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Scientometric Analysis of Mammalian Microbiome Research

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Abstract:

Over the past few decades, microbiota research has been gaining the attention of the researchers working on the concepts of health–enhancement and overall–wellbeing. The mammalian microbiome has been progressively acknowledged as a developing research area resulting in an increased number of publications. This study intends to use scientometric and bibliometric analysis to evaluate the research development and evolution of publication patterns in the field of mammalian microbiome between 2007 and 2020. We retrieved 512 published articles from the Web of Science Core Collection and were analyzed. We assessed the quantity and quality of research output through statistical methods of bibliometric indicators, comprising a number of publications, citations, productive authors, journals and countries, using a bibliometric analysis. Scientometric analysis was performed using main path analysis, bibliometric coupling, co-word co-occurrence and co-author analysis, systematically characterizing and visualizing the trend and delivering a pivotal review of the mammalian microbiome research status quo. The results identified an increase in the number of publications over time showing the rapid research growth, with top productive countries recording the highest number of research outcomes with influential research. The bibliographic coupling revealed the most shared papers that form landmark papers and the co-author analysis indicated the most influential authors in mammalian microbiome research. The evolutionary path of the mammalian microbiome research was traced using the main path analysis identifying the milestone papers. The frequently occurred words were enumerated from co-word, co-occurrence networks. The information from this study could be a transcript for a comprehensive understanding of current mammalian microbiome research and can also direct the future and emerging trends in this research realm.

Keywords: Mammalian microbiome, Bibliometric, Scientometric, Bibliographic coupling, Main path analysis, Co-author analysis, Co-word co-occurrence.

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1. Introduction

Microbiome encompasses the whole pool of both symbiotic and pathogenic microorganisms living in and on a host organism. The history of microbiome reverts to 1800s, with Sergei Winogradsky, the founder of modern microbiology and the first microbiology ecologist, pointing out the interaction of microbes among themselves and within the environment [1]. The usage of the term 'microbiome' dates back to 1988 [2] [3]. In early 1965, Dubos, R and colleagues [4] identified the bacterial flora of gastrointestinal tract to be symbiotic and to have been established as true autochthonous flora. Initial research established the relationship of indigenous microflora to its host and its effect on diet, environment and host body [5]. Further research revealed the mutualism and co-evolution of the microflora with its host [6] [7]. Continuous studies on microbiome subsequently led to the discovery of the influence of microbiome on host immune system, diet and environment, which suggested that the modification of microbiome influences the host's homeostasis. Thus, microbiome research emerged as a promising area as an indicator of host health and disease [8] [9] [10].

An intimation of research development which includes tackling a scientific problem to discover distinguished solutions is presented to the public only through a publication. The publication of the research work provides the scientific community with the information and the trend of research. While enabling a scientific problem to be solved, it also creates a flow of scientific knowledge in the community. An indication of scientific growth in a research area can be assessed by the number of publications in that area. Scientometric and bibliometric analysis have been used in various fields for research evaluation. Scientometric analysis has been used to summarize the research output and elucidate the status of research [11] [12] and bibliometric analysis provides information about influential authors, countries, journals and publications [13] [14] [15] [16] [17].Therefore, both the approaches intimate to the researchers the area to be focused on for more productive outcomes. More than 330 clinical studies have been documented worldwide with an explicit emphasis on the microbiome [15]. The microbiome is a growing area of research in pursuance of attaining the means of measure of an organism's health and homeostasis. The microbiome research has leapt towards microbiome-wide association studies (MWAS) to find associations between the metagenome and phenotypic traits [18]. This immense role of microbiomes on the host physiology could be exploited to consider the microbiome measure to be a digital assessment of host health [19]. For a better application of the research outcomes on mammals, the research on general microbiome is narrowed down to mammalian microbiome. This study aims to compile and assess the research trends on mammalian microbiome using scientometric and bibliometric analysis. This provides new opportunities to find the scientific activities, active scientists, productive countries and journals, enabling the researchers to find the research gaps, research trends, and the least explored area for further exploration.

2. Material and Methods

2.1 Data retrieval

The data published till date regarding microbiome were collected from Web of Science core collection via Boolean search, using keywords "Microbiome" and "Mammalian Microbiome". The full record and cited reference of the retrieved documents were saved in plain text format to be loaded on to the software for further analysis.

2.2 Analytical tools and methods

Bibliometric analysis of the retrieved data was conducted using software including BibExcel [20], Pajek [21] [22], Sci2 (Science of Science) Tool [23] and Gephi [24].

The BibExcel analyses bibliographic information to structure a textual data to a comparable format. Bibliometric analysis is used to unveil the authors, journals, institutions, and the most influential countries on the subject. We obtained the document types, total citation, productive year, journal, keywords and influential countries on the research area.

2.3 Network Construction:

The Science of Science tool (Sci2) was used to conduct fundamental scientometric analysis on the retrieved data. The built-in algorithms of Sci2 tool were applied to produce network analysis-both text based and citation based methods. The data was prepared by normalizing and pruning to obtain the unambiguous illustration of the scientometric

data of our research area and the networks constructed was viewed using visualization tools.

The text based method used was Co-word Co-Occurrence analysis, which corresponded to the research area revealing the topic structure. The Bibliometric coupling and total citation analysis were done which also revealed the relatedness of the research works thus assessing the quality and productivity of the research area. Both the Co-word Co-Occurrence and the bibliometric coupling were visualized in Gephi software.

To trace the evolution of the research domain, Main Path Analysis (MPA) was conducted from the data of citation and co-citation records, which was processed in Sci2 software. Pajek was used to create the Main path analysis to trace out the core papers, milestone papers and emerging trend in the area of Microbiome.

3. Results and Discussion
3.1 Article distribution analysis

A total of 512 relevant records were retrieved using Boolean search from the Web of Science core collection. Of the 512 total records, 356 (69.5%) were classified as articles, 142 (27.7%) as reviews and the others as book chapters, editorial materials, proceedings or meeting abstracts (Fig 1). The analysis revealed a total of 18735 references appended to 512 publications on mammalian microbiome, and there were 9174 total citations for the publications. The status of a number of publications on Microbiome research per year (Fig.2), the top science research domains which implemented Microbiome studies in them (Fig3) and year wise number of citations on each research domains (Fig 4) are presented. Almost 488 (95.3%) of the 512 total research publication on microbiome were from the year 2014 which indicated the increasing attraction of the scientific community towards the microbiome researches (Fig. 2). This increasing trend of scientific research publications in various research domains also showed the wide acceptance and application of microbiome research in different domains of science (Fig.3). This showed the trend in the involvement of microbiome studies in various science research domains. The study showed an increase in the number of publications per year in the area of mammalian microbiome research (Fig 2). A similar pattern of increase was also seen in the number of citations per year in the major research domains, which pointed to widespread acceptance of Microbiome studies in different domains of Science (Supplementary file: 1). Microbiology turned out to

be the significant research stream out of all domains of science as this research domain had a maximum number of citations and contributed to most of the publications in the microbiome research. The top cited papers with the authors are shown in Table 1 [26] [27] [28] [29] [30] [31] [31] [33] [34] [35].

