome (21). These dietary approaches exemplify the profound influence of nutrition on DM management, demonstrating that carefully chosen diets can significantly enhance the overall health of those living with diabetes.

Additionally, compounds such as polyphenols are especially promising to reduce the risk of T2DM development. Flavonoids, a type of polyphenol, influence the absorption of glucose and the secretion of and sensitivity to insulin (22). It is also emerging as a promising non-pharmacological therapeutic for patients with DM.

Lastly, microbiome-modulating nutraceuticals such as prebiotics, probiotics, synbiotics and postbiotics have also been shown to provide potential health benefits in the management of DM. Prebiotics are non-digestible food ingredients, such as dietary fibers, inulin, and fructooligosaccharides, which promote growth and activity of beneficial gut bacteria, such as *Bifidobacteria*, a decline in which is associated with T2DM (23,24). Probiotics are viable organisms that have shown to mediate numerous health benefits, such as boosting the immune system and regulating glycemic control (25). Synbiotics is a combination of prebiotics and probiotics, which improves the stability of the probiotic, and facilitates the improvement of glycemic control and the reduction of inflammation (25). Postbiotics are functional bioactive compounds derived from inanimate microorganisms, and associated structures and molecules. Although consistent data is scant, postbiotics seem to be potentially promising as a therapeutic for DM (26). These advances in microbiome science reflect a growing appreciation for the complex interactions between diet, gut microbial ecology, and metabolic health.

Thus, it becomes imperative to study the impact of diet and the gut microbiota on DM. It is, thereby, important to realize that research in this field can provide insights to treating DM to a further reduce the burden on healthcare and associated costs. A deep understanding of the mechanism of their interaction is required to tailor these aspects to benefit patients with DM and reduce the global burden of DM on the world economy. For this purpose, we undertook bibliometric analysis to chart the evolution and progress within this domain. We meticulously selected 640 publications for analysis to discern patterns and trends that can inform future studies. Our analysis encompassed the top journals, leading countries, prominent organizations, and the nature of collaborations in this field. Additionally, we examined the most-cited articles, study designs, and experimental subjects used. We also explored the co-occurrence of author keywords and assessed the prevailing focus of studies on DM, particularly concerning the gut microbiota profile, dietary patterns, and probiotic interventions. Finally, we also discussed the potential of dietary and microbiome alterations as having a plausible therapeutic value and benefiting patients living with this chronic condition.

## 2. Methods

### *2.1. Database Search*

A literature search was conducted using Web of Science for articles published earlier to and including December 31, 2022. The search was designed using Boolean keywords, targeting terms for "diet", "gut microbiota", "diabetes", and their corresponding synonyms. No filters were used in the search for date or language. A total of 4099 studies that contained the targeted terms were exported into Covidence to remove duplicates (n=3) and further manage the screening phase. The search query was conducted as seen below:

((((TS=(gut OR intestin* OR gastrointestin*)) AND TS=(microbio* OR microflora OR flora OR bacteria* OR dysbiosis OR microecology OR 16Sr* OR metagenome)) OR TS=(prebiotic* OR probiotic* OR synbiotic* OR symbiotic* OR postbiotics* OR parabiotics*)) AND TS=(diet* OR Nutrition*)) AND TS=(diabetes OR diabetic* OR IDDM OR NIDDM OR MODY OR T1D OR T1DM OR T2D OR T2DM)

### *2.2. Title and Abstract Screening Phase*

Covidence was used for the primary screening process. A total of 4096 titles and abstracts were independently reviewed by two researchers. Conflicts were resolved by a third-party researcher from the team not involved in the screening of the conflicted paper. Screening and conflict resolution yielded in the exclusion of 2745 studies; 1351 studies remained for full-text screening (Figure 1). Studies were included based on the following criteria:

1. The scope of the study includes all three of the following aspects: a) diet in the form of nutrition, prebiotics, probiotics, postbiotics, parabiotics, synbiotics/symbiotics, or compounds derived from natural sources, b) gut microbiota, and c) diabetes, including but not limited to T1DM, T2DM, GDM, prediabetes, and complications or comorbidities related to DM.
2. Articles published between January 1, 2012 and December 31, 2022.
3. The study language was in "English".

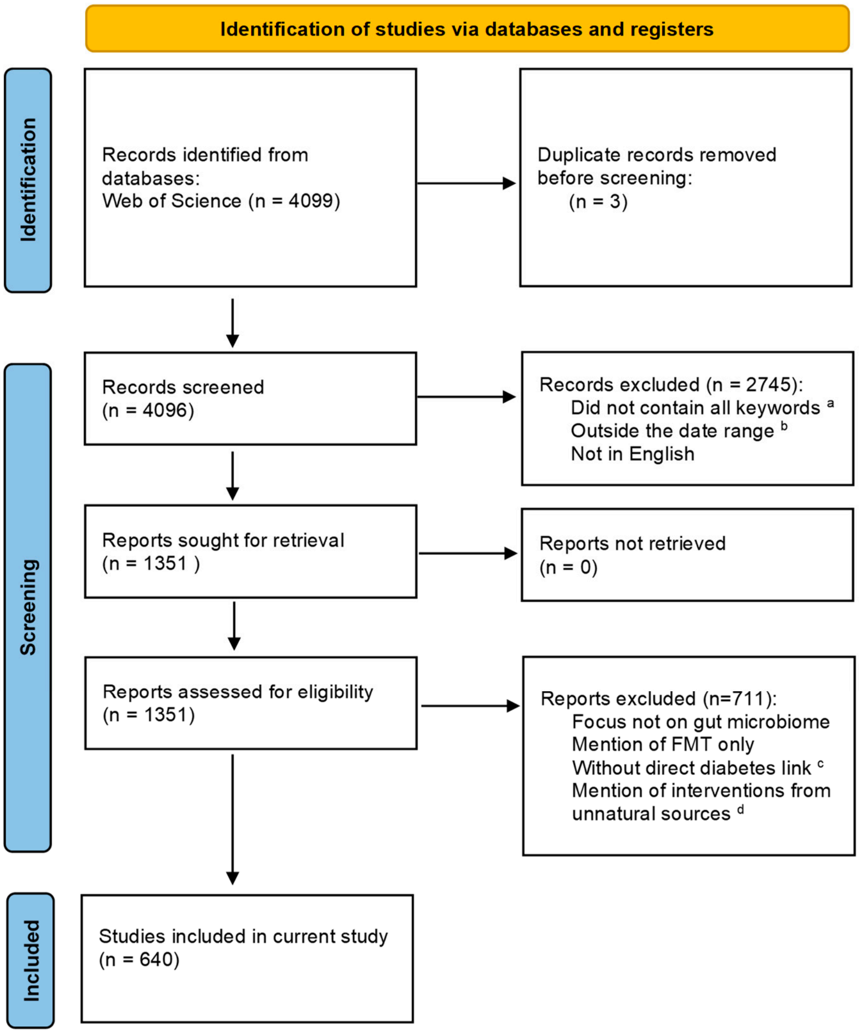

**Figure 1.** PRISMA flowchart entailing the screening strategy. **A**: Studies containing only one or two of the following: diet, gut microbiota, diabetes; **B**: Studies published outside the data range of 2012-2022; **C**: Mention of insulin resistance, metabolic syndrome, and other disorders *without* direct link to DM; **D**: Studies that mentioned medicines or chemical compounds derived from an unnatural source; FMT: Fecal Microbiota transplant.

### *2.3. Full Text Screening Phase*

Two researchers independently reviewed a total of 1351 studies. Conflicts were, again, resolved by a third-party researcher from the team not involved in screening the conflicted paper. The process resulted in a total of 640 papers for data extraction (Figure 1). Studies were included based on the following criteria, in addition to the criteria used for the title and abstract screening phase:

1. The microbiota discussed in the study pertained to the naturally occurring gut flora, not to those artificially transplanted.
2. Conditions such as insulin resistance, metabolic syndromes or other disorders should be associated with DM.
3. The term ‘diet’ should only include nutrition, prebiotics, probiotics, postbiotics, parabiotics, synbiotics/symbiotics, or compounds derived from natural sources. We excluded all studies discussing medications, or chemical compounds not derived directly from a natural source (such as fruits, food items, etc.).

### *2.4. Extraction Phase*

The studies included in the current study (n=640) were comprehensively extracted using Microsoft Excel 2016. Data regarding the authors, the authors' institutions, the journal the paper was published in, the number of times the paper was cited, the type of study, country, funding, along with the diet used, gut microorganisms discussed, and the type of DM was extracted from the studies. Figure 1 summarizes the screening process of the total search results into the final articles extracted and analyzed.

