Keping Sun

Department of Ecology
Northeast Normal University
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EDUCATION

Ph.D. (Environmental Science). "Molecular Phylogeny of Rhinolophidae bats in China." (Jiang Feng, advisor). Northeast Normal University, Changchun, Jilin Province, 2008.

B.A. (Ecology). Northeast Normal University, Changchun, Jilin Province, 2003.

RESEARCH INTERESTS

The main research focuses on molecular and evolutionary ecology of animals, using bats as a model organism to systematically investigate speciation, adaptive evolution, and host-microbe-pathogen interaction mechanisms.

PROFESSIONAL POSITIONS

Professor. Northeast Normal University, Department of Ecology. 2018.6-present.

Associate Professor. Northeast Normal University, Department of Ecology. 2013 – 2018.6.

Ph. D. Advisor. Northeast Normal University, Department of Ecology. 2014-present.

Assistant Professor. Northeast Normal University, Department of Environmental Sciences. 2010 – 2012.

Lecturer. Northeast Normal University, Department of Environmental Sciences. 2008 - 2010.

Visiting Scholar. University of Florida, Department of Biology. 2012-2013.

Visiting Scholar. University of Maryland, Department of Biology. 2019-2020.

PUBLICATIONS

Zhu, Yue, Liu, Sen*, Jianying, Du, Yanhong, Xiao, **Sun, Keping***. Hepatic transcriptome variations among different evolutionary lineages of *Rhinolophus ferrumequinum* during hibernation, 2026, Biology, 15(5):425.

Huang, Long, Pu, Yingting, Zhao, Yanhui, Sun, Xiaoyu, Zhu, Yue, Lu, Yaping, Leng, Haixia, Feng, Jiang, Jin, Longru*, **Sun, Keping***. Diet and environmental factors jointly drive the gut microbiome, resistome, and virulome of urban bats. 2026, npj Biofilms Microbiomes 12(1):61.

Lu, Yaping, Zhu, Yue, Huang, Long, Pu, Yingting, Sun, Xiaoyu,Feng, Jiang*. **Sun, Keping***. Antifungal mechanism of ketone volatile organic compounds against *Pseudogymnoascus destructans*. 2025, Virulence, 16(1): 2569627.

Da, Yanqing, Liu, Mingxuan, Zhu, Yangshuang, Wang, Weixu, Lu, Yaping, **Sun, Keping*** Isolation of antagonistic bacterial strains and their antimicrobial volatile organic compounds against *Pseudogymnoascus destructans* in *Rhinolophus ferrumequinum* wing membranes. 2025, Ecology and Evolution, 15(7): e71628.

Jin, Longru, Zhang, Pai, **Sun, Keping***, Wang, Haitao*. Gut microbiota dynamics and their impact on body condition in nestlings of the yellow-rumped flycatchers, *Ficedula zanthopygia*. 2025, Frontiers in Microbiology, 16:1595357.

Leng, Haixia, Li, Aoqiang, Li, Zhongle, Joseph R. Hoyt,Dai, Wentao, Xiao, Yanhong, Feng, Jiang*, **Sun, Keping***Variation and assembly mechanisms of *Rhinolophus ferrumequinum* skin and cave environmental fungal communities during hibernation periods. 2025, Microbiology Spectrum, 13(3): 02233-1-24.

Wang, Denghui, Wang, Fan, Huang, Zihao, Li, Aoqiang, Dai, Wentao, Leng, Haixia, Jin, Longru, Li, Zhongle*, **Sun, Keping***, Feng, Jiang. Structure and assembly process of skin fungal communities among bat species in northern China. 2024, Frontiers in Microbiology, 15:1458258-1-11.

Lu, Yaping, Ren, Huilan, Li, Zhongle, Leng, Haixia, Li, Aoqiang, Dai, Wentao, Huang, Long, Feng, Jiang*, **Sun, Keping***. Microbiota diversity and anti-*Pseudogymnoascus destructans* bacteria isolated from *Myotis pilosus* skin during late hibernation. 2024, APPL ENVIRON MICROB, 90(8): 1-12.

Zhao, Yanhui, Wang, Lei, Liu, Sen, Pu, Yingting, **Sun, Keping***, Xiao, Yanhong*, Feng, Jiang. Adaptive evolution of the greater horseshoe bat AANAT: insights into the link between AANAT and hibernation rhythms. 2024, Animals, 14(10): 1426-1-20.

Dai, Wentao, Leng, Haixia, Li, Jun, Li, Aoqiang, Li, Zhongle, Zhu Yue, Li, Xiaolin, Jin, Longru*, **Sun, Keping***, Feng, Jiang. The role of host traits and geography in shaping the gut microbiome of insectivorous bats. 2024, Msphere, 9(4):00087-24-1-17.