3.2 Country analysis

Research groups from 57 countries were involved in the publication of 512 articles on the microbiome research in mammals. Some of the research were done as collaboration involving different countries, the paper from such collaboration was taken as an individual count for each countries involved, totaling the number of records to 753 instead of 512. The USA, the UK, Canada, People's Republic of China and 10 other countries published more than 10 research papers each on Microbiome (Table 2). The leading country with the maximum number of records was the United States of America, which figured up to 41.7% (314/753) of the total; followed by the UK with 6.5%(49/753), Canada with 5.3%(40/753) and People's Republic of China with 5%(39/753). Besides, Wikoff WR, from Scripps Research Institute, published the highest number of cited papers with 1116 citations, followed by Chang PV, Yale University, with 545 citations, both from the USA. Of the research publications with more than 10 citations (n=261), 88 (33.7%) where from the USA. 26 other countries had 2-9 publications, and 16 other countries had 1 publication each (details not shown), indicating the widespread recognition of Mammalian microbiome research across the globe.

3.3 Journal analysis

Of the 512 articles on mammalian microbiome published in 273 journals, around 78(15.2%) were published in 5 prominent journals. The journals with the largest number of articles on mammalian microbiome research were published in PlosOne (n=20), Frontiers in Microbiology (n=18), Proceedings of the National Academy of Sciences of the United States of America (n=16), Scientific Reports (n=13), and mBio (n=11) journals. 18 out of 273 journals had publications above 2 to 10 articles (Table 3). All of the top journals covered the influential research areas, and the number of publication on mammalian microbiome research in these journals indicated the recognition of the research community in this area.
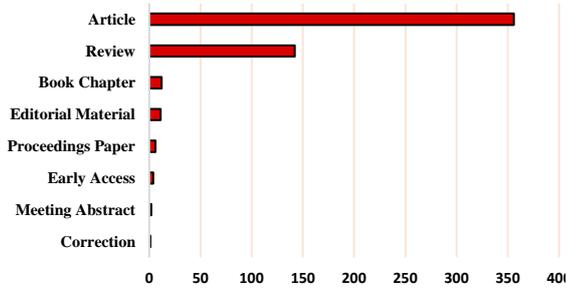
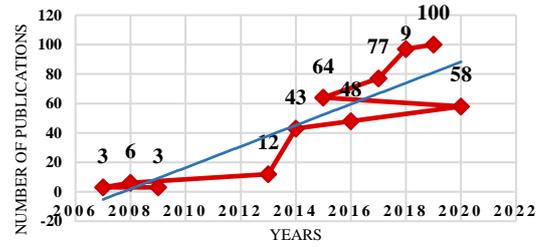**Fig. 1: Document types of publications on Microbiome from Web of Science**

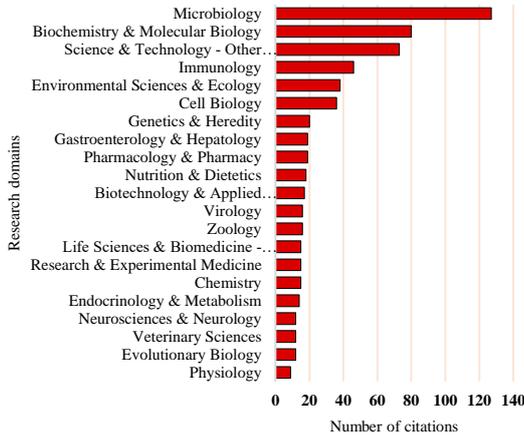**Fig. 2: Number of publications in each year**

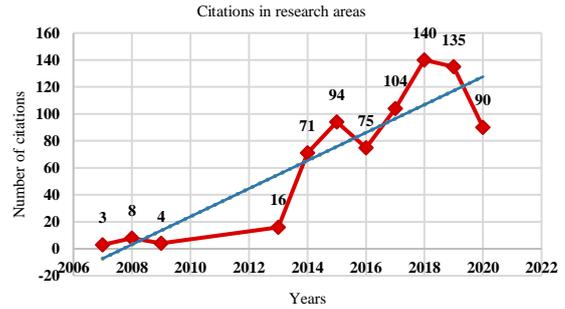**Fig. 3: Top research domains with more than 10 citations**

Fig. 4: Total publications per year in all research domains involving microbiome studies

Top 10 most cited publications on microbiome research

Author	Title	Year of publication	Number of Citation
Wikoff WR; Anfora AT; Liu J *et al.*	Metabolomics analysis reveals large effects of gut microflora on mammalian blood metabolites.	2009	1116
Chang PV; Hao LM; Offermanns S; Medzhitov R	The microbial metabolite butyrate regulates intestinal macrophage function via histone deacetylase inhibition.	2014	545
Gensollen T; Iyer SS; Kasper DL; Blumberg RS	How colonization by microbiota in early life shapes the immune system.	2016	409
Jones BV; Begley M; Hill C; Gahan CGM; Marchesi JR	Functional and comparative metagenomic analysis of bile salt hydrolase activity in the human gut microbiome.	2008	380
Martin FPJ; Dumas ME; Wang YL; Legido-Quigley C; Yap IKS *et al.*	A top-down systems biology view of microbiome-mammalian metabolic interactions in a mouse model.	2007	329
Rowland I; Gibson G; Heinken A; Scott K; Swann J; Thiele I; Tuohy K	Gut microbiota functions: metabolism of nutrients and other food components.	2018	263
Albenberg LG; Wu GD	Diet and the Intestinal Microbiome: Associations, Functions, and Implications for Health and Disease.	2014	251
Cahenzli J; Koller Y; Wyss M; Geuking MB; McCoy KD	Intestinal Microbial Diversity during Early-Life Colonization Shapes Long-Term IgE Levels.	2013	237
Knight R; Vrbanac A; Taylor BC *et al.*	Best practices for analysing microbiomes.	2018	210
Hacquard S; Garrido-Oter R; *et al.*	Microbiota and Host Nutrition across Plant and Animal Kingdoms.	2015	187

Table 2
Countries with most cited papers (record ≥ 10)

Country	Number of publication
USA	314
UK	49
Canada	40
Peoples R China	39
Germany	38
Australia	30
France	22
Italy	19
Switzerland	15
Ireland	15
Japan	13
Czech Republic	12
Spain	11
Israel	10
India*	4

*Exhibiting the number of publications from India with 4 publications. There are 14 other countries with publication between 10 and 4 which are not depicted here.

