



OPEN

DATA DESCRIPTOR

A dataset of distribution and diversity of blood-sucking mites in China

Fan-Fei Meng^{1,2}, Qiang Xu^{1,2}, Jin-Jin Chen¹, Yang Ji¹, Wen-Hui Zhang¹, Zheng-Wei Fan¹, Guo-Ping Zhao¹, Bao-Gui Jiang¹, Tao-Xing Shi¹, Li-Qun Fang¹ & Wei Liu¹

Mite-borne diseases, such as scrub typhus and hemorrhagic fever with renal syndrome, present an increasing global public health concern. Most of the mite-borne diseases are caused by the blood-sucking mites. To present a comprehensive understanding of the distributions and diversity of blood-sucking mites in China, we derived information from peer-reviewed journal articles, thesis publications and books related to mites in both Chinese and English between 1978 and 2020. Geographic information of blood-sucking mites' occurrence and mite species were extracted and georeferenced at the county level. Standard operating procedures were applied to remove duplicates and ensure accuracy of the data. This dataset contains 6,443 records of mite species occurrences at the county level in China. This geographical dataset provides an overview of the species diversity and wide distributions of blood-sucking mites, and can potentially be used in distribution prediction of mite species and risk assessment of mite-borne diseases in China.

Background & Summary

Vector-borne infections (VBI) are defined as infectious diseases transmitted by the bite or mechanical transfer of arthropod vectors. They constitute a significant proportion of the global infectious disease burden. Ticks and mosquitoes are recognized as the most important vectors in the transmission of bacterial and viral pathogens to humans and animals worldwide¹. High priority of VBIs mainly include malaria, dengue, chikungunya virus infection, Zika virus disease, lymphatic filariasis, Lyme disease, tick-borne spotted fever and tick-borne encephalitis, etc., which are primarily transmitted by ticks or mosquitoes, while mite-borne infections were often considered as neglected diseases. According to the recent studies, many infectious diseases transmitted by the bite or mechanical transfer of mite vectors²⁻⁴, including scrub typhus⁵, hemorrhagic fever with renal syndrome (HFRS)⁶ and plague⁷, are of global importance. Moreover, mites can parasitize vertebrates, including livestock, birds, rodents, and other wild animals⁸⁻¹⁰, with intrinsic vector competence to transmit various pathogens of medical and veterinary importance^{11,12}. Therefore, mites have caused a major threat to human and animal health.

Currently, more than 55,000 species of mites are known to exist in the world¹³, with complex living environment in both outdoor and indoor, which differed in accordance with their hosting habitats. Mites usually have a wide geographical distribution with low host specificity. Mammals, birds, reptiles, amphibians and even some other arthropods are reported to be the hosts of mites¹⁴. The larvae of mites are often found on the body surface of small mammals, especially rodents (rats, mice and voles) which are the most common hosts of mites¹⁵. For instance, more than 30 species of small mammals and birds have been reported to be the hosts of *Leptotrombidium delicense*¹⁶. The feeding habits of mites are complicated. Some of the domestic mite species found in indoor environments and in warm or tropical regions, such as house dust mite, are well known for causing allergic disorders and not to suck blood. Most of the parasitic mites with medical importance are related to human and animal and are blood-sucking¹⁷⁻¹⁹. Gamasid mites, chigger mites and oribatid mites are among the most commonly seen mite species that bite and transmit pathogens²⁰.

The Chinese climatic and environmental conditions provide suitable conditions for many mite species, among which a large number of mite species are blood-sucking, having negative influences on human and animal health. Against a true baseline estimate of the geographic distributions of mite species, we can then prepare for the new

