

Global Research on DNA methylation from 2000 to 2019: Bibliometric Analysis and Visualization

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Abstract

Introduction: DNA methylation is the most common epigenetic feature in human somatic cells, it has played a crucial role in regulating related genes and diagnosing cancer. However, few studies used bibliometric method to systematically analyze the development of DNA methylation. The purpose of this study was to systematically analyze the trends of DNA methylation research from 2000 to 2019.

Methods: The published studies were searched between January, 2000 and December 31st, 2019 in the Web of Science. We only included peer-reviewed reviews and articles. The language was limited to English, and no species limitations were specified. A total of 11,127 publications met the inclusion criteria. CiteSpace V was used to analyze the trends of DNA methylation research.

Results: The results showed the publications had a statistical increase over time in the DNA methylation research ($P < 0.005$) by linear regression analyses. USA had the largest number of published papers (4263). Plos One contributed to the most publications (4.52%). The most prolific institution is Chinese Acad Sci (237). In accordance with subject categories of Web of Science, Genetics Heredity subject category had the largest number of publications (2,516) and citations (119,113). Biochemistry Molecular Biology subject category had the highest number of H-index (154). On the basis of the co-citation map of references, the "specific dna methylation" was labeled as the largest cluster. Most recent burst keywords were as follows: "pregnancy" (2017~2019), "obesity" (2017~2019), "growth" (2017~2019).

Conclusions: This study provides useful information for DNA methylation researchers to find fresh viewpoints related to collaborators, cooperative institutions, popular topics. It also reminds us to pay attention to some new research trends.

Introduction

More recently, an increasing number of researches focus on the development of DNA methylation, which is involved in a large quantity of knowledge about biological information. Currently, the most common epigenetic feature in human somatic cells is DNA methylation (1). Adding a methyl groups to the c5 (5meC) cytosine- followed- by-guanine dinucleotide (CG or CpG site) eventually leads to DNA methylation. It has the characteristics of stability and heredity (2). DNA methylation is a dynamic process that occurs in a temporal, spatial, and cell type-specific manner. The removal of methylation can be done either passively or actively, with the ultimate function being to respond to environmental stimuli (3).

The impact of methylation in biological information is enormous. We are just beginning to study the role of methylation in changing the activity of enhancers, insulators, and other regulatory elements (4). However, it has been well studied in transcriptional inhibition, genomic imprinting, dynamic biological process and selective splicing of pre-mRNA(5-7). DNA methylation regulates genes that are highly involved in memory formation and precisely regulates cognitive function in humans (8). Studies of DNA

methylation continue to demonstrate the richness and complexity of epigenetic gene regulation in the central nervous system and provide potential therapeutic targets for the treatment of neuropsychiatric disorders (9). DNA methylation can be used as a biomarker for aging (10) and cancer (11) as well as for predicting age (12) and participate in pathophysiological in disease (e.g., multiple sclerosis) (3, 13).

The study of DNA methylation has attracted researchers and academic journals' much attention in recent ten years, however, few published articles used systematic analysis to report the trends of scholarly production in this field. Bibliometric study is a quantitative method of published articles, which has been widely used to study trend in research activity over time (14-16). At present, bibliometric study has also been used for assessing the trends of plenty of genes and diseases, for example, long noncoding RNA (17), miRNAs and lncRNAs, exosome (18, 19), cancer (20, 21), pain (22-24), heart disease (25, 26), obesity (27, 28).

The purpose of our study is to systematically assess the trends of DNA methylation research from 2000 to 2019. The CiteSpace V (Drexel University, Philadelphia, United States) is used to conduct a bibliometric study in Web of Science Core Collection, which is one of the frequently-used bibliometric method tools to analyze the trends in scientific research (16, 29). In our study, the trends of the DNA methylation research involve the number of published articles, the collaborations between countries/ institutions/ authors, co-citation analysis of authors and references, a citation-burst analysis of keywords (15, 30). Our findings would offer valuable information to scientific researchers, funding agencies and policy makers.

Methods

2.1 Sources of the data

Publications are limited to be between January 1, 2000 and December 31st, 2019. The data were downloaded and extracted from the Science Citation Index Expanded (SCI- Expanded) of Web of Science Core Collection, and used as secondary analysis data.

The following words were used: Title = (methylation) and Title = (DNA or Deoxyribonucleic acid) AND Language: (English).

2.2 Inclusion criteria

First, regarding manuscript types, we only included peer-reviewed reviews and articles and excluded conference presentations, conference abstracts, case reports, expert opinions and editorials. Second, language was limited to English. Third, we included studies that were related to DNA methylation. No species restrictions were considered. The resultant expanded dataset comprises 11,127 records, which were reviewed on 19 Jan 2020.

2.3 Data extraction

The authors (Xuan Su) independently extracted the published papers, and made use of EndNote (EndNote X7, Bld 7072, Thomson Research Soft, Stamford) to conduct the downloaded publications. The txt data were imported into CiteSpace V, which were downloaded from SCI-Expanded.

The included papers of this study were recorded the following characteristics, such as journal, institution, country. And we extracted these information (for example, publication count, citation frequency, H-index, essential science indicators top papers) as bibliometric indicators. H-index refers to the fact that a researcher or research institution has H papers that have been cited at least H times respectively (31). For example, the H-index of a certain researcher is 20, which indicates that among his published papers, a total of 20 papers have been cited more than 20 times. The higher the H-index, the greater the influence of the papers. Essential science indicators (ESI) (32) top papers include hot papers (last two years) and highly cited papers (last ten years) for 22 broad subject categories in ESI database of Web of Science. According to the included studies, we would choose and analyses the top 15 subject categories of Web of Science categories. Research areas are classified into five broad categories in Web of Science Categories, and there are 225 subject categories in the five broad categories, such as cell biology, oncology, physiology.

2.4 Statistical methods

The Microsoft Excel 2020 was utilized for analyzing and predicting the publications of DNA methylation. We used the predicted model ($f(x) = ax^3+bx^2+cx+d$) to calculate the trends of publications and to forecast the cumulative volume in the crosstalk between DNA methylation. The symbol x indicated the year, and $f(x)$ denotes the quantity of published papers by the year. The Microsoft Excel 2020 was also used for drawing the world map about the distribution of papers on DNA methylation. CiteSpace is an appropriate choice of method to perform a bibliometric analysis, facilitating the analysis of the trends and patterns in a knowledge structure. The CiteSpace V were used to 1) analyse the distribution by journals, years, countries, authors and institutions, 2) evaluate the collaborations between countries, institutions and authors, 3) put through analysis of citations, H-index, ESI top papers, 4) analyze the reference and keywords to predict future research trend. To analyses whether the number of articles published each year significantly increased or decreased over time, we used the linear regression analyses with the year as the independent variable and publications as the dependent variables. The linear regression analysis was conducted with IBM SPSS Statistics 22.0 software (SPSS, Inc, Chicago, USA). When P value is less than 0.05, it is considered statistically significant.