Table 3
Top 10 most productive journals having a sizeable number of publications on mammalian microbiome

No. of records	Journals
20	Plos One
18	Frontiers in Microbiology
16	Proceedings of the National Academy of Sciences of the United States of America
13	Scientific Reports
11	mBio
8	Microbiome
8	ISME journal
8	Nature Communications
8	Cell Host & Microbe
6	Frontiers in Immunology

3.4 Main path analysis

The main path analysis was done to reveal core papers of microbiome research domain which were considered to be the base papers for the evolution of the research area. Analysis of the main path resulted in a representative path in the citation network, which described the evolutionary path exhibiting the knowledge flow. An acyclic directed network is constructed using global main path search algorithm, removed loops and calculated traverse weight using Search Path Link Count (SPLC) and thus obtained the most significant citation chain, which trace the knowledge trajectory. Herein, revealed the core papers of the

mammalian microbiome research exhibiting the knowledge flow and also revealed the divergence-convergence in the research area [36]. The milestone papers which lead to the recent research domains and the papers on the emerging trend of the research were also shown in this network (Fig. 5). The main path analysis map showed two major network clusters, and the recent research on mammalian microbiome were evolved through these major clusters of research publications. The network node numbers 116 [26], 222 [37] of the big cluster and 99 [30] of the other cluster formed the three base papers which commenced the track of knowledge flow on mammalian microbiome researches. The large network cluster with two clusters of base papers of node number 116 and 222, is connected with four papers with node number 165 [38], node number 36 [39], node number 33 [40], and 27 [41]. The node number 192 [42] were the paper which seeded the main path of the large network cluster. The link from node number192 to node number 205 [43] carried highest traverse weight (0.70) suited this document to be the milestone paper with its rich descendants till date. From the second cluster, node numbers 168 [29] and 183 [44] had their link carrying traverse weight of 0.14 each, which were connected to node 53 [26] with traverse weight of 0.14 with successful descendants making it to be the significant paper from which the knowledge flow progressed.

3.5 Bibliographic coupling

The bibliographic coupling was performed to find the related papers based on shared references from the data set. The nodes are the papers and edges are the shared references. From this analysis, we obtained 496 nodes and 30244 edges. The data was pruned by selecting the edges which had at least one shared reference. 468 nodes and 13057 edges were selected to construct the network of bibliographic coupling. The details of the analysis with the most shared and most cited references are provided in the Supplementary file: 2. The modularity algorithm [45] was performed to find the clusters which were well connected with one another, and the top papers were found using global citation metrics by counting the number of times a paper was cited. The most cited papers were in modularity class 7(orange color), dealing with microbiome core researches, and the most cited paper was one of the milestone papers [26] which became a core reference paper for the recent research works.
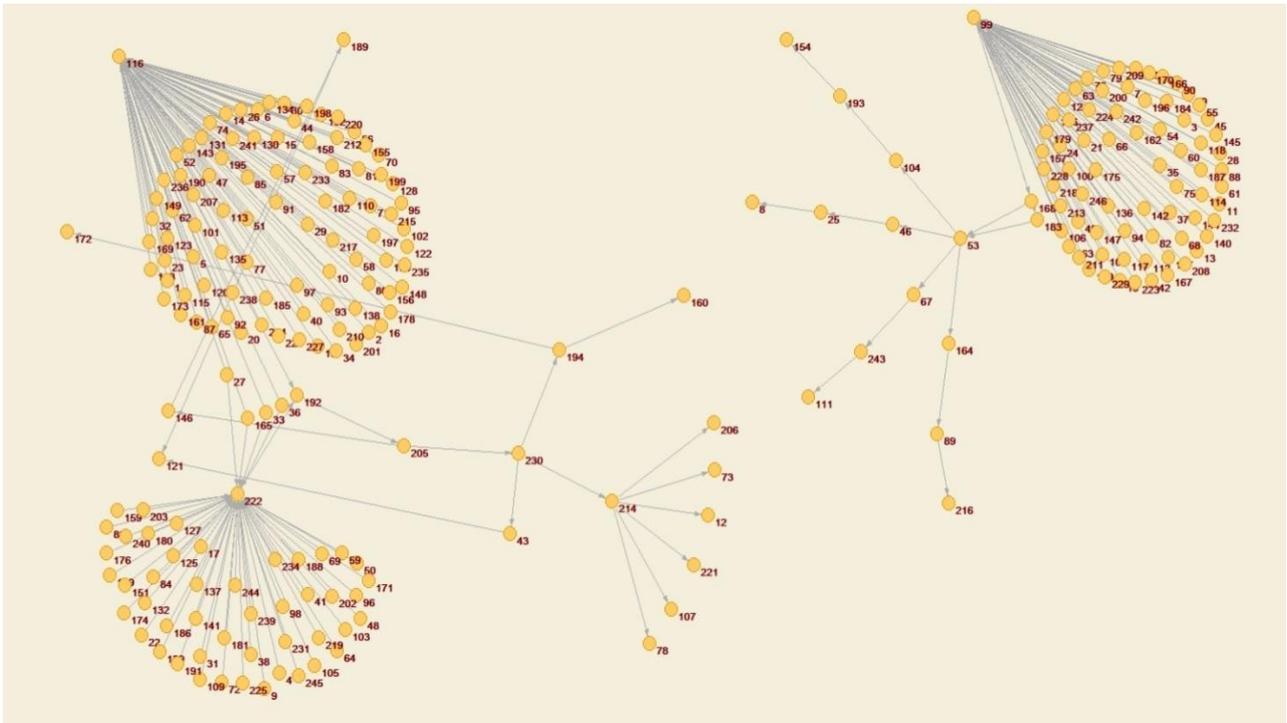
Fig 5: The main path network with the core papers in the microbiome

*Key papers – with node numbers 116 (Delsuc F, 2014), 222 (Eilam O, 2014), 99 (Martin, 2007), 192 (Sanders Jg, 2015), 205 (Groussin M, 2017), 230 (Nishida Ah, 2018), 168 (Jones Bv, 2008), 183 (Yap Iks, 2008) and 53 (Wikoff W, 2009).
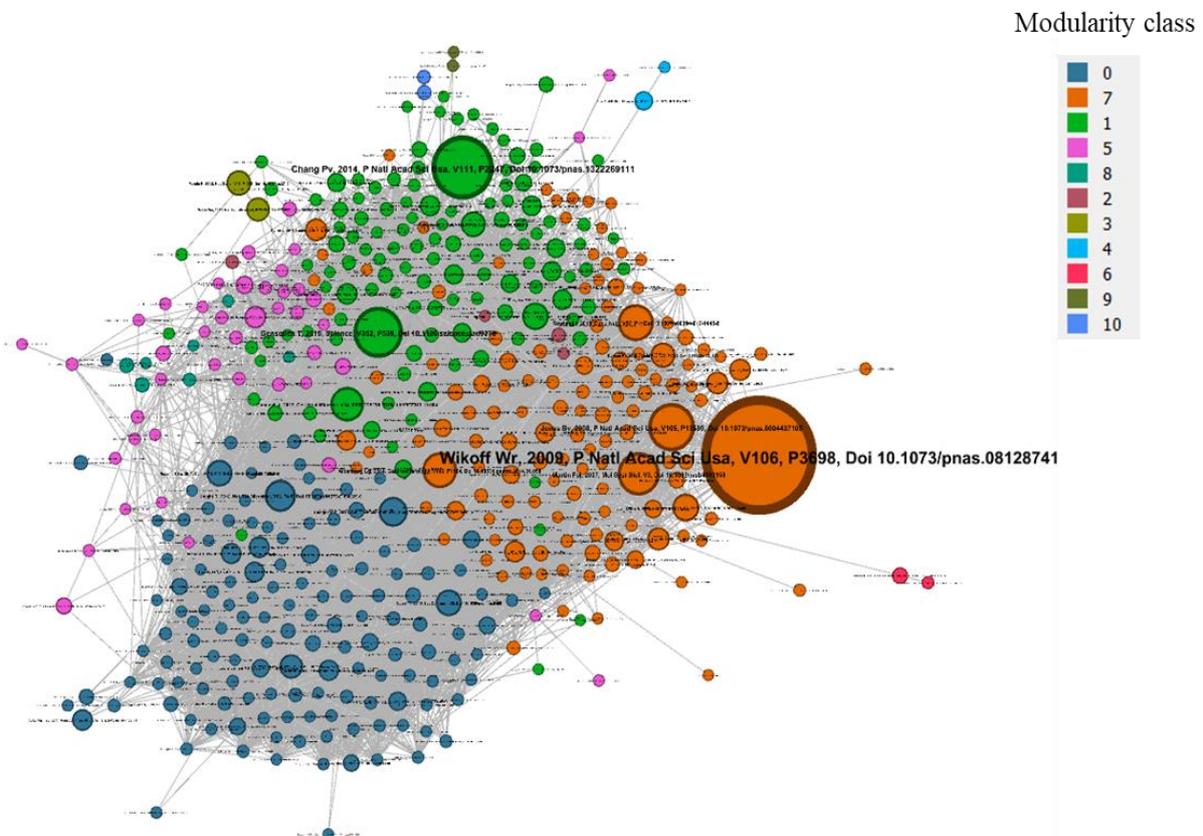

