Non-coding RNA Research 7 (2022) 77–88

Contents lists available at ScienceDirect

Non-coding RNA Research

journal homepage: www.keaipublishing.com/en/journals/non-coding-rna-research

Review Article

Hotspots and development frontiers of circRNA based on bibliometric analysis

Chunlei Zhang [a,1], Yindong Kang [a,1], Feiyan Kong [b,1], Qi Yang [a,**], Dehui Chang [a,*]

[a] Department of Urology, The 940 Hospital of Joint Logistics Support Force of Chinese PLA, Lanzhou, 730050, China
[b] Department of Urology, Beijing Fengtai Hospital of Integrated Traditional Chinese and Modern Medicine, Beijing, 100072, China

ARTICLE INFO

Keywords:
circRNA
Biblioshiny
Bibliometric analysis

ABSTRACT

Background and purpose: Circular RNAs (circRNAs) are a big group of members of the noncoding RNA family following long non-coding RNA and microRNA. They play a regulatory role in many biological processes. Analyzing their current research status and future development trends is conducive to a more comprehensive understanding of circRNAs and contributes to the dedication to the biological field.

Methods: The literature on circRNA from 2000 to 2021 in the Web of Science Core Collection of the Web of Science database with "circular RNA" as the subject was searched. R Studio's Bibliometrix package and biblioshiny software were used for publication trend analysis, citation analysis, keyword analysis, author analysis, research institution analysis, source analysis, country analysis, and collaboration analysis for all documents and highly cited documents.

Results: From 2000 to 2021, 3,186 circRNA-related articles were published worldwide, of which 193 were highly cited. The number of published articles had shown an explosive increase after 2013. These articles were mainly from Chinese research institutions and authors, but the country with the highest average number of citations per year in highly cited documents was Germany. Scientific research institutions came from countries represented by Germany, USA, China, Australia and Canada all had different degrees of cooperation. The theme and key points of the research had evolved over time from expression to the role and mechanism of circRNA in diseases, especially in cancer. CDR1as, circFOXO3, circHIPK3, circITCH, circMTO1, circSMARCA5 and circZNF609 are circRNAs that are mainly studied currently, their studies mainly involve cell biology, biological functions and cancer. The future research direction and trend would still be the application of circRNA in diseases.

Conclusion: The basic situation and development trend of circRNA related research we described provide a direction for future research.

1. Introduction

Circular RNAs (circRNAs) are RNAs with special circular structure formed by covalently joining the 5′end and 3′end of a linear RNA precursor through a reverse splicing mechanism. As early as the 1970s, circRNAs were first discovered in RNA viruses [1,2]. However, it is considered to be a garbage sequence caused by mistranslation due to its low expression abundance. At the beginning of this century, the research of circRNA has gradually attracted attention while only sporadic reports were shown limited by the level of sequencing technology. With the continuous improvement and development of second-generation sequencing, the important functions of circRNA have gradually been recognized by the public since Memczak et al. [3] revealed that circRNA was widely present in animal cells. Recent years, especially in the past five years, the number of research on circRNA increases explosively . Researchers have not only made outstanding contributions in revealing the formation, characteristics, regulation, mechanism of function, and elimination of circRNA [4–7], but also clarified the important role of

Abbreviations: circRNA, circular RNA; CDR1as, antisense to the cerebellar degeneration-related protein 1 transcript; FOXO3, forkhead box O3; HIPK3, homeodomain interacting protein kinase 3; ITCH, itchy E3 ubiquitin protein ligase; MTO1, mitochondrial tRNA translation optimization 1; SMARCA5, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5; ZNF609, zinc finger protein 609; USA, The United States of America.

* Corresponding author.
** Corresponding author.
E-mail addresses: fimmu_edu_cn@163.com (Q. Yang), chdhui@126.com (D. Chang).
[1] These authors contributed equally to this paper.

https://doi.org/10.1016/j.ncrna.2022.03.001
Received 28 December 2021; Received in revised form 13 March 2022; Accepted 14 March 2022
Available online 21 March 2022

Table 1
Main information about data of all articles and H-cited articles related to circRNA.

Main information about data		
Description	Total articles	H-cited articles
Timespan	2000:2021	2011:2021
Sources (Journals, Books, etc)	650	83
Documents	3186	193
Average years from publication	1.79	3.66
Average citations per documents	31.43	271.5
Average citations per year per doc	7.583	49.2
DOCUMENT CONTENTS		
Keywords Plus (ID)	3,534	487
Author's Keywords (DE)	5,740	392
AUTHORS		
Authors	6,247	1,154
Author Appearances	21,870	1,774
Authors of single-authored documents	21	1
Authors of multi-authored documents	6,226	1,153
AUTHORS COLLABORATION		
Single-authored documents	22	1
Documents per Author	0.51	0.167
Authors per Document	1.96	5.98
Co-Authors per Documents	6.86	9.19
Collaboration Index	1.97	6.01

circRNA in cell biology, including proliferation, apoptosis, aging, etc. [8–12]. On the other hand, researchers have also discovered that circRNA plays an important role in diseases of many systems, including the nervous system, digestive system, circulatory system, respiratory system, urinary system, and motor system [13–18], especially its outstanding position in cancer [19,20], which made us deeply realize the value of circRNA. Therefore, what are the research contents and directions of circRNA in the past 20 years? What is the current research status of circRNA? Where will circRNA's research go in the future? The answers to these questions are of great help to the research of circRNA.

Bibliometric analysis is a discipline that uses document system and measurement characteristics as the research object, and uses mathematics, statistics and other measurement methods to explore certain structures, characteristics and laws of science and technology [21]. Through literature statistics, we can analyze the research content and research status of a certain research field well, and predict the future development direction, which has high reference value for scientific researchers. Therefore, we used this method to conduct a statistical analysis of all articles and highly cited (H-cited) articles published in the past 20 years with circRNA as the main research content, including main information, the number of articles published each year, the annual citations, the main keywords, the sources, the authors, the institutions and countries, the evolution and trend of the themes, the cooperation relationship of the studies, circRNAs that are mainly studied currently, etc. The article is going to describe the basic situation and development trend of circRNA-related research and provide direction for research in this field by revealing these contents.

2. Data and methods

2.1. Data

The relevant literature of circRNA in the Web of Science Core Collection of the Web of Science (WoS) database was searched and collected. The search strategy was: ((((((((((TI=(circRNA)) OR TI=(circular RNA)) OR TI= (circRNA*)) OR TI=(circular noncoding RNA)) OR TI=(circular noncoding RNA)) OR TI=(circular ncRNA)) OR TI=(circular nonprotein-coding RNA)) OR TI=(circular nonprotein coding RNA)) RNA)) OR TI=(circular nontranslated RNA)) OR TI=(circular untranslated RNA)) AND PY=(2000–2021)) AND DT=(Article)) AND LA=(English). The document type was limited to article, the language was English, and the time was set from 2000 to 2021. A total of 3,186 documents were finally retrieved, among which 193 were highly cited (H-cited) documents. H-cited papers were defined as papers that have been cited in the top 1% in the last 10 years. The complete record of each article, including title, abstract, keywords, publication year, author, nationality, journal name, research direction, publishing organization, and references, were downloaded from the Web of Science database in BibTex file format.

2.2. Inclusion and exclusion criteria

2.2.1. Inclusion criteria

The publication year of the literature was from January 1, 2000 to September 30, 2021; the language of the literature was English; the type of the literature was articles; the research topic of the literature was circRNA.

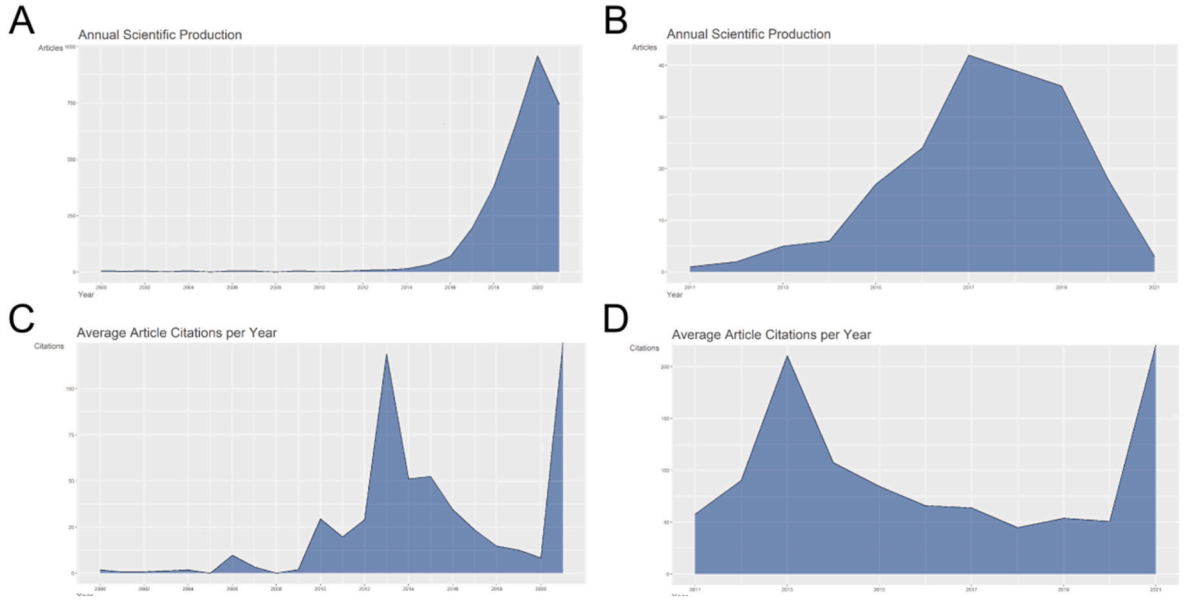

Fig. 1. Annual publication and citation of articles related to circRNA. A) annual scientific production of total published articles; B) annual scientific production of H-cited published articles; C) average article citations per year of total published articles; D) average article citations per year of H-cited published articles.