Results

3.1 Publication outputs and growth trends prediction

A total of 11,127 publications met the inclusion criteria. The characteristic of annual published papers was demonstrated in different periods (Figure 1A). In general, the research interest on DNA methylation has slowly gone up in the past 20 years, as the publication number raised from 101 publications in 2000 to 1273 publications in 2019. Figure 1B showed a statistical correlation ($R^2 = 0.939$) between publication year and the cumulative number of publications by model fitting curve of the publication growth. Using the cumulative number of published papers from 2000 to 2019, it is calculated that the number of publications were up to 1372 in 2020.

In addition, the consequence of linear regression analyses revealed that the percentages increased statistically over time in the past twenty years ($t=16.625$, $P < 0.001$). In the four 5-years (2000-2004; 2005-2009; 2010-2014; 2015-2019), 2015-2019 had the biggest number of papers (5657) and citations (25,750), 2010-2014 had the biggest number of citations (171,825), ESI papers (83) and the highest value of H-index (168), 2005-2009 had the biggest number of citations per paper (85.58). The details can be found in figure 2.

3.2 Distribution by journals

A total 11,127 papers on DNA methylation research were bring out in 1864 academic journals. Of the top 15 journals by the number of published papers (Table 1), Plos One, which IF 2018 was 2.776, conducted to the most publications on DNA methylation research (504 publications, 4.52%), followed by Epigenetics (IF, 4.173; 406 publications; 3.65%), Clinical Epigenetics (IF, 5.496; 267 publications; 2.40%), and Proceedings of Scientific Reports (IF, 4.011; 228 publications; 2.05%). Among the 15 top journals, most journals were Q1 or Q2 in journal IF quartile of Web of Science. From Figure 3, in terms of co-citation coupled with centrality, the Nature, Cell, P Natl Acad Sci USA, Nat Genet, Nucleic Acids Res, and Genome Biol are the most influential in the association of DNA methylation research.

3.3 Distribution by countries and institutions

A total of 11,127 papers on DNA methylation research were published in 107 countries/territories. A widespread collaboration between countries/territories was showed in figure 4A. Among the top ten countries (Table 2), according to the publication of the papers, USA had the largest number of published papers (4263), citations (235,449), citations per paper (55.23), ESI top papers (117), and the highest value of H-index (216). This shows that the United States plays an important role and occupies a high position in the field of DNA methylation research. Based on the number of publications, Figure 5 showing the distribution of published papers in countries around the world.

The 11,127 papers on DNA methylation research were contributed by more than 7,000 institutions. These institutions accounted for 5.999% of the total quantity of DNA methylation studies among the top 10 institutions. The table 3 indicated number of papers, citations, citations per paper, open access papers, H-index and ESI top papers in top 10 institutions. Chinese Acad Sci had the highest number of publications

(237), Harvard Univ had the highest number of citations (25,526), the highest number of open access papers (198) and the highest value of H-index (76), Univ So Calif had the highest number of citations per paper (137.48). The Figure 4B showed network map of institutions engaged in DNA methylation research.

3.4 Subject categories of Web of Science

In 11,127 papers on DNA methylation research, fields of study were assigned to 143 scientific network disciplines. Among the top 21 subject categories, the most representative and influential was Genetics Heredity, with 2,516 published papers and 119,113 citations. The subject category with the highest number of H-index (154) is Biochemistry Molecular Biology. Developmental Biology subject category had the largest number of citations per paper (70.43). Multidisciplinary Sciences subject category had the largest number of ESI top papers (31). The number of papers, citations, citations per paper, H-index and ESI top papers of the top 10 subject categories of Web of Science were shown in Figure 6.

3.5 The distribution of authors

A total of 44633 authors devoted to 11,127 published papers. The cooperation between authors were outlined by network map (Figure 7A). The Table 4 showed the top ten authors who had the most published papers. Among the top ten authors, ANDREA A BACCARELLI had the most published papers (66), followed by MOSHE SZYF (46), MANEL ESTELLER (42), and CARMEN J MARSIT (42). A network map was presented for information on authors citation by using CiteSpace V (Figure 7B). In the midst of the top 10 co-cited authors (Table 4), JONES PA (2277 citations), followed by ESTELLER M (1409 citations), BIRD A (1216 citations), and LISTER R (1025 citations).

3.6 Analysis of references

Reference analysis was considered as a significant indicator in bibliometrics study. Figure 8 a showed the map for co-citation of references, suggesting the association of the published studies on DNA methylation research. The modularity Q value was 0.8963 (greater than 0.5), indicating that it is reasonable to divide the co-cited graph into coupling clustering. All clusters were traced by index terms extracted from the references. As shown in the figure, we can see that labeled as the largest cluster is "specific DNA methylation", and labeled as the second largest cluster #1 is "DNA methylation dynamics". "non-conventional DNA methylation" was labeled the third largest cluster, and finally "lung cancer" was labeled the fourth largest cluster. A timeline view was showed for the top 12 clusters (Figure 8B).

3.7 Analysis of keywords

CiteSpace V was used to extract keywords from the 11,127 published studies. The top 77 most-cited keywords are delineated in Figure 10. The top five keywords with strongest citation bursts were as

supersedes: “de novo methylation” (2000-2010), “cpg island” (2001- 2010), “cpg island methylation” (2000-2010), “inactivation” (2000- 2011), “promoter hypermethylation” (2001-2013). Figure 9 shows the keyword co- occurrence network diagram of DNA methylation research from 2000 to 2019.

3.8 Characteristics of top 10 papers with the highest citation frequency

The top ten papers on DNA methylation scientific research with the most citation frequency was put on the Table 5. The article by Bird A et al. come out in 2002 was the most cited (4205 times) paper, was entitled “DNA methylation patterns and epigenetic memory.” published in GENE DEV. In the thick of the top 10 papers, six were bring out in journals with impact factor ≥ 40 (NAT REV GENET , NATURE), one in journals with $20 \leq$ Impact factor <40 (NAT GENET), two in journals with $10 \leq$ Impact factor <20 (TRENDS BIOCHEM SCI, GENOME BIOL), one journal with $1 \leq$ Impact factor <10 (GENE DEV).

Discussion

4.1 Global trends in DNA methylation research

Over time, the tendency in global publications has keep on rising in DNA methylation research. According to the observed increase of publications on DNA methylation research, our findings disclosed two periods in publication year. The first period (2000-2004) was considered as a germination period of the DNA methylation research. Although the first paper on DNA methylation research was published in 1963, these papers systematically describe the process of enzyme methylation of RNA and DNA (33, 34). This is enough to prove that the topic is very research-oriented. In this period, the number of publications contributed to 6.36% of the total number of publications on DNA methylation research. Over time, it has grown by almost twice every five years. The second period (2015-2019) could be regarded as a golden period for DNA methylation research, as 50.84% of papers were published during this period. Though the H-index has fallen by nearly half since the previous five years, but citations in 2019 are the highest.

The top 15 journals by the number of published papers, contributed to 2,611 publications on DNA methylation research. *Plos One* had the most published papers on DNA methylation research (504 publications, 4.53%), followed by *Epigenetics* (406 publications; 3.65%), *Clinical Epigenetics* (267 publications; 2.40%). Top of the citations per paper (108.21) was *Cancer Research* (IF 2018, 8.378). *Plos One* (IF 2018, 2.776) had the most citations (15463) and highest value of H-index (60). *Genome Biology* (IF 2018, 14.028) is an excellent organization with the largest number of ESI top level papers (6).

