Fifty Years of Research on Camelids and the Contribution of Genetics and Genomics: A Scientometrics Evaluation

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Summary

The population and importance of camels in human life have improved in recent years. As genetics and genomics are becoming a more comprehensive section of life sciences, studying genetic/genomic aspects of the camelid nutrition, milk production, reproduction, immunity, disease and racing ability has become common in recent years. This study was conducted based on text mining and scientometrics techniques. To employ relevant information from Web of Science (WoS), a search strategy was developed to retrieve the "genetics or genomics" and words/phrases related to "camelids". The statistical population of this study included 3830 publications over a period of 50 years (1971–2020). A total of 3830 publications were retrieved that included 3269 research articles (85.35% of the publications) and 224 review articles (5.85% of the publications). The most frequent subject groups were "Veterinary Sciences" including 862 publications. In total, articles on camelid genomics were published in 1345 journals. Moreover, 127 countries contributed to these 3830 publications, with the USA being the leading country both in number of publications and international collaboration. During the 1971–2010 time period, the phrases "MERS-CoV" and "coronavirus" did not exist in the literature at all, while in the last decade, with 140 and 63 times (5.36% and 2.41%, respectively), they were the most frequent keywords. In general, the most important topics studied from the perspective of camelid genomics have been population genetics and pathogens and their diagnosis, as well as camelid immunity. Future studies should pay special attention to the specificity of camelid genomics for hosting the coronavirus. Furthermore, the special structure of humoral immunity in camels makes this section attractive in immunogenetics research.

Key words

dromedary camels, bactrian camels, llama, alpaca, camelidae; genome

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Received: February 23, 2022 | Accepted: April 28, 2022

Introduction

Ancestors of camelids appeared almost 20 million years ago and phylogenetically Old World and New World camelids were derived from their ancestors about 15 million years ago (Heintzman et al., 2015; Burger, 2016; Wu et al., 2014). Domestic Old World camelids include one-humped or dromedary camels (*Camelus dromedarius*), and two-humped including Bactrian (*Camelus bactrianus*), and wild Bactrian camels (*Camelus ferus*). Besides them, New World camelids are llamas (*Lama glama*), alpacas (*Vicugna pacos*), vicunas (*Vicugna vicugna*), and guanacos (*Lama guanicoe*) (Ruvinskiy et al., 2019; Gentry et al., 2004). Compared with other livestock animals, including cattle, sheep, goats and even chickens, camelids are not widely distributed around the world. However, they are well adapted to harsh environments, from the hot climates of South West Asia and the African Sahara to the cold uplands in Tibet and South America. Camelids have a very close relationship with humans and are considered as multi-purpose livestock. They are usually reared for their milk and meat (Zarin et al., 2020); however, their fiber (Wang et al., 2015) should be taken into account. While the adverse forces, including changes in human lifestyle, are working to decrease camelid populations, the global population of camelids has increased over the last two decades (Fig. 1), maybe due to increasing global drought and the camels' adaptation to the arid and harsh environments (Watson et al., 2016). Except for Asia, during the last two decades, the global population of camelids has been growing, mainly due to the increased population of dromedary camels in Africa (Faye, 2020). Over the last two decades, Old World camels have received specific attention as sustainable livestock, very unique in their morphology, physiology, and immunological characterization, and are valuable for providing vital products, especially for economically developing and underdeveloped countries. This is the main reason for a considerable increase in their number in Africa. Estimated camelid population in North America is about 3000 heads (Faye, 2020), but for Oceania it has not been reported (population size ≈ 0). The population of camels in Europe in 2018 was reported as 6560 heads (FAO, 2019), with Ukraine seeming to be the main host of the camelids in Europe and a limited number of camels kept in the Netherlands (for milk production), and in Western Europe (as tourist attractions) (Faye, 2020). Therefore, data from these continents are not presented in Fig. 1.

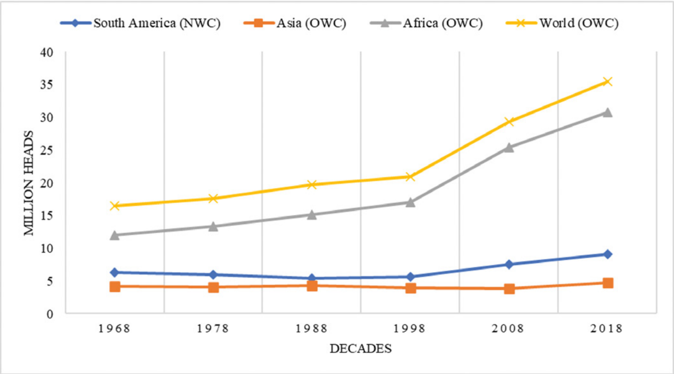

Figure 1. Change in camelid populations during the last 5 decades according to the FAO-STAT (2018). Abbreviations: NWC: New World camels, and OWC: Old World camels

Besides the limited population of European camels in recent years, a fifty-year history of the camelid population shows a very sharp downward trend. Considering 10-year periods, including 1969–1978, 1979–1988, 1989–1998, 1999–2008, and 2009–2018 time periods, the European camel population was 268,688, 248,700, 90,000, 7619, and 7274. In fact, in the recent decade, the camelid population in Europe has decreased dramatically to less than 3% of that in the 1961–1968 period.

