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Scientometric analysis of kidney disease and gut microbiota from 2001 to 2020 based on Web of Science

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Abstract

This study aims to demonstrate current research priorities and predict future trends in the link between kidney disease and gut microbiota by means of scientometric analysis. We collected nearly 20 years (2001–2020) of publications related to kidney disease and gut microbiota in the Web of Science database. CiteSpace was used to evaluate the knowledge mapping. There are 965 manuscripts about kidney disease and gut microbiota in total, and faster growth after 2016. The country, institution, and author who posted the most are the USA, Univ Calif Irvine, and DENISE MAFRA, respectively. The frequencies are 109, 16, and 17. The most important of them are FRANCE (0.23), Fed Univ Parana UFPR (0.13), and VAZIRI ND (1.14), owing to their highest centrality. In addition, the cited documents that have contributed the most to the co-citations are Wong J (2014); the most key cited reference is Rossi M (2016); the most commonly used keywords are chronic kidney disease, gut microbiota and indoxyl sulfate. Through scientometric analysis of the past 20 years, we obtained the knowledge map of this information, which has important guiding significance for accurately and quickly locating trends in this field.

Abbreviations: CKD = chronic kidney disease, IF = impact factor, IS = indoxyl sulfate, PCS = p-cresol sulfate, WOS = Web of Science.

Keywords: CiteSpace, gut microbiota, kidney disease, knowledge mapping, scientometric analysis

1. Introduction

The main characteristics of chronic kidney disease (CKD) are decreased glomerular filtration rate and progressive impairment of renal function. It has become a global public health problem; prevalence is about 8% to 16%.[1] More than 2000 species of commensal bacteria live in the intestinal tract in a natural balance. Recent studies have suggested that the gut microbiota is one of the pathogenic factors in kidney disease.[2] CKD patients may suffer from multiple complications, including increased anemia, blood pressure, cardiovascular mortality. More and more evidence shows a strong and pathophysiological connection between the microbiota and the host.[2,3] It is very important to master the research activities of kidney disease and gut microbiota. Due to the rapid growth of kidney disease and gut microbiota research, it is particularly important to fully understand its research status and hot spots.

Service networks for sustainable business research in the big data era have received more attention in the development of advanced theories and new technologies for adaptation to a dynamic and turbulent business environment.[4,5] Scientometrics is a quantitative analysis in a specific discipline including different databases (PubMed,[6] Web of Science [WOS]),[7] Scopus,[8] Derwent,[9] etc). Among them, WOS is analyzed by different software: Histcite,[10] CiteSpace,[9] VOSviewer,[11] etc. Readers can completely understand the hot spots, trends and frontiers and in this field through CiteSpace software, which helps us to illustrate the development background of certain areas of research.[12] CiteSpace is a mature visualization software with Java language.[13] It can explore knowledge turning points and changes in subject areas. CiteSpace includes coauthor, co-citation, and co-occurrence analysis.[14] There are 3 concepts, which include burst detection, betweenness centrality, and heterogeneous network.[15] Therefore, the scientometric analysis

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of kidney disease and gut microbiota through CiteSpace can gain the research trend and knowledge mappings. Researchers engaged in this field can use it to accurately grasp research hotspots.

There is currently no bibliometric method to study the relationship between kidney disease and gut microbiota. Therefore, the researchers used CiteSpace software to analyze the global role and trend of the relationship between the gut microbiota and CKD in the WOS database from 2001 to 2020, and established a field knowledge map in this study.

2. Methods

2.1. Source of literature

We input the WOS database with the following subject words: TS = (Uremia* OR kidney disease* OR CKD) AND TS = (gut microbiota* OR gut-kidney axis* OR gut microbiome* OR gut bacteria). The search scope of the database is from 2001 to 2020. Through a literature search, 965 records were gained. After CiteSpace eliminated duplication, 215 literatures were used for quantitative analysis. The WOS database comes from the Shanxi Bethune Hospital database in China.