Among the top 10 countries, the United States has made outstanding contributions to DNA methylation research, with the highest number of papers (4,263), citations (23,5449), citations per paper, H-index (216), and the highest number of ESI top papers (117). Among the top 10 countries, there were two Asia-Pacific countries, five European countries, one American country and one Oceania country. In addition, based on the number of publications, we can see that eight organizations were from North America (the United States has seven) and two were from Asia Pacific countries. It can be seen that American research in this field has a certain influence.

Researchers interested in this field can pay more attention to the research direction of relevant institutions in the United States.

4.2 Emerging trends of DNA methylation research

In accordance with the latest Web of Science category, the hot research areas among 11,127 papers chiefly concentrated on Genetics Heredity, Biochemistry Molecular Biology and Oncology for the DNA methylation research. As shown in figure 6, in terms of the number of publications Genetics Heredity (2516 publications) led the first research echelon, followed by "Biochemistry Molecular Biology" (2286 publications), "Oncology" (1836 publications), "Cell Biology" (1148 publications), and "Multidisciplinary Sciences" (1063 publications).

On the basis of the co-citation map of references, we noticed that "specific dna methylation" was labeled as the largest cluster, followed by "dna methylation dynamics", "non-conventional dna methylation", and "lung cancer". Ambrosi C et al. showed that DNA methylation can directly affect gene expression patterns and cell recognition, linking promoters to gene activity dynamics (35). Pitto L et al. suggested that the range and environment of methylation might help regulate gene expression (36). Mehta A et al. showed that DNA methylation is the most intensively studied epigenetic marker of human cancer, and that some cancers occur and develop as a result of interactions between permanent genetic and dynamic epigenetic changes (37).

Among the top 10 most cited papers, the paper wrote by Bird A et al. published in *Gene Dev* was the most cited paper (4205 times), which focus on DNA methylation, involving not only the generation of methylation patterns in mammalian genomes, but also genetic and biological knowledge (8). Jones P et al. published the paper entitled "Functions of DNA methylation: islands, start sites, gene bodies and beyond." in *NAT REV GENET*, they reveal we can evaluate DNA methylation in different genomic contexts: transcriptional start sites with or without CpG islands, in gene bodies, at regulatory elements and at repeat sequences (4).

The burst keywords, which break out frequently and appear within a certain period, are thought to be the indicators of frontier topics or jumped-up trends(38). CiteSpace can be used to detect burst keywords. Figure 10 shows the top 77 keywords, which with the strongest bursts in their appearances, from 2000 to 2019. By the end of 2019, the most recent burst keywords were as follows: "brain"(2014~2019), "stem

cell”(2014~2019), “epigenome wide association”(2015~2019), “oxidative stress”(2016~2019) , “inflammation”(2016~2019), “methylome”(2016~2019), “pregnancy”(2017~2019), “obesity”(2017~2019), “growth”(2017~2019). Among them, the keyword “blood”, which emerged starting from 2015, has the strongest citation burst (42.1367). We observed that the research related to DNA methylation is more deeply studied and more widely developed. We found that different DNA methylation in the brain is associated with many psychiatric diseases (39), and not only that, it also plays an important role in stem cells pluripotency and differentiation (40). From 2017 to 2019, the key words that started to explode, We have learned that blood DNA methylation during pregnancy has been shown to be sensitive to air pollutants and to affect the health of the fetus (41). DNA methylation is used to explain genetic variability in obesity (42). Some evidence suggests that DNA methylation is associated with (i) changes in lipid and glucose metabolism, (ii) diabetes and (iii) size and composition in children (43). Hence, further DAN methylation research are needed to focus on these keywords.

4.3 Strengths and limitations

We are the first research team to analyze on the trends of the DNA methylation research from 2000 to 2019 in SCI-Expanded of Web of Science through visual analysis. Furthermore, the trends analysis of the DNA methylation research include the quantity of publications, academic journals, the distribution and collaborations between countries/ institutions/ authors, H-index and ESI papers, co-citation analysis on authors and journal, analysis of keywords, which could offer valuable information for DNA methylation researchers to discover new areas connected with companions, cooperative institutions, research frontiers.

There are some limitations in this study. Only SCI-Expanded of Web of Science is searched and analyzed, and the other electronic database such as PubMed, Scopus, Cochrane library, Embase, are not searched and analyzed. Besides, non-English publications, which were few in number and may not change the conclusions, were excluded during retrieval. This study focuses on quantitative analysis but less qualitative analysis. Another limitation is that influential papers were not quoted with frequent times. Because some potential influential papers would be cited with high citation frequency until the findings were well known. Other influential and relevant papers could be published recently, may not be quoted with high citation frequency.

Conclusions

Here, for the first time, we performed a bibliometric analysis of the scientific literature on DNA methylation. From 2000 to 2019, we conducted quantitative and qualitative analyses of global scientific papers on these topics. This will help researchers understand the trends of DNA methylation. The top three countries that contributed to the largest number of publications were USA, Peoples R China, and Germany, Plos One, Epigenetics, and Clinical Epigenetics were the top three journals engaged in DNA methylation research. The most prolific institution is Chinese Acad Sci, followed by Harvard University,

Johns Hopkins Univ. We can choose these institutions for Cooperation and communication. The latest research frontier may be “pregnancy”, “obesity”, and “growth”. The development trends in the applications of DNA methylation as revealed by the hot topics and research frontiers discussed in this study. The related studies may pioneer this field in the next few years and may help researchers to identify new directions with renewed focus. In conclusion, this study provides an insight into DNA methylation and valuable information for researchers to identify new perspectives concerning potential collaborators and cooperative institutions, hot topics, and research frontiers.

Declarations

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Author Contributors: XQ. Wang designed the study. All authors whose names appear on the submission contributed substantially to the acquisition of data, or the analysis and interpretation of the data. Xuan Su wrote the first draft of the manuscript, and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

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Tables

Table 1. The top 15 journal of origin of papers in the DNA methylation research.