¹State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing, 100071, People's Republic of China. ²These authors contributed equally: Fan-Fei Meng, Qiang Xu. ✉e-mail: fang_lq@163.com; liuwei@bmi.ac.cn

disease threats associated with mite-bite. However, most of the recent studies have been carried out to report the identification of novel mite species²¹, the novel endemic regions²², novel mite-borne diseases⁶, or even the genomics and developmental transcriptomics analyses of certain mite species²³. For those reports on the geographic distributions of mite species, the publication language was usually in Chinese. The geographic scope was rather limited and recorded in a patchy way²⁴, or with low spatial resolutions and representing an aggregate of geographical points and time points²⁵. The available dataset is far from adequate to attain a complete understanding of the distributions of mites in China. Moreover, many historical collection of mite-related records were documented in Chinese, and the largest two datasets were (China Economic Entomology, 《中国经济昆虫志》²⁶; Atlas of Epidemiology of Natural Focus Diseases in China, 《中国自然疫源性疾病预防学图集》²⁷) compiled by Institute of Zoology, Chinese Academy of Sciences and our institute (Beijing Institute of Microbiology and Epidemiology). A study on breaking language barriers for a more complete picture of mite landscapes in China would be useful for future disease risk analysis and modelling experiments. To better identify the geographic distributions of the major mite species in China, we reviewed the prevalence, geographical distributions, and zoonotic potential of blood-sucking mites in China. Both English and Chinese records were reviewed, which were collectively composed into the dataset that comprised 6,443 records of geo-referenced mite occurrence without repetition at county level reported from 1978 to 2020, involving 551 mite species in 759 locations across China. The most frequently reported mite species are *Haemolaelaps glasgowi* and *Laelaps echidninus*.

Methods

Data Collection. The aim of the data assembly was to build a comprehensive database of reports on the distributions of mites in the mainland of China, with the study subject focusing on the blood-sucking mites. A systematic literature review on the distributions of blood-sucking mites in China was performed according to the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) statement guidelines²⁸. The literature search was conducted in both Chinese and English literature databases, mainly through China National Knowledge Infrastructure (CNKI) (<http://www.cnki.net/>), Wan Fang Database (<http://www.wanfangdata.com.cn/>), VIP Database (<http://www.cqvip.com/>), PubMed Database (<https://pubmed.ncbi.nlm.nih.gov/>), related domestic zoological works and research data on the distribution of mites in our laboratory over the years. After the first-round literature search, we made double check to find the publications that were overlapped in three Chinese databases (CNKI, Wan Fang database, and VIP database). There might also be duplicated references in PubMed with Chinese core journal database, which were checked by the method provided in Giovanni Herrera *et al.*²⁹, and with the English literature included only. Although the literature search was made during the period from 1950 to 2020, the earliest one can be traced back to 1978 and the latest was reported on October 15th, 2020. The terms (“螨” or “螨虫”) were used in Chinese journal databases, and (‘mite’ and ‘China’) were used in PubMed search. No language restrictions were placed on these searches.

To attain a valid information extraction, we followed the three-step guideline for data screening. For the first step screening, totally 24,738 publications, including 22,899 Chinese and 1,839 English abstracts were retrieved for initial screening using the key words searching. For the second-step screening, the abstracts of all returned references were reviewed to exclude those reporting only clinical case or laboratory data and without mentioning any specific mite species. For the third step screening, we reviewed the full text of all the 308 Chinese references and 60 English references in detail, from which a total of 153 Chinese references and 27 English references were determined to be eligible for data extraction (Fig. 1). The earliest Chinese and English publications were published in 1978 and 1990, respectively, and an abrupt increase of references that reported mite records was seen after 1990 (Fig. 2).

The key data we extracted from the literature included: (i) name of the mite genera, (ii) name of the mite species, (iii) the reported geographic location information (province, city and county), (iv) time of publication, (v) source of literature. After the initial data entrance, a twice re-check by two researchers was performed to avoid errors and duplicates. Each record represents the distribution of one mite species in one certain district. Among them, 4,101 records were extracted from Chinese journals and 282 records from English journals. In addition, 2,060 records were extracted from China Economic Entomology and Atlas of Epidemiology of Natural Focus Diseases in China, two books that have involved a large number of field surveys since 1980 in 31 provinces (autonomous regions and municipalities) across the country, which have supplemented the distribution of mites in the mainland of China. In total, 6,443 records were compiled at the county level, and differences of the number of records between provinces and over years were shown in Fig. 3.