2.2. Statistical methods

All literature on kidney disease and gut microbiota were scientifically analyzed; the frequency is mainly used to observe core countries or regions, institutions, authors, keywords, and cited documents.[16–19]

2.3. Results and discussion

2.3.1. Analysis of the publications outputs During the research period, the total number of articles increased and fluctuated. From Figure 1, the research is divided into 3 stages: 2001 to 2012 is the first stage, from 2013 to 2015 is the second stage, and 2016 to 2020 is the third stage. The third stage was a speed development period. The publications published were 4 references in 2015, rising to 20 references in 2016, and in 2019, this number grew to 55. These results indicate that interaction between intestinal microbiota and kidney disease is receiving increasing attention in research for the last 5 years.

2.4. Analysis of document type

There were 6 document types in the 965 references. The most was original articles (240, 24.9%). Next was reviews (158, 16.4%; Table 1). The most cited article is "Expansion of Urease-and Uricase-Containing, Indole-and p-Cresol-Forming, and Contraction of Short-Chain Fatty Acid-Producing Intestinal Microbiota in ESRD."[18] In that article, the author found the patients with end-stage renal disease showed a significant expansion of the microbiota family. Changes in intestinal microbial metabolites include indoxyl sulfate (IS), p-cresol sulfate (PCS), and urea-derived ammonia. The beneficial effects of short-chain fatty acids contribute to uremic toxicity and inflammation.[18]

2.5. Analysis of country and institution

A country map was generated that had 63 nodes and 116 links (Fig. 2). Research groups in 27 countries published 965 references. The USA, PEOPLES R CHINA, ITALY, BRAZIL, and FRANCE are the top 5 countries (Table 2). FRANCE (0.23) and England (0.13) are the top 2 countries from centrality (purple round). An analysis from publication and centrality shows that FRANCE, ENGLAND, and BRAZIL were the main research forces in kidney disease and gut microbiota. The USA, China, Italy, the United Kingdom, Brazil, Australia, and France have continued to increase their research interest in this field. The research is mainly distributed in developed countries and regions. The outer circle is purple-red, indicating that the amount

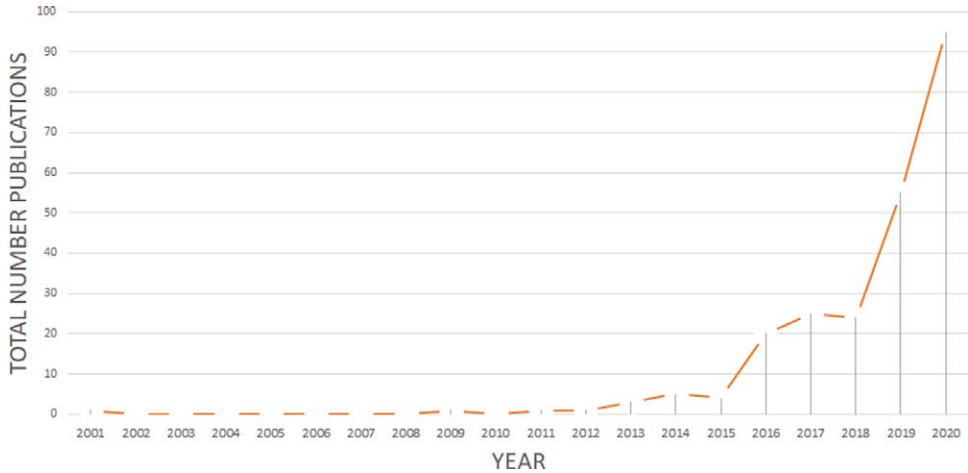

Figure 1. The number of kidney disease and gut microbiota publications indexed by WOS from 2001 to 2020. WOS = Web of Science.

Table 1

Document types for documents referencing kidney disease and gut microbiota.