Journals	Papers	Citations WoS	Citations per paper	WoS categories	IF 2018	Quartile	H-index	ESI top paper
Plos One	504	15463	30.68	Multidisciplinary Sciences	2.776 (IF 2018)	Q2	60	4
Epigenetics	406	11474	28.26	Biochemistry & Molecular Biology; Genetics & Heredity	4.173	Q2; Q1	56	1
Clinical Epigenetics	267	3579	13.4	Genetics & Heredity; Oncology	5.496	Q1; Q1	29	1
Scientific Reports	228	2590	11.36	Multidisciplinary Sciences	4.011	Q1	23	0
Nucleic Acids Research	189	10901	57.68	Biochemistry & Molecular Biology	11.147	Q1	53	3
Epigenomics	161	3500	21.74	Genetics & Heredity	4.404	Q1	32	1
BMC Genomics	113	2547	22.54	Applied Microbiology; Genetics & Heredity	3.501	Q2 ; Q2	29	0
Proceedings of The National Academy Of Sciences of The United States of America	111	11757	105.92	Multidisciplinary Sciences	9.58	Q1	55	5
Oncotarget	105	1380	13.14	Cell Biology & Oncology	5.168	Q2;Q1	19	0
Plos Genetics	94	8265	87.93	Genetics & Heredity	5.224	Q1	51	2
Journal of Biological Chemistry	93	6972	74.97	Biochemistry & Molecular Biology	4.106	Q2	48	0
Genome Biology	91	7431	81.66	Biotechnology & Applied Microbiology; Genetics & Heredity	14.028	Q1; Q1	44	6
International Journal of Cancer	85	3383	39.8	Oncology	4.982	Q1	35	0
Genome Research	84	8405	100.06	Biochemistry & Molecular Biology ; Biotechnology & Applied Microbiology; Genetics & Heredity	9.944	Q1; Q1;Q1	51	2
Cancer Research	78	8440	108.21	Oncology	8.378	Q1	50	1

Table 2. The top 10 countries of origin of papers in the DNA methylation research.

Country	Papers	Citations WoS	Citations per paper	Open access	H-index	ESI top paper
USA	4263	235449	55.23	3332	216	117
Peoples R China	2263	39512	17.46	1241	83	20
Germany	1028	51363	49.96	684	111	32
England	919	44003	47.88	720	102	36
Japan	901	34918	38.75	522	94	4
Canada	635	27367	43.1	428	80	14
Austria	496	18388	37.07	346	71	15
France	485	23263	47.96	318	79	11
Italy	462	17924	38.8	286	69	11
Spain	445	20068	45.1	288	71	10

Table 3. The top 10 institutions of origin of papers in the DNA methylation research.

Institutions	Papers	Citations WoS	Citations per paper	Open access	H-index	ESI top paper
Chinese Acad Sci	237	8927	37.67	157	52	4
Harvard Univ	223	25526	114.47	198	76	23
Johns Hopkins Univ	207	13397	64.72	171	58	10
Columbia Univ	179	8595	48.02	164	44	5
Univ Calif Los Angeles	176	23829	135.39	142	67	13
McGill Univ	173	8389	48.49	117	52	6
Univ Michigan	161	6362	39.52	134	43	2
Univ Tokyo	154	5338	34.66	94	43	0
Univ So Calif	152	20897	137.48	117	72	8
Emory Univ	151	7781	51.53	129	44	3

Table 4. The top 10 authors, co-cited authors, and co-cited references in the DNA methylation research.

Author	Count	Co-cited Author	Count	Co-cited Reference	Count
Andrea A Baccarelli	66	Jones PA	2377	Jones PA,2012, Nat Rev Genet, V13, P484	680
Moshe Szyf	46	Esteller M	1409	Lister R,2009, Nature, V462, P315	590
Manel Esteller	42	BIRD A	1216	Houseman EA, 2012, BMC Bioinformatics, V13, P0	479
Carmen J Marsit	36	Lister R	1025	Aryee MJ,2014, Bioinformatics, V30, P1363	376
Caroline L Relton	35	HERMAN JG	845	Irizarry RA,2009, Nat Genet, V41, P178	373
Michael S Kobor	34	Feinberg AP	621	Bibikova M, 2011, Genomics, V98, P288	353
Lifang Hou	32	Houseman EA	515	Horvath S, 2013, Genome Biol, V14, P0	340
Andrea Baccarelli	28	Baylin SB	514	Law JA, 2010, Nat Rev Genet, V11, P204	340
Karl T Kelsey	27	Robertson KD	490	Meissner A, 2008, Nature, V454, P766	335
E Andres Houseman	25	Teschendorff AE	448	Jones PA,2007, Cell, V128, P683	327

Table 5. The top 10 papers with the most citation frequency in the DNA methylation research.

Title	First author	Journal	Impact factor	Year	Citations WoS	WoS categories	Category ranking
DNA methylation patterns and epigenetic memory	Bird A	Gene Dev	8.99	2002	4205	Cell Biology; Developmental Biology; Genetics & Heredity	22/193;3/43;11/174
Functions of DNA methylation: islands, start sites, gene bodies and beyond	Jones P	Nat Rev Genet	43.704	2012	2381	Genetics & Heredity	1/174
Establishing, maintaining and modifying DNA methylation patterns in plants and animals	Law J	Nat Rev Genet	43.704	2010	1645	Genetics & Heredity	1/174
DNA methylation landscapes: provocative insights from epigenomics	Suzuki M	Nat Rev Genet	43.704	2008	1639	Genetics & Heredity	1/174
Genome-scale DNA methylation maps of pluripotent and differentiated cells	Meissner A	Nature	43.07	2008	1623	Multidisciplinary Sciences	1/69
Genomic DNA methylation: the mark and its mediators	Klose RJ	Trends Biochem SCI	16.889	2006	1552	Biochemistry & Molecular Biology	4/299
DNA methylation and human disease	Robertson KD	Nat Rev Genet	43.704	2005	1527	Genetics & Heredity	1/174
The Polycomb group protein EZH2 directly controls DNA methylation	Vire E	Nature	43.07	2008	1364	Multidisciplinary Sciences	1/69