### *2.5. Analysis of the Data*

The data extracted was analyzed using Microsoft Excel 2016 and a bibliometric analysis tool VOSviewer (version 1.6.19). The included 640 studies were selected from the Web of Science database and imported into VOSviewer in plain text file format. Several bibliometric indicators were used: most cited publications in journals, organizations and countries, the collaborative networks among authors (using Density Visualization), organizations and countries, and co-occurrence of author keywords from the 640 selected publications from the screening phase.

## 3. Results

We analyzed 640 selected papers using Microsoft Excel 2016 and VOSviewer software. A compilation of the diet and type of DM, and gut microbiota extracted from each study can be accessed in Supplementary Table 1 [ (27), (28), (29), (30), (31), (32), (33), (34), (35), (36), (37), (38), (39), (40), (41), (42), (43), (44), (45), (46), (47), (48), (49), (50), (51), (52), (53), (54), (55), (56), (57), (58), (59), (60), (61), (62), (63), (64), (65), (66), (67), (68), (69), (70), (71), (72), (73), (74), (75), (76), (77), (78), (79), (80), (81), (82), (83), (84), (85), (86), (87), (88), (89), (90), (91), (92), (93), (94), (95), (96), (97), (98), (99), (100), (101), (102), (103), (104), (105), (106), (107), (108), (109), (110), (111), (112), (113), (114), (115), (116), (117), (118), (119), (120), (121), (122), (123), (124), (125), (126), (127), (128), (129), (130), (131), (132), (133), (134), (135), (136), (137), (138), (139), (140), (141), (142), (143), (144), (145), (146), (147), (148), (149), (150), (151), (152), (153), (154), (155), (156), (157), (158), (159), (160), (161), (162), (163), (164), (165), (166), (167), (168), (169), (170), (171), (172), (173), (174), (175), (176), (177), (178), (179), (180), (181), (182), (183), (184), (185), (186), (187), (188), (189), (190), (191), (192), (193), (194), (195), (196), (197), (198), (199), (200), (201), (202), (203), (204), (205), (206), (207), (208), (209), (210), (211), (212), (213), (214), (215), (216), (217), (218), (219), (220), (221), (222), (223), (224), (225), (226), (227), (228), (229), (230), (231), (232), (233), (234), (235), (236), (237), (238), (239), (240), (241), (242), (243), (244), (245), (246), (247), (248), (249), (250), (251), (252), (253), (254), (255), (256), (257), (258), (259), (260), (261), (262), (263), (264), (265), (266), (267), (268), (269), (270), (271), (272), (273), (274), (275), (276), (277), (278), (279), (280), (281), (282), (283), (284), (285), (286), (287), (288), (289), (290), (291), (292), (293), (294), (295), (296), (297), (298), (299), (300), (301), (302), (303), (304), (305), (306), (307), (308), (309), (310), (311), (312), (313), (314), (315), (316), (317), (318), (319), (320), (321), (322), (323), (324), (325), (326), (327), (328), (329), (330), (331), (332), (333), (334), (335), (336), (337), (338), (339), (340), (341), (342), (343), (344), (345), (346), (347), (348), (349), (350), (351), (352), (353), (354), (355), (356), (357), (358), (359), (360), (361), (362), (363), (364), (365), (366), (367), (368), (369), (370), (371), (372), (373), (374), (375), (376), (377), (378), (379), (380), (381), (382), (383), (384), (385), (386), (387), (388), (389), (390), (391), (392), (393), (394), (395), (396), (397), (398), (399), (400), (401), (402), (403), (404), (405), (406), (407), (408), (409), (410), (411), (412), (413), (414), (415), (416), (417), (418), (419), (420), (421), (422), (423), (424), (425), (426), (427), (428), (429), (430), (431), (432), (433), (434), (435), (436), (437), (438), (439), (440), (441), (442), (443), (444), (445), (446), (447), (448), (449), (450), (451), (452), (453), (454), (455), (456), (457), (458), (459), (460), (461), (462), (463), (464), (465), (466), (467), (468), (469), (470), (471), (472), (473), (474), (475), (476), (477), (478), (479), (480), (481), (482), (483), (484), (485), (486), (487), (488), (489), (490), (491), (492), (493), (494), (495), (496), (497), (498), (499), (500), (501), (502), (503), (504), (505), (506), (507), (508), (509), (510), (511), (512), (513), (514), (515), (516), (517), (518), (519), (520), (521), (522), (523), (524), (525), (526), (527), (528), (529), (530), (531), (532), (533), (534), (535), (536), (537), (538), (539), (540), (541), (542), (543), (544), (545), (546), (547), (548), (549), (550), (551), (552), (553), (554), (555), (556), (557), (558), (559), (560), (561), (562), (563), (564), (565), (566), (567), (568), (569), (570), (571), (572), (573), (574), (575), (576), (577), (578), (579), (580), (581), (582), (583), (584), (585), (586), (587), (588), (589), (590), (591), (592), (593), (594), (595), (596), (597), (598), (599), (600), (601), (602), (603), (604), (605), (606), (607), (608), (609), (610), (611), (612), (613), (614), (615), (616), (617), (618), (619), (620), (621), (622), (623), (624), (625), (626), (627), (628), (629), (630), (631), (632), (633), (634), (635), (636), (637), (638), (639), (640), (641), (642), (643), (644), (645), (646), (647), (648), (649), (650), (651), (652), (653), (654), (655), (656), (657), (658), (659), (660), (661), (662), (663), (664), (665), (666) ]

We conducted an analysis of the annual publication trends in the fields of diet, nutraceuticals, gut microbiome, and DM to gauge the research topic's popularity. As Figure 2 illustrates, we have observed a steady increase in the number of studies published annually over the last decade (2012 – 2022). Despite a minor decline in publications in 2013, there has been a rapid and consistent upward trend every year since. Our analysis was based on 640 selected papers only, however, it indicates that this field is gaining increasing interest and will likely continue attracting attention in the coming years.

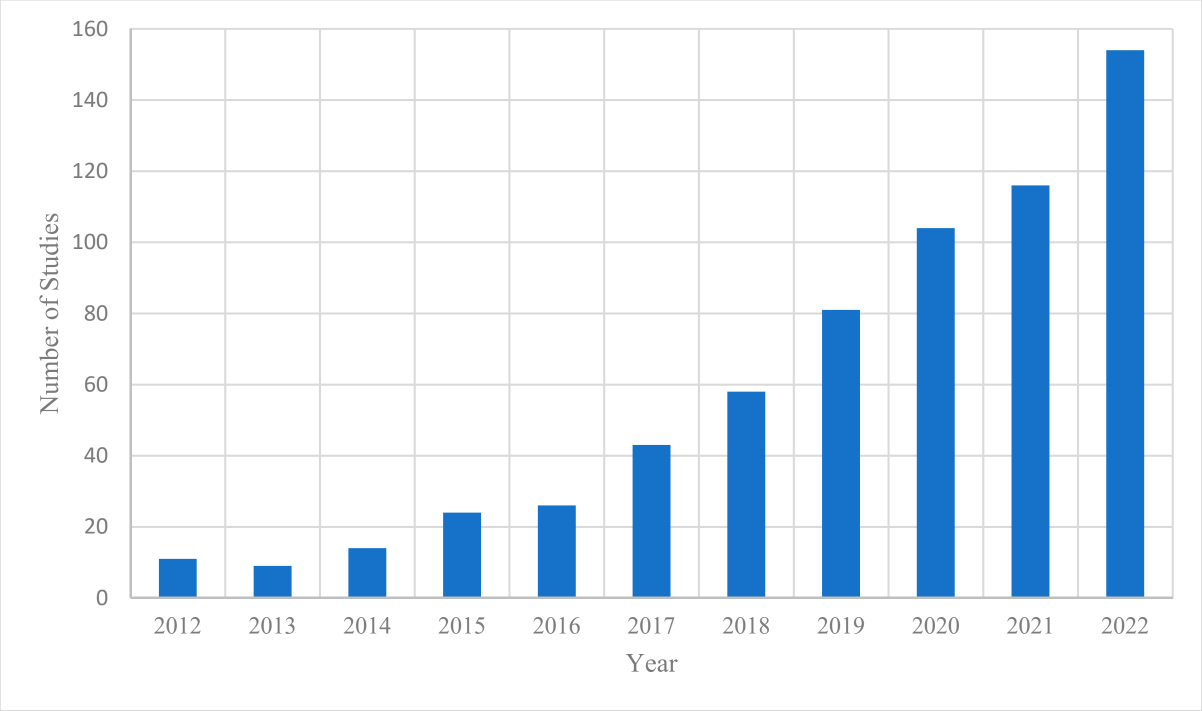

**Figure 2.** Number of studies on Diet, Nutraceuticals, Gut Microbiome and DM, 2012 – 2022.

### *3.1. Top Journals in this field*

The analysis of the top journals with the highest number of publications in this field was analyzed using Microsoft Excel 2016. Per Table 1, the top 2 journals with the highest number of publications were *Nutrients* with 63 documents and *Food & Function* followed with 34 documents. The rest of the Journals in Table 1 did not reach the first two journals but were considerably higher than the other Journals that did not make it into this category.