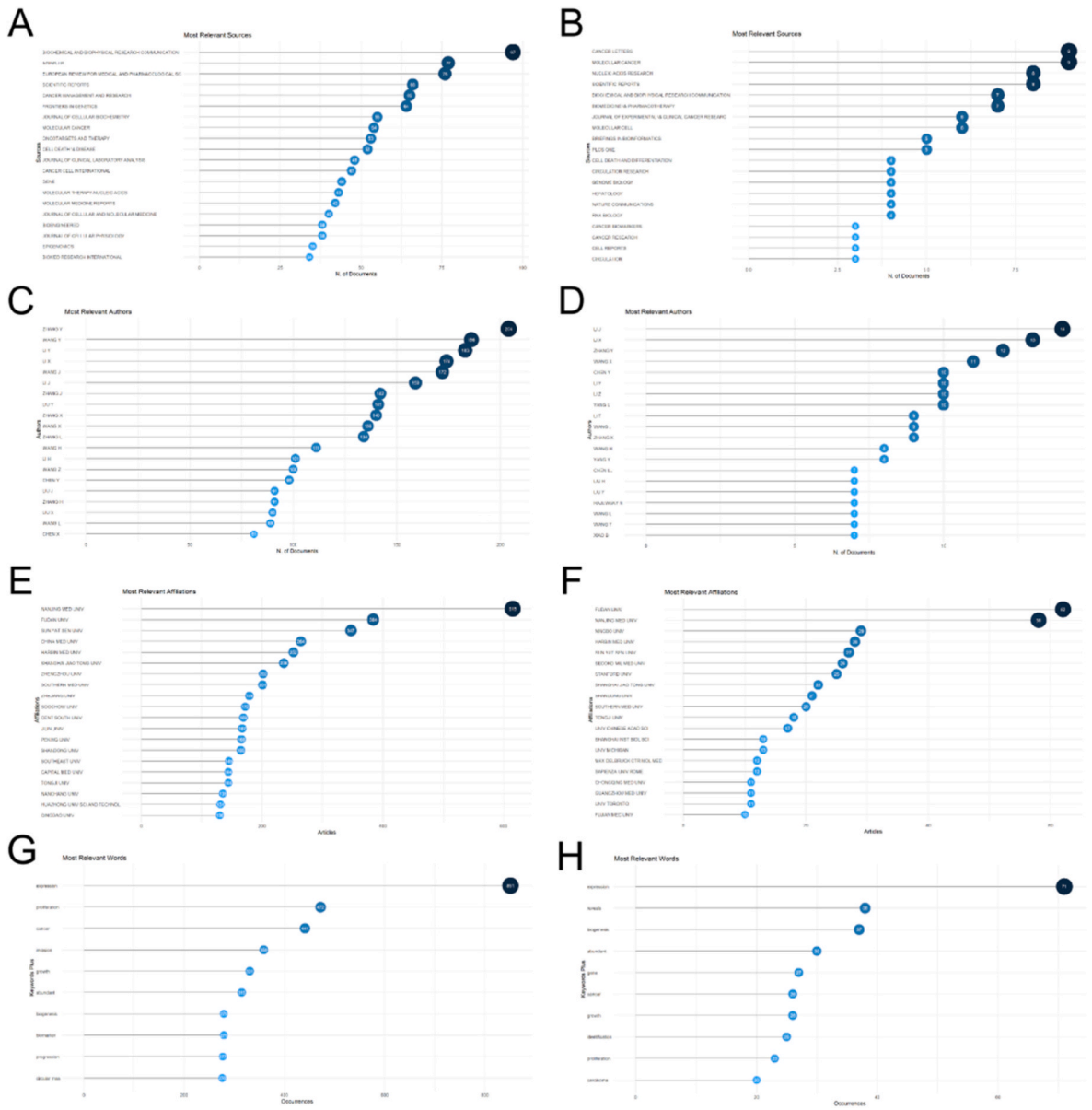

Fig. 2. Relevant information of published articles related to circRNA. A) top 20 most relevant sources of total published articles; B) top 20 most relevant sources of H-cited published articles; C) top 20 most relevant authors of total published articles; D) top 20 most relevant authors of H-cited published articles; E) top 20 most relevant affiliations of total published articles; F) top 20 most relevant affiliations of H-cited published articles; G) top 10 most relevant key words of total published articles; E) top 10 most relevant key words of H-cited published articles.

2.2.2. *Exclusion criteria*

The types of documents were conferences and reports; the documents did not use circRNA as the research topic; non-English circRNA related documents.

2.2.3. *Statistics and visual analysis*

R Studio's Bibliometrix package and biblioshiny software [22,23] were used to analyze the main information of all published articles and H-cited articles, including the amount of articles published each year, the annual citation situation, the main keywords, the sources, the authors, the institutions and countries, and the subject terms evolution and trends, the cooperative relationships. All index frequency was measured by number of documents. Cooperation index means the average number of authors in co-authored articles. Keywords plus means the keywords related to the original article added by WoS while the authors did not add, in order to increase the hit rate of the article under related topics. Trend topics parameters: field was keywords plus, world minimum frequency was 5, number of words per year was more or equal to 5. Thematic evolution and thematic map parameters: field was key words plus, number of words was more or equal to 250 , minimum cluster frequency (per thousand docs) was more or equal to 5, weight index was inclusion index weighted by word occurrences and minimum weight index was more or equal to 0.1.

3. Results

3.1. *Main information of the published articles*

From 2000 to 2021, a total of 3,186 circRNA-related articles were published, of which 193 were H-cited. Among all published articles, there were a total of 650 sources (Journals, Books, etc.), average years from publication was 1.79, average citations per documents was 31.43, average citations per year per doc was 7.583, and the number of keywords plus, author's keywords, authors, co-authors per document was

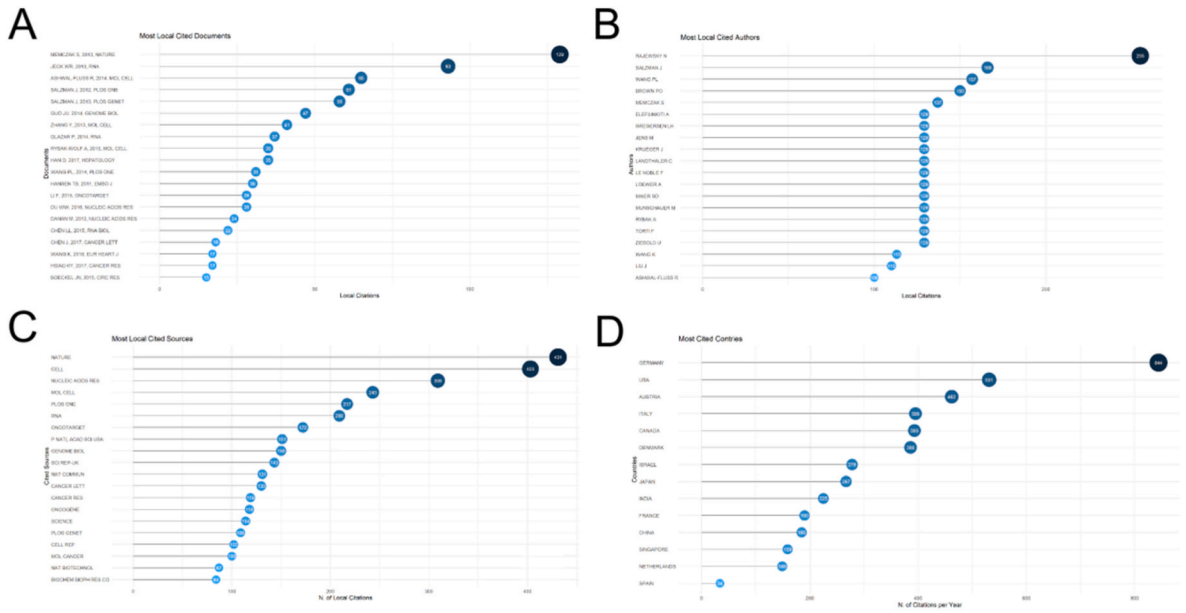

Fig. 3. Citation of H-cited published articles related to circRNA. A) top 20 most local cited documents; B) top 20 most local cited authors; C) top 20 most local cited sources; D) 14 most cited countries (average citations per year).