Figures

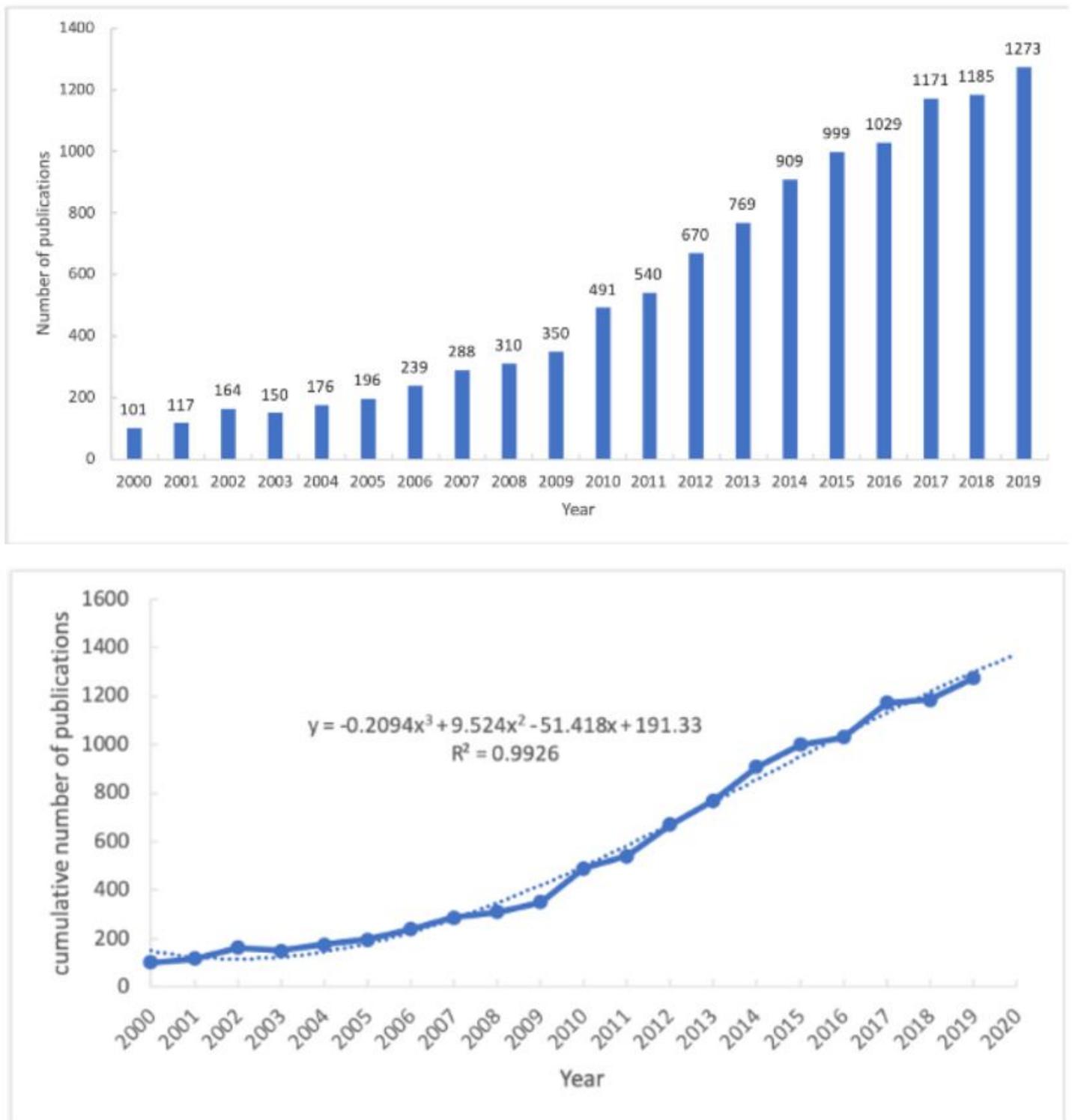


Figure 1

Publication outputs and growth prediction. (A) The number of annual publications on DNA methylation research from 2000 to 2019; (B) The model fitting curve of growth trend of DNA methylation publications.

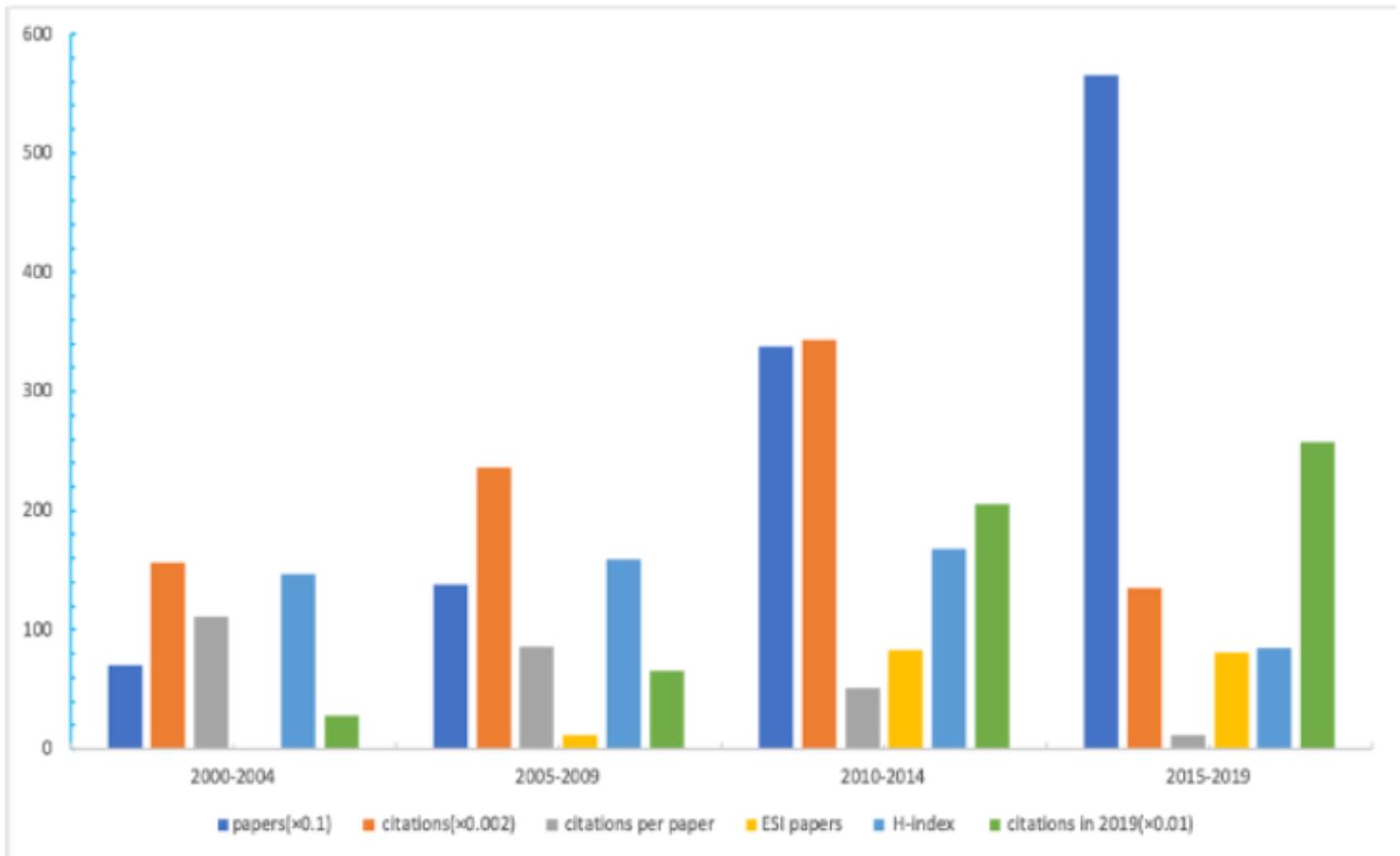


Figure 2

Number of papers, citations, citations per paper, ESI top paper, H- index and citations in 2019 for each 5-year time period.