Ranking	Type	Counts (%)
1	Article	240 (24.9)
2	reviews	158 (16.4)
3	Meeting Abstract	13 (1.3)
4	Editorial Material	12 (1.2)

of research in this field in these countries is likely to continue to grow in the future. The United States posted the highest number of 109 articles, followed by 83 articles published in mainland China. At the same time, the thinner connections between countries indicate weak cooperation.

An institution map was generated that had 99 nodes and 119 links (Fig. 3). The 965 publications have been published in 99 research institutions. The Univ Calif Irvine, Chang Gung Univ, Karolinska Inst, Katholieke Univ Leuven, and Kaohsiung Med Univ are the top 5 institutions (Table 2). In terms of centrality, the top 3 institutions were Fed Univ Parana UFPR (0.13), Univ Fed Fluminense (0.12) and Karolinska Inst (0.12). In addition, the links between institutions are relatively thin, indicating that cooperation is weak.

2.6. Analysis of journals and co-cited journals

The top 10 academic journals related to kidney disease and gut microbiota are listed in Table 3. They are specialized journals in these field. The average impact factor (IF) is 9.83.

Some articles are highly cited, such as the Circulation Research article that was cited 72 times, and they reported identified trimethylamine-N-oxide are produced by gut microbiota and proved gut microbiota-associated trimethylamine-N-oxide formation in the development and progression of CKD.[21] Megan Rossi's study shows that synbiotics could decrease the microbial production of PCS, and indoxyl sulfate to the form or function of the gut microbiota.[22] In addition, Dorothy A's research found that in the high amylose maize-resistant starch type 2-fed rats, IS and p-cresol in the urine the was reduced by 66% and 47%, respectively. Therefore, they suggest that gut microbial metabolism plays an important role in regulating host kidney function.[23] Ramezani A's research shows that CKD disrupts gut barrier function, leading to inflammation, CKD exacerbations and related cardiovascular diseases (IF = 9.274).[24]

A co-citation journal map was generated that had 31 nodes and 40 links (Fig. 4). KIDNEY INT, PLOS ONE, J AM SOC NEPHROL, NEPHROL DIAL TRANSPL and NATURE are the top 5 co-cited journals; KIDNEY INT, PLOS ONE, NATURE, J AM SOC NEPHROL and NEPHROL DIAL TRANSPL are the top 5 centrality (Table 4, Fig. 4). In an analysis of publication, centrality and co-citation counts, the core journal for the kidney disease and gut microbiota research field is the KIDNEY INT, the published literatures reflect the current state of research in this field.

2.7. Analysis of author and co-cited author

The information about influential researchers is provided by knowledge map. A coauthor map was generated that had 116 nodes and 257 links (Fig. 5). A total of 116 research authors published 965 articles. The top ten authors with published articles about kidney disease and gut microbiota are listed in Table 5. They are experts in this field. The top author DENISE MAFRA is based at the Fluminense Federal University and reviews kidney disease and gut microbiota from the Resistant starch. They reviewed the potential role of the gut microbiota on CKD patients.[25]

An author co-citation map was generated that had 116 nodes and 257 links (Fig. 6). VAZIRI ND, RAMEZANI A, TANG WHW, WONG J and ROSSI M are the top 5 co-cited authors, and the top 3