Shi, Xiaoxiao, Li, Jun, Liu, Tong, Zhao, Hanbo, Leng, Haixia, **Sun, Keping***, Feng, Jiang*Divergence of cochlear transcriptomics between reference-based and reference-free transcriptome analyses among *Rhinolophus ferrumequinum* populations. 2023, PLOS ONE, 18(7):e0288404.

Li, Aoqiang, Li, Zhongle, Leng, Haixia, Jin, Longru, Xiao, Yanhong, **Sun, Keping***, Feng, Jiang*. Seasonal assembly of skin microbiota driven by neutral and selective processes in the greater horseshoe bat. 2023, Molecular Ecology, 32(16):4695-4707.

Dai, Wentao, Li, Aoqiang, Chang, Yang, Liu, Tong, Zhang, Lin, Li, Jun, Haixia, Leng, Li, Zhongle, Jin, Longru*, **Sun, Keping***, Feng, Jiang. Diet composition, niche overlap and partitioning of five sympatric rhinolophid bats in Southwestern China during summer. 2023, Frontiers in Ecology and Evolution, 11:1108514-1-12.

Li, Xiaolin, Liu, Tong, Li, Aoqiang, Xiao, Yanhong, **Sun, Keping***, Feng, Jiang*. Diversifying selection and climatic effects on major histocompatibility complex class II gene diversity in the greater horseshoe bat. 2023, Evolutionary Applications, 16(3):688-704.

Li, Jun, **Sun, Keping***, Dai, Wentao, Leng, Haixia, Feng, Jiang.Divergence in interspecific and intersubspecific gene expression between two closely related horseshoe bats (*Rhinolophus*). 2023, Journal of Mammalogy, 104(1):62-75.

Li, Aoqiang, Leng, Haixia, Li, Zhongle, Jin, Longru, **Sun, Keping***, Feng, Jiang*. Temporal dynamics of the bat wing transcriptome: insight into gene-expression changes that enable protection against pathogen, Virulence, **2022**, 14(1):2156185.

Li, Jun, **Sun, Keping***, Dai, Wentao, Leng, Haixia, Li, Aoqiang, Feng, Jiang*. Extensive adaptive variation in gene expression within and between closely related horseshoe bats (Chiroptera, Rhinolophus) revealed by three organs, Animals, **2022**, 12(23):3432.

Li, Zhongle, Li, Aaqiang, Dai, Wentao, Leng, Haixia, Liu, Sen, Jin, Longru, **Sun, Keping***, Feng, Jiang*. Skin microbiota variation among bat species in China and their potential defense against pathogens, Frontiers in Microbiology, **2022**, 13:808788-1-13.

Li, Aaqiang, Li, Zhongle, Dai, Wentao, Parise, Katy L., Leng, Haixia, Jin, Longru, Liu, Sen, **Sun, Keping***, Hoyt, Joseph R.*, Feng, Jiang. Bacterial community dynamics on bats and the implications for pathogen resistance, Environmental Microbiology, **2022**, 24(3):1484-1498.

Li, Zhongle, Li, Aoqiang, Hoyt JR, Dai, Wentao, Leng, Haixia, Li, Yanfei, Li, Wei, Liu, Sen, Jin, Longru, **Sun, Keping***, Feng, Jiang*. Activity of bacteria isolated from bats against Pseudogymnoascus destructans in China, Microbial Biotechnology, **2022**, 15(2):469-481.

Zhang, Lin, **Sun, Keping***, Csorba, Gabor, Hughes, Alice Catherine, Jin, Longru, Xiao, Yanhong, Feng, Jiang*. Complete mitochondrial genomes reveal robust phylogenetic signals and evidence of positive selection in horseshoe bats, BMC Ecology and Evolution, **2021**, 21:199.

Li, Xiaolin, Liu, Tong, Li, Aaqiang, Zhang, Lin, Dai, Wentao, Jin, Longru, **Sun, Keping***, Feng, Jiang*. Genetic polymorphisms and the independent evolution of major histocompatibility complex class II-DRB in sibling bat species Rhinolophus episcopus and Rhinolophus siamensis. Journal of Zoological Systematics and Evolutionary Research, **2021**, 59(4): 887-901.

Liu, Tong, Zhang, Kangkang, Dai, Wentao, Jin, Longru, **Sun, Keping***, Feng Jiang. Evolutionary insights into Rhinolophus episcopus (Chiroptera, Rhinolophidae) in China: Isolation by distance, environment, or sensory system? Journal of Zoological Systematics and Evolutionary Research, **2021**, 59(1):294-310.