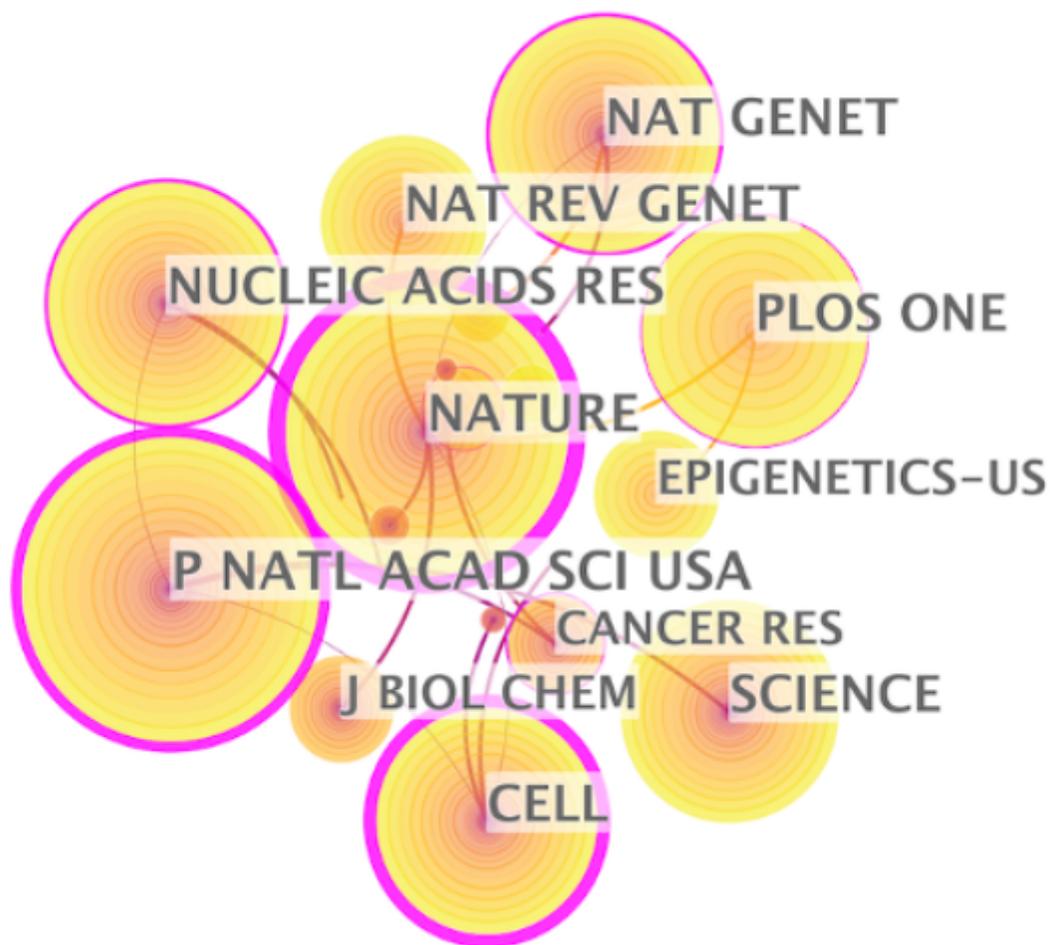


Figure 3

Journal co-citation map related to DNA methylation research from 2000 to 2019.

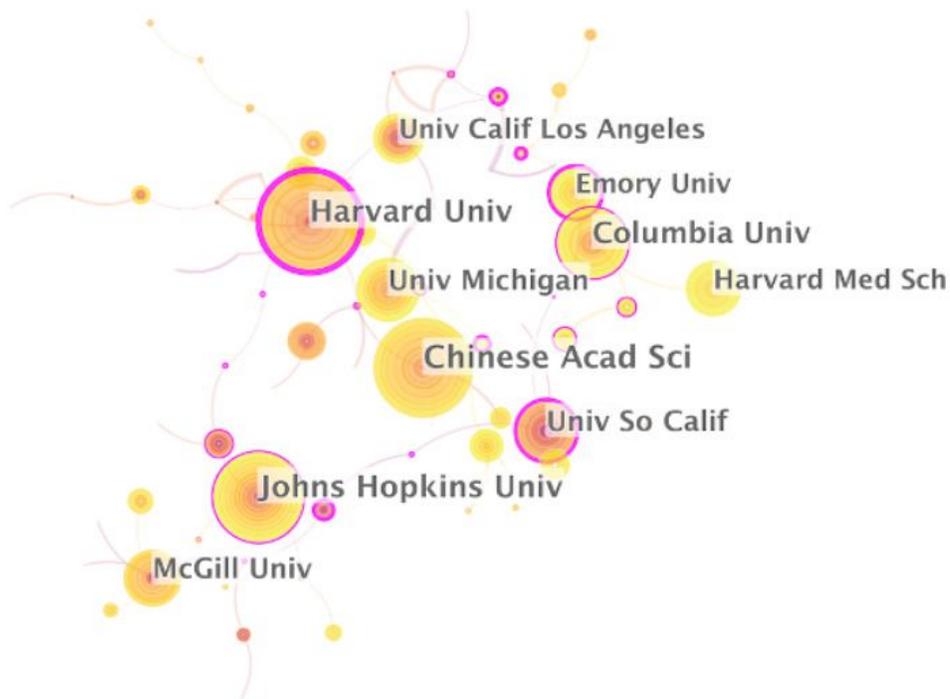
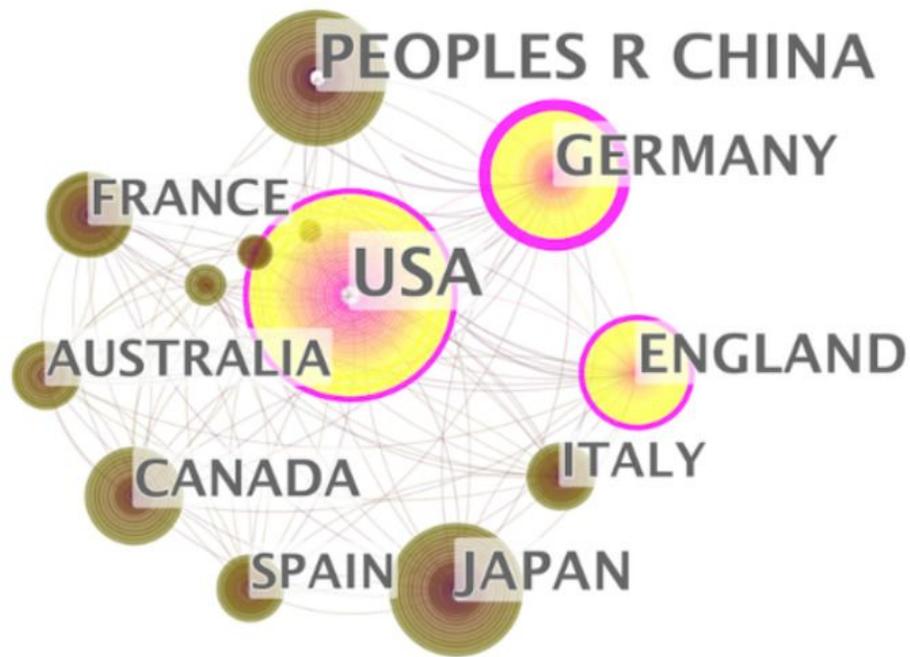


Figure 4

The analysis of countries and institutions. (A) Network map of countries/territories engaged in DNA methylation research; (B) Network map of institutions engaged in DNA methylation research.