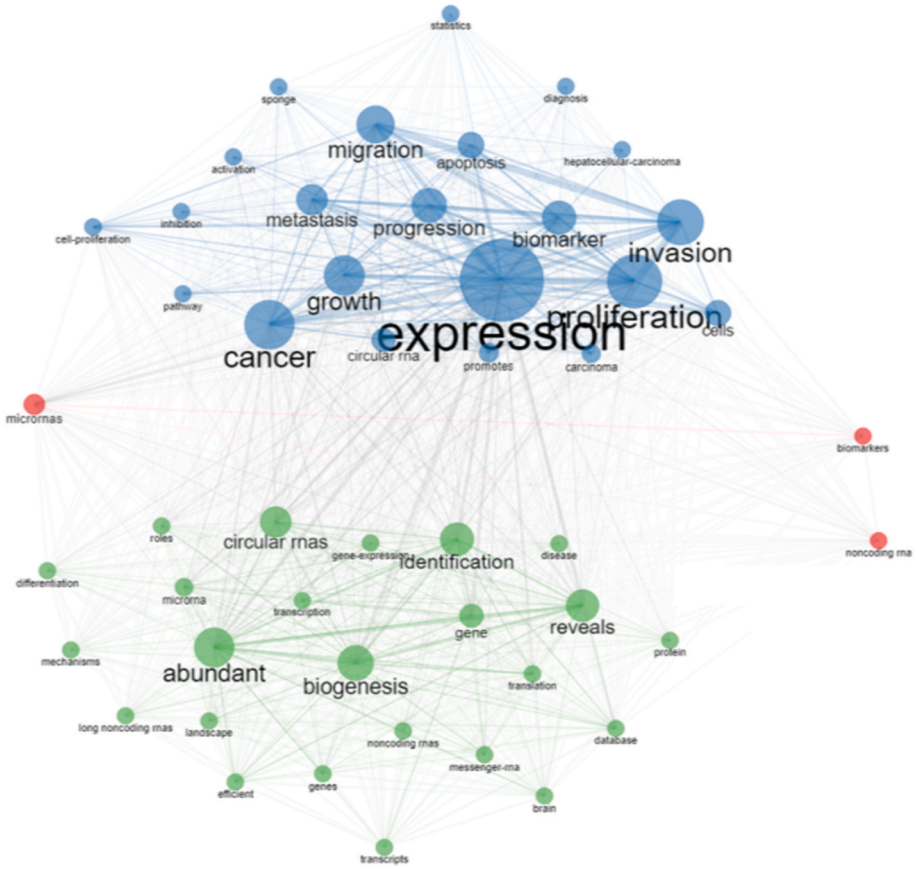

Fig. 4. Co-occurrence network for the keywords in the H-cited literature. Cluster 1 was biological characteristics of circRNA (green part), cluster 2 was biological function of circRNA (blue part), cluster 3 was application of circRNA as a biomarker (red part). (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

3,534, 5,740, 6,247, and 6.86, respectively, the collaboration index was 1.97. Of all H-cited articles published, there were 83 sources (Journals, Books, etc.), average years from publication was 3.66, average citations per documents was 271.5, average citations per year per doc was 49.2, and the number of keywords plus, author's keywords, authors, co-authors per document was 487, 392, 1,154, 9.19, respectively, the

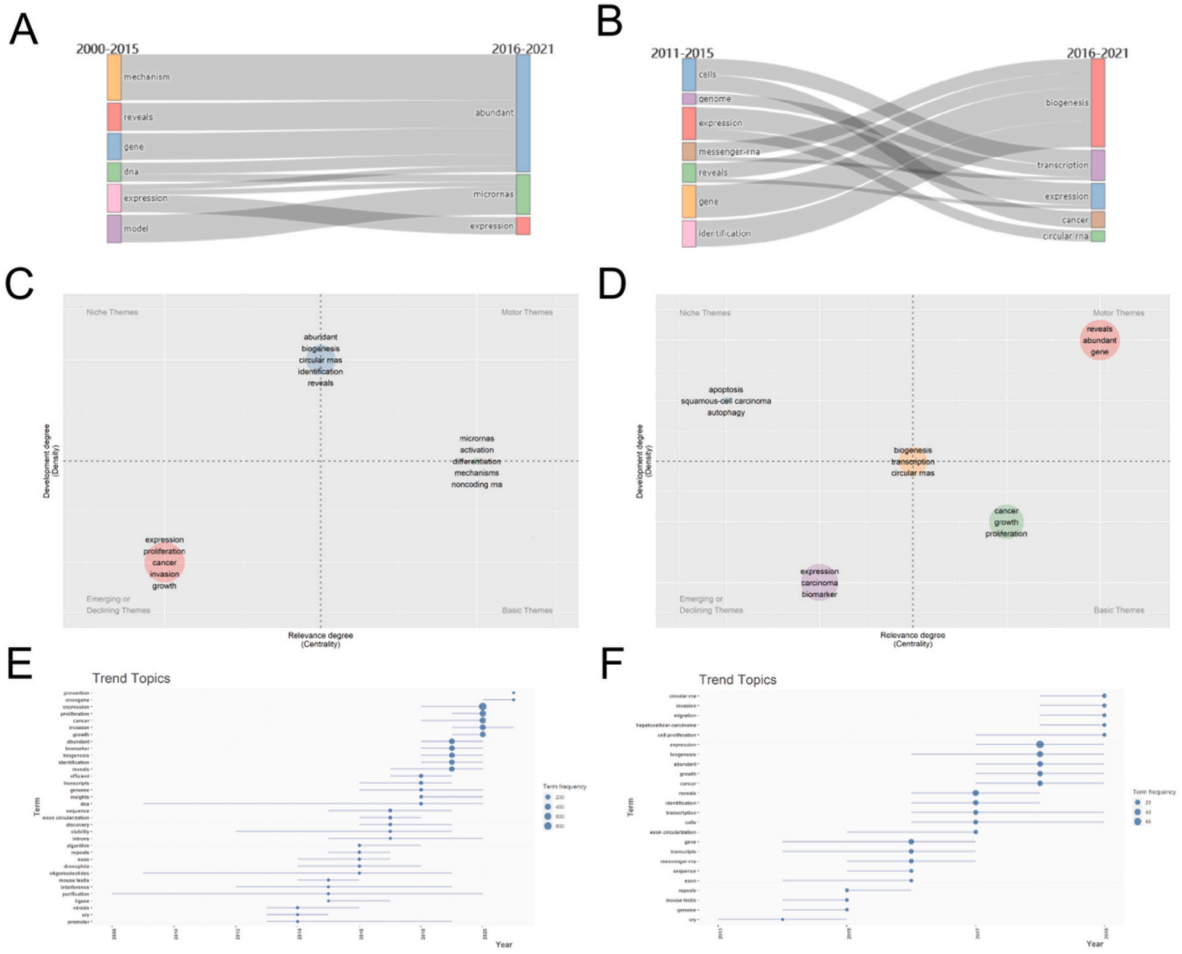

Fig. 5. Theme changes and trend of published articles related to circRNA from 2000 to 2021. A) thematic evolution of total published articles; B) thematic evolution of H-cited published articles; C) thematic map of total published articles; D) thematic map of H-cited published articles; E) trend topics of total published articles; F) trend topics of H-cited published articles.

collaboration index was 6.01. All data were shown in Table 1.

3.2. Annual articles and citations

The number of circRNA-related articles published every year from 2000 to 2013 was less than 10, and no related article was even published in 2005 and 2008. The amount of articles published in 2014 and afterwards had almost increased in an explosive manner and continues to grow. The number of circRNA-related articles published increased from 14 in 2014 to 960 in 2020. Since the total number of articles in 2021 has not yet appeared, it is expected to continue to increase or remain basically the same as before (Fig. 1A). The average number of articles cited per year was ups and downs, with the highest number being 118.89 in 2013 (Fig. 1C). In H-cited articles, the earliest article appeared in 2011, with only one article published in this year. The year with most published articles was 2017, reaching 42 (Fig. 1B). The average number of articles cited per year was 210.48 in 2013 (Fig. 1D).