Geo-positioning. For each record of mite, we extracted the location information at the county level from the selected references. Since the multiple surveys in the same county may be reported in different publications for different research purposes, we summarized all the records reported in the references and deleted the duplicate records of the same species at the same location. For the references that reported no longitude and latitude of the study sites, we used the ArcGIS Desktop 10.7.0.10450 software to extract the geographical coordinates of the center points of the corresponding administrative areas from the digital map, China administrative boundary maps (2015), which were obtained from the Resource and Environment Data Cloud Platform, Chinese Academy of Sciences (<http://www.resdc.cn/data.aspx?DATAID=202/>). In order to accurately demonstrate the spatial precision of each record, we included the ‘location_level’ field in the dataset to ensure that each location was pinned into the correct administrative regions. The standardized data were uploaded to the figshare website for potential data set users to download³⁰. We use RStudio Version 1.2.5001 and ArcGIS Desktop 10.7.0.10450 software to statistically analyze and visualize the obtained geographic data.

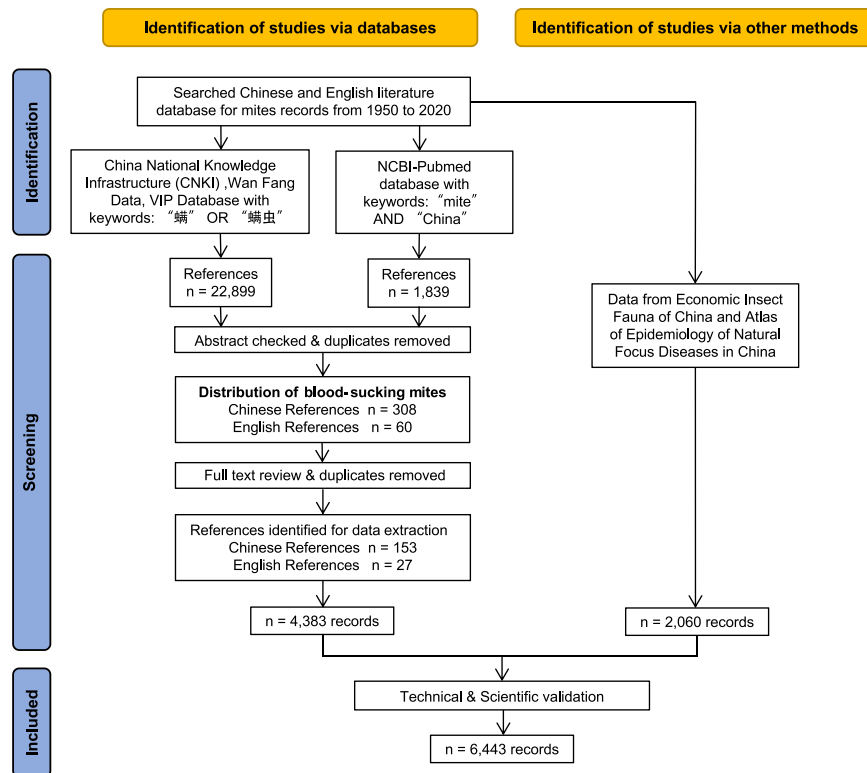


Fig. 1 Schematic diagram of the literature search process and results.

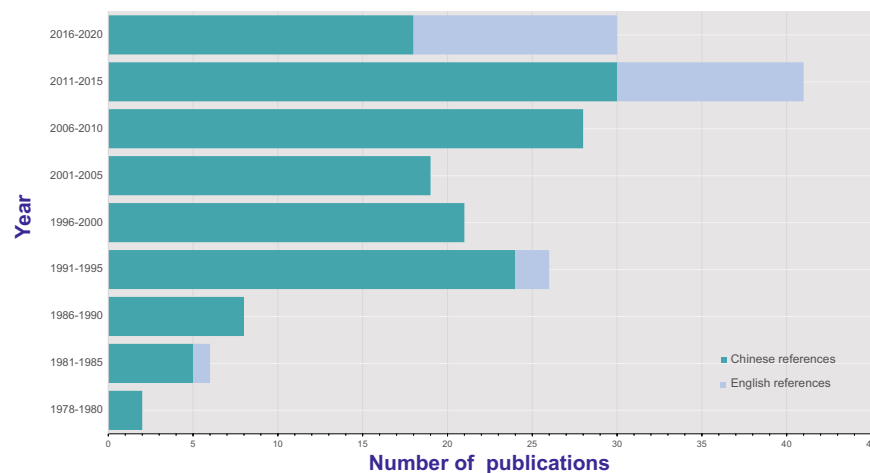


Fig. 2 Numbers of publications that recorded mite obtained from Chinese and English references. An abrupt increase of publications with mite records was seen after 1990.