Given that the population and importance of camels have improved in recent years, studying their production ability and inherent potentials has received more scholarly attention. Studying the characteristics of domestic animals is more established in Europe and North America; at the same time, the population of camelids on these two continents is very small. This poses a challenge to the establishment of research on camelids.

From the researchers 'point of view, camelids' nutrition (Emmanuel et al., 2015; Johnson, 1994), milk production and ingredients (Bekele et al., 2019; Wang et al., 2018; Ryskaliyeva et al., 2018), meat production (Neely et al., 2001; Rawdah et al., 1994; Yousif & Babiker, 1989), morphological characteristics (Abdel-Maksoud et al., 2019; Zhaxi et al., 2014; Hajinezhad-Bamroud et al., 2020), reproduction (El-Malky et al., 2018), immunity (Romão et al., 2018; Elbanna et al., 2018), disease diagnosis and treatment (Dubey & Schuster, 2018; Alshukairi et al., 2018), and racing ability (Maghsoudi et al., 2020; Soman & Tinson, 2016; Spencer et al., 2010) are mainly considered. While different research areas are recognized, most of the research areas overlap. One of the most progressive research areas (subject groups) in life sciences is "genetics and heredity". Geneticists study inherent factors influencing the performance of animals and their characteristics. Therefore, studying genetic/genomic aspects of camelid nutrition (Gharechahi & Salekdeh, 2018), genes associated with camel milk production (Nagy et al., 2017), genetics of meat (Favia et al., 2019), genetics of camelid reproduction (Fellows et al., 2012), immunogenetics (Nunes-Silva et al., 2014), genetics in veterinary sciences (Fischer et al., 2013; Chu et al., 2018), and the genetic potential of camels for racing (Spencer et al., 2010) has become common in recent years. However, some studies have only focused on camelid genomics (Ruvinskiy et al., 2019; Khalkhali-Evrigh et al., 2018; Ming et al., 2016; Sani et al., 2020). Nevertheless, rather than camelid-exclusive potentials, research on camelid genetics/genomics including population genetics, domestication, and phylogenetics is understudied (Khalkhali-Evrigh et al., 2018; Ruvinskiy et al., 2019). Advances in laboratory methods and utilization of technology in genetics are advancing our knowledge on the camelid genome. Recently, the camelid origin of domestication and historical perspective have become clearer in the light of molecular genetics (Almathen et al., 2016; Burger, 2016; Wu et al., 2016). Genomics also provides opportunities to utilize camelid potential in medicine (Ali et al., 2019). Due to the specific molecular structure of camelid antibodies, researchers are interested in studying humoral immunization in camels (Hamers-Casterman et al., 1993; Muyldermans et al., 2013; Ghahroudi et al., 1993). Genomic high-throughput data provide an opportunity to differentiate genes groups related to the immune performance of camels (Lado et al., 2020). Most of the studies on camelid populations were species level-based. However, differences in morphological and biochemical characteristics of camel breeds, including within-species and between-breeds differences, should be taken into account (Hajinezhad-Bamroud et al., 2020). Molecular genetic markers and developing a genomic data analysis of camels will provide reliable methods to separate breeds.

Measurement and analysis of scientific publications are known as scientometrics. Scientometrics is considered as a text mining-based research methodology as well. In scientometrics, researchers employ quantitative variables to describe the scientific output of the authors, institutions, and countries. Their findings are usually considered as useful tools to evaluate scientific activities, leading to the research path. In addition to quantifying the research and scientific publications, scientometrics evaluates other scientific criteria such as budget and position and determines the efficiency of organizations, universities, and scientific centers. Quantifying scientific productions, making scientific policy, scientific collaboration, and mapping of science are some of other topics in this field. Moreover, the purpose of scientometrics is to evaluate the latest developments in scientific research activities in different trends of science and the factors affecting their growth. Scientometrics can be a useful and efficient tool for scientific managers and planners to manage financial and human resources with the highest efficiency. Scientometrics-based studies have risen in recent years (Maghsoudi et al., 2020), and camels are included in the scientometrical assays (Charbonnier & Marti, 1999; Rathinasabapathy & Rajendran, 2015; Gupta et al., 2015).

The aim of this study is to use scientometrics techniques to integrate information from publications on research on camelids, especially the contribution of genetics/genomics. We are looking for the relationship between countries, research institutions, and researchers to draw an insight on how researchers have collaborated to study camelid genetics/genomics. Moreover, co-occurrence of keywords (retrieved from published articles) over time is another aim of the current study to provide relevant insight and find policies of the future research establishment.