An analysis on VOSviewer was done to assess which of the Journals with a minimum of 3 documents in this field was the most cited by other authors. A minimum of 3 citations was necessary to qualify for this analysis. The output from VOSviewer is shown in Figure 3.

**Table 1.** Top 11 Journals with the highest number of publications in this field.

| Journals | Documents, *n* |
|---|---|
| Nutrients | 63 |
| Food & Function | 34 |
| Frontiers in Nutrition | 19 |
| Journal of Agricultural and Food Chemistry | 19 |

| | |
|---|---|
| International Journal of Molecular Sciences | 18 |
| Molecular Nutrition & Food Research | 17 |
| Journal of Functional Foods | 15 |
| Food Research International | 14 |
| Scientific Reports | 12 |
| FOODS | 11 |
| Frontiers in Microbiology | 11 |
| Biomedicine & Pharmacotherapy | 8 |
| Frontiers in Endocrinology | 8 |

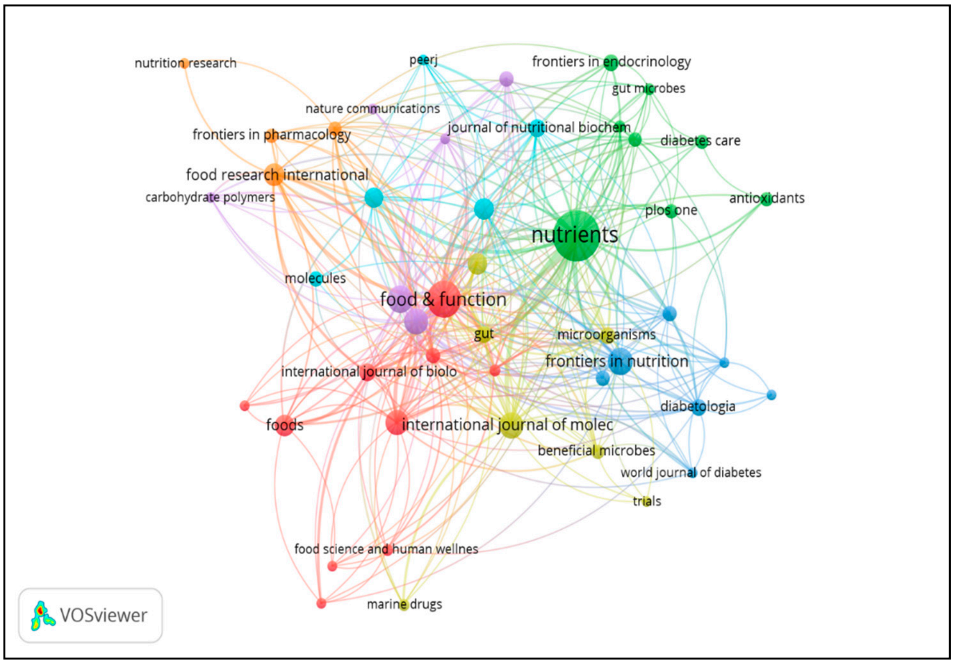

**Figure 3.** Journals with Most Cited Publications in this field.

The journals *Nutrient* and *Food & Function* are still at the top with the most citations of 2343 and 1234, respectively. Both of these journals have the highest total link strength of 140 and 133, respectively. *International Journal of Molecular Sciences* and *Journal of Agricultural and Food Chemistry* follow next with 782 and 385 citations and 65 and 58 total link strength, respectively. Although *Frontiers in Nutrition* has a total of 19 documents, it has only 64 citations and a total link strength of 43, and is therefore further down in the list.

These analyses collectively highlight that Nutrients and Food & Function are leading journals in this research domain in terms of publication volume and citation impact, signaling their central role in advancing the field of dietary influence on metabolic health.

### *3.2. Top Organizations and Collaborations in this field*

To assess for the organizations that produced the most cited publications in this field, VOSviewer was used with the set criteria of a minimum of 5 documents and 3 citations per organization, as shown in Figure 4A. A total of 45 organizations met the criteria, among which China Agricultural University (documents: 25, citations: 1045, total link strength: 111) came out as top with Fujian Agriculture & Forestry University (documents: 12, citations: 420, total link strength: 87) as the second highest cited organization. Jiangnan University was a close third with 14 documents and 452 citations but a lower total link strength of 57.

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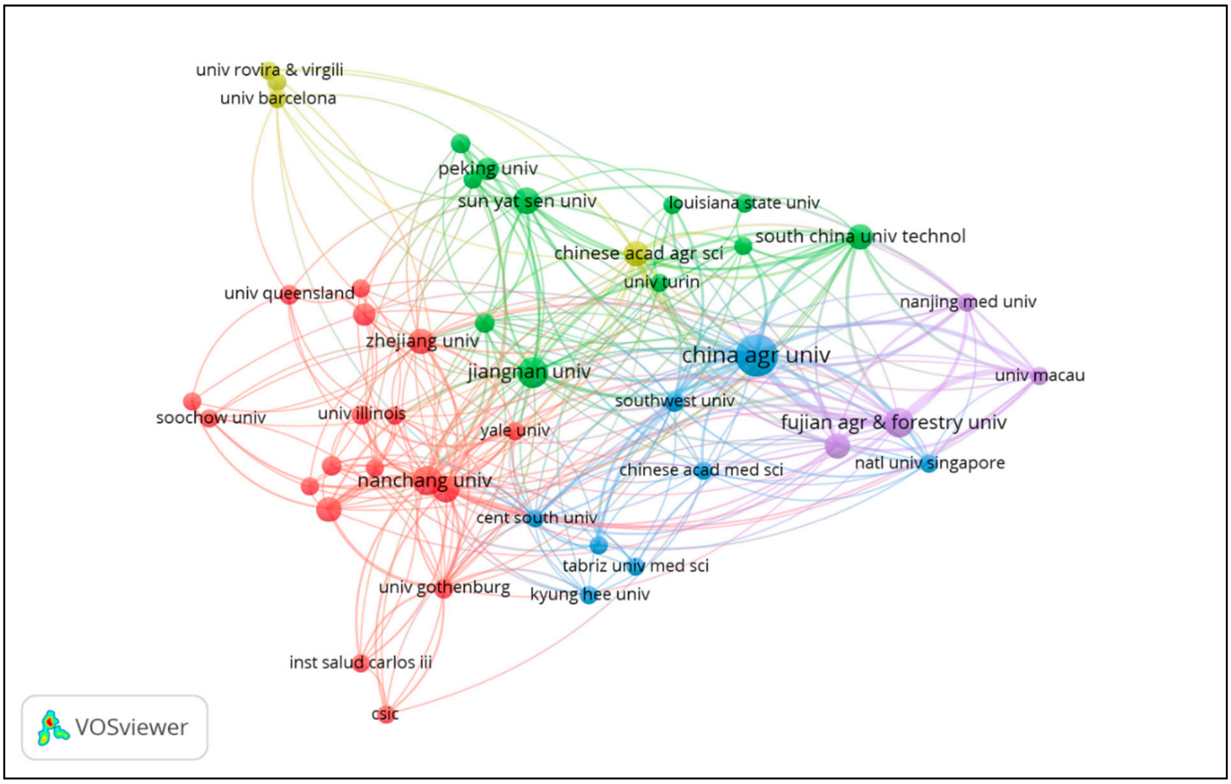