Fig 7: Bibliographic coupling analysis on microbiome publications. The size of the node is according to the global citation, and the size of the node shows the global citation count, node color indicates the modularity class

3.6 Co-author analysis

The co-author analysis was performed to assess the research trend and to identify prominent scientists and their areas of work. This identified the scientific collaborations, which indicated the flourishing of research in and out of the domain, pointing out the focus of the scientist fraternity [46]. A co-authorship analysis gave 2779 authors of the publication (nodes) and 13738 co-authored
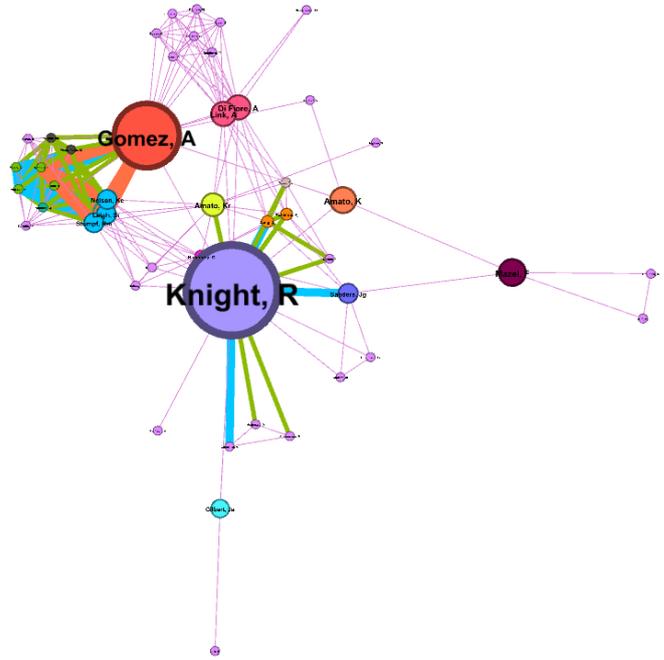
Table 2 Top 20 authors from the co-author network

Label	Number of authored works	Times cited	Betweenness centrality
Knight, R	14	1011	0.40
Gomez, A	8	154	0.27
Mazel, F	4	104	0.09
Amato, K	3	31	0.08
Di Fiore, A	3	114	0.07
Link, A	3	114	0.07
Amato, Kr	5	162	0.07
Sanders, Jg	6	464	0.05
Nelson, Ke	7	180	0.05
Leigh, Sr	6	169	0.05
Stumpf, Rm	6	169	0.05
Gilbert, Ja	3	82	0.04
Humphrey, G	3	94	0.02
Song, Sj	4	249	0.01
Mckenzie, Vj	3	118	0.01
Metcalf, Jl	3	244	0.002
White, Ba	5	127	0.0004
Modry, D	4	80	0.0004
Vlckova, K	4	80	0.0004
Todd, A	3	75	0.0004

or shared authorship (edges). The whole network had 18 clusters from the total co-authorship analysis. The largest connected node cluster was selected to create the network. This cluster had 735 nodes and 5254 edges. The statistical analysis of the co-author network was performed using 'betweenness centrality' metrics which provided us with the dominant node in a given network and its interaction with other nodes of network. The top 20 authors having maximum shared publications are shown in table 2. In the current network, the 'central' node with the highest level of betweenness centrality was 'Knight, R' (0.40) having the highest number of co-authorships in microbiome domain (Fig 5). This was followed by 'Gomez, A' (0.27), Mazel, F (0.09), Amato, K (0.08) and Di Fiore, A (0.07).

Fig 5: Co-author network on microbiome research. Each node represents an author and is connected when each of them shares the authorship of a paper. The size of the node shows the degree of 'betweenness centrality' and the thickness of the edges indicates the number of co-authored works

From the study, the author 'Knight, R' with maximum centrality metrics, 14 research papers on the microbiome, and 1011 citations were found to be the most influential author in the mammalian microbiome research. This author had the maximum collaborative works indicating the boom in microbiome research domain productivity. Following him was the author 'Gomez, A', who had 8 research papers and 154 citations, turning out to be an influential author with the research domain of microbiome of non-human primates. Recently published research article co-authored by 'Knight, R' in 2020 [47], highlights the recent research trend in microbiome as phylosymbiosis and its convergence in organisms according to physiological mechanisms, pointing out the trend of research domain. By following this trend, researchers can pay attention to the areas to be focused and find out the gaps in their researches.

3.7 Co-Word Co-Occurrence analysis

A total of 1638 keywords were mined from the data. The co-word serves as the indicator of the relatedness of the research. From the analysis, 1638 keywords (nodes) and 18094 co-occurrences (edges) were unveiled. The data were pruned to reject the weak clusters and select the strongest cluster which had 178 nodes and 488 edges in them. A statistical test was performed to find out the bond between keywords and the frequently used words.

Table3 The most used 25 keyword in the analyzed data

Label	Occurrences	Betweenness centrality
Gut	163	0.44
Microbiome	163	0.37
Microbiota	83	0.11
Metabolism	43	0.07
Host	66	0.05
Intestine	46	0.04
Mammalian	61	0.04
Disease	34	0.04
Human	46	0.03
Function	29	0.03
Immunology	30	0.02
Microbiology	47	0.02
Acid	14	0.02
Interaction	28	0.02
Effect	22	0.01
Diverse	19	0.01
Model	23	0.01
Small	12	0.01
Bile	8	0.01
Specific	10	0.01

Of the centrality metrics, 'betweenness centrality' metrics were applied which provided us with the prominent keyword which acted as the intermediator and mediator in the entire network. The keyword with the highest level of betweenness centrality was 'Gut' (0.44), followed by 'Microbiome' (0.37), 'Microbiota' (0.11), 'Host' (0.05) and 'Intestine' (0.04) Table 3. And these were the most influential keywords of the whole network.