Materials and Methods

This study was conducted to evaluate scientific publications (published scientific papers) on camelids while considering the genetics and genomics contributions using scientometrics techniques. The statistical population of this study included 3830 publications, over a period of 50 years (1971–2020) that were retrieved from the Web of Science (WoS) database. To find these publications, the following search strategy was used in the WoS advance search service: "TS = ((“gene*” OR “genom*” OR genotype OR DNA OR RNA OR “transcript*”) AND (“*Camelus bactrianus*” OR “*Camelus dromedarius*” OR “*Camelus ferus*” OR “*Lama glama*” OR “*Lama guanicoe*” OR “*Lama vicugna*” OR “lamoid species” OR “*Vicugna pacos*” OR “*Vicugna vicugna*” OR camel OR camelid OR Alpaca OR Camelidae OR Dromedary OR Guanaco OR Lamii OR Llama OR Vicugna OR vicuna OR “Feral Bactrian”))”. This search strategy appropriately led us to camelid genetics and genomics. To finalize the search strategy, consultation of expert geneticists was considered. Preparation of publications from 1971 to 1 September 2020 was conducted through Bibexcel software (2016, Leuven, Belgium). Next, the number of researchers, type of publications, language and publications with/without citations were extracted. Additionally, scientific collaborations between countries, researchers, and organizations were retrieved to draw scientific networks and betweenness and closeness centrality through NetDraw (version 2.153, Kentucky, USA; Borgatti, 2002) and UCInet (version 6.581, Kentucky, USA; Borgatti et al., 2002) software. In other words, in a scientific collaboration network, the degree of centrality of each node indicates the degree of scientific cooperation of that node with other nodes (in Fig. 3: collaboration between researchers). Further, the betweenness centrality of a node indicates how many nodes are placed in the shortest path between the other two nodes. Nodes with the highest betweenness centrality are important in a network due to their role in information transferring and nodes' connections. The closeness centrality of a node represents the average length of the shortest paths between that node and other nodes in the network. Nodes with high closeness centrality have more access to other groups in the network and play a more influential role in the network (Erfanmanesh et al., 2014). Finally, VOSviewer software (release 1.6.1, Leiden, Netherland) was used to draw scientific maps and cluster topics and keywords (Van Eck et al., 2010).

Results

Trends in the Research of Camelid Genomics

Using the search strategy, a total of 3830 publications were retrieved including 3269 research articles (85.35% of the publications) and 224 review articles (5.85% of the publications). Other types of publications are presented in Table 1.

Table 1. The publication types associated with camelid genomics

Publication Type	No.	%
Article	3269	85.35
Review	224	5.85
Proceedings Paper	192	5.01
Book Chapter	53	1.38
Meeting Abstract	27	0.70
Early Access	24	0.63
Editorial Material	10	0.26
Correction	9	0.23
Letter	8	0.21
Note	8	0.21
Data Paper	3	0.08
Retracted Publication	1	0.03
Book Review	1	0.03
News Item	1	0.03

No = number of publications; % = percentage of publications

Corrections (nine publications) were not evaluated in this study. Moreover, one of the publications was retracted and therefore discarded from final analyses. The first article on camelid genetics/genomics was published 50 years ago by Melgar et al., (1971) entitled "DNA of the alpaca: composition of its bases".

The dominant language was English with 3706 publications (96.76%), and other publications were in Spanish (1.44%), German (0.60%), French (0.37%), Turkish (0.31%), Russian (0.18%), Hungarian (0.10%), and Polish (0.08%) (Table 2). The first paper on camelid genomics was published in Spanish (Melgar et al., 1971).

Table 2. Languages of publications associated with camelid genomics

Language	Frequency	%
English	3706	96.76
Spanish	55	1.44
German	23	0.60
French	14	0.37
Turkish	12	0.31
Russian	7	0.18
Hungarian	4	0.10
Polish	3	0.08
Chinese	2	0.05
Portuguese	2	0.05
Indonesian	1	0.03
Unspecified	1	0.03

% = percentage of publications

The research on camelids dramatically increased after the 1990s and has received a great deal of attention during the last two decades. Therefore, according to the WoS database, publications from almost 45 in 2000, reached more than 360 in 2019 (Fig. 2).

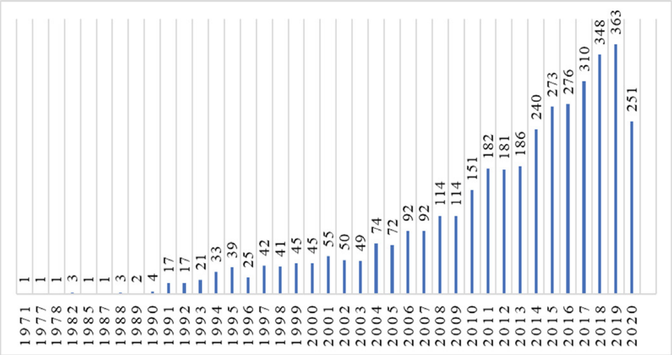

Figure 2. Publications/year on camelid genomics

Subject Groups

According to the WoS database, publications were categorized in different subject groups. The ten top subject groups were "Veterinary Sciences" (862 publications), "Biochemistry & Molecular Biology" (394), "Agriculture, Dairy & Animal Science" (390), "Parasitology" (289), "Microbiology" (263), "Biotechnology & Applied Microbiology" (226), "Immunology" (199), "Multidisciplinary Sciences" (188), "Genetics & Heredity" (187), and "Food Science & Technology" (165). Moreover, among the 3830 publications, there were 119 common publications in "Veterinary Sciences" and "Agriculture, Dairy & Animal Science". Followed by these two subject groups, "Parasitology" and "Tropical Medicine" (78), and "Parasitology" and "Veterinary Sciences" (58) have the most common publications.