**Figure 4A.** Organizations with Most Cited Publications in this field.

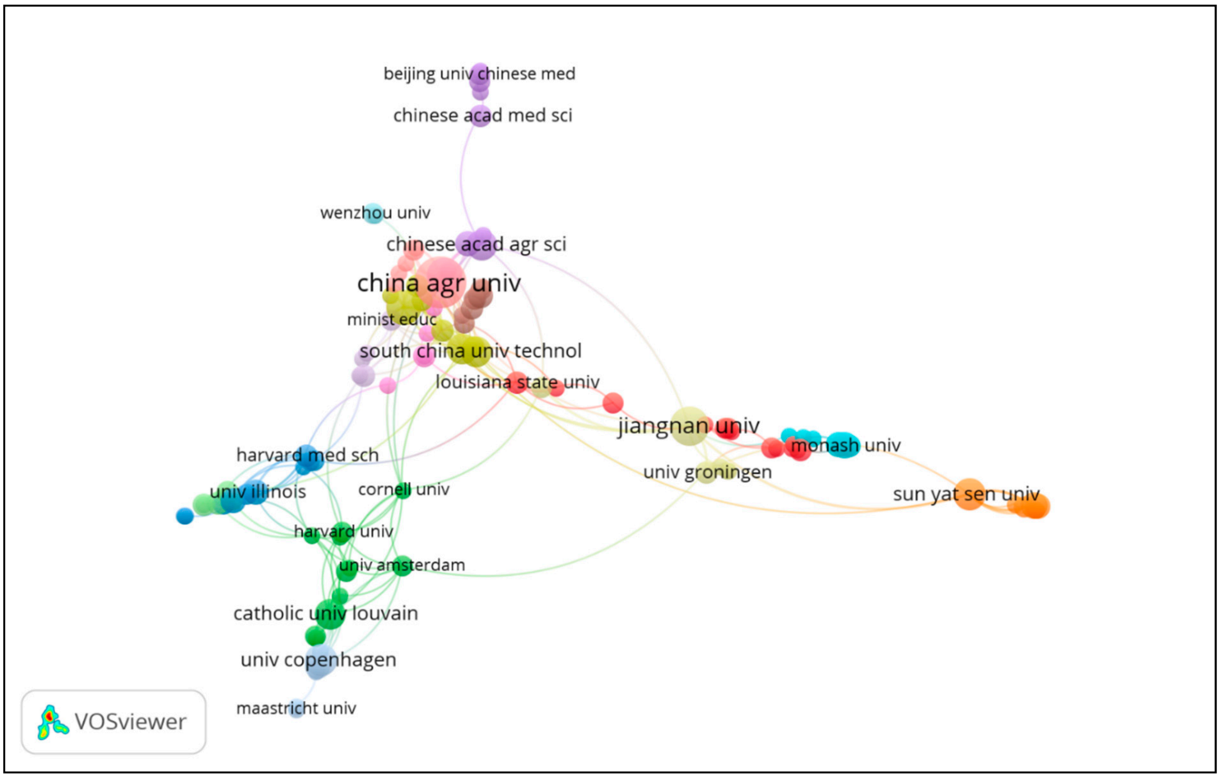

**Figure 4B.** Analysis of Collaborations between Organizations in this field.

Next, VOSviewer was also used to assess the collaborations between organizations in this field with at least 3 documents and at least 3 citations per organization (Figure 4B). The top 2 organizations with the most collaborations are China Agricultural University (documents: 25, citations 1045, total link strength: 35) and Fujian Agriculture & Forestry University (documents: 12, citations 420, total link strength: 29). China Agricultural University has the strongest collaboration with Fujian Agriculture & Forestry University, South China University of Technology, University of California, Davis, Louisiana State University and other universities such as Jiangnan University and Sun Yat-Sen University. A second cluster can be seen around University of Copenhagen and Catholic University of Louvain.

Our results show that China Agricultural University leads in the most cited publications and collaboration networks in this field, with Fujian Agriculture & Forestry University as a close second, highlighting a solid collaboration ecosystem among top-performing institutions.

### *3.3. Top Countries in this field*

A similar assessment was done with the countries as with organizations. Table 2 shows the countries of origin from where the most publications in this field emerged. China takes the bulk of publications and leads with a significant margin with 188 documents published in this field. The United States comes in second with 41 publications with Japan and South Korea following next with 13 publications each. The rest of the countries had a lower number of publications than the top 4. VOSviewer was used to analyze the countries with the most cited publications and the cross-country collaborations (Figure 5A,B). A total of 39 countries fit into the criteria of a minimum of 3 documents and 3 citations per country. China and the United States are the highest with 6289 and 7554 citations and 1070 and 667 total link strength, respectively. Italy, Canada, France, and England follow next in terms of total link strength.

**Table 2.** Top 10 Countries with highest number of publications in this field (n = 360).

| Country | Frequency Tally |
|---|---|
| China | 188 |
| United States | 41 |
| Japan | 13 |
| South Korea | 13 |
| Iran | 7 |
| Spain | 7 |
| Australia | 6 |
| Canada | 6 |
| France | 6 |
| Poland | 6 |

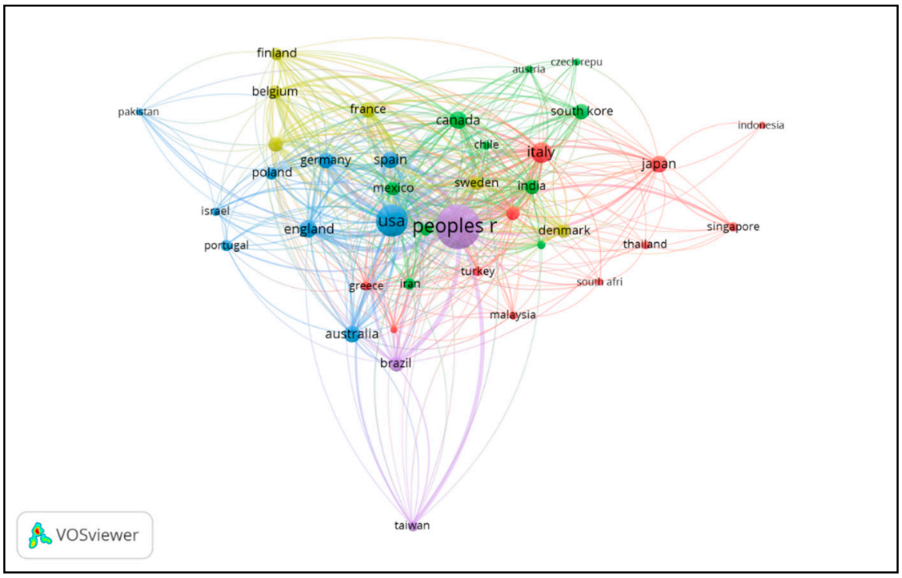

**Figure 5A.** Countries with Most Cited Publications in this field.

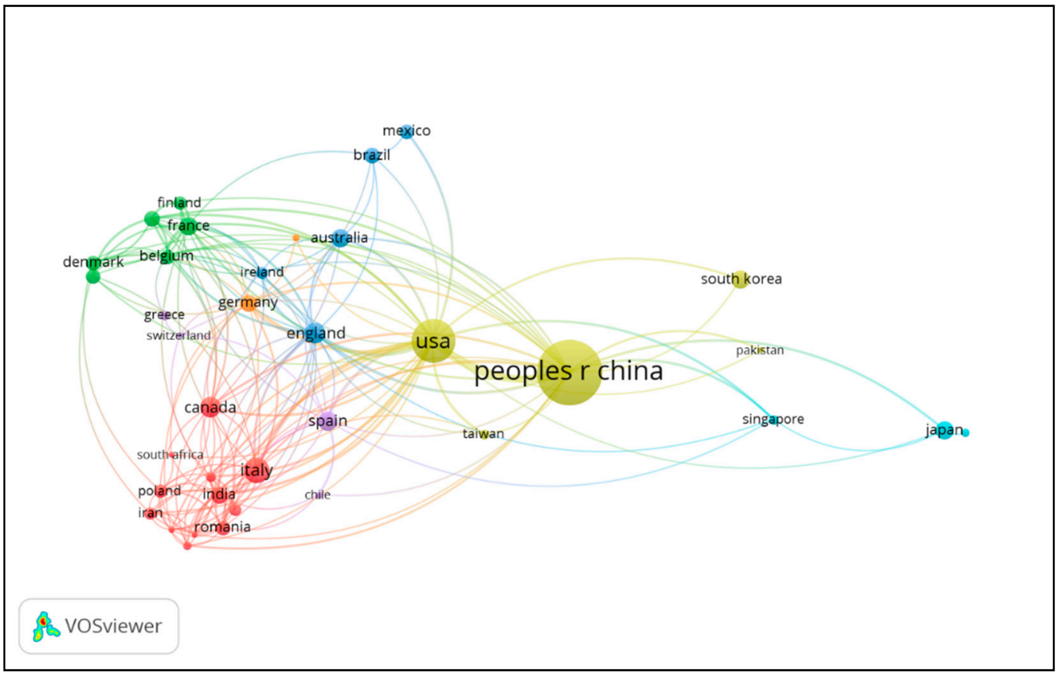

**Figure 5B.** Analysis of Cross-Country Collaborations in this field.

In terms of the cross-country collaboration (Figure 5B), set with the criteria of a minimum 3 documents and 3 citations per country, the United States shows the most collaborations with the strongest total link of 104. The United States shows a collaboration with almost all countries, the highest being with China and England. China comes in second with a total link strength of 70, with the highest being with the United States and Taiwan. It is interesting to note here that South Korea has only two cross-country collaborations, highest being China and second being with the United States.

In sum, our results indicate that China emerges as the foremost contributor to publications in this field. At the same time, the United States leads in citations and international collaborations, reflecting a dynamic global research network with China and the U.S. at its core.