3.3. Sources, authors, institutions and main keywords of the articles

Among all the indexes with the most published articles in all articles, the top 5 journals were *BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS*, *AGING-US*, *EUROPEAN REVIEW FOR MEDICAL AND PHARMACOLOGICAL SCIENCES*, *SCIENTIFIC REPORTS*, *CANCER MANAGEMENT AND RESEARCH*, with number of 97, 77, 76, 66 and 65, respectively (Fig. 2A). The top 5 authors were Zhang Y, Wang Y, Li Y, Li X, and Wang J, with number 204, 186, 183, 174, and 172, respectively (Fig. 2C). The top 5 institutions were Nanjing Med Univ, Fudan Univ, Sun Yat Sen Univ, China Med Univ and Harbin Med Univ, with number of 615, 384, 347, 264 and 252, respectively (Fig. 2E). And the top 5 related keywords were expression, proliferation, cancer, invasion, growth, with the number of occurrences were 851, 472, 441, 359 and 331, respectively (Fig. 2G). In the H-cited articles, the top 5 journals were *CANCER LETTERS*, *MOLECULAR CANCER*, *NUCLEIC ACIDS RESEARCH*, *SCIENTIFIC REPORTS*, *BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS*, with number of 9, 9, 8, 8 and 7, respectively (Fig. 2B). The top 5 authors were Li J, Li X, Zhang Y, Wang X and Chen Y, with number of 14, 13, 12, 11 and 10, respectively (Fig. 2D). The top 5 institutions were Fudan Univ, Nanjing Med Univ, Ningbo Univ, Harbin Med Univ and Sun Yat Sen Univ, with number of 62, 58, 29, 28 and 27, respectively (Fig. 2F). And the top 5 related keywords were expression, reveals, biogenesis, abundant, gene, with the number of occurrences were 71 , 38 , 37 , 30 and 27, respectively (Fig. 2H).

3.4. Authors, sources, institutions and keywords of highly cited articles

Among all the H-cited articles with most cited times, the top 5 articles were "Memczak S, 2013, *NATURE*" [3], "Jeck WR, 2013, *RNA*" [24], "Ashwal-Fluss R, 2014, *MOL CELL*" [25], "Salzman J, 2012, *PLOS ONE*" [26], "Salzman J, 2013, *PLOS GENET*" [27], the number of local citations were 129, 93, 65, 61 and 58, respectively (Fig. 3A). The top 5 authors were Rajewsky N, Salzman J, Wang P, Brown P and Memczak S, the number of citations were 255, 166, 157, 150 and 137, respectively

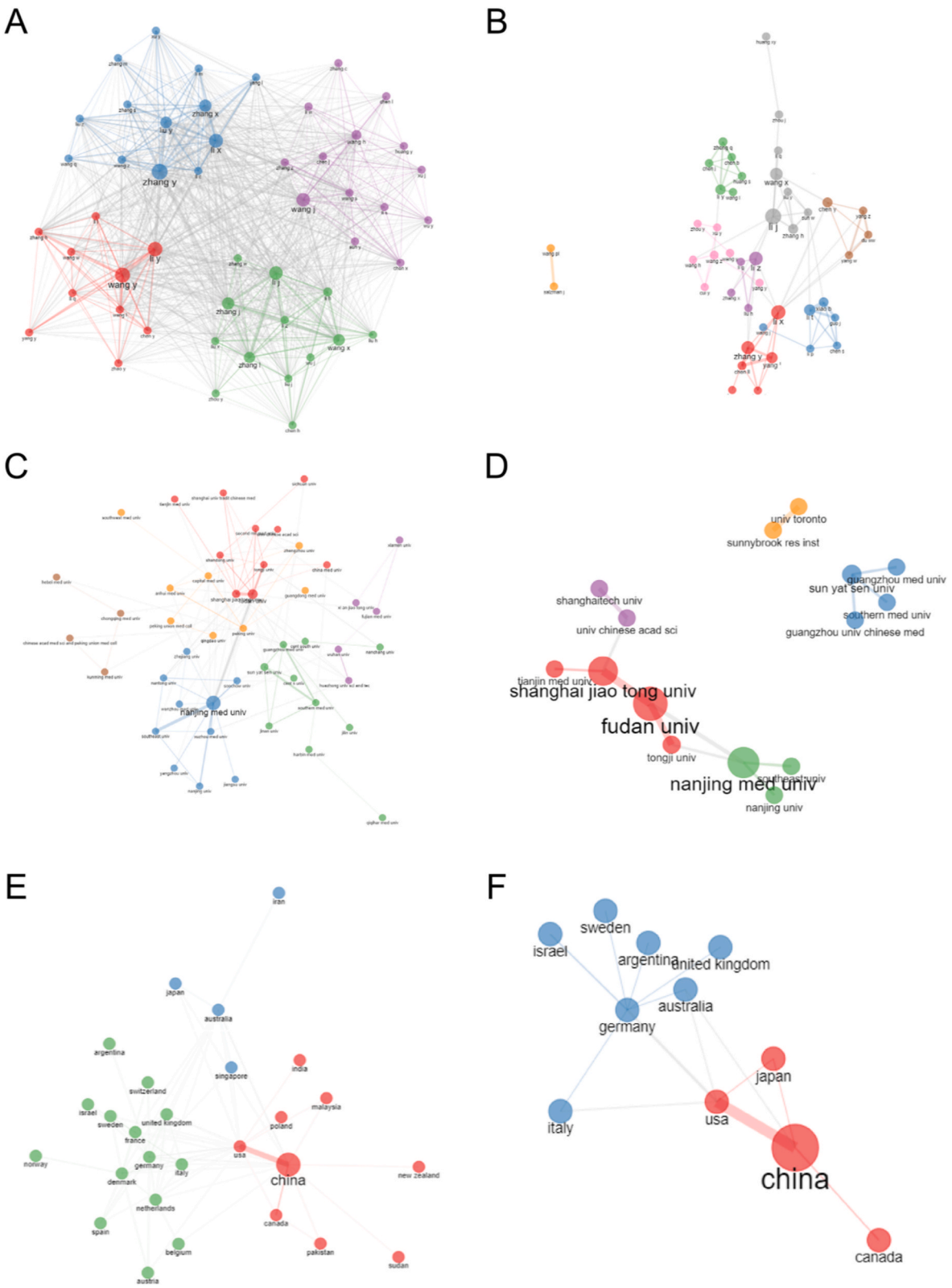

Fig. 6. Cooperative relationship of published articles. A) authors cooperative relationship in total published articles; B) authors cooperative relationship in H-cited published articles; C) affiliations cooperative relationship in total published articles; D) affiliations cooperative relationship in H-cited published articles; E) countries cooperative relationship in total published articles; F) countries cooperative relationship in H-cited published articles.

Table 2
Top 20 authors with collaboration.

Authors with collaboration					
Total articles			H-cited articles		
Node	Cluster	Betweenness	Node	Cluster	Betweenness
Li Y	1	36.8	Li J	8	438.3
Li X	2	34.6	Wang H	7	270.4
Wang Y	1	33.0	Wang Z	7	237.0
Zhang Y	2	32.7	Li Z	4	225.4
Li J	3	27.7	Sun W	8	205.4
Wang J	4	25.1	Zheng Q	3	175.0
Zhang X	2	24.8	Li X	1	155.4
Wang X	3	18.0	Wang X	8	132.6
Wang H	4	17.3	Chen Y	6	91.0
Liu Y	2	16.3	Zhang Y	1	86.2
Zhang J	3	15.7	Li T	2	70.0
Li H	3	11.5	Xiao B	2	70.0
Zhang L	3	10.7	Cui Y	7	46.4
Wang Z	2	9.8	Li P	2	39.0
Li Z	3	7.1	Li Y	3	39.0
Wang S	4	6.9	Zhou J	8	39.0
Liu X	3	6.6	Wang Y	7	37.6
Wang L	1	5.7	Xu Y	7	24.4
Liu J	3	5.2	Zhou Y	7	23.4
Chen J	4	5.1	Liu H	4	2.6

(Fig. 3B). The top 5 sources were *NATURE*, *CELL*, *NUCLEIC ACIDS RES*, *MOL CELL* and PLOS ONE, and the number of citations were 431, 403, 309, 243 and 217, respectively (Fig. 3C). The top 5 countries with the most average article citations per year were Germany, USA, Austria, Italy and Canada, with a total number of citations per year of 844, 531, 462, 395 and 393, respectively (Fig. 3D). We constructed the co-occurrence network for the keywords in the H-cited literature. It could be seen that the circRNAs in the H-cited articles mainly consist of 3 clusters, cluster 1 was biological characteristics of circRNA (green part in Fig. 4), cluster 2 was biological function of circRNA (blue part in Fig. 4), cluster 3 was application of circRNA as a biomarker (red part in Fig. 4).

3.5. Theme evolution and trend

In all the published literature, thematic evolution has gradually developed from mechanism, reveals, gene, DNA, expression, and model in 2000–2015 to abundant, microRNAs, and expression in 2016–2021 (Fig. 5A). In the H-cited literature, themes have evolved from cells, genome, expression, messenger-RNA, reveals, gene, identification in 2000–2015 to biogenesis, transcription, expression, cancer and circular RNA in 2016–2021 (Fig. 5B). In the thematic map of all articles, themes between the first and second quadrants were absolute, biogenesis, circular RNAs, identification, reveals, between the second and third quadrants were microRNAs, activation, differentiation, mechanisms, and noncoding RNA, located in the fourth quadrant were expression, proliferation, cancer, invasion and growth (Fig. 5C). In the thematic map of H-cited articles, themes in the first quadrant were reveals, absolute and gene, in the second quadrant were apoptosis, squamous-cell carcinoma and autophagy, in the third quadrant were expression, carcinoma and biomarker, and in the fourth quadrant were cancer, growth and proliferation (Fig. 5D). In all the literature, the trend topics in the past two years were ranked in order of prevention, oncogene, expression, proliferation, cancer, invasion and growth (Fig. 5E). In the highly cited literature, the trend topics in the past two years were ranked in the order of circular RNA, invasion, migration, hepatocellular-carcinoma, cell proliferation (Fig. 5F).