Countries

In total, 127 countries contributed to the publication of 3830 research papers on camelids. The size of the circles indicates the number of publications of that country and the thickness of the lines indicates the number of collaborations between the two countries (Fig. 3). Therefore, the leading countries were the USA, China, Egypt, Saudi Arabia and Germany with 792, 364, 284, 280, and 269 publications, respectively. Considering international collaborations between countries, Saudi Arabia and Egypt stay at the top with 119 publications. China with the USA, the UK with the USA, the USA with Saudi Arabia, and the USA with Egypt with, respectively, 68, 63, 41, and 37 publications are in the next rank. Fig. 3 only demonstrates the number of publications and their quality (the publication/journal impact factor) was not considered. Therefore, some countries (as Austria) which appear in Fig. 3 are not ranked as top proliferative countries.

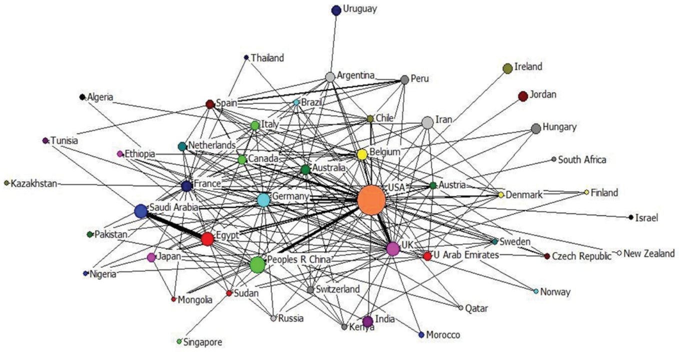

Figure 3. Scientific collaborations among countries involving camelid genomics (threshold of at least 10 joint publications)

Research Institutions

Considering at least five collaborations, there were 3782 research institutions that contributed to the publications. "King Saud University" (109 publications), "Vrije Universiteit Brussel" (81), "Central Veterinary Research Laboratory at United Arab Emirates" (67), "The University of Hong Kong" (56), "Vlaams Instituut voor Biotechnologie at Belgium" (VIB) (54), "National Research Center" (54), "Cairo University" (53), and "King Faisal University" (50) had more than 50 publications (Fig. 4).

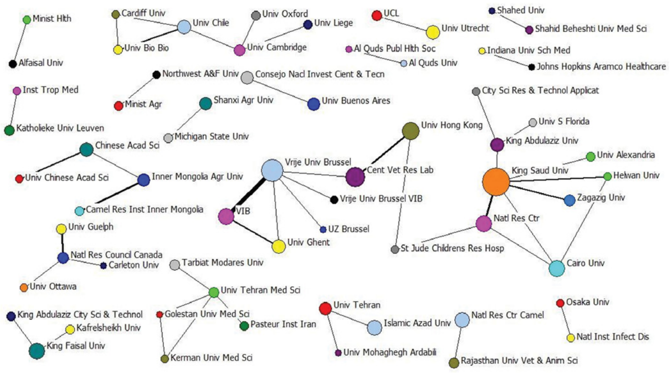

Figure 4. Scientific collaborations among research institutions involving camelid genomics (threshold of at least 5 joint publications)

The most frequent collaboration between research institutions was between "Vlaams Instituut voor Biotechnologie at Belgium" and "Vrije Universiteit Brussel" with 42 common publications, followed by "Central Veterinary Research Laboratory" and "The University of Hong Kong" (17 publications), and "King Saud University" and "National Research Center" (16 publications).

Researchers

A total of 14,538 researchers contributed to the publication of 3830 articles. The most proliferative researchers (with more than 25 publications) were Muyldermans S (with 90 publications), Wernery U (63), Faye B (31), Woo PCY (30), Lau SKP (27), Kinne J (26), and Burger PA (25). Considering scientific collaboration in the field of camelid genomics, Lau SKP with Woo PCY, Woo PCY with Yuen KY, and Yuen KY with Lau SKP had 27, 18, and 18 collaborations, respectively (Fig. 5). While the number of publications for each researcher is an important scientific factor based on network indices, researchers with the highest number of publications were not involved in Table 3.

Co-Occurrence of Keywords

Uniform keywords were used to draw density maps (Fig. 6). To understand the chronological trends in keywords, three time periods, namely before 2000 (≤ 2000), 2001–2010, and 2011–2020, were considered. Considering the co-occurrence of keywords, "alpaca" and "llama" appeared 40 times together during the last 50 years, followed by "camel" with "PCR", "camel" with "*Trypanosoma evansi*" (each 19 times), and "nanobody" with "phage display" (16 times). For the 3830 retrieved publications, 15,328 keywords were included with approximately 4 keywords per publication. To assess the trends of research topics and trends during the time periods, 20 top keywords were extracted in terms of repetition of use in articles. The information of the most frequent keywords is presented in Table 4.