This finding shows that many quantitative studies were carried out on the top keywords with a high frequency of co-occurrence like 'gut', 'microbiome', 'microbiota', 'metabolism', 'Intestine', and 'mammalian'. The reason for the high frequency occurrence of the word 'Gut' and 'microbiome' is possibly the focus of microbiome study on the gut microbiota as a non-invasive approach. We could also find the occurrence of 'metabolism', 'host', and 'intestine' in lower frequency in the top word list, indicating the comparatively lower number of studies in these areas, which are the emerging areas that could be focused on in future. Also, the word 'Mammalian' which was found to be in lower frequency and on
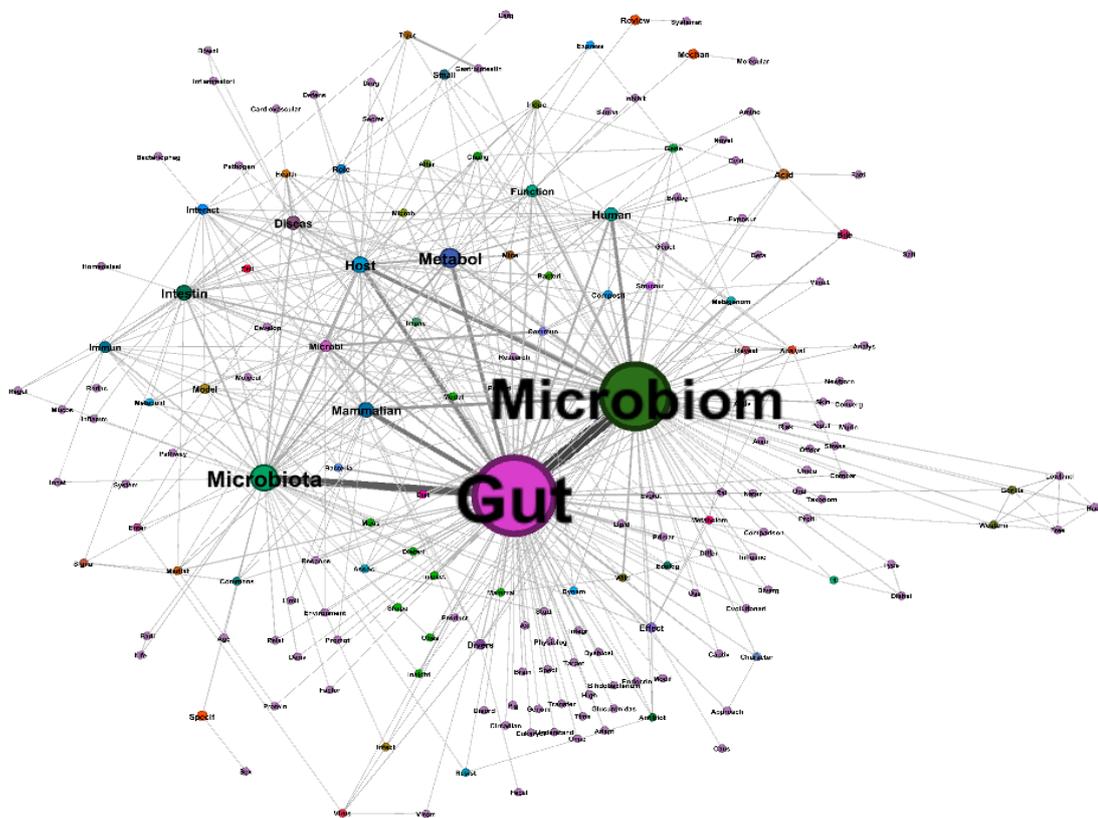

Fig 6: The network of Co-word Co-Occurrence showing the most frequently used words in microbiome literature. The size of the node shows the degree of 'betweeness centrality', and the thickness of the edges indicates the frequency of the word used

which not much significant research has been conducted, could be focused on as a major domain of research. The words like 'age', 'endocrine', 'drug', 'virome', 'skin', and 'environment' were not in the top word list as they were found to be in the lower centrality range, which could possibly be due to the lower research done so far. They can also be considered the emerging area of the research domain.

4. Discussion

In this study, we identified and analyzed 512 original articles related to microbiome research published from 2007 to 2020. The scientometric analysis intended an inclusive summary of the research trend and development in the mammalian microbiome research, which revealed a steady increase in the microbiome related scientific productions since 2014. Almost 95.3% of the total publications on the mammalian microbiome research were published during this period.

The USA, the UK and five other countries contributed more than 20 publications each, while 49 other countries published 1-20 mammalian microbiome studies each from 2007 to 2020 (Table 2). This widespread pattern of publication on microbiome across different countries showed the recognition and strong potentials of microbiome research, which could be explored for the wellbeing of the community and its ecosystem. Likewise, the major papers cited were funded by eminent bodies like National Institute of Health (NIH), USA, and other premier funding agencies of the top productive countries (Supplementary file: 3), marking the significance of the microbiome research as a burgeoning area of research.

As increasing citations represents the accreditation of a paper [48], the current study analyzed the total citation count, which provided us with 9174 citations for total 512 publications considered. Out of the 512 publications, 261(34.9%) publications had more than 10 citations and all had works related to the mammalian microbiome research progress.

From the main path analysis, the evolutionary path of mammalian microbiome research was meticulously displayed and the trajectory of the knowledge flow with SPLC count was identified. In the light of the fact that a document is considered a significant paper when such a document has successful and varied descendants; the work published by Groussin M *et al.,* 2017 (node number 205) [43] was found to be a significant paper from the larger network cluster as shown as in Fig.5. As the source paper to node

number 205 the resource trajectory on mammalian microbiome was from the studies which depicted the microbiome community convergence of its composition and diversity on the influence of diet, body mass and phylogeny of the host. The significant discoveries from the studies by Sanders J G ,2015 - node number 192 had been cited by Groussin M,2017 -node number 205, pointing out the possibility of considering the host and associated microbiome as holobiont, hinting at the co-speciation of the microbial taxa providing a phylogenetic signal in the divergence of microbiome in a host. This was further extensively taken up and studied by Nishida, A.H in 2018 [49] in their work, with an expanded sampling of the mammalian host. The study in a wide range of mammals showed the diversification of the microbiome with respect to host physiology and ecological factors across evolutionary time period. This knowledge flow was taken up by Amato K R, 2019 [50], which had the link traverse weight with 0.42, and had 6 studies which indicated the emerging trend in the mammalian microbiome research ([51] [47] [52] [53] [54] [55]). The other influential link from node number 230 with traverse weight 0.14, to node number 194 [56], had further studies taken up by node number 160 [57], node number 121[58] and node number 172 [59]. The second cluster of the main path analysis map dealt with the microbial-mammalian co-metabolism, mainly focusing on the complex biochemical interaction between host and microbiome symbionts, node number 99 [30], as the source paper of the cluster. This path showed the trajectory of the research knowledge focusing on the influence of microbiome on hosts' general lipid metabolism and energy balance, impacting ultimately the host health. The bile acid metabolism was intensively emphasized. Further, study was extensively taken up by node number 168 [29] and node number 183 [44], showing a traversal weight of 0.14, addressing the influence of modification of bile acid and metabolites respectively on the host health and diseases. Node number 53 [26], was the significant paper in this cluster with surplus descendants. The study comprehensively dealt with the profiling of intricate chemistry between mammalian and microbial metabolic processes using metabolomics as a powerful tool.