3.6. Cooperation

The cooperation network of authors, institutions, and countries in all published articles and H-cited articles was analyzed. The size of the dots in the figure represents the amount of articles published by the authors in this field, and the thickness of the lines represents the closeness of cooperation between authors. The results showed that among all published articles, the top 5 authors with the most partnerships were Li Y, Li X, Wang Y, Zhang Y and Li J (Fig. 6A, Table 2); the top 5 institutions with the most partnerships were Fudan Univ, Nanjing Med Univ, Shanghai Jiao Tong Univ, Peking Univ, and Southern Med Univ (Fig. 6C, Table 3); the top 5 countries for the number of published articles were China, USA, Germany, Canada and Spain, with number of published articles 2,735, 129, 54, 24, and 24 (Table 4), the proportions of multiple country publications were 0.0706, 0.3023, 0.3519, 0.75, 0.3333, respectively (Fig. 7A, Table 4); the top 5 countries with the most partnerships were China, USA, Germany, Denmark and Australia (Fig. 6E, Table 5); the top 5 cooperation relationship of countries were from China to USA, from China to Canada, from China to Australia, from USA to Germany, and from China to Germany, the number of articles published were 152, 33,

Table 3
Top 20 affiliations with collaboration.

affiliation with collaboration					
Total articles			H-cited articles		
Node	**Cluster**	**Betweenness**	**Node**	**Cluster**	**Betweenness**
Fudan Univ	1	367.3	Shanghai Jiao Tong Univ	1	17
Nanjing Med Univ	2	264.2	Fudan Univ	1	16
Shanghai Jiao Tong Univ	1	164.5	Nanjing Med Univ	3	13
Peking Univ	5	118.7	Univ Chinese Acad Sci	4	7
Southern Med Univ	3	117.1	Sun Yat Sen Univ	2	3
Fujian Med Univ	4	89.7	Tongji Univ	1	0
Guangzhou Med Univ	3	87.2	Tianjin Med Univ	1	0
Tongji Univ	1	78.5	Southern Med Univ	2	0
Capital Med Univ	5	78.0	Guangzhou Med Univ	2	0
Shandong Univ	1	66.9	Guangzhou Univ Chinese Med	2	0
Sun Yat Sen Univ	3	62.8	Southeast Univ	3	0
Xiamen Univ	4	45.0	Nanjing Univ	3	0
Harbin Med Univ	3	45.0	Shanghaitech Univ	4	0
Second Mil Med Univ	1	26.6	Univ Toronto	5	0
Chongqing Med Univ	6	21.8	Sunnybrook Res Inst	5	0
Huazhong Univ Sci And Technol	4	19.1			
Nanchang Univ	3	18.8			
Peking Union Med Coll	5	14.3			
Xuzhou Med Univ	2	11.6			
Kunming Med Univ	6	8.0			

Table 4
Top 20 countries with the most published articles.

Countries with the most published articles									
Total articles						H-cited articles			
Country	**Articles**	**SCP**	**MCP**	**MCP_Ratio**	**Country**	**Articles**	**SCP**	**MCP**	**MCP_Ratio**
China	2735	2542	193	0.07	China	144	124	20	0.14
USA	129	90	39	0.30	USA	19	14	5	0.26
Germany	54	35	19	0.35	Germany	12	6	6	0.50
Canada	24	6	18	0.75	Canada	4	1	3	0.75
Spain	24	16	8	0.33	Italy	3	1	2	0.67
Italy	22	10	12	0.55	Denmark	2	1	1	0.50
Japan	21	20	1	0.05	Israel	2	2	0	0
Denmark	19	13	6	0.32	Austria	1	1	0	0
India	18	15	3	0.17	France	1	0	1	1
Australia	15	8	7	0.47	India	1	1	0	0
France	15	6	9	0.60	Japan	1	1	0	0
Iran	14	11	3	0.21	Netherlands	1	0	1	1
Netherlands	11	6	5	0.45	Singapore	1	1	0	0
Malaysia	9	4	5	0.56	Spain	1	0	1	1
Russia	8	8	0	0.00					
Korea	7	7	0	0.00					
Switzerland	7	2	5	0.71					
United kingdom	7	3	4	0.57					
Austria	5	2	3	0.60					
Brazil	5	5	0	0.00					

Tips: SCP: single country publications, MCP: multiple country publications.

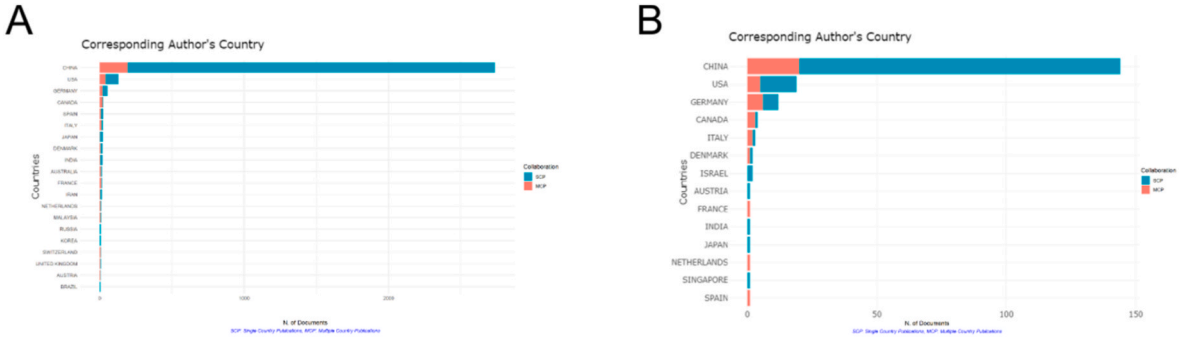

Fig. 7. Countries with the highest number of published articles related to circRNA. A) total published articles; B) H-cited articles.

Table 5
Top 20 countries with collaboration.

countries with collaboration					
Total articles			H-cited articles		
Node	**Cluster**	**Betweenness**	**Node**	**Cluster**	**Betweenness**
China	1	116.0	Germany	2	30.5
USA	1	97.6	USA	1	18.6
Germany	3	74.1	China	1	9.5
Denmark	3	32.3	Australia	2	0.4
Australia	2	27.9	Canada	1	0
Netherlands	3	3.5	Japan	1	0
France	3	3.1	Italy	2	0
United kingdom	3	0.8	Israel	2	0
Italy	3	0.4	Argentina	2	0
Canada	1	0.2	Sweden	2	0
Spain	3	0.1	United kingdom	2	0
India	1	0			
Malaysia	1	0			
Poland	1	0			
Pakistan	1	0			
New zealand	1	0			
Sudan	1	0			
Japan	2	0			
Iran	2	0			
Singapore	2	0			

Table 6
Top 20 world countries collaboration.

world country collaboration					
Total articles			H-cited articles		
From	**To**	**Frequency**	**From**	**To**	**Frequency**
China	USA	152	China	USA	20
China	Canada	33	USA	Germany	5
China	Australia	17	China	Canada	3
USA	Germany	16	Germany	Israel	3
China	Germany	11	China	Australia	2
China	United kingdom	10	China	Japan	2
USA	Denmark	10	Germany	Argentina	2
USA	Italy	9	Germany	Australia	2
Germany	United kingdom	8	Germany	Italy	2
China	Japan	7	Germany	Sweden	2
Germany	Australia	7	Germany	United kingdom	2
China	Pakistan	6	USA	Australia	2
Germany	Netherlands	6	USA	Italy	2
USA	India	6	USA	Japan	2
Canada	Pakistan	5	Argentina	Korea	1
Germany	France	5	Argentina	Sweden	1
Germany	Italy	5	Argentina	United kingdom	1
USA	Australia	5	Australia	Argentina	1
USA	Canada	5	Australia	Denmark	1
China	Denmark	4	Australia	France	1

17, 16, and 11, respectively (Table 6). Among all published H-cited articles, the top 5 authors with the most partnerships were Li J, Wang H, Wang Z, Li Z, and Sun W (Fig. 6B, Table 2); the top 5 institutions with the most partnerships were Shanghai Jiao Tong Univ, Fudan Univ, Nanjing Med Univ, Univ Chinese Acad Sci, and Sun Yat Sen Univ (Fig. 6D, Table 3); the top 5 countries for the number of published articles were China, USA, Germany, Canada, and Italy, with the number of published articles 144, 19, 12, 4, and 3 (Table 4), the proportions of multiple country publications were 0.139, 0.263, 0.5, 0.75, 0.667, respectively (Fig. 7B, Table 4); the top 5 countries with the most partnerships were Germany, USA, China, Australia, and Canada (Fig. 6F, Table 5); the top 5 cooperation relationship of countries were from China to USA, from USA to Germany, from China to Canada, from Germany to Israel, from China to Australia, the number of articles published were 20, 5, 3, 3, and 2, respectively (Table 6).