Table 3. The top proliferative researchers associated with camelid genomics

Researcher	Institution	Number of Publications	Degree	Closeness	Betweenness
Lau SKP	Univ Hong Kong, Li Ka Shing Fac Med, Dept Microbiol, Hong Kong, Peoples R China	27	11.688	1.449	0.171
Woo PCY	Univ Hong Kong, Li Ka Shing Fac Med, Dept Microbiol, Hong Kong, Peoples R China	30	11.688	1.449	0.171
Yuen KY	Univ Hong Kong, Li Ka Shing Fac Med, State Key Lab Emerging Infect Dis, Hong Kong, Peoples R China	20	11.688	1.449	0.171
Wernery U	Cent Vet Res Lab, Dubai, U Arab Emirates	63	7.792	1.448	0.026
Anderson GP	USN, Res Lab, Ctr Bio Mol Sci & Engn, Washington, USA	17	3.896	1.333	0.000
Goldman ER	Ctr Bio Mol Sci & Engn, Naval Res Lab, Washington, USA	17	3.896	1.333	0.000
Liu JL	Naval Res Lab, Ctr Biomol Sci & Engn, Washington, USA	17	3.896	1.333	0.000
Pardon E	VIB, Dept Biol Struct, Brussels, Belgium	17	1.299	1.299	0.000
Steyaert J	Vrije Univ Brussel, Struct Biol Brussels, Brussels, Belgium	21	1.299	1.299	0.000
Zabetakis D	US Navy, Res Lab, Ctr Bio Mol Sci & Engn,Washington, USA	11	3.896	1.333	0.000
Wong EYM	Univ Hong Kong, Dept Microbiol, Hong Kong, Peoples R China	11	5.195	1.448	0.000
Ahmadvand D	Iran Univ Med Sci, Fac Appl Med Sci, Dept Med Biochem, Tehran, Iran	11	1.299	1.299	0.000
Rahbarizadeh F	Tarbiat Modares Univ, Dept Med Biotechnol, Fac Med Sci, Tehran, Iran	19	1.299	1.299	0.000

The results show that 3830 articles on camelid genomics were published in 1345 journals. Table 5 shows the information of the top 20 journals in terms of the number of articles published in the field of camelid genomics. These 20 journals, with 781 articles out of 3830 articles, have published more than 20% of the total number of articles. The "Journal of Camel Practice and Research" is ranked first with 170 articles. Among the top 20 journals, most of them were published in the Netherlands and the USA (each with six journals), followed by the UK (four journals), India (two), and Switzerland and Germany (each with one). More information can be found in Table 5.

Table 6 presents articles with more than 300 citations related to camelid genetics/genomics, along with the year of publication and the number of citations received. It should be noted that the phrase "camelid genomics" may not be seen in the titles listed in Table 6; however, each word/phrase included in our search strategy certainly occurred in the papers' abstracts or keywords.

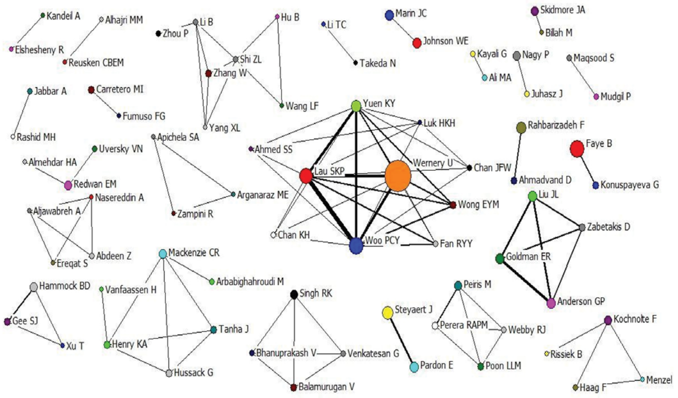

Figure 5. Scientific collaborations among researchers involving camelid genomics (threshold of at least 7 joint publications)

Table 4. The keywords frequencies and percentages during three time periods (≤2000, 2001–2010, and 2011–2020)

Rank	Keyword	≤2000		2001–2010		2011–2020		Total	
		N	%	N	%	N	%	N	%
1	Camel	29	9.76	102	11.23	282	10.80	413	10.78
2	Alpaca	8	2.69	61	6.72	134	5.13	203	5.30
3	Nanobodies	0	0	13	1.43	139	5.33	152	3.97
4	MERS-CoV	0	0	0	0	140	5.36	140	3.66
5	Llama	18	6.06	50	5.51	51	1.95	119	3.11
6	Milk	2	0.67	22	2.42	92	3.52	116	3.03
7	PCR	8	2.69	33	3.63	72	2.76	113	2.95
8	Camelids	7	2.36	29	3.19	59	2.26	95	2.48
9	Genes	4	1.35	13	1.43	78	2.99	95	2.48
10	Single-domain antibodies	3	1.01	19	2.09	70	2.68	92	2.40
11	Dromedary camel	2	0.67	8	0.88	82	3.14	92	2.40
12	VHH	0	0	17	1.87	71	2.72	88	2.30
13	Antibodies	4	1.35	17	1.87	64	2.45	85	2.22
14	Dromedary	7	2.36	17	1.87	60	2.30	84	2.19
15	*Camelus dromedaries*	4	1.35	11	1.21	60	2.30	75	1.96
16	*Trypanosoma evansi*	5	1.68	21	2.31	48	1.84	74	1.93
17	Microsatellites	0	0	27	2.97	45	1.72	72	1.88
18	Phage display	2	0.67	17	1.87	51	1.95	70	1.83
19	Echinococcus granulosus	4	1.35	30	3.30	36	1.38	70	1.83
20	Coronavirus	0	0	0	0	63	2/41	63	1.75
	Total articles	297		908		2610		3830	