Hoyt, Joseph R.*, Langwig, Kate E., **Sun Keping***, Parise, Katy L., Li, Aaoqiang, Wang, Yujuan, Huang, Xiaobin, Worledge, Lisa, Miller, Helen, White, J. Paul, Kaarakka, Heather, Redell, Jennifer, Görföl, Tamas, Boldogh, Sandor Andras, Fukui, Dai, Sakuyama, Muneki, Yachimori, Syuuji, Sato, Akiyoshi, Dalannast, Munkhnast, Jargalsaikhan, Ariunbold, Batbayar, Nyambayar, Yossi, Yovel, Amichai, Eran, Natradze, Ioseb, Frick, Winifred F., Foster, Jeffery, Feng, Jiang*, Kilpatrick A. Marm. Environmental reservoir dynamics predict global infection patterns and population impacts for the fungal disease white-nose syndrome, Proceedings of the National Academy of Sciences of the United States of America, **2020**, 117(13): 7255-7262.

Wang, Hui#, Zhao, Hanbo#, **Sun, Keping***, Huang, Xiaobin, Jin, Longru, Feng, Jiang*. Evolutionary basis of high-frequency hearing in the cochleae of echolocators revealed by comparative genomics, Genome Biology and Evolution, **2020**, 12: 3740-3753.

Zhao, Hanbo, Wang, Hui, Liu, Tong, Liu, Sen, Jin, Longru, Huang, Xiaobin, Dai, Wentao, **Sun Keping***, Feng, Jiang*. Gene expression vs. sequence divergence: comparative transcriptome sequencing among natural *Rhinolophus ferrumequinum* populations with different acoustic phenotypes, Frontiers in Zoology, **2019**, 16: 37-1-15.

Liu, Tong, **Sun, Keping***, Csorba Gabor, Zhang, Kangkang, Zhang, Lin, Zhao, Hanbo, Jin, Longru, Thong, Vu Dinh, Xiao, Yanhong, Feng, Jiang*. Species delimitation and evolutionary reconstruction within an integrative taxonomic framework: A case study on Rhinolophus macrotis complex (Chiroptera: Rhinolophidae), Molecular Phylogenetics and Evolution, **2019**, 139: 106544.

Zhang, Lin, **Sun, Keping***, Liu, Tong, Zhao, Hanbo, Csorba Gabor, Jin, Longru, Thong, Vu Dinh, Feng, Jiang*. Multilocus phylogeny and species delimitation within the *philippinensis* group (Chiroptera: Rhinolophidae), Zoologica Scripta, **2018**, 47:655-672.

Li, Shi, **Sun, Keping***, Lu, Guanjun, Li, Aiqing, Jiang, Tinglei, Jin, Longru, Hoyt, Joseph R., Feng, Jiang*. Mitochondrial genetic differentiation and morphological difference of *Miniopterus fuliginosus* and *Miniopterus magnater* in China and Vietnam, Ecology and Evolution, **2015**, 5(6): 1214-1223.

Sun, Keping, Meiklejohn, Kelly, Faircloth, Brant, Glenn, Travis, Braun, Edward, Kimball, Rebecca*. The evolution of peafowl and other taxa with ocelli (eyespots): a phylogenomic approach. Proceedings of the Royal Society of London Series B-Biological Sciences, **2014**, 281: 20140823.

Lu, Guanjun, Lin, Aiqing, Luo, Jinhong, Blondel, Dimitri, Meiklejohn KA, **Sun, Keping*** and Feng, Jiang*. Phylogeography of the Rickett's big- footed bat, *Myotis pilosus* (Chiroptera: Vespertilionidae): a novel pattern of genetic structure of bats in China, BMC Evolutionary Biology, **2013**, 13: 241.

GRANTS

2022.01-2025.12.

Research on dynamic variations and potential functions of skin microbial communities of greater horseshoe bats, funded by National Natural Science Foundation of China (leader).

2018.1-2021.12.

Research on adaptive differentiation of *Rhinolophus macrotis* species complex, funded by National Natural Science Foundation of China (leader).

2014.1-2017.12.

Speciation and Differentiation of sister species in *Rhinolophus* bats, funded by National Natural Science Foundation of China (leader).

2010.1-2012.12.

Population genetic structure and molecular phylogeoraphy of *Rhinolophus ferrumequinum* in China, funded by National Natural Science Foundation of China (leader).

2008.1-2010.12.

Population genetic structure and molecular phylogeoraphy of the endemic bats of *Myotis* in China, funded by National Natural Science Foundation of China (participator).

HONORS

The First Prize for Technology Progress of Jilin Province, The third contributor. 2009.
Talent Plan in Jilin Province in the New Century. 2013.

ACADEMIC POSITIONS

Members of the Chinese Zoological Society
Executive Council Member of the Jilin Provincial Society of Zoology
Vice Chairperson of the Changchun Society of Zoology