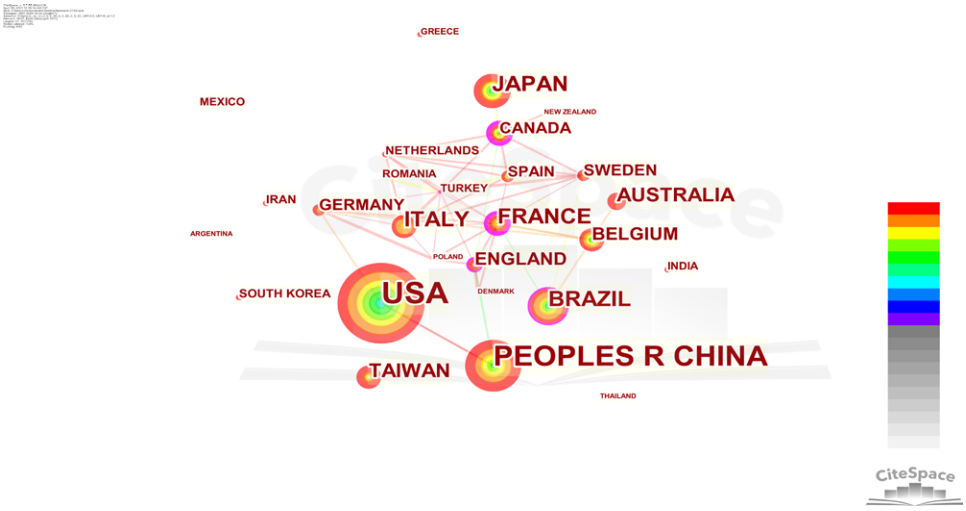

Figure 2. Network of territories or countries on between kidney disease and gut microbiota.

Table 2

Top 10 prolific countries and institutions researching kidney disease and gut microbiota.

Ranking	Country	Publications	Rank	Institution	Publications
1	USA	109	1	Univ Calif Irvine	16
2	PEOPLES R CHINA	83	2	Chang Gung Univ	11
3	ITALY	28	3	Karolinska Inst	7
4	BRAZIL	28	4	Katholieke Univ Leuven	7
5	FRANCE	24	5	Kaohsiung Med Univ	7
6	JAPAN	24	6	Univ Bari Aldo Moro	6
7	TAIWAN	20	7	Ghent Univ Hosp	6
8	AUSTRALIA	20	8	Kaohsiung Chang Gung Mem Hosp	6
9	BELGIUM	14	9	Fed Univ Parana UFPR	6
10	ENGLAND	13	10	Sichuan Univ	5

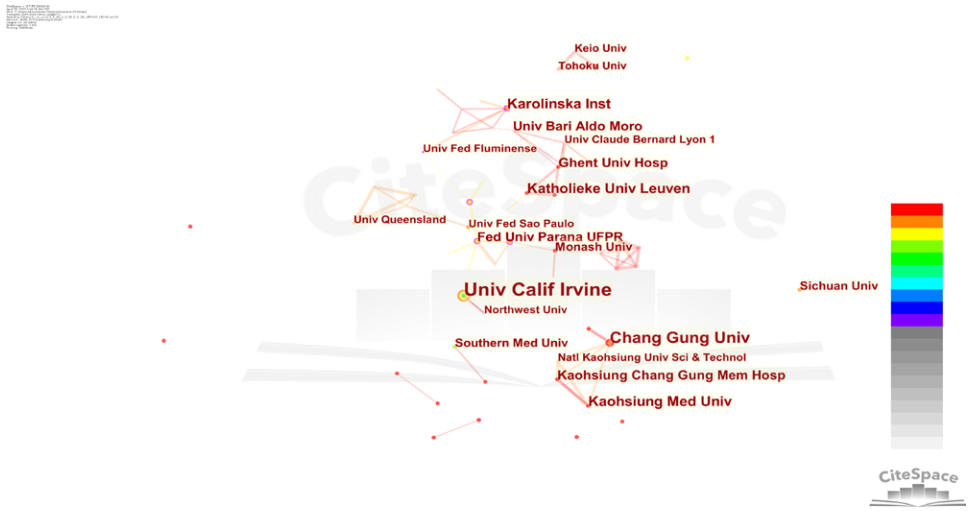

Figure 3. Institutional map researching kidney disease and gut microbiota from 2001 to 2020.

Table 3

Top 10 scholarly journals related to research kidney disease and gut microbiota.