N = number of articles that used keywords during this period; % = percentage of using keywords in all articles in the time period

Table 5. The most frequent journals that published articles on camelid genomics

Journal Name	Country	IF (2019)	Publications	Ratio (%)
Journal of Camel Practice and Research	India	0.137	170	4.44
PloS One	USA	2.740	75	1.96
Small Ruminant Research	Netherlands	1.273	63	1.64
Veterinary Parasitology	Netherlands	2.157	58	1.51
Tropical Animal Health and Production	Netherlands	1.333	47	1.23
Veterinary Microbiology	Netherlands	3.030	41	1.07
Scientific Reports	UK	3.998	28	0.73
Animal Reproduction Science	Netherlands	1.660	25	0.65
Journal of Biological Chemistry	USA	4.238	25	0.65
Parasitology Research	Germany	1.641	25	0.65
Parasites & Vectors	UK	2.824	24	0.63
Journal of Dairy Science	USA	3.333	24	0.63
Parasitology	UK	2.783	24	0.63
Acta Tropica	Netherlands	2.555	23	0.60
Journal of Veterinary Diagnostic Investigation	USA	1.135	23	0.60
Viruses-Basel	Switzerland	3.816	22	0.57
Indian Journal of Animal Sciences	India	0.278	22	0.57
Journal of Virology	USA	4.501	22	0.57
Molecular Immunology	UK	3.641	20	0.52
PNAS *	USA	9.412	20	0.52

* Proceedings of the National Academy of Sciences of the United States of America

Table 6. The most cited articles

Title	Year	Citations
Naturally-occurring antibodies devoid of light-chains (Hamers-Casterman et al., 1993)	1993	1572
Structure of a nanobody-stabilized active state of the β(2) adrenoceptor (Rasmussen et al., 2011)	2011	1075
Nanobodies: Natural single-domain antibodies (Muyldermans et al., 2013)	2013	675
Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG) (Matthijnssens et al., 2011)	2011	578
Phylogenetic analysis of Cryptosporidium parasites based on the small-subunit rRNA gene locus (Xiao et al., 1999)	1999	506
Selection and identification of single domain antibody fragments from camel heavy-chain antibodies (Ghahroudi et al., 1997)	1997	475
Origin and evolution of pathogenic coronaviruses (Cui et al., 2019)	2019	411
A versatile nanotrap for biochemical and functional studies with fluorescent fusion proteins (Rothbauer et a., 2008)	2008	386
Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range (Henderson et al., 2015)	2015	377
Targeting and tracing antigens in live cells with fluorescent nanobodies (Rothbauer et al., 2006)	2006	375
Evidence for Camel-to-Human Transmission of MERS Coronavirus (Azhar et al., 2014)	2014	361
Consensus proposals for classification of the family Hepeviridae (Smith et al., 2014)	2014	353
Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses (Su et al., 2016)	2016	326
Middle East respiratory syndrome (Zumla et al., 2015)	2015	324
Sequence and structure of VH domain from naturally-occurring camel heavy-chain immunoglobulins lacking light-chains (Muyldermans et al., 1994)	1994	324
Middle East respiratory syndrome coronavirus in dromedary camels: an outbreak investigation (Haagmans et al., 2014)	2014	320
Molecular evidence from retroposons that whales form a clade within even-toed ungulates (Shimamura et al., 1997)	1997	308