The bibliographic coupling networks were constructed based on the shared references among the selected articles on mammalian microbiome research. This network provided the most vital

research paper representing the current research. The bibliographic coupling was considered to be the maximum degree when an article shared the knowledge of the research area with the maximum number of other articles. The reference at node number 53 [26], dealt with the recent research trend and the paper was significant in the main path analysis that had the maximum coupling strength along with maximum citations. All these analyses showed that the metabolomics was the hot research area in the mammalian microbiome studies.

The research area was broadened when there was admittance to different specializations of research through interaction and collaboration of scientists and an exchange of their research contexts. The Co-author analysis was performed to find the most productive and influential authors whose works were shared the most, in order to find the influential structure of scientific collaborations. Knight R, had the maximum potential partners for the mammalian microbiome researches with the maximum of 48 co-authored papers. The works on the mammalian microbiome from this influential author had the most collaborative works indicating the influence of this author in the field of mammalian microbiome. The highest centrality measure also supported the significance of Knight R.

The co-word co-occurrence provided us with the textual interpretation of the recent research trends in the mammalian microbiome research [60] [61]. This analysis estimated the relationship between the most occurred in the papers. From the analysis of the mammalian microbiome studies, it was deduced that 'Gut' and 'Microbiome' were the most co-occurred words. This showed the emphasis of the research trend, and significant areas focused on. The mammalian microbiome had so far focused on the gut microbiome researches. The word 'metabolism', 'microbiota', and 'host' were the smaller node of co-occurred words, indicating the emerging and recent trend in research. This was supported by the significant research trend in main path analysis.

Our study comprised extensive review on the mammalian microbiome research from 2007 till date using a scientometric approach. This summarized the status and progress of the research on the mammalian microbiome. Since the data for the study was retrieved from the Web of Science core collection, this study could be taken as providing vital information on the mammalian microbiome evolutions. Furthermore, the evolutionary path of the research area was depicted which provided the real emergence and trend of the topic. The limitation of our study was that the data was retrieved from only Web of Science Core Collection database. We might have missed out on the papers from other database. It is noteworthy; however, that we used the database which most of the scientific community reliably depended on for the data retrieval, for most bibliometric analyses.

5. Conclusion

The present study analyzed 512 articles on mammalian microbiome studies by Scientometric approach. The results from this study provided us with information on the research trends, productivity over the years, influential countries, authors and their works, most cited works, and top used words and evolutionary path of the mammalian microbiome research. This study enabled us to envision those areas of research where collaborations and funding were concerted. The results also helped to trace out the trending research and point out gaps to indicate areas which called for a greater focus if there had to be an expansion in the research area.

Conflict of Interest: All authors declare that they do not have conflicts of interest.

References

[1]. Martin Dworkin, David Gutnick, (2012). Sergei Winogradsky: a founder of modern microbiology and the first microbial ecologist, FEMS Microbiology Reviews, Volume 36, Issue 2, March, Pages 364–379. https://doi.org/10.1111/j.1574-6976.2011.00299.x.

[2]. Prescott, S. L. (2017). History of medicine: Origin of the term microbiome and why it matters. Human Microbiome Journal, 4, 24–25. https://doi.org/10.1016/j.humic.2017.05.004.

[3]. Eisen JA. (2015). what does the term microbiome mean? And where did it come from? A bit of a surprise. Microbiol Built Environ Netw, Available at http://www.microbe.net/2015/04/08/what-does-the-term-microbiome-mean-andwhere-did-it-come-from-a-bit-of-a-surprise/.

[4]. Dubos, R., Schaedler, R. W., Costello, R., & Hoet, P. (1965). Indigenous, Normal, and Autochthonous Flora of the Gastrointestinal. The Journal of Experimental Medicine, 122, 67–76. https://doi.org/10.1084/jem.122.1.67.

[5]. Savage, D. C. (1977). Microbial ecology of the gastrointestinal tract. Annual Review of Microbiology, 31(70), 107–133. https://doi.org/10.1146/annurev.mi.31.100177.000543.

[6]. Brune, A., & Friedrich, M. (2000). Microecology of the termite gut: Structure and function on a microscale. Current Opinion in Microbiology, 3(3), 263–269. https://doi.org/10.1016/S1369-5274(00)00087-4.

[7]. Bäckhed, F., Ley, R. E., Sonnenburg, J. L., Peterson, D. A., & Gordon, J. I. (2005). Host-bacterial mutualism in the human intestine. Science, 307(5717), 1915–1920. https://doi.org/10.1126/science.1104816.

[8]. Orlich, M. J., Siapco, G., & Jung, S. (2017). Vegetarian Diets and the Microbiome. Vegetarian and Plant-Based Diets in Health and Disease Prevention, 429–461. Doi:10.1016/b978-0-12-803968-7.00024-1.

[9]. Taneja, V. (2017). Microbiome: Impact of Gender on Function & Characteristics of Gut Microbiome. Principles of Gender-Specific Medicine: Gender in the Genomic Era: Third Edition, 569–583. https://doi.org/10.1016/B978-0-12-803506-1.00027-9.

[10]. Bucci, M. (2020). Modulating the microbiota. Nature Chemical Biology, 16(9), 933. https://doi.org/10.1038/s41589-020-0635-5.

[11]. Shamszadeh, S., Asgary, S., & Nosrat, A. (2019). Regenerative Endodontics: A Scientometric and Bibliometric Analysis. Journal of Endodontics, 45(3), 272–280. Doi:10.1016/j.joen.2018.11.010.

[12]. Zhong, B., Wu, H., Li, H., Sepasgozar, S., Luo, H., & He, L. (2019). A scientometric analysis and critical review of construction related ontology research. Automation in Construction, 101, 17–31. Doi:10.1016/j.autcon.2018.12.013.

[13]. Zyoud, Sa'ed H., Waring, W. S., Al-Jabi, S. W., & Sweileh, W. M. (2017). Global cocaine intoxication research trends during 1975-2015: A bibliometric analysis of Web of Science publications. Substance Abuse: Treatment, Prevention, and Policy, 12(1), 1–15. https://doi.org/10.1186/s13011-017-0090-9.

[14]. Aazami, H., DehghanBanadaki, H., Ejtahed, H. S., Fahimfar, N., Razi, F., Soroush, A. R., Hasani-Ranjbar, S., Pasalar, P., Ahmadi Badi, S., Siadat, S. D., & Larijani, B. (2020). The landscape of microbiota research in Iran; a bibliometric and network analysis. Journal of Diabetes and Metabolic Disorders, 19(1), 163–177. https://doi.org/10.1007/s40200-020-00488-2.

[15]. Zyoud, Sa'Ed H., Smale, S., Waring, W. S., Sweileh, W. M., & Al-Jabi, S. W. (2019). Global research trends in microbiome-gut-brain axis during 2009-2018: A bibliometric and visualized study. BMC Gastroenterology, 19(1), 1–11. https://doi.org/10.1186/s12876-019-1076-z.

[16]. Albuquerque, P. C., Castro, M. J. C., Santos-Gandelman, J., Oliveira, A. C., Peralta, J. M., & Rodrigues, M. L. (2017). Bibliometric Indicators of the Zika Outbreak. PLoS Neglected Tropical Diseases, 11(1), 1–6. https://doi.org/10.1371/journal.pntd.0005132.