3.7. Articles of circRNAs that have been mainly investigated

In order to better demonstrate the role and function of circRNAs, we listed 7 circRNAs that are currently mainly studied, including CDR1as [3,32–35], circFOXO3 [36–40], circHIPK3 [41–45], circITCH [46–50], circMTO1 [50–55], circSMARCA5 [56–60] and circZNF609 [61–65]. Moreover, we showed the top 5 most cited articles for these circRNAs (Table 7). These studies mainly involve cell biology, such as properties of circRNAs [32], cell cycle [36], cell apoptosis [38]and cell growth [41]; biological functions, such as miRNA sponge [3], brain function [33,35], insulin transcription and secretion [34], and cardiac senescence [37]. The main research area of these circRNAs is tumor study, including prostate cancer [39,40,57], bladder cancer [42,46,52,56], colorectal cancer [43,53,60,64], hepatocellular carcinoma [45,47,51], thyroid cancer [48], breast cancer [49], ovarian carcinoma [50], cervical cancer [54], lung adenocarcinoma [55,61], non-small cell lung cancer [58], multiple myeloma [59], cholangiocarcinoma [62], glioma [63], and gastric cancer [65]. Study of diabetes mellitus was also reported in one article [44].

4. Discussion

Since 2000, thousands of articles that are obviously related to circRNA have been published. According to the main information of the published articles, each article is cited 7.583 times per year on average, each of H-cited articles is cited even 49.2 times per year, indicating that circRNA has been one of the focus of attention in the research field in the past 20 years. This phenomenon has become more obvious after 2013, especially Memczak et al. [3] revealed that circRNA is widely present in animal cells and may function through miRNA sponge adsorption. The important role of circRNA in biology is gradually recognized, and researchers began to pay attention to the mechanism study of circRNA. After Jeck et al. [24] revealed that circRNA has special ALU repeats, and Zhang et al. [28] revealed that circRNA loops through complementary sequences, research on the structural characteristics of circRNA and the mechanism of circular structure formation began to gain attention. The number of circRNA articles published reaches nearly 1000 per year, these articles give us a deep understanding of the characteristics and the biological function of circRNA in disease research.

JThe main journals that publish circRNA are comprehensive journals related to RNA biology and cancer, and the publishing organization are mainly Chinese university research institutions, indicating that Chinese researchers have made major contributions in the field of circRNA research. However, when sorted by the number of citations, this situation has changed. The published articles mainly come from top comprehensive journals such as *Nature* and *Cell*. The main authors of the published articles are mainly non-Chinese scholars, and the source countries are mainly Germany, the United States, Australia, Italy and Canada. It shows that although authors and institutions from China have published a large number of circRNA-related articles, lack of leading articles is a big shortcoming. This phenomenon is especially manifested in the fact that Chinese authors pay more attention to the biological role of circRNA in cancer and other diseases, rather than studying the mechanism and function of circRNA itself. Of course, there are also a few articles from Chinese researchers that are also very meaningful. For example, articles represented by the Chen LL team on the mechanism of circRNA are also researches with relatively high scientific value [29–31].

From the evolution and trend of the themes, we can see that the research topic of circRNA has gradually developed from the expression and abundance analysis to the biogenesis, transcription and function mechanism of circRNA, such as microRNA sponge in the past five years. Research of circRNA's identification and abundance, biogenesis, and its function such as influencing cell apoptosis and autophagy has been well developed. The functions of circRNA in cancer cells such as proliferarion, invasion, growth and migration are still the most important and promising study themes. This is especially manifested in hepatocellular carcinoma research. Of course, we need to be soberly aware that Chinese research occupies a dominant position in all research, and the published research is mostly circRNA and cancer-related research, which has led to this research trend-oriented. More in-depth and valuable research such as the new function and the mechanism of circRNA formation and function are still worth exploring.

The five main countries with multi-country cooperative scientific research are China, USA, Germany, Denmark, and Australia. Among them, China and the United States have the highest number of cooperative publications. The number of articles published jointly by China and the United States are the most. Although China ranks first in the number of articles published, the proportion of articles on multi-country cooperation is only 0.07, which is significantly less than that of the other four countries. In the H-cited literature, the proportion of China's cooperation with other countries has increased significantly, indicating that multi-country cooperation may increase the value of research.

Currently, studies of circRNAs involve cell biology, biological functions, and disease (especially cancer) are still cited mostly. CDR1as, circFOXO3, circHIPK3, circITCH, circMTO1, circSMARCA5, and

Table 7
Articles of circRNAs that have been mainly investigated.

First author, year	circRNA	host gene	title	topic	Ref.
Memczak S, 2013	CDR1as	CDR1	Circular RNAs are a large class of animal RNAs with regulatory potency	miRNA sponge	[3]
Guo J, 2014	CDR1as	CDR1	Expanded identification and characterization of mammalian circular RNAs	properties of circRNAs	[32]
Piwecka M, 2017	CDR1as	CDR1	Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function	brain function	[33]
Xu H, 2015	CDR1as	CDR1	The circular RNA Cdr1as, via miR-7 and its targets, regulates insulin transcription and secretion in islet cells	insulin transcription and secretion	[34]
Kleaveland B, 2018	CDR1as	CDR1	A network of noncoding regulatory RNAs acts in the mammalian brain	mammalian brain	[35]
Du W, 2016	circFOXO3	FOXO3	Foxo3 circular RNA retards cell cycle progression via forming ternary complexes with p21 and CDK2	cell cycle	[36]
Du W, 2017	circFOXO3	FOXO3	Foxo3 circular RNA promotes cardiac senescence by modulating multiple factors associated with stress and senescence responses	cardiac senescence	[37]
Du W, 2017	circFOXO3	FOXO3	Induction of tumor apoptosis through a circular RNA enhancing Foxo3 activity	tumor apoptosis	[38]
Shen Z, 2020	circFOXO3	FOXO3	Reduction of circular RNA Foxo3 promotes prostate cancer progression and chemoresistance to docetaxel	prostate cancer	[39]
Kong Z, 2020	circFOXO3	FOXO3	Circular RNA circFOXO3 promotes prostate cancer progression through sponging miR-29a-3p	prostate cancer	[40]
Zheng Q, 2016	circHIPK3		Circular RNA profiling reveals an abundant circHIPK3 that regulates cell growth by sponging multiple miRNAs	cell growth	[41]
Li Y, 2017	circHIPK3	HIPK3	CircHIPK3 sponges miR-558 to suppress heparanase expression in bladder cancer cells	bladder cancer	[42]
Zeng K, 2018	circHIPK3	HIPK3	CircHIPK3 promotes colorectal cancer growth and metastasis by sponging miR-7	colorectal cancer	[43]
Shan K, 2017	circHIPK3	HIPK3	Circular noncoding RNA HIPK3 mediatesretinalvascular dysfunction in diabetes mellitus	diabetes mellitus	[44]
Chen G, 2018	circHIPK3	HIPK3	circHIPK3 regulates cell proliferation and migration by sponging miR-124 and regulating AQP3 expression in hepatocellular carcinoma	hepatocellular carcinoma	[45]
Yang C, 2018	circITCH	HIPK3	Circular RNA circ-ITCH inhibits bladder cancer progression by sponging miR-17/miR-224 and regulating p21, PTEN expression	bladder cancer	[46]
Guo W, 2017	circITCH	ITCH	Polymorphisms and expression pattern of circular RNA circ-ITCH contributes to the carcinogenesis of hepatocellular carcinoma	hepatocellular carcinoma	[47]
Wang M, 2018	circITCH	ITCH	CircRNA circ-ITCH suppresses papillary thyroid cancer progression through miR-22–3p/CBL/beta-catenin pathway	thyroid cancer	[48]
Wang S, 2019	circITCH	ITCH	Circ-ITCH regulates triple-negative breast cancer progression through the Wnt/beta-catenin pathway	breast cancer	[49]
Hu J, 2018	circITCH	ITCH	The circular RNA circ-ITCH suppresses ovarian carcinoma progression through targeting miR-145/RASA1 signaling	ovarian carcinoma	[50]
Han D, 2017	circMTO1	MTO1	Circular RNA circMTO1 Acts as the Sponge of MicroRNA-9 to Suppress Hepatocellular Carcinoma Progression	hepatocellular carcinoma	[51]
Li Y, 2019	circMTO1	MTO1	Circular RNA circMTO1 suppresses bladder cancer metastasis by sponging miR-221 and inhibiting epithelial-to-mesenchymal transition	bladder cancer	[52]
Ge Z, 2018	circMTO1	MTO1	CircMTO1 inhibits cell proliferation and invasion by regulating Wnt/beta-catenin signaling pathway in colorectal cancer	colorectal cancer	[53]
Chen M, 2019	circMTO1	MTO1	circMTO1 promotes tumorigenesis and chemoresistance of cervical cancer via regulating miR-6893	cervical cancer	[54]
Zhang B, 2019	circMTO1	MTO1	A regulatory circuit of circ-MTO1/miR-17/QKI-5 inhibits the proliferation of lung adenocarcinoma	lung adenocarcinoma	[55]
Tan Y, 2019	circSMARCA5	SMARCA5	Circular RNA SMARCA5 is overexpressed and promotes cell proliferation, migration as well as invasion while inhibits cell apoptosis in bladder cancer	bladder cancer	[56]
Kong Z, 2017	circSMARCA5	SMARCA5	Androgen-responsive circular RNA circSMARCA5 is up-regulated and promotes cell proliferation in prostate cancer	prostate cancer	[57]
Tong S, 2020	circSMARCA5	SMARCA5	Circular RNA SMARCA5 may serve as a tumor suppressor in non-small cell lung cancer	non-small cell lung cancer	[58]
Liu H, 2019	circSMARCA5	SMARCA5	Circ-SMARCA5 suppresses progression of multiple myeloma by targeting miR-767–5p	multiple myeloma	[59]
Miao X, 2020	circSMARCA5	SMARCA5	Circ-SMARCA5 suppresses colorectal cancer progression via downregulating miR-39–3p and upregulating ARID4B	colorectal cancer	[60]
Zuo Y, 2020	circZNF609	ZNF609	Circular RNA Circ-ZNF609 Promotes Lung Adenocarcinoma Proliferation by Modulating miR-1224–3p/ETV1 Signaling	lung adenocarcinoma	[61]
Guan C, 2021	circZNF609	ZNF609	YY1 and eIF4A4 are mediators of the cell proliferation, migration and invasion in cholangiocarcinoma promoted by circ-ZNF609 by targeting miR-432–5p to regulate LRRC1	cholangiocarcinoma	[62]
Du S, 2021	circZNF609	ZNF609	Circular RNA ZNF609 promotes the malignant progression of glioma by regulating miR-1224–3p/PLK1 signaling	glioma	[63]
Wu L, 2018	circZNF609	ZNF609	Circ-ZNF609 promotes migration of colorectal cancer by inhibiting Gli1 expression via microRNA-150	colorectal cancer	[64]
Liu Z, 2019	circZNF609	ZNF609	Circ-ZNF609 promotes carcinogenesis of gastric cancer cells by inhibiting miRNA-145–5p expression	gastric cancer	[65]