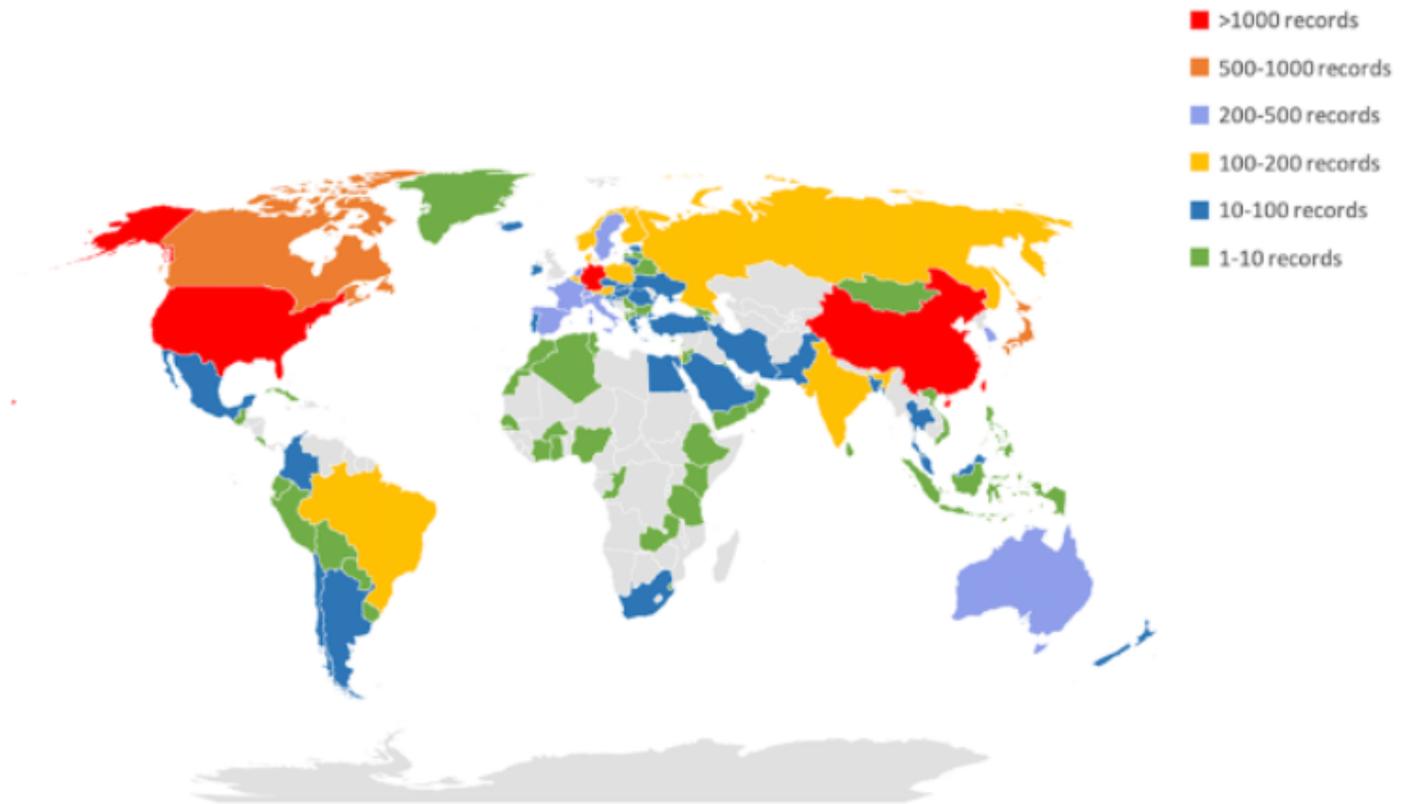


Figure 5

World map of total country output based on DNA methylation research. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

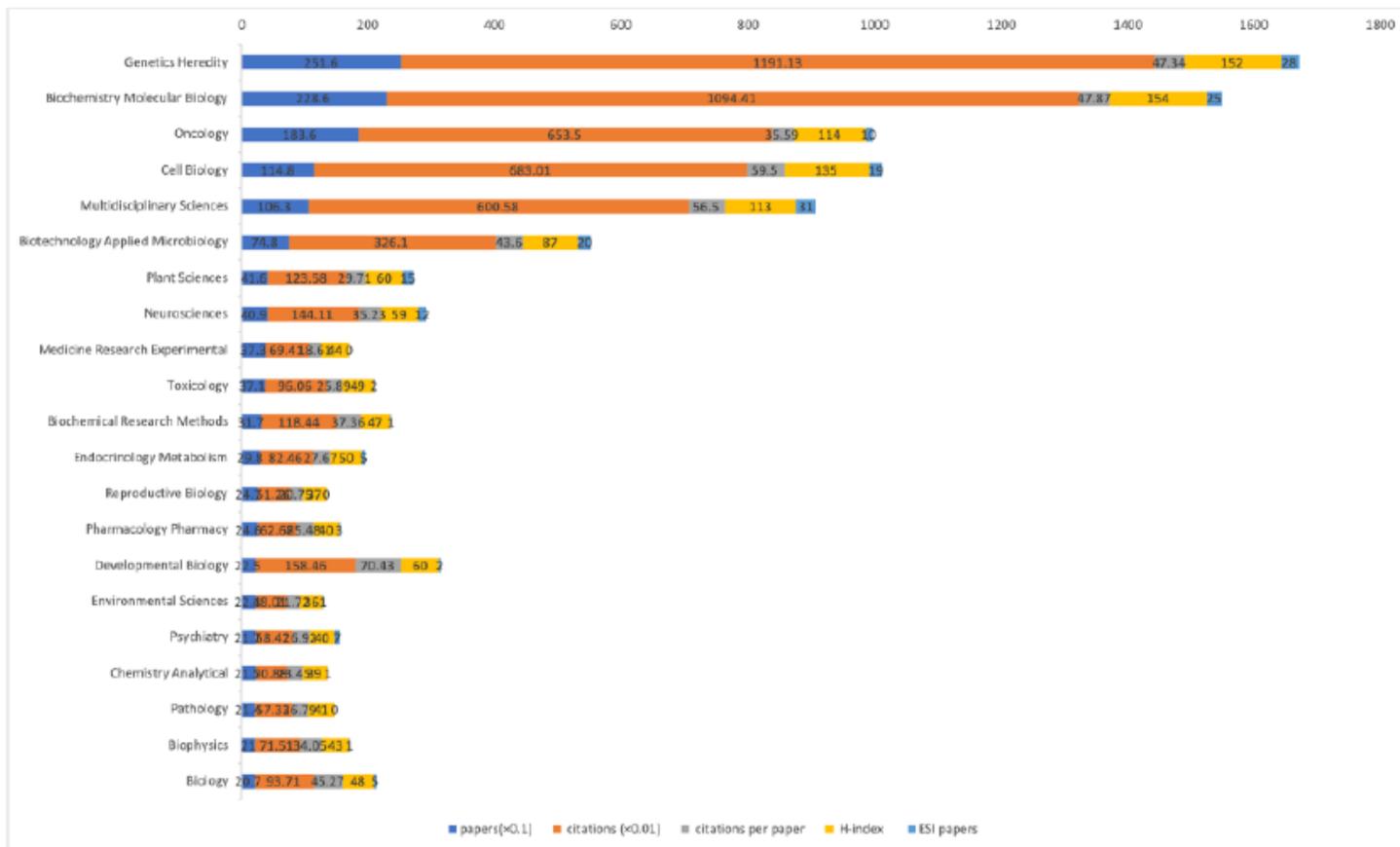


Figure 6

The number of papers, citations, citations per paper, H-index and ESI top papers of the top 10 subject categories of Web of Science.