Ranking	Journal	Publications	IF (2020)
1	KIDNEY INT	267	8.945
2	PLOS ONE	257	2.74
3	J AM SOC NEPHROL	250	9.274
4	NEPHROL DIAL TRANSPL	221	4.531
5	NATURE	197	42.778
6	CLIN J AM SOC NEPHRO	155	6.628
7	SCI REP-UK	153	3.998
8	AM J KIDNEY DIS	145	6.618
9	P NATL ACAD SCI USA	120	9.412
10	AM J NEPHROL	118	3.411

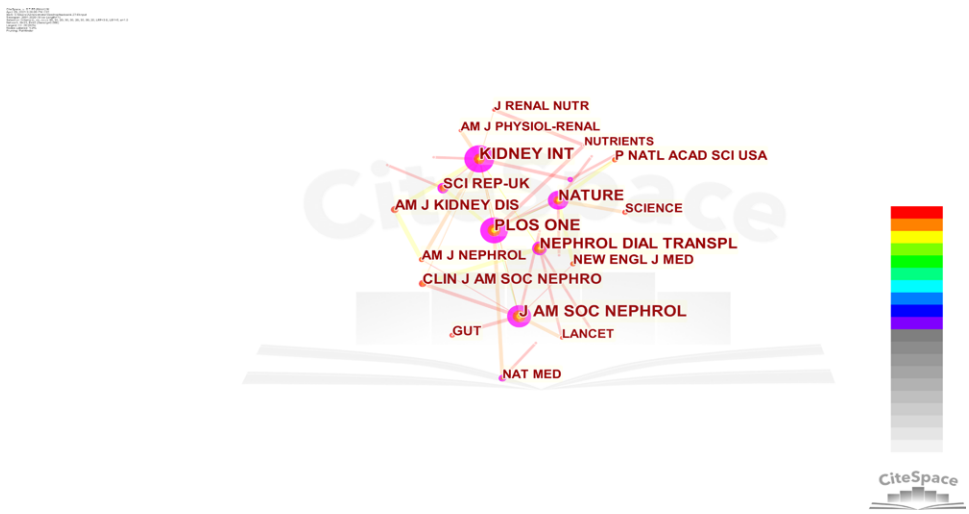

Figure 4. Co-citation map of journal related to kidney disease and gut microbiota research from 2001 to 2020.

Table 4

Top 5 cocited journals and centrality related to kidney disease and gut microbiota research from 2001 to 2020.

Ranking	Cocitation counts	Cited journal	Ranking	Centrality	Cited journal
1	267	KIDNEY INT	1	0.82	KIDNEY INT
2	257	PLOS ONE	2	0.74	PLOS ONE
3	250	J AM SOC NEPHROL	3	0.47	NATURE
4	221	NEPHROL DIAL TRANSPL	4	0.44	J AM SOC NEPHROL
5	197	NATURE	5	0.14	NEPHROL DIAL TRANSPL