Data Records

The dataset of distributions and diversity of blood-sucking mites in China is available on figshare³⁰. Each row of the dataset represents a distinct record, which records one specific mite species in a specific location by a scientific literature at a specific time. The columns contained in the dataset are shown as follows:

1. **Genus:** Identifying the genus of mites.
2. **Species:** Identifying the species of mites.
3. **Province:** Provincial level information of mites reported location, including names of 34 provinces, autonomous regions, municipalities or special administrative regions of China.
4. **City:** City level information of mites reported location, including names of 333 prefectural-level cities or autonomous prefectures.
5. **County:** County level information of mites reported location, including names of 382 counties.

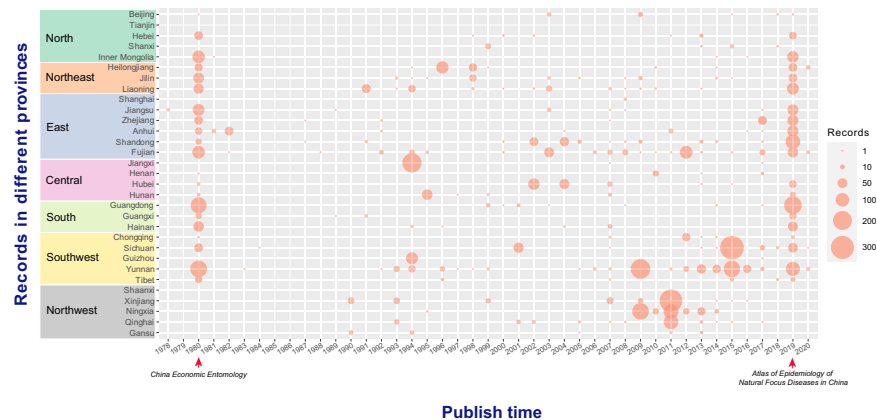


Fig. 3 The number of reported records for mites in different provinces between 1978 and 2020. The bubble diagram was used with the size of bubble indicating the number of records. The abrupt increase of publications in 1980 and 2019 was due to the supplementation of the data collected from the two books in Chinese (Economic Entomology and Atlas of Epidemiology of Natural Focus Diseases in China).

6. **Province_code:** Adopt 2018 China's administrative division province name code.
7. **City_code:** Adopt 2018 China's administrative division city name code.
8. **County_code:** Adopt 2018 China's administrative division county name code.
9. **GPS_xx:** Longitude of reported county coordinates.
10. **GPS_yy:** Latitude of reported county coordinates.
11. **Location_level:** The geographic scale of location (1 = provincial level, 2 = city level, 3 = county level).
12. **Duplicate_name:** If species name has duplicate names (0 = no, 1 = yes).
13. **Data_source:** Details about whether location data were extracted from literature data or research site survey data (1 = Chinese literature data, 2 = English literature data, 3 = data from China Economic Entomology and Atlas of Epidemiology of Natural Focus Diseases in China).
14. **Publish_time:** The year of publication.
15. **References:** The full name of references identified for data extraction.

Technical Validation

This dataset contains 6,443 records that were extracted from 153 Chinese references and 27 English references, as well as from China Economic Entomology and Atlas of Epidemiology of Natural Focus Diseases in Chinese. All records were extracted and entered under the same standard by the same person at the initial stage. The data were subsequently double checked by another member, with the emphasis on screening the duplicate data and correcting the ambiguous data, and supplementing the missing data. Data were strictly checked to ensure that accuracy and extraction criteria were met, by an approach similar to that used in Herrera *et al.*²⁹. In the process of confirming the geographic location information, an independent third-party was designated to re-check the geographic location information of the data. The verification process refers to the same standard in the data entry process to re-check the accuracy of the data, by a similar approach to that used in Battle *et al.*³¹. In order to unify the geographic location information that was extracted from references with no uniform standard to the county level, ArcGIS software was used to determine the coordinates of the central points of the counties, which were marked on Baidu Map (<https://map.baidu.com/>) to ensure that each coordinate point corresponds to an accurate administrative region in China. The resulting locations of mite occurrence as depicted in Fig. 4 agree well with the previous findings and maps.