Figure 7

The analysis of authors. (A) Network map of active authors contributed to DNA methylation research; (B) Network map of co-cited authors contributed to DNA methylation research.

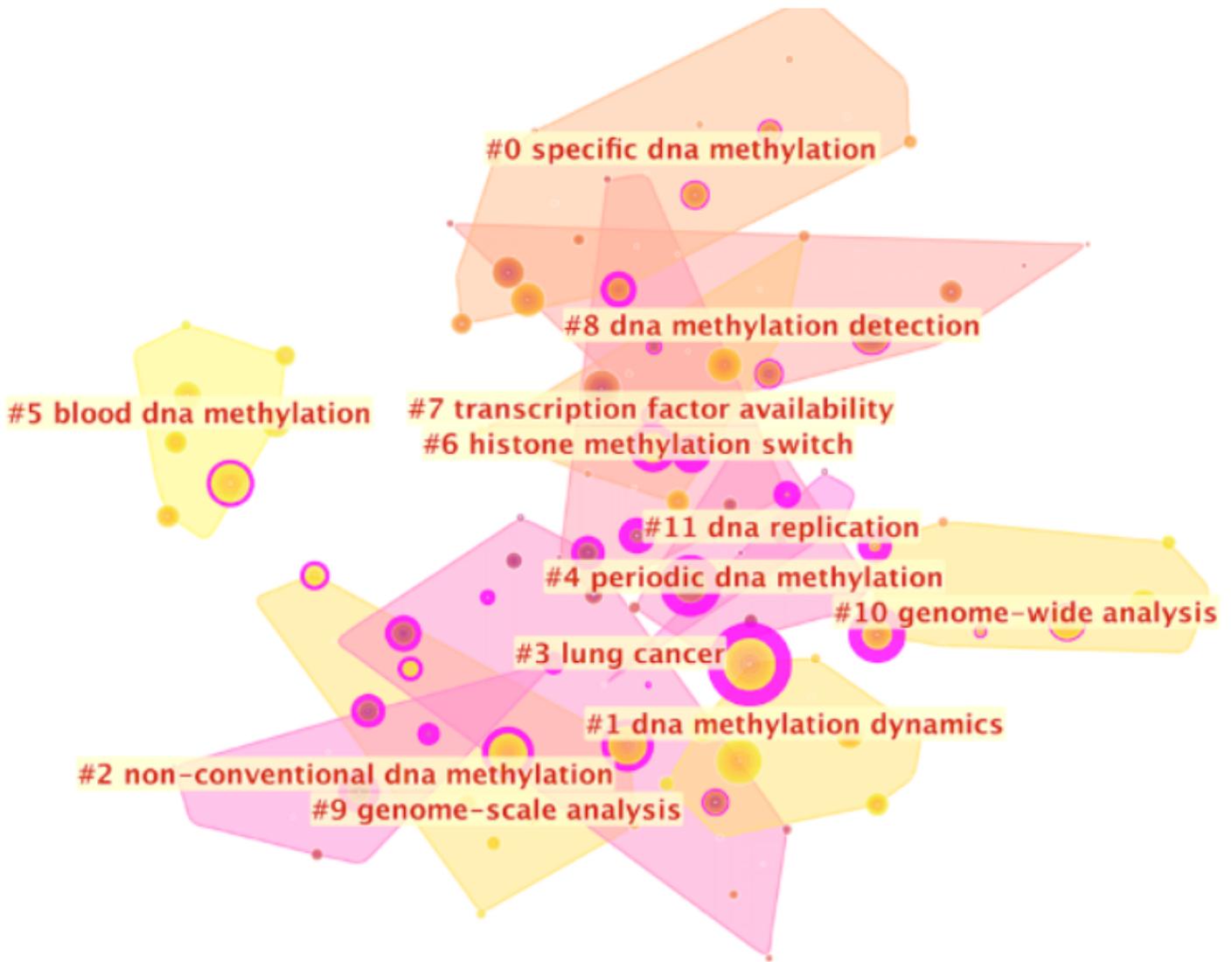


Figure 8

The analysis of references. (A) Co-citation map of references from publications on DNA methylation research; (B) Co-citation map (timeline view) of references from publications on DNA methylation research.

Top 77 Keywords with the Strongest Citation Bursts

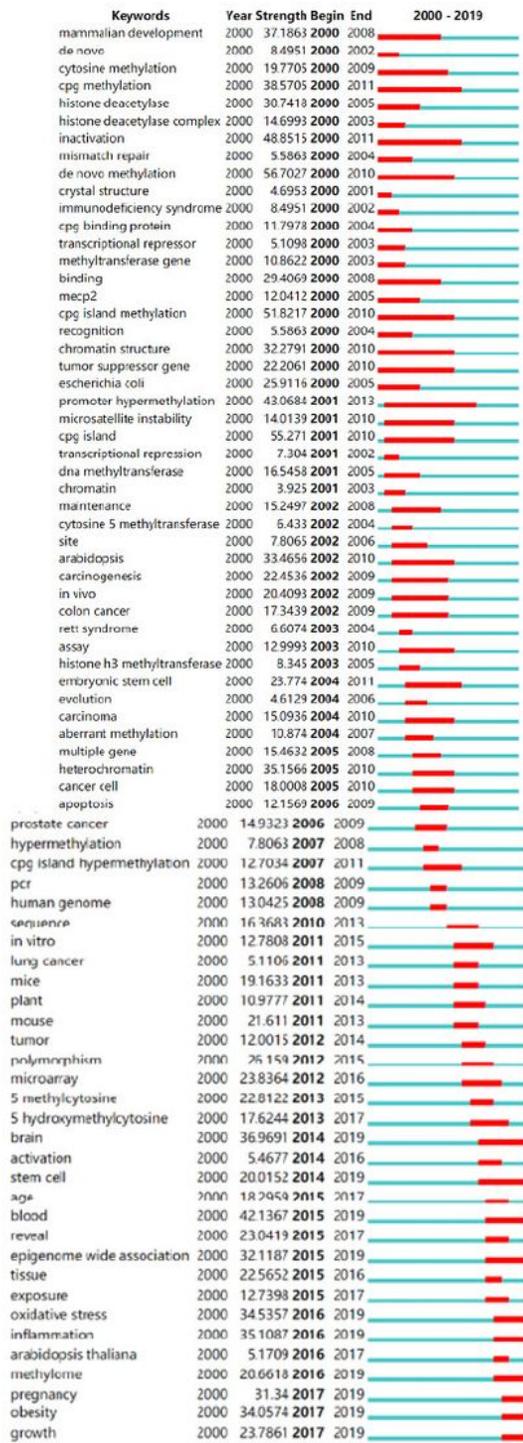


Figure 10

The keywords with the strongest citation bursts of publications on DNA methylation research.