### *3.4. Author Collaborations in this field*

The VOSviewer software was also employed to analyze the collaborations between authors that produce publications in this field using the Density Visualization tool (Figure 6). We set a criterion for authors to have a minimum of 3 documents and at least 3 citations. There were not many authors that collaborated among other authors in this field. Nevertheless, it is evident that P D Cani (documents: 9, citations: 1650, total link strength: 26) has the highest collaboration with M Van Hul and C Druart. N M Delzenne (documents: 7, citations: 1542, total link strength: 23) has the second strongest collaboration with L Geurts, C Druarts and M Van Hul. It should be noted that there seems to be a strong collaboration between H Herrema, M Nieuwdorp and F Backhed, and an especially stronger one between the former two.

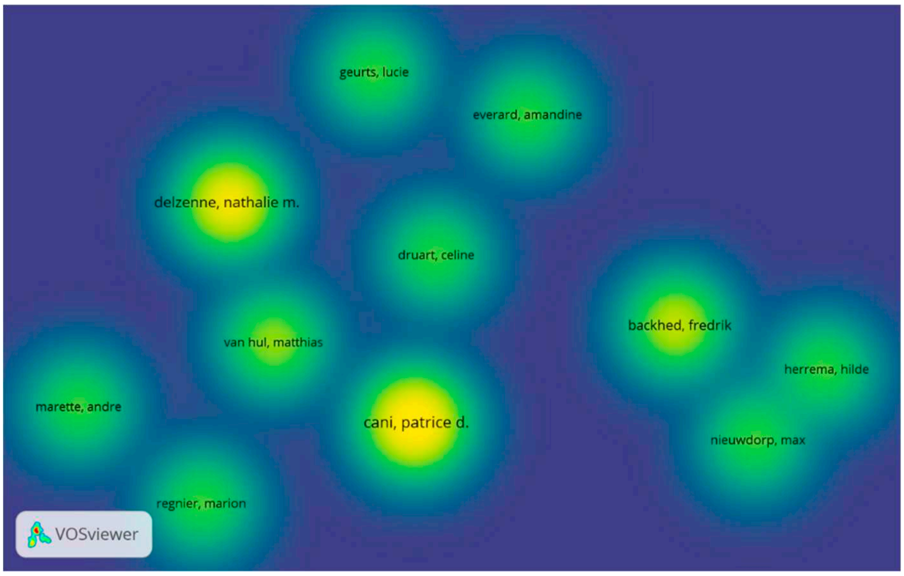

**Figure 6.** Analysis of Collaborations between Authors in this field (Density Visualization).

### 3.5. Top Cited Articles in this field

Microsoft Excel 2016 was used to analyze the top cited articles in this field. According to Table 3, Tremaroli et al. (471), Zeevi et al. (609) and Singh et al. (416) are the top 3 most cited publications with 2704, 1214 and 1008 citations respectively. Plovier et al. and Anhe et al. also follow closely with 932 and 700 citations, respectively.

### 3.6. Top Study Designs in this field

Microsoft Excel 2016 was also used to analyze the top study designs of the publications in this field. It is evident by Table 4 that the top 2 study designs are randomized controlled trials and literature reviews comprising of 32.3% and 24.5% of publications, respectively. Non-randomized experimental studies and case control studies follow next, comprising 8.4% and 8.3% of the publications, respectively.

### 3.7. Top Experimental Subjects in this field

Microsoft Excel 2016 was also used to evaluate the types of experimental subjects used for the study or whether the study was done *in vitro* (Table 5). These studies also include reviews which mention studies utilizing an animal, human or the study performed *in vitro*. Only 434 studies utilized animals in their studies. Out of 434 studies, 64.1% of the studies used animals, 31.8% used human subjects and 3.2% of the studies mentioned the use of both human and animal subjects. Table 6 provides a detailed breakdown of the animals used in the 434 studies. It is evident that mice, human subjects and rats were the top 3 experimental subjects mentioned in 42.6%, 32.0% and 19.3% of the publications respectively out of the total 434 studies.

Overall, we found that most of the studies in this field predominantly use mice, followed by human subjects and rats, with a small percentage involving both human and animal subjects.

**Table 3.** Top 10 Cited Publications in this field.

| Author | Title of the Paper | Times cited | References |
|---|---|---|---|
| Tremaroli et al., 2012 | Functional interactions between the gut microbiota and host metabolism | 2704 | (471) |
| Zeevi et al., 2015 | Personalized Nutrition by Prediction of Glycemic Responses | 1214 | (609) |
| Singh et al., 2017 | Influence of diet on the gut microbiome and implications for human health | 1008 | (416) |
| Plovier et al., 2017 | A purified membrane protein from Akkermansia muciniphila or the pasteurized bacterium improves metabolism in obese and diabetic mice | 932 | (355) |
| Anhe et al., 2015 | A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation in association with increased Akkermansia spp. population in the gut microbiota of mice | 700 | (37) |
| Serino et al., 2012 | Metabolic adaptation to a high-fat diet is associated with a change in the gut microbiota | 416 | (401) |
| Fraga et al., 2019 | The effects of polyphenols and other bioactives on human health | 399 | (121) |
| Hartstra et al., 2015 | Insights Into the Role of the Microbiome in Obesity and Type 2 Diabetes | 378 | (168) |
| Marino et al., 2017 | Gut microbial metabolites limit the frequency of autoimmune T cells and protect against type 1 diabetes | 366 | (279) |
| Ussar et al., 2015 | Interactions between Gut Microbiota, Host Genetics and Diet Modulate the Predisposition to Obesity and Metabolic Syndrome | 348 | (480) |

**Table 4.** Top 9 Study Designs in this field.

| Study Design | Frequency |
|---|---|
| Randomized controlled trial | 207 |
| Literature review | 157 |
| Non-randomized experimental study | 54 |
| Case control study | 53 |
| Systematic review | 26 |
| Experiment | 25 |
| Cohort study | 19 |
| Cross-sectional study | 13 |
| Meta-analysis/Systematic review | 7 |

**Table 5.** Types of Experimental subjects used in these Publications, (n = 434).

| Type of experimental subject | Frequency Tally |
|---|---|
| Animal | 278 |
| Human | 138 |
| Human, animal | 14 |
| *In Vitro*, mice | 2 |
| *In Vitro*, rats | 1 |

| | |
|---|---|
| *In Vitro*, human | 1 |

**Table 6.** Breakdown of Animal/Human subjects used in these Publications, (n = 434).

| Animal/Human subjects | Frequency Tally |
|---|---|
| Mice | 183 |
| Human | 138 |
| Rats | 83 |
| Mice, Humans | 7 |
| Mice, Rats | 4 |
| Mice, Rats, Humans | 3 |
| Animal, Human | 2 |
| Hamsters | 1 |
| Mice, Piglets | 1 |
| Mice, Rabbits, Humans | 1 |
| Mice, Rats, Rodents | 1 |
| Pigs (piglets & swine) | 1 |
| Rats, Human | 1 |
| Rodents | 1 |
| Rodents, Swine | 1 |
| Animals (unspecified) | 2 |

### *3.8. Co-occurrence of author keywords*

VOSviewer was used to assess the number of times author keywords that have co-occurred with a minimum of 5 occurrences, which yielded 73 studies that met the threshold (Figure 7). Overall, the most frequent keywords are 'gut microbiota' (occurrences: 241, total link strength: 468) and 'diabetes' (occurrences: 104, total link strength: 241). Figure 8 shows the top 20 Author Keywords based on their frequency of occurrence and also maps the co-occurrence of these Author Keywords.