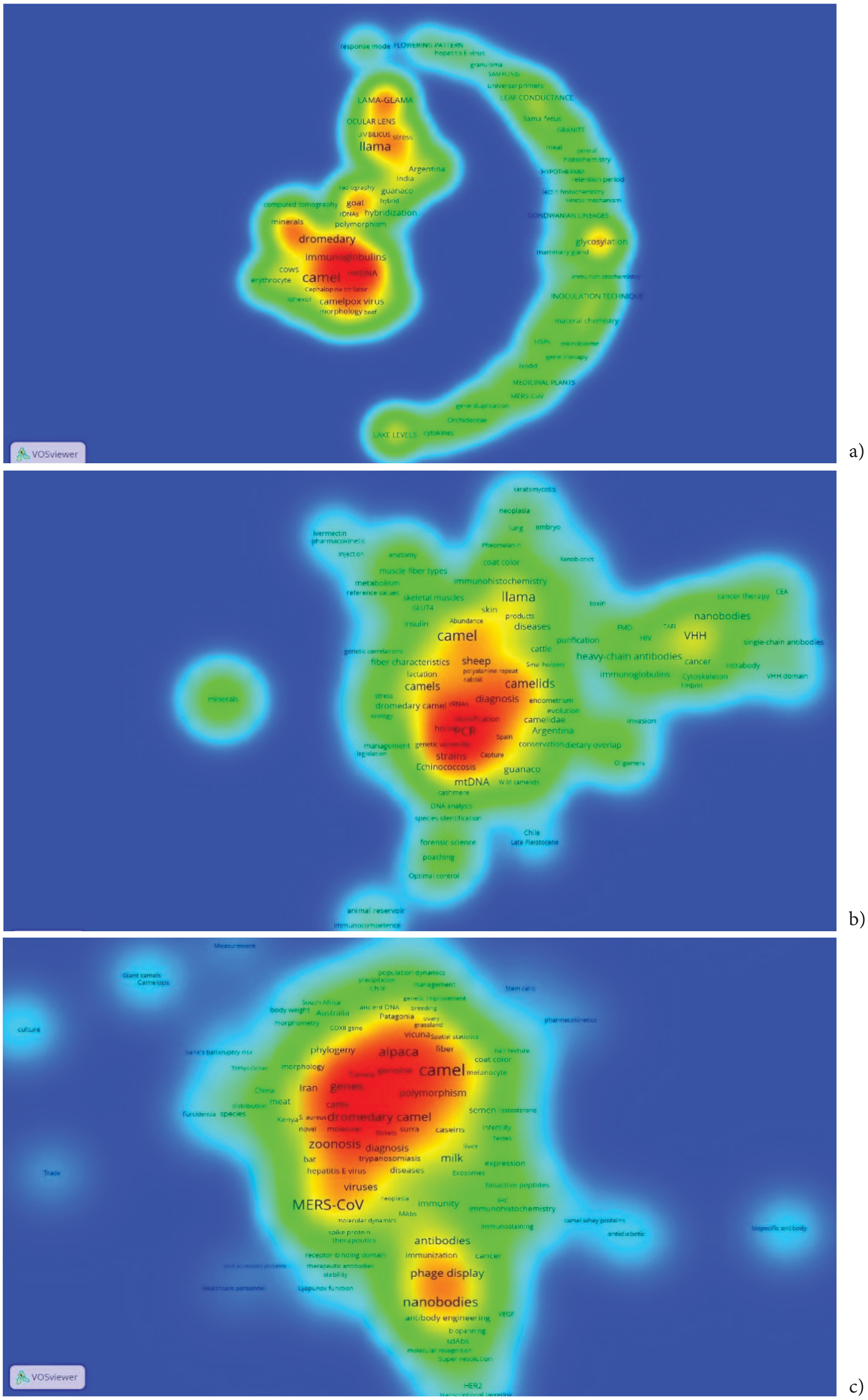

Figure 6. Density map of keywords in three time periods including (a) before 2000 (≤2000), (b) 2001–2010, and (c) 2011–2020

Discussion

Considering the research strategy, it seems that "Genetics & Heredity" is among the top subject groups. However, the number of publications is not a relevant criterion for grading the rank of a subject group, because publications may have been indexed in a variety of subject groups. As a matter of fact, papers with a genetic/genomic context may be published in any subject group. For example, "PloS ONE", which includes 75 papers on camelid genomics (Table 5), covers four subject groups including "Agricultural and Biological Sciences", "Biochemistry & Molecular Biology", "Medicine", and "Multidisciplinary". However, the genetic variability of three dromedary camels was published in this journal (Khalkhali-Evrigh et al., 2018).

Ignoring the first rank of collaborations between Saudi Arabia and Egypt (which are the main countries of camel breeding), the USA has collaborated with China, the UK, Saudi Arabia, and Egypt (Fig. 3). Therefore, based on our search strategy, the USA has a key role in the research on camelid genomics, even though the population of camelids in the USA is very small (≈ 3000 heads; Faye, 2020). The infrastructure and extent of the biological research in USA institutions give the opportunity to researchers from other countries to establish research on camelids in the USA. Considering the collaboration of the USA with other countries, it reveals that American scientists are interested in research on both Old World camelids (collaboration with Saudi Arabia, Unites Arab Emirates, Iran, Qatar, Jordan, India, China, Egypt, Kenya, and Sudan, which all are home of Old World Camelids), and New World camelids (collaboration with Chile, Argentina, Brazil, and Peru, which all are home of New World Camelids) (Fig. 3). Considering between-researchers collaborations, collaboration between Chinese researchers is considerable.

Between researchers, Lau SKP, Woo PCY, and Yuen KY, with a centrality degree of 11.688, have the most scientific activity in the field of camelid genomics. They also have the highest closeness centrality and between centrality at 1449 and 0.171, respectively (Table 3). The centrality indicators actually examine the position of the node in the network (Shekofteh & Hariri, 2013). The centrality of a node in a network refers to the number of direct connections of a node with other adjacent nodes (Qin et al., 2011). In Fig. 5, between researchers' collaboration is shown. In this network, each researcher (node) indicates the degree of scientific cooperation of that researcher with other researchers, which indicates the degree of centrality. Scientific collaboration associated to the same problem (here camelid genomics) can reflect the importance of a problem between several research institutes/universities. Therefore, for future studies, newcoming researchers can directly involve in a research group or can find originality of research funds.

In order to determine the trend of research topics and trends in each field, in addition to the words/phrases used in the title and abstract, keywords employed by the researchers of those articles were also considered. Journal editors commonly recommend using different keywords from those included in the title of the article, in order to make that study more retrievable. Keywords also reflect the scientific importance of an article since they reflect the opinion of experienced researchers in that field. The VOS viewer software utilizes distance-based methods to draw density maps. More adjacent keywords have close distances in the map and more frequent keywords with the highest density are revealed in a red context, while rare keywords have a blue context. According to the frequency (density) of each keyword, green to yellow colors' tonality appear between blue and red colors.