[17]. Zongyi Y, Dongying C, Baifeng L. (2016). Global regulatory T-cell research from 2000 to 2015: a bibliometric analysis. PLoS One.; 11(9):e0162099.

[18]. Gilbert JA, Quinn RA, Debelius J, Xu ZZ, Morton J, Garg N, Jansson JK, Dorrestein PC, Knight R. (2016). Microbiome-wide association studies link dynamic microbial consortia to disease. Nature, 535(7610), 94–103. https://doi.org/10.1038/nature18850.

[19]. Nath, K., & Thaiss, C. A. (2019). Digitalizing the Microbiome for Human Health. MSystems, 4(3), 1–4. https://doi.org/10.1128/msystems.00129-19.

[20]. Persson, O., R. Danell, J. Wiborg Schneider. (2009). How to use Bibexcel for various types of bibliometric analysis. In Celebrating scholarly communication studies: A Festschrift for Olle Persson at his 60th Birthday, ed. F. Åström, R. Danell, B. Larsen, J. Schneider, Leuven, Belgium: International Society for Scientometrics and Informetrics. p 9–24.

[21]. Batagelj, V., & Mrvar, A. (1998). Pajek-program for large network analysis. Connections, 21(2), 47–57.

[22]. De Nooy, W., Mrvar, A., & Batagelj, V. (2018). Exploratory social network analysis with Pajek (3rd Ed.). Cambridge: Cambridge University Press.

[23]. Sci2 Team: Science of Science (Sci2) Tool, http:// sci.slis.indiana.edu (2009) Indiana University and SciTech Strategies.

[24]. Bastian, M., Heymann, S., & Jacomy, M. (2009). Gephi: An open source software for

exploring and manipulating networks. BT - International AAAI Conference on Weblogs and Social. International AAAI Conference on Weblogs and Social Media, 361–362.

[25]. Liu, J. S., Lu, L. Y. Y., & Ho, M. H. C. (2019). A few notes on main path analysis. Scientometrics, 119(1), 379–391. https://doi.org/10.1007/s11192-019-03034-x.

[26]. William R. Wikoff, Andrew T. Anfora, Jun Liu, Peter G. Schultz, Scott A. Lesley, Eric C. Peters, Gary Siuzdak. (2009). Metabolomics analysis reveals large effects of gut microflora on mammalian blood metabolites. Proceedings of the National Academy of Sciences, 106 (10) 3698-3703; Doi: 10.1073/pnas.0812874106.

[27]. Chang, P. V., Hao, L., Offermanns, S., & Medzhitov, R. (2014). The microbial metabolite butyrate regulates intestinal macrophage function via histone deacetylase inhibition. Proceedings of the National Academy of Sciences of the United States of America, 111(6), 2247–2252. https://doi.org/10.1073/pnas.1322269111

[28]. Gensollen, T., Iyer, S. S., Kasper, D. L., & Blumberg, R. S. (2016). How colonization by microbiota in early life shapes the immune system. Science (New York, N.Y.), 352(6285), 539–544. https://doi.org/10.1126/science.aad9378

[29]. Brian V. Jones, Máire Begley, Colin Hill, Cormac G. M. Gahan, Julian R. Marchesi. (2008). Functional and comparative metagenomic analysis of bile salt hydrolase activity in the human gut microbiome. Proceedings of the National Academy of Sciences Sep, 105 (36) 13580-13585; Doi: 10.1073/pnas.0804437105.

[30]. Martin, F. P., Dumas, M. E., Wang, Y., Legido-Quigley, C., Yap, I. K., Tang, H., Zirah, S., Murphy, G. M., Cloarec, O., Lindon, J. C., Sprenger, N., Fay, L. B., Kochhar, S., van Bladeren, P., Holmes, E., & Nicholson, J. K. (2007). A top-down systems biology view of microbiome-mammalian metabolic interactions in a mouse model. Molecular systems biology, 3, 112. https://doi.org/10.1038/msb4100153

[31]. Rowland, I., Gibson, G., Heinken, A., Scott, K., Swann, J., Thiele, I., & Tuohy, K. (2018). Gut microbiota functions: metabolism of nutrients and other food components. European journal of nutrition, 57(1), 1–24. https://doi.org/10.1007/s00394-017-1445-8

[32]. Albenberg, L. G., & Wu, G. D. (2014). Diet and the intestinal microbiome: associations, functions, and implications for health and disease. Gastroenterology, 146(6), 1564–1572. https://doi.org/10.1053/j.gastro.2014.01.058

[33]. Julia Cahenzli, Yasmin Köller, Madeleine Wyss, Markus B. Geuking, Kathy D. McCoy, (2013).Intestinal Microbial Diversity during Early-Life Colonization Shapes Long-Term IgE Levels. Cell Host & Microbe. 14(5), 559-570. https://doi.org/10.1016/j.chom.2013.10.004

[34]. Knight, R., Vrbanac, A., Taylor, B. C., Aksenov, A., Callewaert, C., Debelius, J., Gonzalez, A., Kosciolek, T., McCall, L. I., McDonald, D., Melnik, A. V., Morton, J. T., Navas, J., Quinn, R. A., Sanders, J. G., Swafford, A. D., Thompson, L. R., Tripathi, A., Xu, Z. Z., Zaneveld, J. R., … Dorrestein, P. C. (2018). Best practices for analysing microbiomes. Nature reviews. Microbiology, 16(7), 410–422. https://doi.org/10.1038/s41579-018-0029-9

[35]. Stéphane Hacquard, Ruben Garrido-Oter, Antonio González, Stijn Spaepen, Gail Ackermann, Sarah Lebeis, Alice C. McHardy, Jeffrey L. Dangl, Rob Knight, Ruth Ley, Paul Schulze-Lefert. (2015). Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host & Microbe, 17(5), 603-616, https://doi.org/10.1016/j.chom.2015.04.009.

[36]. Delsuc, F., Metcalf, J. L., Wegener Parfrey, L., Song, S. J., González, A., & Knight, R. (2014). Convergence of gut microbiomes in myrmecophagous mammals. Molecular Ecology, 23(6), 1301–1317. https://doi.org/10.1111/mec.12501.

[37]. Eilam O, Zarecki R, Oberhardt M, Ursell LK, Kupiec M, Knight R, Gophna U, Ruppin E. (2014). Glycan degradation (GlyDeR) analysis predicts mammalian gut microbiota abundance and host diet-specific adaptations. Mbio. Doi: 10.1128/mBio.01526-14.

[38]. Yatsunenko T, Rey FE, Manary MJ, Trehan I, Dominguez-Bello MG, Contreras M, et al. (2012). Human gut microbiome viewed across age and geography. Nature. 486:222–7. Doi: 10.1038/nature11053.

[39]. Muegge, B. D., Kuczynski, J., Knights, D., Clemente, J. C., González, A., Fontana, L., Henrissat, B., Knight, R., & Gordon, J. I. (2011). Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. Science, 332(6032), 970–974. https://doi.org/10.1126/science.1198719.

[40]. Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., Fierer, N., & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the National Academy of Sciences of the United States of America, 108(SUPPL. 1), 4516–4522. https://doi.org/10.1073/pnas.1000080107.