circZNF609 have shown extraordinary value in the research of various tumor diseases. Their important role in the study of other diseases will remain an area worth exploring in the future.

Although this article is a good display of the research progress of circRNA in the past 20 years, it is limited to the selection of materials. In order to accurately analyze the content of the literature and limit the number of documents, only the articles in the Web of Science Core Collection of the Web of Science and the articles in English are selected. These factors have caused the lost of the articles whose main research is circRNA.

5. Conclusion

This article analyzes the research of circRNA from expression analysis to biological function and mechanism in the past 20 years, and proposes that the function and mechanism of circRNA in many diseases

including cancer are still important research directions in the future. Multi-country and multi-team cooperation will help to make breakthroughs in the field of circRNA research.

Data availability

The datasets analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

Chunlei Zhang, Yindong Kang and Feiyan Kong contributed equally to this work. Chunlei Zhang, Yindong Kang and Feiyan Kong carried out the literature and statistical analysis, and wrote the article. Qi Yang helped edit and correct the manuscript. Dehui Chang conceived the ideas for the article and helped draft the manuscript. Qi Yang, Chunlei Zhang, and Dehui Chang provided funding support. All of the authors read and approved the final manuscript.

Funding

This work was supported by Chinese People's Liberation Army Health Project (grant number 21BJZ43) and In-hospital project of The 940 Hospital of Joint Logistics Support Force of Chinese PLA (grant number 2021yxky017, 2021yxky034, 2021yxky041 and 2021yxky057).

Declaration of competing interest

The authors declare that they have no conflicts of interest.