Before 2000, the density map included two separate islands. The crescent-shaped island includes keywords with approximately the same density appearing mainly in a green context. In another island, two separated red (dense) zones can be seen clearly, including "llama" and "camel" as main keywords. Considering co-occurrence of keywords, during the early 30 years of research on camelid genomics (1971–2000), the main topics were immunity (keyword: immunoglobulin) and population genetics (keyword: mtDNA) (Fig. 6a). Before 2000, immunogenetics and immunogenomics were not yet well developed as they were only established in recent years (Lado et al., 2020); thus, the keyword "immunoglobulin" was the main representative of camelid immunity. Including other species such as goat and cows in keywords, might refer to research on the comparative population genetics, which corresponded with the development of molecular genetics techniques in the 20th century.

During 2001–2010, the central hot keyword in the red context was "Polymerase Chain Reaction" (PCR) (Fig. 6b). The importance of PCR in studying camelid genomics is obviously recognizable. Meanwhile, the distances of keywords "camel", "camels", "camelids", and "dromedary camels", and even "llama" and other mammals ("horse", "sheep", and "rabbits"), are close to "PCR". In this time period, population genetics (representative keywords: "mtDNA" and "genetic variability") was still important. However, instead of immunoglobulin in the previous time period (≤ 2000), "echinococcus", "diagnosis", and probably "identification" appear, which refers to the animals' health and immunity.

Considering the 2011–2020 time period, in addition to a new comers' area, a dense red area appeared (Fig. 6c). Compared with two previous time periods, in the 2011–2020 time period, the distance between Old and New World camelids became closer, whereas "vicuna", "alpaca", "dromedary camel", and "camel" appeared together in the red context zone. Genetic-based keywords/phrases also included "genome", "genes", "polymorphism", and "phylogeny", which somehow reflects the continuing importance of population genetics in recent decades. Camelid-originated foods, particularly "meat" and "milk", mainly assumed major importance and attracted the attention of animal geneticists during this time period (2011–2020). According to the global human population rise during the last decade, the importance of camelid meat and milk is considerable. Moreover, the genetic study of camelid fiber production has assumed major importance in recent years (Liu et al., 2018), as "fiber" and "coat color" are becoming important according to Fig. 6c. In fact, in recent decades, researchers have been studying multidimensional potentials of camelids. Besides, some countries presented in the density map, including "Iran", "China", "Kenya", and "Chile", referred to the importance of camelid research in these countries (Khalkhali-Evrigh et al., 2018).

Zoonoses assume major importance in camelid genomic research, while keywords including "diagnosis", "disease", "MERS-CoV", and "viruses" appear in the red zone and near genes and genome. Compared to other ruminants, camels have a very close relationship with their owners. This is why common diseases between humans and camels are of particular importance. The Middle East respiratory syndrome virus (MERS-CoV) is one of the viruses that camels are responsible for. During 1971–2010, the phrase "MERS-CoV" did not exist in the literature at all, while in the last decade with 140 times (5.36%), it was one of the most frequent keywords (Table 4). Such as "MERS-CoV", the keyword "coronavirus" is presented in the 2011–2020 time period and, with 2.41%, it is one of the most frequent keywords in this time period. The camel genome provided a potential medium to host the virus and transmit it to humans (Cui et al., 2019; Azhar et al., 2014; Su et al., 2016; Zumla et al., 2015; Haagmans et al., 2014). All of these studies were published before the COVID-19 virus pandemic in 2019–2020. In other words, researchers in this field were paying special attention to the diagnosis and treatment of acute respiratory diseases in camels in the last decade. Immunogenetics studies are under way to diagnose and treat infectious diseases (Premraj et al., 2013).

In addition to the extended large red context in Fig. 6-c, a newcomerrs' region is forming: camelid immunity (keywords: "nanobodies", "phage display", "antibodies", "antibody engineering", and "immunization"). Therefore, the genetic study of immunity in camelids was seriously and professionally followed in the last decade (Lado et al., 2020; Daouam et al., 2016). The special structure of antibodies in camels made this attractive (Hamers-Casterman et al., 1993; Ghahroudi et al., 1997). Nanobodies are considered as a transformed shape of well-known IgGs missing their L-chain (Muyldermans et al., 2013). Camel-derived nanobodies are widely utilized in human disease treatment (Rasmussen et al., 2011) and antibody engineering (Hattori et al., 2012).

Conclusion

In general, the most important topics studied from the perspective of camelid genomics have been the study of population genetics and the genetic study of pathogens and their diagnoses, as well as the study of camelid immunogenetics. With the development of devices and technologies used in the study of molecular genetics, new methods have been used in the study of population genetics. Over the past 50 years, along with the development of the findings of researchers in the field of immunogenetics, the study of immunity in camels has also evolved. In future studies, special attention may be paid to the "camel genome" capacity to host the corona virus. Furthermore, the special structure of humoral immunity in camels makes this section attractive in immunogenetics research.

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