Curriculum Vitae

Ming Li, Ph.D.

Assistant Professor, Evolutionary Biology, Department of Biology,
University of Konstanz, 78457, Konstanz, Germany
Phone: +49 0174 5606764
Email: minnglee@163.com / ming.li@uni-konstanz.de
ORCID: https://orcid.org/0000-0001-7049-8666
ResearchGate: https://www.researchgate.net/profile/Ming_Li359
GitHub: https://github.com/MinngLi
Google Scholar: https://scholar.google.com/citations?user=62Sw600AAAA

Citation: 1,605; H-index: 16 (Last update: July 2025)

EDUCATION

1). 01/09/2015 – 18/06/2021: Ph.D. of Animal Genetics Breeding and Reproduction (Minor: Molecular evolution and Evolutionary genetics), Northwest A&F University, Yangling, China. (Advisor: Prof. Yu Jiang)

2). 01/09/2011 – 30/06/2015: B.Eng., (Bioinformatics), Huazhong University of Science and Technology, Wuhan, China.

POSITIONS HELD TO DATE

01/06/2025 – present: Assistant Professor, University of Konstanz, Germany.

15/09/2021 – 31/05/2025: Postdoctoral Research Fellow, University of Konstanz, Germany. (Advisor: Prof. Axel Meyer)

AWARDS AND FELLOWSHIPS

2022: Humboldt Research Fellowship for Postdocs

RESEARCH EXPERIENCES

My research mainly focuses on evolutionary genomics, with particular interest in the genetic basis of phenotypic diversity. In an effort to better understand the origin and maintenance of diversity, I mostly use comparative genomics, genome-wide association analysis, pangenome, population genetics, and other omics approaches to ask how many and what kind of genetic changes accompany phenotypic differentiation among populations and species, and its evolutionary process. My previous projects involved chicken, duck, goat, and sheep which are important domestic animals with enormous phenotypic diversity. And my current project focuses on the Midas cichlid species complex, an ideal system for rapid sympatric speciation studies. I also collaborated extensively with other researchers on many genomics-related projects.

PEER-REVIEWED PUBLICATIONS

Mainly contributed papers (#equally contributing authors *Corresponding author)

1). Dou M.#, **Li M.#**, Zheng Z.#, Chen Q., Wu Y., Wang J., Shan H., Wang F., Dai X., Li Y., Yang Z., Tan G., Luo F., Chen L., Shi Y.S., Wu J.W., Luo X.-J., Asadollahpour Nanaei H., Niyazbekova Z., Zhang G., Wang W., Zhao S., Zheng W., Wang X., Jiang Y. 2023. A missense mutation in

RRM1 contributes to animal tameness. ***Science Advances***. 9(25) doi: 10.1126/sciadv.adf4068.

2). **Li M.#**, Sun C.-J.#, Xu N.-Y.#, Bian P.-P.#, Tian X.-M.#, Wang X.-H.#, Wang Y.-Z.#, Jia X.-Z., Heller R., Wang M.-S., Wang F., Dai X.-L., Luo R.-S., Guo Y.-W., Wang X.-N., Yang P., Hu D.-X., Liu Z.-Y., Fu W.-W., Zhang S.-J., Li X.-C., Wen, C.-L., Lan F.-R., Siddiki A.-Z., Suwannapoom C., Zhao X., Nie Q.-H., Hu X.-X.*, Jiang Y.*, Yang N.* *De novo* assembly of 20 chicken genomes reveals the undetectable phenomenon for thousands of core genes on micro-chromosomes and sub-telomeric regions. ***Molecular Biology and Evolution*** (2022) doi: https://doi.org/10.1093/molbev/msac066

3). Wang M.-S.#, Zhang J.-J.#, Guo X.#, **Li M.#**, Meyer R.#, Ashari H.#, Zheng Z.-Q., Wang S., Peng M.-S., Jiang Y., Thakur M., Suwannapoom C., Esmailizadeh A., Hirimuthugoda N.-Y., Zein M.-S.-A., Kusza S., Kharrati-Koopaee H., Zeng L., Wang Y.-M., Yin T.-T., Yang M.-M., Li M.-L., Lu X.-M., Lasagna E., Ceccobelli S., Gunwardana H.-G.-T.-N., Senasig T.-M., Feng S.-H., Zhang H., Bhuiyan A.-K.-F.-H., Khan M.-S., Silva G.-L.-L.-P., Thuy L.-T., Mwai O.-A., Ibrahim M.-N.-M., Zhang G.-J., Qu K.-X., Hanotte O., Shapiro B., Bosse M.*, Wu D.-D.*, Han J.-L.*, Zhang Y.-P.* Large-scale genomic analysis reveals the genetic cost of chicken domestication. ***BMC Biology*** (2021) doi: https://doi.org/10.1186/s12915-021-01052-x

4). Li R.#, Yang P.#, **Li M.#**, Fang W.-W., Yue X.-P., Nanaei H.-A., Gan S.-Q., Du D., Cai Y.-D., Dai X.-L., Yang Q.-M., Cao C.-N., Deng W.-D., He S.-G., Li W.-R., Ma R.-L., Liu M.-J., Jiang Y.* A Hu sheep genome with the first ovine Y chromosome reveal introgression history after sheep domestication. ***SCIENCE CHINA Life Sciences*** (2020) doi: 10.1007/s11427-020-1807-0