References

[1] H.L. Sanger, G. Klotz, D. Riesner, H.J. Gross, A.K. Kleinschmidt, Viroids are single-stranded covalently closed circular RNA molecules existing as highly base-paired rod-like structures, Proc. Natl. Acad. Sci. U. S. A. 73 (11) (1976) 3852–3856.
[2] A.C. Arnberg, G.J. Van Ommen, L.A. Grivell, E.F. Van Bruggen, P. Borst, Some yeast mitochondrial RNAs are circular, Cell 19 (2) (1980) 313–319.
[3] S. Memczak, M. Jens, A. Elefsinioti, et al., Circular RNAs are a large class of animal RNAs with regulatory potency, Nature 495 (7441) (2013) 333–338.
[4] L.L. Chen, L. Yang, Regulation of circRNA biogenesis, RNA Biol. 12 (4) (2015) 381–388.
[5] X. Li, L. Yang, L.L. Chen, The biogenesis, functions, and challenges of circular RNAs, Mol. Cell 71 (3) (2018) 428–442.
[6] L.S. Kristensen, M.S. Andersen, L. Stagsted, K.K. Ebbesen, T.B. Hansen, J. Kjems, The biogenesis, biology and characterization of circular RNAs, Nat. Rev. Genet. 20 (11) (2019) 675–691.
[7] Y. Lee, J. Choe, O.H. Park, Y.K. Kim, Molecular mechanisms driving mRNA degradation by m(6)a modification, Trends Genet. 36 (3) (2020) 177–188.
[8] J. Salzman, Circular RNA expression: its potential regulation and function, Trends Genet. 32 (5) (2016) 309–316.
[9] L.L. Chen, The expanding regulatory mechanisms and cellular functions of circular RNAs, Nat. Rev. Mol. Cell Biol. 21 (8) (2020) 475–490.
[10] J. Li, D. Sun, W. Pu, J. Wang, Y. Peng, Circular RNAs in cancer: biogenesis, function, and clinical significance, Trends Cancer 6 (4) (2020) 319–336.
[11] C.M. Weigelt, R. Sehgal, L.S. Tain, et al., An insulin-sensitive circular RNA that regulates lifespan in drosophila, Mol. Cell 79 (2) (2020) 268–279, e5.
[12] C. Zhao, G. Li, J. Li, Non-coding RNAs and cardiac aging, Adv. Exp. Med. Biol. 1229 (2020) 247–258.
[13] J.Q. Sheng, L. Liu, M.R. Wang, P.Y. Li, Circular RNAs in digestive system cancer: potential biomarkers and therapeutic targets, Am. J. Cancer Res. 8 (7) (2018) 1142–1156.
[14] M.Y. Zhou, J.M. Yang, X.D. Xiong, The emerging landscape of circular RNA in cardiovascular diseases, J. Mol. Cell. Cardiol. 122 (2018) 134–139.
[15] S.L. Mehta, R.J. Dempsey, R. Vemuganti, Role of circular RNAs in brain development and CNS diseases, Prog. Neurobiol. 186 (2020) 101746.
[16] D. Mei, W. Tan, Y. Tay, A. Mukhopadhyay, W. Wong, Therapeutic RNA strategies for chronic obstructive pulmonary disease, Trends Pharmacol. Sci. 41 (7) (2020) 475–486.
[17] S. Patil, K. Dang, X. Zhao, Y. Gao, A. Qian, Role of lncRNAs and circRNAs in bone metabolism and osteoporosis, Front. Genet. 11 (2020) 584118.
[18] L. Yang, X. Zou, J. Zou, G. Zhang, Functions of circular RNAs in bladder, prostate and renal cell cancer (Review), Mol. Med. Rep. 23 (5) (2021).
[19] Y. Zhong, Y. Du, X. Yang, et al., Circular RNAs function as ceRNAs to regulate and control human cancer progression, Mol. Cancer 17 (1) (2018) 79.
[20] M. Lei, G. Zheng, Q. Ning, J. Zheng, D. Dong, Translation and functional roles of circular RNAs in human cancer, Mol. Cancer 19 (1) (2020) 30.
[21] O. Farideh, Bibliometrics. Citation analysis and co-citation analysis: a review of literature I, Libri. 46 (2009) 149–158.
[22] M. Gagolewski, Bibliometric impact assessment with R and the CITAN package, J. Inf. 5 (2011) 678–692.
[23] A. Massimo, C. Corrado, Bibliometrix: an R-tool for comprehensive science mapping analysis, J. Inf. 11 (2017) 959–975.
[24] W.R. Jeck, J.A. Sorrentino, K. Wang, et al., Circular RNAs are abundant, conserved, and associated with ALU repeats, RNA 19 (2) (2013) 141–157.
[25] R. Ashwal-Fluss, M. Meyer, N.R. Pamudurti, et al., circRNA biogenesis competes with pre-mRNA splicing, Mol. Cell 56 (1) (2014) 55–66.
[26] J. Salzman, C. Gawad, P.L. Wang, N. Lacayo, P.O. Brown, Circular RNAs are the predominant transcript isoform from hundreds of human genes in diverse cell types, PLoS One 7 (2) (2012), e30733.
[27] J. Salzman, R.E. Chen, M.N. Olsen, P.L. Wang, P.O. Brown, Cell-type specific features of circular RNA expression, PLoS Genet. 9 (9) (2013), e1003777.
[28] X.O. Zhang, H.B. Wang, Y. Zhang, X. Lu, L.L. Chen, L. Yang, Complementary sequence-mediated exon circularization, Cell 159 (1) (2014) 134–147.
[29] R. Dong, X.O. Zhang, Y. Zhang, X.K. Ma, L.L. Chen, L. Yang, CircRNA-derived pseudogenes, Cell Res. 26 (6) (2016) 747–750.
[30] C.X. Liu, X. Li, F. Nan, et al., Structure and degradation of circular RNAs regulate pkr activation in innate immunity, Cell 177 (4) (2019) 865–880, e21.
[31] S. Li, X. Li, W. Xue, et al., Screening for functional circular RNAs using the CRISPR-Cas13 system, Nat. Methods 18 (1) (2021) 51–59.
[32] J.U. Guo, V. Agarwal, H. Guo, D.P. Bartel, Expanded identification and characterization of mammalian circular RNAs, Genome Biol. 15 (7) (2014) 409.
[33] M. Piwecka, P. Glažar, L.R. Hernandez-Miranda, et al., Loss of a mammalian circular RNA locus causes miRNA deregulation and affects brain function, Science 357 (6357) (2017).
[34] H. Xu, S. Guo, W. Li, P. Yu, The circular RNA Cdr1as, via miR-7 and its targets, regulates insulin transcription and secretion in islet cells, Sci. Rep. 5 (2015) 12453.
[35] B. Kleaveland, C.Y. Shi, J. Stefano, D.P. Bartel, A network of noncoding regulatory RNAs acts in the mammalian brain, Cell 174 (2) (2018) 350–362, e17.
[36] W.W. Du, W. Yang, E. Liu, Z. Yang, P. Dhaliwal, B.B. Yang, Foxo3 circular RNA retards cell cycle progression via forming ternary complexes with p21 and CDK2, Nucleic Acids Res. 44 (6) (2016) 2846–2858.
[37] W.W. Du, W. Yang, Y. Chen, et al., Foxo3 circular RNA promotes cardiac senescence by modulating multiple factors associated with stress and senescence responses, Eur. Heart J. 38 (18) (2017) 1402–1412.
[38] W.W. Du, L. Fang, W. Yang, et al., Induction of tumor apoptosis through a circular RNA enhancing Foxo3 activity, Cell Death Differ. 24 (2) (2017) 357–370.
[39] Z. Shen, L. Zhou, C. Zhang, J. Xu, Reduction of circular RNA Foxo3 promotes prostate cancer progression and chemoresistance to docetaxel, Cancer Lett. 468 (2020) 88–101.
[40] Z. Kong, X. Wan, Y. Lu, et al., Circular RNA circFOXO3 promotes prostate cancer progression through sponging miR-29a-3p, J. Cell Mol. Med. 24 (1) (2020) 799–813.
[41] Q. Zheng, C. Bao, W. Guo, et al., Circular RNA profiling reveals an abundant circHIPK3 that regulates cell growth by sponging multiple miRNAs, Nat. Commun. 7 (2016) 11215.
[42] Y. Li, F. Zheng, X. Xiao, et al., CircHIPK3 sponges miR-558 to suppress heparanase expression in bladder cancer cells, EMBO Rep. 18 (9) (2017) 1646–1659.
[43] K. Zeng, X. Chen, M. Xu, et al., CircHIPK3 promotes colorectal cancer growth and metastasis by sponging miR-7, Cell Death Dis. 9 (4) (2018) 417.
[44] K. Shan, C. Liu, B.H. Liu, et al., Circular noncoding RNA HIPK3 mediates retinal vascular dysfunction in diabetes mellitus, Circulation 136 (17) (2017) 1629–1642.
[45] G. Chen, Y. Shi, M. Liu, J. Sun, circHIPK3 regulates cell proliferation and migration by sponging miR-124 and regulating AQP3 expression in hepatocellular carcinoma, Cell Death Dis. 9 (2) (2018) 175.
[46] C. Yang, W. Yuan, X. Yang, et al., Circular RNA circ-ITCH inhibits bladder cancer progression by sponging miR-17/miR-224 and regulating p21, PTEN expression, Mol. Cancer 17 (1) (2018) 19.
[47] W. Guo, J. Zhang, D. Zhang, et al., Polymorphisms and expression pattern of circular RNA circ-ITCH contributes to the carcinogenesis of hepatocellular carcinoma, Oncotarget 8 (29) (2017) 48169–48177.
[48] M. Wang, B. Chen, Z. Ru, L. Cong, CircRNA circ-ITCH suppresses papillary thyroid cancer progression through miR-22-3p/CBL/β-catenin pathway, Biochem. Biophys. Res. Commun. 504 (1) (2018) 283–288.
[49] S.T. Wang, L.B. Liu, X.M. Li, et al., Circ-ITCH regulates triple-negative breast cancer progression through the Wnt/β-catenin pathway, Neoplasma 66 (2) (2019) 232–239.
[50] J. Hu, L. Wang, J. Chen, et al., The circular RNA circ-ITCH suppresses ovarian carcinoma progression through targeting miR-145/RASA1 signaling, Biochem. Biophys. Res. Commun. 505 (1) (2018) 222–228.
[51] D. Han, J. Li, H. Wang, et al., Circular RNA circMTO1 acts as the sponge of microRNA-9 to suppress hepatocellular carcinoma progression, Hepatology 66 (4) (2017) 1151–1164.
[52] Y. Li, B. Wan, L. Liu, L. Zhou, Q. Zeng, Circular RNA circMTO1 suppresses bladder cancer metastasis by sponging miR-221 and inhibiting epithelial-to-mesenchymal transition, Biochem. Biophys. Res. Commun. 508 (4) (2019) 991–996.
[53] Z. Ge, L.F. Li, C.Y. Wang, Y. Wang, W.L. Ma, CircMTO1 inhibits cell proliferation and invasion by regulating Wnt/β-catenin signaling pathway in colorectal cancer, Eur. Rev. Med. Pharmacol. Sci. 22 (23) (2018) 8203–8209.
[54] M. Chen, G. Ai, J. Zhou, W. Mao, H. Li, J. Guo, circMTO1 promotes tumorigenesis and chemoresistance of cervical cancer via regulating miR-6893, Biomed. Pharmacother. 117 (2019) 109064.

[55] B. Zhang, M. Chen, N. Jiang, K. Shi, R. Qian, A regulatory circuit of circ-MTO1/miR-17/QKI-5 inhibits the proliferation of lung adenocarcinoma, Cancer Biol. Ther. 20 (8) (2019) 1127–1135.
[56] Y. Tan, T. Zhang, C. Liang, Circular RNA SMARCA5 is overexpressed and promotes cell proliferation, migration as well as invasion while inhibits cell apoptosis in bladder cancer, Transl. Cancer Res. 8 (5) (2019) 1663–1671.
[57] Z. Kong, X. Wan, Y. Zhang, et al., Androgen-responsive circular RNA circSMARCA5 is up-regulated and promotes cell proliferation in prostate cancer, Biochem. Biophys. Res. Commun. 493 (3) (2017) 1217–1223.
[58] S. Tong, Circular RNA SMARCA5 may serve as a tumor suppressor in non-small cell lung cancer, J. Clin. Lab. Anal. 34 (5) (2020), e23195.
[59] H. Liu, Y. Wu, S. Wang, et al., Circ-SMARCA5 suppresses progression of multiple myeloma by targeting miR-767-5p, BMC Cancer 19 (1) (2019) 937.
[60] X. Miao, Z. Xi, Y. Zhang, et al., Circ-SMARCA5 suppresses colorectal cancer progression via downregulating miR-39-3p and upregulating ARID4B, Dig. Liver Dis. 52 (12) (2020) 1494–1502.
[61] Y. Zuo, W. Shen, C. Wang, N. Niu, J. Pu, Circular RNA Circ-ZNF609 promotes lung adenocarcinoma proliferation by modulating miR-1224-3p/ETV1 signaling, Cancer Manag. Res. 12 (2020) 2471–2479.
[62] C. Guan, L. Liu, Y. Zhao, et al., YY1 and eIF4A3 are mediators of the cell proliferation, migration and invasion in cholangiocarcinoma promoted by circ-ZNF609 by targeting miR-432-5p to regulate LRRC1, Aging (N Y) 13 (23) (2021) 25195–25212.
[63] S. Du, H. Li, F. Lu, S. Zhang, J. Tang, Circular RNA ZNF609 promotes the malignant progression of glioma by regulating miR-1224-3p/PLK1 signaling, J. Cancer 12 (11) (2021) 3354–3366.
[64] L. Wu, J. Xia, J. Yang, et al., Circ-ZNF609 promotes migration of colorectal cancer by inhibiting Gli1 expression via microRNA-150, J BUON 23 (5) (2018) 1343–1349.
[65] Z. Liu, H.M. Pan, L. Xin, et al., Circ-ZNF609 promotes carcinogenesis of gastric cancer cells by inhibiting miRNA-145-5p expression, Eur. Rev. Med. Pharmacol. Sci. 23 (21) (2019) 9411–9417.