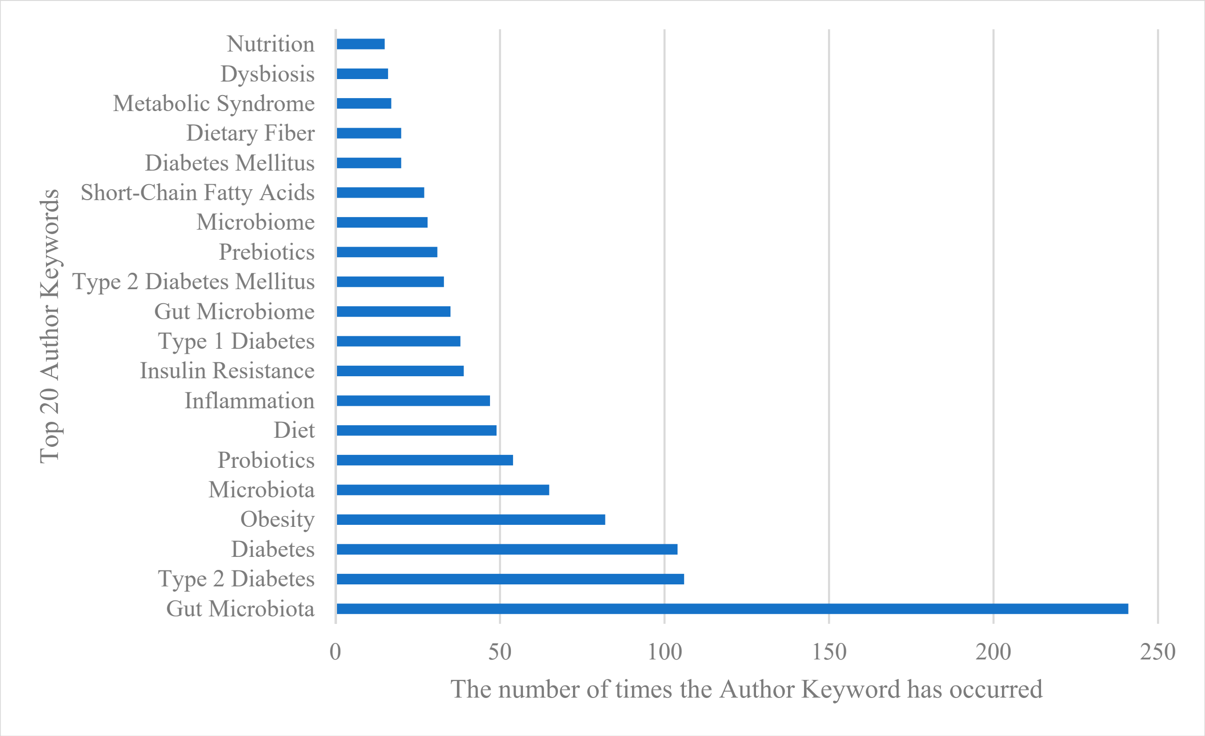

**Figure 7.** The Top 20 Author Keywords based on Number of Occurrences.

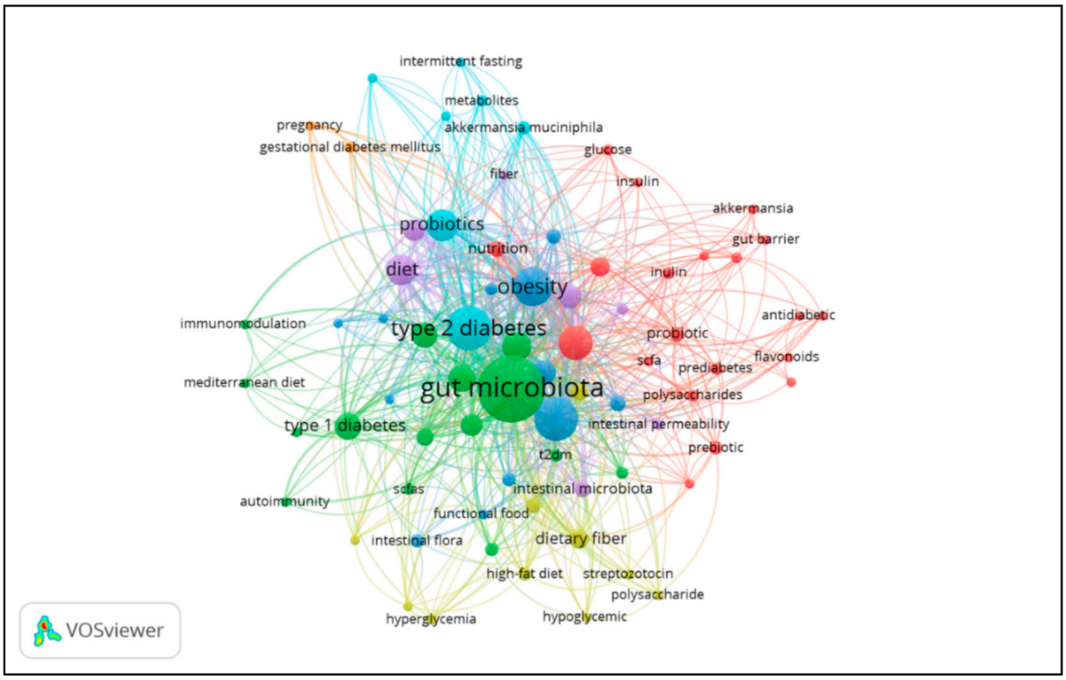

**Figure 8.** Analysis of Co-occurrences of Author Keywords.

### 3.9. Diet, DM and Gut Microbiota

All 640 studies were extracted to yield information on diet, type of DM and gut microbiota. Diet was further subdivided into specific diets such as Mediterranean Diet, Ketogenic Diet, etc., food and food products, probiotics, prebiotics, synbiotics, postbiotics, parabiotics and compounds from natural sources. Since no studies mentioned the use of parabiotics, we excluded this category from Supplementary Table 1. The type of DM from each study was analyzed on Microsoft Excel 2016 (Table 7). Majority of the studies mentioned only T2DM at 62.0%. T1DM came in second with 10.8%. GDM and prediabetes followed next with both being at 2.7%. A total of 2.3% studies mentioned both T1DM and T2DM, 1.09% studies mentioned T2DM and prediabetes, and 1% of papers mentioned GDM and T2DM both, and only Diabetic Nephropathy.

**Table 7.** Top 8 Types of DM mentioned in these Publications in this field.

| Type of Diabetes | Frequency Tally |
|---|---|
| Type 2 Diabetes | 397 |
| Type 1 Diabetes | 69 |
| Gestational Diabetes Mellitus | 17 |
| Prediabetes | 17 |
| Type 1 Diabetes, Type 2 Diabetes | 15 |
| Type 2 Diabetes, Prediabetes | 7 |
| Diabetic Nephropathy | 6 |
| Gestational Diabetes Mellitus, Type 2 Diabetes | 6 |

We observed that the gut microbiota composition varied across the studies, primarily based on the main outcomes they investigated. Some of the common organisms mentioned were Firmicutes, *Bifidobacterium*, Bacteroidetes, *Lactobacillus*, *Prevotella*, Proteobacteria and *Akkermansia muciniphila*. Interestingly, no specific diet, food and food product, probiotic, prebiotic, synbiotic, postbiotic, parabiotic or compound from a natural source was mentioned as a majority in the analyzed publications. Nevertheless, diets containing fats and carbohydrates, the Mediterranean Diet, and diets containing fiber were among the most common diets used in the articles. *Bifidobacterium* and *Lactobacillus* were among the most commonly used probiotics, along with *Akkermansia muciniphila*. VSL#3 ((containing three species of *Bifidobacterium* (B. longum, B. infantis, and B. breve), four species of *Lactobacillus* (L. acidophilus, L. paracasei, L. delbrueckii subsp. bulgaricus, and L. plantarum), and Streptococcus thermophilus)) was the most common formulation used in these studies. Prebiotics used in the studies were varied but several studies included dietary fibers, inulin, β-glucans and carbohydrates such as oligosaccharides. The only study that utilized postbiotics in the study used *Bifidobacterium* (141).

Overall, our analysis of 640 studies revealed a predominant focus on T2DM and a varied gut microbiota profile, with no single dietary intervention being prominently featured. Bifidobacterium and Lactobacillus emerge as the most frequently used probiotics, reflecting their significant role in this research area.

## 4. Discussion

### *4.1. Research Overview*

DM is becoming increasingly prevalent, and is associated with significant morbidity and mortality (667). Central to this exploration is the gut microbiota, now recognized as a crucial health indicator due to its role in metabolizing dietary components and producing metabolites that can influence an individual's diabetic status (668). For instance, individuals who showed a higher prevalence of *Roseburia hominis*, *Paraprevotella unclassified* and *Porphyromonas bennonis*, and lower levels of *Bifidobacterium longum*, *Veillonella dispar* and *Coprobacillus unclassified* were seen to develop T2DM in the future, when compared to matched controls (669). These microbial populations are deeply entwined with various critical physiological pathways, not only affecting the permeability of the intestinal wall and signaling pathways but also modulating host inflammation, metabolism, insulin resistance, and lipid metabolism, all of which contribute to an individual's response to DM treatments. It follows that dysbiosis of the gut microbiota can precipitate a range of pathological consequences and functional disturbances (670), highlighting the importance of microbial balance in managing DM.

On the other hand, diet is another modifiable risk factor for DM. Diet modification has shown to provide several benefits to people with DM, and is also associated with favorable birth outcomes in women with GDM (671,672). The volume, composition and quality of the food incorporated into the diet are important factors that dictate the effect of the diet on DM. A diet rich in red meat, sweets and fried foods is associated with an increased risk of developing insulin resistance and T2DM. In contrast, a diet rich in fruits and vegetables is seen to be protective against developing T2DM due to the presence of several antioxidants, nutrient and fiber (673). This protective effect partially stems from the gut microbiota's metabolic processing of ingested food, producing metabolites that can either worsen or alleviate various pathological processes in the body. Thus, grasping the synergistic relationship between diet and gut microbiota becomes crucial in developing comprehensive and effective DM prevention and treatment strategies.