Due to the wide time span of the literature search (1978–2020), the classification and naming of some mite species have changed. After a thorough re-evaluation, the standard synonymisations were followed: *Hypoaspis* (*Laelaps*) *pavloskii* as synonym of *Androlaelaps pavlovskii*³²; *Laelaps jettmari* as synonym of *Laelaps huaihoensis*³³; *Hypoaspis freemani*, *Haemolaelaps magaventralis* and *Haemolaelaps haemorrhagicus* as synonyms of *Haemolaelaps casalis*³⁴; *Haemolaelaps microti*, *Haemolaelaps morhvae* and *Haemolaelaps scalopi* as synonyms of *Haemolaelaps glasgowi*³⁴; *Hyperlaelaps microti* as synonym of *Hyperlaelaps aravalis*³⁴; *Hypoaspis murinus* and *Hypoaspis smithii* as synonym of *Hypoaspis* (*Geolaelaps*) *lubrica*³⁴; *Cosmolaelaps gurabensis* as synonym of *Hypoaspis* (*Cosmolaelaps*) *miles*³⁴; *Hypoaspis sinicus* as synonym of *Hypoaspis* (*Geolaelaps*) *praesternalis*³⁴; *Haemolaelaps angustiscutis* as synonym of *Haemolaelaps fragilis*³⁵; *Haemogamasus macrodentilis* as synonym of *Haemogamasus daliensis*^{36,37}; *Proctolaelaps pygmaeus* as synonym of *Hypoaspis ovatus*^{38,39}; *Proctolaelaps fiseri* as synonym of *Proctolaelaps yinchuanensis*⁴⁰; *Pachylaelaps siculus* as synonym of *Pachylaelaps xinghaiensis*^{41,42}.

Usage Notes

Blood-sucking mites are important vectors of infectious diseases of global concern. Being aware of the distribution of blood-sucking mites is of great significance to prevent and manage relevant diseases. To the best of our knowledge, this dataset represents the first and the most comprehensive database for the blood-sucking mite species, together with their distribution at multiple scales in China. Compared to previous studies, this database contains a total of 6,443 pieces of data, recording the distributions of 551 species of mites from 759 counties that

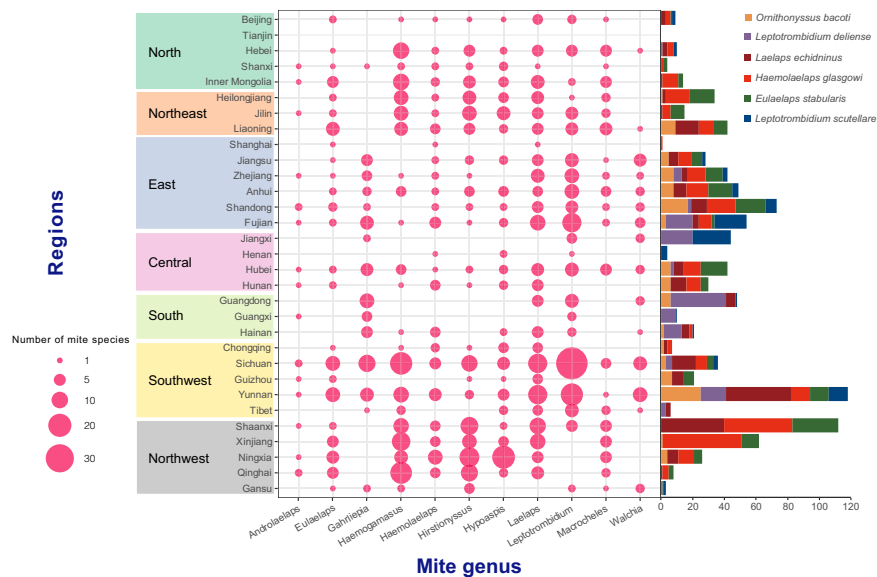


Fig. 4 The number of blood-sucking mite species of eleven main mite genera reported in different provinces with the size of red bubble indicating the number of mite species. The bar chart indicates the distribution of 6 major mite species that carry pathogens.

spanned from 1978 to 2020. To make the dataset easily filter or aggregate for investigation purposes and methodologies, each record of the mites was paired with relevant geo-positioning and timeline variables.