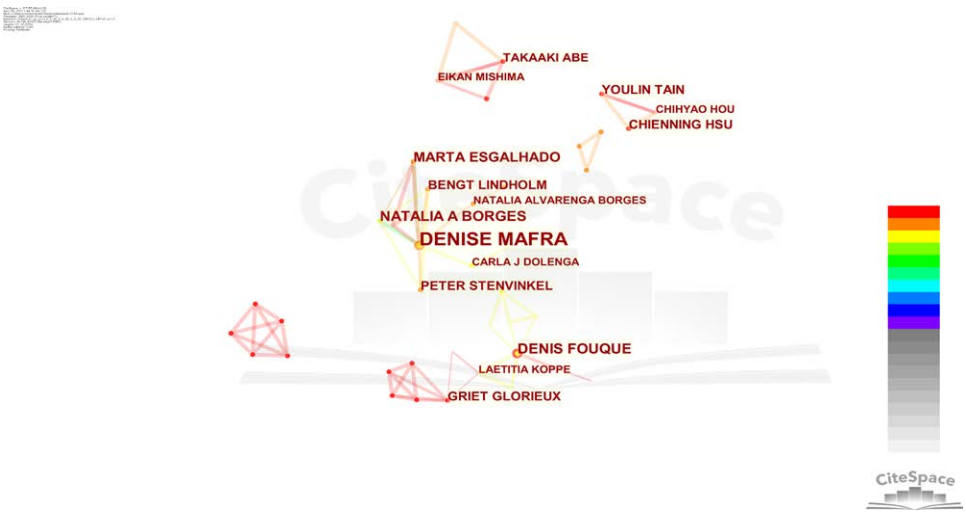

Figure 5. A coauthor map related to kidney disease and gut microbiota research from 2001 to 2020.

Table 5

Top 10 active authors in kidney disease and gut microbiota research from 2001 to 2020.

Ranking	Author	Publications
1	DENISE MAFRA	17
2	NOSRATOLA D VAZIRI	13
3	NATALIA A BORGES	8
4	DENIS FOUQUE	8
5	MARTA ESGALHADO	7
6	PETER STENVINKEL	6
7	CHIENNING HSU	6
8	GRIET GLORIEUX	6
9	YOULIN TAIN	6
10	BENGT LINDHOLM	6

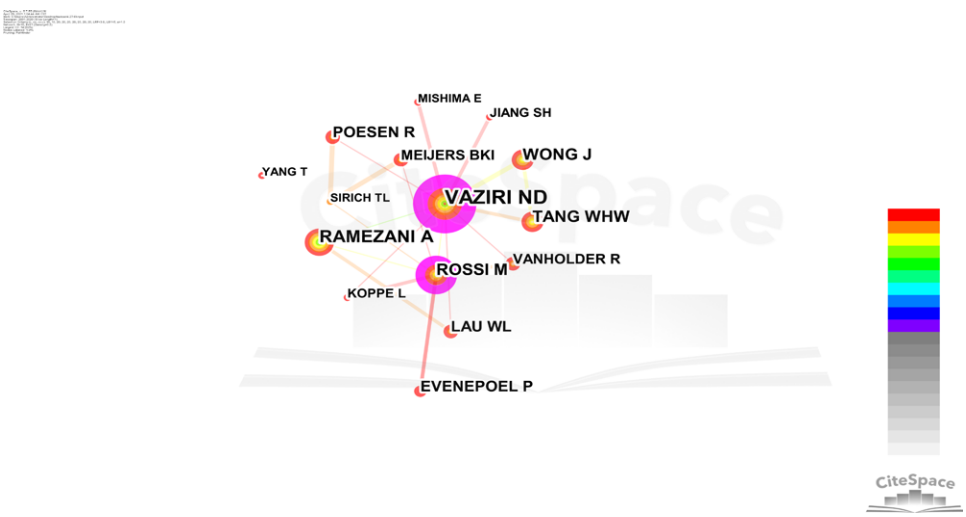

Figure 6. A co-citation map of author related to kidney disease and gut microbiota research from 2001 to 2020.

authors by centrality were VAZIRI ND, ROSSI M and RAMEZANI A (Table 6, Fig. 6). An analysis by centrality and co-citation counts revealed that VAZIRI ND, ROSSI M and RAMEZANI A were "core strength" researchers. They had an important influence in this field. VAZIRI ND is based at the California Irvine University (the USA), studies kidney disease and gut microbiota by the effect of synbiotic therapy on gut microbiome in patients with CKD.[26,27]

2.8. Co-citation analysis

A map of co-citation was generated that had 40 nodes and 60 links (Fig. 7). An analysis from co-citation centrality and counts (Tables 7 and 8, Fig. 7) revealed that the data usually comes like random trials and reviewed this topic in the past 20 years.

Table 6

Top 5 cocited authors in kidney disease and gut microbiota research in terms of cocitations and centrality.