Building on the interaction between diet and gut health, the use of probiotics like the VSL#3 formulation, frequently investigated in numerous studies included in our analysis, has shown promise for DM treatment. This probiotic blend is beneficial due to its ability to increase acetate and butyrate levels, thereby improving the SCFA composition in mice. This increase was associated with a decrease in the glycemic level, reduction in inflammation and decreased insulin resistance in T2DM models of mice. Alterations in the gut microbiota composition was also observed, showing increased abundance of microbiota producing SCFA (674). It was also noted that diets that were supplemented with prebiotics or synbiotics also improved lipid and glucose metabolism in patients with T2DM (675), further highlighting the complex interplay between diet, gut microbiota, and metabolic health.

The implications of these findings extend far into the future, especially for non-pharmaceutical interventions in metabolic disorders such as DM. Hence, the necessity of conducting a bibliometric

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analysis becomes evident as it is crucial for assessing the growth and trajectory of this research field. The surge in publications over the past decade, with a notable increase from 2017 onwards, indicates escalating interest and recognition of this topic. This trend aligns with Zhang et al. (676), which traced DM and gut microbiota research trends from 2011 to 2021, further affirming the field's expanding frontiers. In light of this notable trend, we must recognize the traits of such articles that have played a key role in disseminating these findings, shaping our current understanding, and guiding the future trajectory of research in this critical field.

### *4.2. Characteristics of Publications*

Moving into the characteristics of publications, it is pertinent to recognize the journals that have been instrumental in sharing these insights. In terms of the top journals publishing the highest number of articles and the most cited journals in this field, *Nutrients* boasts high visibility across various databases such as Web of Science, Scopus, PubMed, etc. Importantly, it stands out in the first quartile for papers on nutrition, food, and diet, maintaining a position as the most productive journal in this field, as confirmed by other bibliometric studies on DM and gut microbiota (615,676).

Transitioning from academic publications to institutional contributions, an organization-wise analysis of the most cited publications revealed that the top spots have been taken by organizations from China, such as China Agricultural University, Fujian Agriculture & Forestry University and Jiangnan University, have emerged prominently, a trend not previously observed. It is also worthy of note that the highest number of collaborations with an increased number of publications also came within the organizations in China, and between China and the United States, consistent with previous studies (676).

Moreover, the most productive countries in this field were China and the USA, producing the most cited articles and the most collaborations (615,676). This may be due to the fact that DM is a major health concern in these two countries due to its growing prevalence. The prevalence of DM increased from 10.9% to 12.4% from 2013 to 2018 in China with high estimated cost burden, among which many were unaware or undiagnosed and several with uncontrolled or untreated DM (677,678). In the United States, the prevalence of DM was 28.2 million, of which 2.9% was undiagnosed (667).

The University of Copenhagen and Catholic University of Louvain also ranked as one of the top collaborators in this field, mirroring the results of other bibliometric studies (676,679). This correlation can be explained by the fact that the authors that collaborated the most were also from these universities such as P D Cani, N M Delzenne, L Geurts and A Everard from the Catholic University of Louvain. These authors, along with F Backhed and M Nieuwdorp have been highly collaborative, producing significant work on DM and gut microbiota (615,676,679). DM is also very prevalent in European countries with the highest rates seen in Belgium, England and The Netherlands in persons aged up to 44 years, and may explain the extensive collaboration among these authors (680).

Interestingly, it was also observed that the most cited articles in the selection of 640 articles for this bibliometric analysis was from Tremaroli et al. (471), Zeevi et al. (609) and Singh et al. (416). The first two papers are also listed among the highest cited articles in Zhang et al. (676). It is interesting to note that the first and third articles were reviews which was the second most popular study design in this selection. Another commonality was attributed to the type of DM studies in these three articles. This was T2DM, which was also the most common type of DM studied in this selection of 640 articles. This may be due to the increased prevalence of T2DM as compared to other DM types. The proportion of T2DM is estimated to be at 90%. The remaining 10% is attributed to other types of DM, the major proportion of which is T1DM (681). However, since this selection includes articles published very recently in 2022, this analysis might not accurately reflect the most cited articles, as older articles tend to accumulate more citations than newly published ones over time.

The experimental subjects most used in these studies were mice, human subjects, and rats. Mice were used in considerably more studies than rats, supporting the current trend. This can be attributed to the plethora of different strains of mice to choose from as compared to rats, and the ease of producing genetically modified versions of mice than rats. Rats are also less economical than mice and take up more space and are expensive to manage. There are also better diagnostic tools for mice models than rats. However, the use of rats is still high in our selection, which may due to the rats sharing more similarities to humans than mice (682).

The analysis of author-used keywords, based on how frequently they appear or co-occur in the papers, reveals a similar pattern. 'Gut Microbiota', 'Type 2 Diabetes', 'Diabetes' and 'Obesity' were the most frequent, likely because authors more often used keywords related to gut microbiota and DM than to nutraceuticals. The most commonly used keyword in terms of nutraceuticals is 'Probiotics', which is the 6th common keyword in top 20 most occurring keywords used by authors. Interestingly, 'Obesity' was a commonly occurring keyword even though our study did not specifically focus on obesity. This likely reflects the close relatedness of DM and obesity and the increased prevalence of metabolic syndrome in obese individuals.

The gut microbiota composition mentioned by these publications were diverse and were dependent mainly on the type of outcome studied by these publications. However, Firmicutes, *Bifidobacterium*, Bacteroidetes, *Lactobacillus*, *Prevotella*, Proteobacteria and *Akkermansia muciniphila* were some of the most commonly mentioned gut bacteria in the publications. The relative abundances of Firmicutes, Bacteroidetes and Proteobacteria are altered in patients with T2DM, causing a decrease in the F:B (Firmicutes:Bacteroidetes) ratio. The levels of Proteobacteria were also increased in patients with T2DM. *Prevotella* was also seen to be decreased in patients with T2DM (683). *Bifidobacterium* and *Lactobacillus* are important to assess both as a probiotic and a resident bacterium in the gut. The levels of these two bacteria genera is seen to be increased with treatment of T2DM with metformin (683). The abundance of these gut bacteria dictate the production of various metabolites such as SCFA, which then modulate the various metabolic pathways in pathological states, such as DM. Additionally, *Bifidobacterium* improves the permeability of the intestinal barrier by reducing inflammation and circulating levels of endotoxins. It also improves glucose tolerance and insulin sensitivity (683). *Akkermansia muciniphila* is a bacterium that can be provided as a probiotic or may be present as a resident gut bacterium. It plays a protective role against the development of T2DM, and is important to maintain the integrity of the mucin layer. Mucins play a significant role in protecting the lumen of the gastrointestinal tract and helps in reducing the translocation of the gut microbiota. It improves storage and metabolism of lipids and glucose homeostasis, while also reducing inflammation (683). The emphasis of these microorganisms specifically underscores the critical interplay between gut microbiota and the management of metabolic diseases. Their collective influence on metabolic regulation, immune modulation, and overall homeostasis positions these bacteria as key targets for therapeutic interventions in DM management.

While the analyzed publications did not frequently mention a specific nutraceutical, diets containing fats and carbohydrates, the Mediterranean Diet, and diets containing fiber were some of the most common diets referenced in the selected articles. In the recent years, the current trends have moved towards a healthier diet with increased intake of high-quality carbohydrates and plant proteins such as whole grains and nuts, and polyunsaturated fats, and decreased intake of low-quality carbohydrates (such as added sugars). However, intake of saturated fats has still remained above the recommended level (684). It was noted that intake of low-fat diet increased the abundance *Bifidobacterium* and reduction in fasting glucose levels. Digestible carbohydrates such as glucose, fructose and sucrose fed in high quantities in the form of date fruits to human subjects were also seen to increase the relative abundance of *Bifidobacterium* and *Bacteroides*. Lactose has also been seen to increase the concentration of beneficial SCFAs. Non-digestible carbohydrates or fibers, such as whole grains and wheat bran were seen to increase *Bifidobacteria* and *Lactobacilli*, while reduced fiber intake was linked to reduced SCFA concentration (416). The Mediterranean Diet is characterized by an increased amount of dietary fibers and polyphenols, and is able to induce the production of SCFAs. It promotes gut symbiosis rather than dysbiosis (685). The positive effects of these diets on the gut microbiota is beneficial for patients with DM. These trends may have led to increased research into the possible implications of these diets on the gut microbiota and DM.