The dataset is helpful for understanding the spatial distributions, ecological niches, and geographic co-occurrence patterns of mite species, and can also be used to identify the spatial profile of mite-borne pathogens, with expectation that future health impacts of the mite-borne infections could be projected, and better surveillance and control of mite-borne diseases can be guided in China. The diagrams created in the paper might give a straightforward clue as to which kind of pathogen could be carried by the mites at specific locations. According to the current data review, *Leptotrombidium deliense* (*L. deliense*), *Leptotrombidium scutellare* (*L. scutellare*), *Ornithonyssus bacoti* (*O. bacoti*), *Laelaps echidninus* (*La. echidninus*), *Haemolaelaps glasgowi* (*H. glasgowi*) and *Eulaelaps stabularis* (*E. stabularis*) are the most frequently reported blood-sucking mites with competence to transmit various pathogens, which were widely distributed in China (Fig. 4). *L. deliense* and *L. scutellare* are the main vectors of *Orientia tsutsugamushi* (*O. tsutsugamushi*)^{43,44}, which have been found in more than 15 provinces of China. Both trombiculid and gamasid mites, including *O. bacoti*, *La. echidninus*, *H. glasgowi* and *E. stabularis* are naturally infected with Hantavirus, which might effectively transmit the virus⁴⁵. *L. scutellare* mites, the vector of *O. tsutsugamushi*, had been tested positive for *Rickettsia* by PCR or RT-PCR amplification, including *Rickettsia felis*, *Rickettsia australis* and an unnamed *Rickettsia* sp. TwKM02, according a report from Shandong Province in China⁴⁶.

Additionally, this dataset can be extrapolated and used to guide estimation of the global clinical burden of mite-borne diseases, which is largely unknown. Although some mite species are often limited to specific geographical regions, there might have geographic expansion that increase their potential of re-location elsewhere, probably due to international travel from endemic regions to non-endemic regions by people, animals and cargo shipment or climate change. The contemporary distributions and mapping of the mite species on a fine spatial scale would also benefit the prediction of future trends and possibility of transmission in unaffected regions by applying model construction. This dataset is crucial for developing innovative strategies to control mites and mite-borne diseases.

Code availability

No custom code was made during the collection and validation of this dataset.

Received: 11 January 2021; Accepted: 16 July 2021;

Published online: 05 August 2021

References

- Colwell, D. D., Dantas-Torres, F. & Otranto, D. Vector-borne parasitic zoonoses: emerging scenarios and new perspectives. *Vet. Parasitol.* **182**, 14–21 (2011).
- Guo, L. *et al.* Meta-transcriptomic analysis reveals the virome and viral genomic evolution of medically important mites. *J. Virol.* **95**, e01686–20 (2020).
- Javed, S., Khan, F., Ramirez-Fort, M. & Tying, S. K. Bites and mites: prevention and protection of vector-borne disease. *Curr. Opin. Pediatr.* **25**, 488–491 (2013).
- Van der Geest, L. P. *et al.* Diseases of mites. *Exp. Appl. Acarol.* **24**, 497–560 (2000).
- Kala, D. *et al.* Diagnosis of scrub typhus: recent advancements and challenges. *3 Biotech.* **10**, 396 (2020).
- Jiang, F. *et al.* Meteorological factors affect the epidemiology of hemorrhagic fever with renal syndrome via altering the breeding and hantavirus-carrying states of rodents and mites: a 9 years' longitudinal study. *Emerg. Microbes Infect.* **6**, e104 (2017).