Ranking	Author	Cocitation counts	Centrality	Author
1	VAZIRI ND	191	1.14	VAZIRI ND
2	RAMEZANI A	113	0.63	ROSSI M
3	TANG WHW	81	0.06	POESEN R
4	WONG J	80	0.04	RAMEZANI A
5	ROSSI M	78		

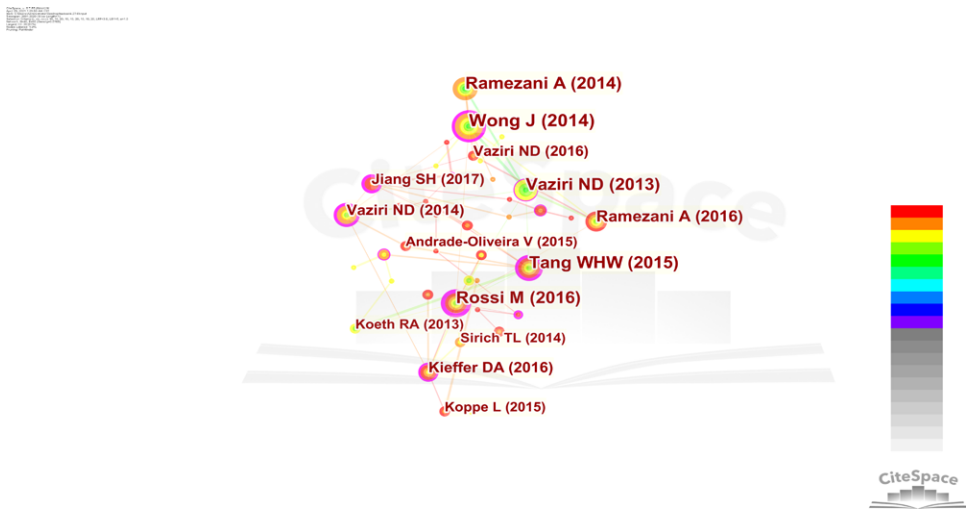

Figure 7. A co-citation map of reference related to kidney disease and gut microbiota research from 2001 to 2020.

Table 7

Top 5 cocited references related to kidney disease and gut microbiota research.

Ranking	Cited reference	Cocitation counts	Representative author (publication year)
1	Expansion of urease- and uricase-containing, indole- and p-cresol-forming and contraction of short-chain fatty acid-producing intestinal microbiota in ESRD	80	Wong J (2014)[18]
2	Gut microbiota-dependent trimethylamine N-oxide (TMAO) pathway contributes to both development of renal insufficiency and mortality risk in chronic kidney disease	72	Tang WHW (2015)[19]
3	Chronic kidney disease alters intestinal microbial flora	69	Vaziri ND, 2013[26]
4	The gut microbiome, kidney disease, and targeted interventions	68	Ramezani A (2014)[21]
5	Synbiotics Easing Renal Failure by Improving Gut Microbiology (SYNERGY): a randomized trial	68	Rossi M (2016)[20]

Table 8

Top 5 cocited references in kidney disease and gut microbiota research in terms of centrality.

Ranking	Cited reference	Centrality	Representative author (publication year)
1	Synbiotics Easing Renal Failure by Improving Gut Microbiology (SYNERGY): a randomized trial	0.66	Rossi M (2016)[19]
2	Expansion of urease- and uricase-containing, indole- and p-cresol-forming and contraction of short-chain fatty acid-producing intestinal microbiota in ESRD	0.44	Wong J (2014)[25]
3	Chronic kidney disease alters intestinal microbial flora	0.43	Vaziri ND (2014)[26]
4	Gut microbiota-dependent trimethylamine N-oxide (TMAO) pathway contributes to both development of renal insufficiency and mortality risk in chronic kidney disease	0.42	Tang WHW (2015)[18]
5	Resistant starch alters gut microbiome and metabolomic profiles concurrent with amelioration of chronic kidney disease in rats	0.24	Kieffer DA (2016)[20]