Some of the most common probiotics mentioned in the selection were *Bifidobacterium*, *Lactobacillus* and *Akkermansia muciniphila*. The specific probiotic formulation, VSL#3 was also commonly used in these studies. This formulation contains various strains of *Bifidobacterium* and

*Lactobacillus* which are important in modulating DM. Interestingly, VSL#3 enriched with Lactobacillaceae was seen to be protective against a T1DM mouse model by affecting the inflammasome at the level of the intestines (686). Interestingly, in our selection of 640 articles, we found one study that utilized postbiotics (141). The study added *Bifidobacterium* to the diet, which is again beneficial for patients with T2DM. Finally, commonly used prebiotics were dietary fibers, inulin, β-glucans and carbohydrates such as oligosaccharides. Dietary fibers, such as cereal fibers, have been shown to reduce the FPG and HbA1c in patients with T2DM (687). Inulin was also shown to significantly reduce the FPG, HbA1c and cholesterol and triglyceride levels in patients with T2DM. Thus, it may aid in controlling DM and its complications as well (688). β-glucans have also shown benefits in treating DM (possibly through the phosphoinositide 3-kinase (PI3K)/protein kinase B (PKB or Akt) pathway) by not only reducing hyperglycemia, hyperlipidemia and hypertension, but also by promoting wound healing and improving injury to the heart via ischemia, thereby also managing the cardiovascular complications of DM (689). Lastly, functional oligosaccharides such as fructo-oligosaccharides, galacto-oligosaccharides, and xylo-oligosaccharides were shown to play a protective role against the development of DM, possibly by improving inhibition by $\alpha$-glucosidase, insulin and leptin resistance, and pancreatic function, while also reducing inflammation and regulating the gut microbiome, gut hormones and risk factors leading to DM (690). The nutraceuticals detailed in the 640 selected articles impact DM and gut microbiota through various mechanisms, demonstrating their interconnected roles in metabolic health. Their multifaceted effects underscore their potential as non-pharmacological treatments for DM and its associated complications, positioning them as integral components of holistic metabolic disease management.

### *4.3. Research Hotspots and Frontiers*

DM research aims to, among other things, determine bodily mechanisms leading to deterioration of insulin homeostasis and development of DM. Among other well-cited risk factors, the dysbiosis of the gut microbiome, a rich community of over a ten trillion bacteria, archaea, and eukaryotes, is a recent hotspot of DM research in the past few decades (691). The human gut houses a diverse microbiome with large compositions of *Bacteroidetes*, *Verrucomicrobia*, *Actinobacteria*, *Fusobacteria*, *Bacteroidetes*, and *Proteobacteria* in proportions that promote physiological balance and function, though various mechanisms including the action of microbiota-produced metabolites. These metabolites, including SCFAs such as propionate and acetate, result from fermentation of indigestible carbohydrates by microbiota and have shown to improve glucose homeostasis in multiple tissues (692).

Depletion of butyrate-producing has especially been repeatedly linked to T2DM (658). A recent study in *Diabetes* analyzing associations between butyrate-producing taxa and measures of insulin homeostasis in both non-Hispanic Whites and African American showed that *Coprococcus* was associated with higher insulin sensitivity and lower rate of dysglycemia; *Flavonifractor* was associated with lower insulin sensitivity and higher dysglycemia prevalence. The authors showed that although most butyrate producers appeared to be metabolically beneficial, and that, instead of targeting all butyrate producers, therapeutic approaches aimed at preventing or treating DM through the microbiome should focus on specific taxa that produce butyrate (693). Butyrate acts by binding to G-protein coupled receptors, GPCR41 and GPCR43, and stimulating the release of GLP-1 and Glucagon-like peptide 2 (GLP-2), thus enhancing insulin, and inhibiting glucagon secretion (691). Further, butyrate has shown to inhibit histone deacetylase, which stimulates the growth and differentiation, enhances the function, and inhibits the death of pancreatic β-cells (658). Hence, targeting specific butyrate-producing bacteria may offer a focused and effective strategy for T2DM treatment, capitalizing on their proven role in metabolic health.

Gut dysbiosis has been linked to increased risk of developing metabolic syndromes including DM (658). In the context of T2DM, *Bifidobacterium*, *Akkermansia*, *Roseburia*, and *Faecalibacterium* have exhibited a negative association, whereas *Fusobacterium*, *Blautia*, and *Ruminococcus* have shown a positive association (691). Migration of gram-negative bacteria such as *Proteobacteria* from the intestines to the tissues is also considered a signal for the development of T2DM.

Various bacteria have been investigated for their probiotic properties for potential benefit in various deranged aspects of T2DM (694–698). *Bifidobacterium lactis* promotes glycogen synthesis and suppresses gluconeogenesis in the liver, in addition to improving glucose uptake. *Lactobacillus gasseri* BNR17 exhibits similar effects in muscles. *Akkermansia muciniphila* and *Lactobacillus plantarum* have shown to repress hepatic flavin monooxygenase 3 thus preventing hyperglycemia in insulin-resistant mice. *A. muciniphila* also impedes carbohydrate breakdown, thereby reducing postprandial hyperglycemia. *Lactobacillus rhamnosus* enhances insulin sensitivity by elevating adiponectin. A multi-strain formulation of probiotic Ecologic® Barrier (consisting of *Bifidobacterium bifidum* W23, *B Bifidobacterium lactis* W52, *Lactobacillus acidophilus* W37, *Levilactobacillus brevis* W63, *Lactobacillus casei* W56, *Ligilactobacillus salivarius* W24, *Lactococcus lactis* W19, and *Lactococcus lactis* W58) has also shown positive results for T2DM (699). Particularly, *Bifidobacterium* and *Lactobacillus* are among the most investigated species for their probiotic properties secondary to their ability to convert primary conjugated bile salts to bile acids that are later deconjugated by producing bile salt hydrolases. These studies not only verify the adverse effects of gut dysbiosis on T2DM but also underline the role of probiotics in mitigating these effects and offering an adjunctive treatment strategy for the disease.

### *4.4. Limitations*

While our findings contribute meaningful insights into the interplay between diet, gut microbiota, and DM, the scope of our analysis was bound by specific parameters that future studies may wish to expand. First, we sourced our papers exclusively from the Web of Science database, potentially overlooking relevant articles not indexed there. Second, our selection was limited to 640 articles. While the broader field of DM and gut microbiota is vast, narrowing our focus to include diet-related keywords significantly reduced the pool of research. The inclusion criteria that the articles were subjected to was also relatively lenient, however only 640 articles could be included due to one of the main criteria being that the articles must include all three keywords (relating to DM, gut microbiota and diet). Third, the specific keywords chosen for our database search might have influenced the relevance of the articles retrieved, causing us to miss key studies not tagged with our selected search terms. Lastly, we excluded studies published outside the 2012–2022 timeframe and those not in English, introducing the potential for bias by omitting pertinent research not captured within these parameters.

## 5. Conclusions

Diet, DM, and the gut microbiota are interconnected and can influence each other via the application of microbiome-modulating dietary nutraceuticals. Such interactions can be exploited to prevent, manage, and possibly even reverse DM, and warrants the importance of continued research in this field. This topic has been garnering increasing attention and more research is needed to sustain the uptrend. Research collaborations between different authors, institutions and countries is impactful in the field of research to establish connections and produce new papers to potentiate a therapeutic in diet and the gut microbiota to target DM. This bibliometric and visual analysis of research trends and important hotspots highlight the diverse qualities of published literature in this field, allowing researchers to identify collaborators, sponsors, new leads, influential journals and authors, as well as the top keywords and research questions for their future research. This study also sheds light on novel areas of research regarding the use of nutraceuticals such as dietary interventions, probiotics, prebiotics, synbiotics and others, which aim to modulate the gut microbiota. This modulation would regulate inflammation and different metabolic pathways to induce, promote or protect against pathological states, to non-pharmacologically manage DM and its complications. By highlighting substantial opportunities for further research, our study promotes the streamlining of efforts toward shared objectives and encourages interdisciplinary and international collaboration to expand upon this field of research.

**Supplementary Materials:** The following supporting information can be downloaded at the website of this paper posted on Preprints.org.

**Author Contributions**: Conceptualization, AC, AS, SuL, IK; Methodology, AC, AS, SaL; Software, AC, AS, SaL; Validation, AC, AS, AK, SuL, IK; Formal Analysis, AC, AS, AK; Investigation, AC, AS, AK, SuL, IK; Resources, AC, SaL; Data Curation, AC, AS, AK, SuL, IK, SaL; Writing – Original Draft Preparation, AC, AS, AK; Writing – Review & Editing, AC, AS, AK, RK, PP; Visualization, AC, AS, AK, RK, PP; Supervision, AC, AS; Project Administration, AC, AS, SaL; Funding Acquisition, AC

**Conflict of interest**: The authors declare no conflict of interest.

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