7. Khosravani, M. The fauna and perspective of rodentia ectoparasites in Iran relying on their roles within public health and veterinary characteristics. *J. Parasit. Dis.* **42**, 1–18 (2018).
8. Wu, Q., Richard, M., Rutschmann, A., Miles, D. B. & Clobert, J. Environmental variation mediates the prevalence and co-occurrence of parasites in the common lizard, *Zootoca vivipara*. *BMC Ecol.* **19**, 44 (2019).
9. Binh, M. D. *et al.* Identification of trombiculid chigger mites collected on rodents from southern Vietnam and molecular detection of Rickettsiaceae pathogen. *Korean J. Parasitol.* **58**, 445–450 (2020).
10. Bassini-Silva, R. *et al.* A checklist of *Macronyssid* species (*Mesostigmata: Macronyssidae*) from Brazil. *J. Med. Entomol.* **58**, 625–633 (2020).
11. Roy, L. *et al.* Evaluating the link between predation and pest control services in the mite world. *Ecol. Evol.* **10**, 9968–9980 (2020).
12. Diaz, J. H. Endemic mite-transmitted dermatoses and infectious diseases in the South. *J. La. State Med. Soc.* **162**(140–145), 147–149 (2010).
13. Liu, D., Yi, T. C., Xu, Y. & Zhang, Z. Q. Hotspots of new species discovery: new mite species described during 2007 to 2012. *Zootaxa* **3663**, 1–102 (2013).
14. Peng, P. Y., Guo, X. G., Ren, T. G., Dong, W. G. & Song, W. Y. An updated distribution and hosts: trombiculid mites (Acari: *Trombidiformes*) associated with small mammals in Yunnan Province, southwest China. *Parasitol. Res.* **115**, 1923–38 (2016).
15. Xiang, R. & Guo, X. G. Research Advances of *Leptotrombidium scutellare* in China. *Korean J. Parasitol.* **59**, 1–8 (2021).
16. Lv, Y., Guo, X. G. & Jin, D. C. Research Progress on *Leptotrombidium deliense*. *Korean J. Parasitol.* **56**, 313–324 (2018).
17. Alexander, L. & Buckley, C. J. *Chigger Bites* (StatPearls, 2021).
18. Feldmeier, H. Treatment of parasitic skin diseases with dimeticone a new family of compounds with a purely physical mode of action. *Trop. Med. Health* **42**, 15–20 (2014).
19. De Luna, C. J. *et al.* The poultry red mite *Dermanyssus gallinae* as a potential carrier of vector-borne diseases. *Ann. N. Y. Acad. Sci.* **1149**, 255–258 (2008).
20. Yu, X. J. & Tesh, R. B. The role of mites in the transmission and maintenance of Hantan virus (Hantavirus: Bunyaviridae). *J. Infect. Dis.* **210**, 1693–1699 (2014).
21. Zhang, X. S., Guo, J. J., Yi, T. C. & Jin, D. C. Two new species of the genus *Onchodellus* (Acari: *Pachylaelapidae*) from China. *Zootaxa* **4801**, zootaxa.4801.3.2 (2020).
22. Huang, X. D. *et al.* Chigger mite (Acari: *Trombiculidae*) survey of rodents in Shandong Province, Northern China. *Korean J. Parasitol.* **55**, 555–559 (2017).
23. Zhang, Y. X. *et al.* Genomic insights into mite phylogeny, fitness, development, and reproduction. *BMC Genomics* **20**, 954 (2019).
24. Chen, L. *et al.* Population genomic data in spider mites point to a role for local adaptation in shaping range shifts. *Evol. Appl.* **13**, 2821–2835 (2020).
25. Lv, Y. *et al.* Relative abundance of a vector of scrub typhus, *Leptotrombidium sialkotense*, in Southern Yunnan Province, China. *Korean J. Parasitol.* **58**, 153–159 (2020).
26. Pan, W. & Deng, G. F. *China Economic Entomology, Book 17 Acarina, Gamasidae* (Science Press, 1980).
27. Cao, W. C. *et al.* *Atlas of Epidemiology of Natural Epidemic Diseases in China, Vol 1, Vol 3* (Science Press, 2019).
28. Moher, D., Liberati, A., Tetzlaff, J., Altman, D. G. & Group, P. Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement. *Int. J. Surg.* **8**, 336–341 (2010).
29. Herrera, G. *et al.* An interactive database of *Leishmania* species distribution in the Americas. *Sci. Data* **7**, 110 (2020).
30. Meng, F. F. *et al.* A dataset of distribution and diversity of blood-sucking mites in China. *figshare* <https://doi.org/10.6084/m9.figshare.13490700.v4> (2020).