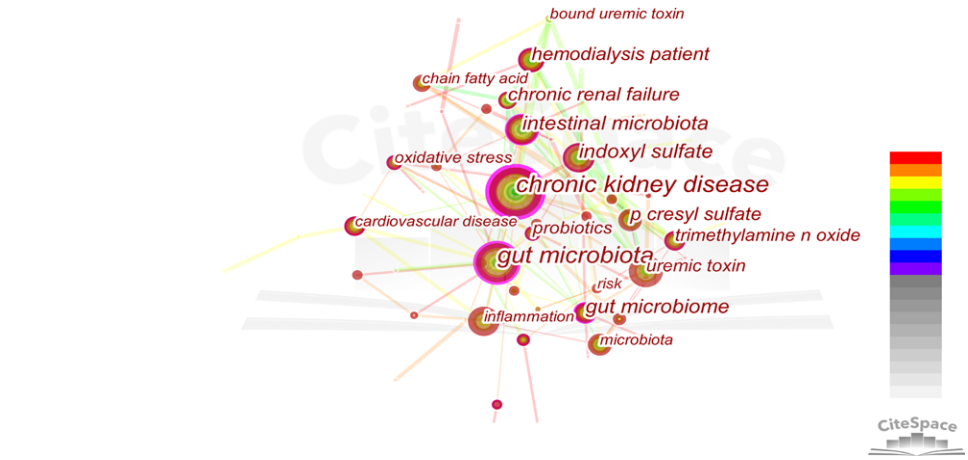

Figure 8. A keyword co-occurrence map of kidney disease and gut microbiota from 2001 to 2020.

2.9. Analysis of keyword co-occurrence

A keyword co-occurrence map could reflect hot topics; burst keywords could reflect frontier topics. A keyword co-occurrence map was generated that had 63 nodes and 116 links (Fig. 8). It shows that the prevalent keywords were CKD, gut microbiota, indoxyl sulfate, inflammation, intestinal microbiota, a uremic toxin, p-cresol sulfate, hemodialysis, hemodialysis patient, microbiota, and cardiovascular. There were the following hot topics: CKD and gut microbiota: the gut microbiota is crucial in the progression of CKD. The fermentation of amino acids tyrosine and tryptophan obtained from food by intestinal microbiota produce indole and p-cresol, respectively, further metabolized to p-indoxyl sulfate and p-cresol sulfate in the liver. These toxins are mainly secreted and excreted through the kidneys. Their increased concentration is associated with kidney impairment and advancing CKD.[29] p-cresol sulfate and indoxyl sulfate: Only 2 solutes from the colon (indoxyl sulfate and p-cresol sulfate) have been extensively studied.[30]

3. Conclusion

Bibliometric analysis of kidney disease and gut microbiota publications from 2001 to 2020 revealed more and more studies have confirmed that toxic substances produced by the prebiotic gut microflora may lead to the progression of CKD and CKD-related complications. The relationship between PCS and IS produced by microbial metabolism and CKD patients is a current research hotspot. FRANCE, England, and BRAZIL, have become the main research forces in this field with high publication rates and centrality, revealing that the relationship between kidney disease and gut microbiota is increasingly accepted by researchers. Many developed countries have the strongest cooperation with well-known institutions, which is conducive to the development of kidney disease and intestinal microbiota research. Because many articles have higher IF, those articles were heavily cited.

In conclusion, this study provides an in-depth understanding with the relationship between kidney disease and gut microbiota for kidney disease to identify new perspectives on collaborating cooperative institutions, potential collaborators, hot topics, and research.

Author contributions

Conception and design: Ran Zhang, Zhong-Biao Nie.
Administrative support: Yan-Yan Li.
Collection and assembly of data: Yan-Miao Ma, Xue-Qin Zhang.
Data analysis and interpretation: Ran Zhang, Yan-Yan Li, Zhong-Biao Nie.
Manuscript writing: All authors.
Final approval of manuscript: All authors.

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