[41]. Ley, R. E., Hamady, M., Lozupone, C., Turnbaugh, P. J., Ramey, R. R., Bircher, J. S., Schlegel, M. L., Tucker, T. A., Schrenzel, M. D., Knight, R., & Gordon, J. I. (2008). Evolution of mammals and their gut microbes. Science (New York, N.Y.), 320(5883), 1647–1651. https://doi.org/10.1126/science.1155725.

[42]. Sanders, J. G., Beichman, A. C., Roman, J., Scott, J. J., Emerson, D., McCarthy, J. J., & Girguis, P. R. (2015). Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. Nature Communications, 6, 1–8. https://doi.org/10.1038/ncomms9285.

[43]. Groussin, M., Mazel, F., Sanders, J. G., Smillie, C. S., Lavergne, S., Thuiller, W., & Alm, E. J. (2017). Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. Nature Communications, 8. https://doi.org/10.1038/ncomms14319.

[44]. Yap, I. K. S., Li, J. V, Saric, J., Martin, F., Davies, H., Wang, Y., Wilson, I. D., Nicholson, J. K., Utzinger, J., Marchesi, J. R., & Holmes, E. (n.d.). (2008). Metabonomic and Microbiological Analysis of the Dynamic Effect of Vancomycin-Induced Gut Microbiota Modification in the Mouse J Proteome Res. 2008; 7(9):3718-3728. Doi: 10.1021/pr700864x.

[45]. Blondel, V. D., Guillaume, J. L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. Journal of Statistical Mechanics: Theory and Experiment, 2008(10), 1–12. https://doi.org/10.1088/1742-5468/2008/10/P10008.

[46]. E Fonseca, B. de P. F., Sampaio, R. B., Fonseca, M. V. de A., & Zicker, F. (2016). Co-authorship network analysis in health research: Method and potential use. Health Research Policy and Systems, 14(1), 1–10. https://doi.org/10.1186/s12961-016-0104-5.

[47]. Song, S. J., Sanders, J. G., Delsuc, F., Metcalf, J., Amato, K., Taylor, M. W., Mazel, F., Lutz, H. L., Winker, K., Graves, G. R., Humphrey, G., Gilbert, J. A., Hackett, S. J., White, K. P., Skeen, H. R., Kurtis, S. M., Withrow, J., Braile, T., Miller, M., … Knight, R. (2020). Comparative analyses of vertebrate gut microbiomes reveal convergence between birds and bats. MBio, 11(1), 1–14. https://doi.org/10.1128/mBio.02901-19.

[48]. Shih, M., Feng, J., & Tsai, C.-C. (2008). Research and trends in the field of e-learning from 2001 to 2005: A content analysis of cognitive studies in selected journals. Computers & Education, 51(2), 955–967. https://doi.org/10.1016/j.compedu.2007.10.004.

[49]. Nishida, A. H., & Ochman, H. (2018). Rates of gut microbiome divergence in mammals. Molecular ecology, 27(8), 1884–1897. https://doi.org/10.1111/mec.14473.

[50]. Amato, K. R., Sanders, J. G., Song, S. J., Nute, M., Metcalf, J. L., Thompson, L. R., Morton, J. T., Amir, A., McKenzie, V. J., Humphrey, G., Gogul, G., Gaffney, J., Baden, A. L., Britton, G. A. O., Cuozzo, F. P., Di Fiore, A., Dominy, N. J., Goldberg, T. L., Gomez, A., … Leigh, S. R. (2019). Evolutionary trends in host physiology outweigh dietary niche instructuring primate gut microbiomes. ISME JOURNAL, 13(3), 576–587. https://doi.org/10.1038/s41396-018-0175-0.

[51]. Garber, P. A., Mallott, E. K., Porter, L. M., & Gomez, A. (2019). The gut microbiome and metabolome of saddleback tamarins (Leontocebus weddelli): Insights into the foraging ecology of a small-bodied primate. American Journal of Primatology, 81(10–11), 1–13. https://doi.org/10.1002/ajp.23003.

[52]. Kartzinel, T. R., Hsing, J. C., Musili, P. M., Brown, B. R. P., & Pringle, R. M. (2019). Covariation of diet and gut microbiome in African megafauna. Proceedings of the National Academy of Sciences of the United States of America, 116(47), 23588–23593. https://doi.org/10.1073/pnas.1905666116.

[53]. Holly L. Lutz, Elliot W. Jackson, Paul W. Webala, Waswa S. Babyesiza, Julian C. Kerbis Peterhans, Terrence C. Demos, Bruce D. Patterson, Jack A. Gilbert. (2019). Ecology and Host Identity Outweigh Evolutionary History in Shaping the Bat Microbiome. mSystems Nov, 4 (6) e00511-19; Doi: 10.1128/mSystems.00511-19.

[54]. Mann, A. E., Mazel, F., Lemay, M. A., Morien, E., Billy, V., Kowalewski, M., Di Fiore, A., Link, A., Goldberg, T. L., Tecot, S., Baden, A. L., Gomez, A., Sauther, M. L., Cuozzo, F. P., Rice, G. A. O., Dominy, N. J., Stumpf, R., Lewis, R. J., Swedell, L., … Wegener Parfrey, L. (2020). Biodiversity of protists and nematodes in the wild nonhuman primate gut. ISME Journal, 14(2), 609–622. https://doi.org/10.1038/s41396-019-0551-4.

[55]. Amato, K. R., Kuthyar, S., Ekanayake-Weber, M., Salmi, R., Snyder-Mackler, N., Wijayathunga, L., Vandercone, R., & Lu, A. (2020). Gut microbiome, diet, and conservation of endangered langurs in Sri Lanka. Biotropica, January, 1–10. https://doi.org/10.1111/btp.12805.

[56]. Knowles, S. C. L., Eccles, R. M., & Baltrūnaitė, L. (2019). Species identity dominates over environment in shaping the microbiota of small mammals. Ecology Letters, 22(5), 826–837. https://doi.org/10.1111/ele.13240.

[57]. Groussin, M., Mazel, F., & Alm, E. J. (2020). Co-evolution and Co-speciation of Host-Gut Bacteria Systems. Cell Host and Microbe, 28(1), 12–22. https://doi.org/10.1016/j.chom.2020.06.013.

[58]. Jha AR, Shmalberg J, Tanprasertsuk J, Perry L, Massey D, Honaker RW (2020) Characterization of gut microbiomes of household pets in the United States using a direct-to-consumer approach. PLoS ONE 15(2): e0227289. https://doi.org/10.1371/journal.pone.0227289.

[59]. Kirsten Grond, Kayce C Bell, John R Demboski, Malia Santos, Jack M Sullivan, Sarah M Hird.(2020). No evidence for phylosymbiosis in western chipmunk species, FEMS Microbiology Ecology, Volume 96, Issue 1, fiz182. https://doi.org/10.1093/femsec/fiz182.

[60]. Lu, K., Yu, S., Yu, M., Sun, D., Huang, Z., Xing, H., Bi, J., Li, Z., Li, Z., Liu, X., Kong, C., & Zhu, Y. (2018). Bibliometric analysis of tumor immunotherapy studies. Medical Science Monitor, 24, 3405–3414. https://doi.org/10.12659/MSM.910724.

[61]. Van Rijsbergen, C. J. (1977). A theoretical basis for the use of co-occurrence data in information retrieval. Journal of Documentation, 33(2), 106–119. https://doi.org/10.1108/eb026637.