31. Battle, K. E. *et al.* Global database of matched *Plasmodium falciparum* and *P. vivax* incidence and prevalence records from 1985–2013. *Sci. Data* **2**, 150012 (2015).
32. Lin, J. Z. *et al.* Investigation of free living gamasid mites in China (VII) (Acari: *Mesostigmata*). *Wuyi Sci. J.* **30**, 41–57 (2014).
33. Ding, L. M. Surveillance of animal carriers of Hantan virus and their ectoparasites at Shanghai coastal harbors. *Chin. J. Vector Biol. Control.* **22**, 4 (2011).
34. Yi, Y. *Taxonomic studies on gamasid mites of rats in Yunnan (Acari: Mesostigmata: Gamasina)*, Master Dissertation. Guizhou University, (2009).
35. Chen, B. F., Bai, X. L. & Gu, Y. M. A newspecies of *Hamolaelaps* (Acari: *Laelapidae*) from Ningxia, China. *Entomotaxonomia* **17**, 228–230 (1995).
36. Zhou, M. S. & Jiang, Z. Y. Description of *Haemogamasus trifurcisetus* sp. nov. (Acarina: *Gamasina*). *Acta Zootax. Sin.* **12**, 58–60 (1987).
37. Tian, J. Two new species of the family *Haemogamasidae* (Acari). *Acta Zootax. Sin.* **15**, 453–456 (1990).
38. Hughes, A. M. The mites of stored food and houses. London: Her Majesty's Stationary Office, 317–320 (1976).
39. Ma, Y., Ning, G. & Wei, Y. W. A new species of the genus *Hypoaspis* from Qinghai, China (Acari, *Laelapidae*). *Acta Zootax. Sin.* **28**, 356–357 (2003).
40. Bai, X. L., Yin, S. G. & Gu, Y. M. A new species and a new record of the genus *Proctolaelaps* from China (Acari: *Blattisocidae*). *Acta Zootax. Sin.* **18**, 174–176 (1993).
41. Costa, M. Mites recovered from the nests of the levant vole (*Microtus guentheri*) in Israel. *Ann. Mag. Nat. Hist.* **4**, 257–282 (1961).
42. Ma, L. M. Three new species of the genus *Pachylaelaps* from Qinghai and Gansu Provinces, China. *Entomotaxonomia* **7**, 337–340 (1985).
43. Xiang, R. & Guo, X. G. Research Advances of *Leptotrombidium scutellare* in China. *Korean J. Parasitol.* **59**, 1–8 (2021).
44. Lv, Y., Guo, X. G. & Jin, D. C. Research Progress on *Leptotrombidium deliense*. *Korean J. Parasitol.* **56**, 313–324 (2018).
45. Yu, X. J. & Tesh, R. B. The role of mites in the transmission and maintenance of Hantan virus (Hantavirus: Bunyaviridae). *J. Infect. Dis.* **210**, 1693–1699 (2014).
46. Huang, Y. *et al.* Detection of a Novel Rickettsia From *Leptotrombidium scutellare* Mites (Acari: *Trombiculidae*) From Shandong of China. *J. Med. Entomol.* **54**, 544–549 (2017).

Acknowledgements

This work was funded by grants from National Science and Technology Major Project (Grant No. 2018ZX10101003-002, 2018ZX10201001 and 2017ZX10303401-006) and the National Key Research and Development Project (No. 2019YFC1200604).

Author contributions

All the authors in the author list were all involved in the preparation and writing process of this paper, and all of them agreed to be responsible for all aspects of the research paper. W.L. and L.Q.F. designed this study; F.F.M., Q.X., J.J.C., Y.J., W.H.Z., Z.W.F. and G.P.Z. collected and tabulated the data; F.F.M., Q.X. and J.J.C. constructed the database and analyzed the data. B.G.J. and Q.X. contributed analysis methods and tools. W.L., L.Q.F. and T.X.S. provided administrative guidance in this study. F.F.M. wrote the original draft. All of the authors reviewed the manuscript and approved the final version.

Competing interests

The authors declare no competing interests.

Additional information

Correspondence and requests for materials should be addressed to L.-Q.F. or W.L.

Reprints and permissions information is available at www.nature.com/reprints.

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.

The Creative Commons Public Domain Dedication waiver <http://creativecommons.org/publicdomain/zero/1.0/> applies to the metadata files associated with this article.

© The Author(s) 2021