5). Zheng Z.-Q.#, Wang X.-H.#, **Li M.#**, Li Y.-J.#, Yang Z.-R.#, Wang X.-L.#, Pan X.-Y., Gong M., Zhang Y., Guo Y.-W., Wang Y., Liu J., Cai Y.-D., Chen Q.-M., Okpeku M., Colli L., Cai D.-W., Wang K., Huang S.-S., Sonstegard T.-S., Esmailizadeh A., Zhang W.-G., Zhang T.-T., Xu Y.-B., Xu N.-Y., Yang Y., Han J.-L., Chen L., Lesur J., Daly K.-G., Bradley D.-G., Heller R., Zhang G.-J., Wang W., Chen Y.-L.*, Jiang Y.* The origin of domestication genes in goats. ***Science Advances*** (2020) doi: 10.1126/sciadv.aaz5216 (cover story)

6). Wang M.-S.#, Thakur M.#, Peng M.-S.#, Jiang Y.#, Frantz L. A. F.#, **Li M.#**, Zhang J.-J., Wang S., Peters J., Otecko N.-O., Suwannapoom C., Guo X., Zheng Z.-Q., Esmailizadeh A., Hirimuthugoda N.-Y., Ashari H., Suladari S., Zein M.-S.-A., Kusza S., Sohrabi S., Kharrati-Koopaee H., Shen Q.-K., Zeng L., Yang M.-M., Wu Y.-J., Yang X.-Y., Lu X.-M., Jia X.-Z., Nie Q.-H., Lamont S.-J., Lasagna E., Ceccobelli S., Gunwardana H.-G.-T.-N., Senasige T.-M., Feng S.-H., Si J.-F., Zhang H., Jin J.-Q., Li M.-L., Liu Y.-H., Chen H.-M., Ma C., Dai S.-S., Bhuiyan A.-K.-F.-H., Khan M.-S., Silva G.-L.-L.-P., Le T.-T., Mwai O.-A., Ibrahim M.-N.-M., Supple M., Shapiro B., Hanotte O., Zhang G.-J., Larson G., Han J.-L.*, Wu D.-D.*, Zhang Y.-P.* 863 genomes reveal the origin and domestication of chicken. ***Cell Research*** (2020) doi: 10.1038/s41422-020-0349-y (cover story)

7). Li C.-Y.#, **Li M.#**, Li X.-Y.#, Ni W.*, Xu Y.-R., Yao R., Wei B., Zhang M.-D., Li H.-X., Zhao Y., Liu L., Ullah Y., Jiang Y.*, Hu S.-W.* Whole-Genome Resequencing Reveals Loci Associated With Thoracic Vertebrae Number in Sheep. ***Frontiers in Genetics*** (2019) doi: 10.3389/fgene.2019.00674

8). Zhou Z.-K.#, **Li M.#**, Cheng H.#, Fan W.-L.#, Yuan Z.-R.#, Gao Q., Xu Y.-X., Guo Z.-B., Zhang Y.-S., Hu J., Liu H.-H., Liu D.-P., Chen W.-H., Zheng Z.-Q., Jiang Y., Wen Z.-G., Liu Y.-M., Chen H., Xie M., Zhang Q., Huang W., Wang W., Hou S.-S.*, Jiang Y.* An intercross population study reveals genes associated with body size and plumage color in ducks. ***Nature communications*** (2018) doi: 10.1038/s41467-018-04868-4

Other papers

1). Tian X.-M., Li M., Meyer A.* 2025. Insights into the genetic basis of bilateral head asymmetry in a scale-eating cichlid fish. Science Advances 11, eadw4406. doi:10.1126/sciadv.adw4406

2). Li C., Liu K., Gu C., **Li M.**, Zhou P., Chen L., Sun S., Li X., Wang L., Ni W., Li M., Hu S. 2024. Gastrointestinal jumbo phages possess independent synthesis and utilization systems of NAD+. **Microbiome**. 12(1):268. doi:10.1186/s40168-024-01984-w

3). Schartl M., Woltering J.M., Irisarri I., Du K., Kneitz S., Pippel M., Brown T., Franchini P., Li J., **Li M.**, Adolfi M., Winkler S., De Freitas Sousa J., Chen Z., Jacinto S., Kvon E.Z., Correa De Oliveira L.R., Monteiro E., Baia Amaral D., Burmester T., Chalopin D., Suh A., Myers E., Simakov O., Schneider I., Meyer A. 2024. The genomes of all lungfish inform on genome expansion and tetrapod evolution. ***Nature***. 634(8032):96-103. doi:10.1038/s41586-024-07830-1

4). Li C., Chen B., Langda S., Pu P., Zhu X., Zhou S., Kalds P., Zhang K., Bhati M., Leonard A., Huang S., Li R., Cuoji A., Wang X., Zhu H., Wu Y., Cuomu R., Gui B., **Li M**., Wang Y., Li Y., Fang W., Jia T., Pu T., Pan X., Cai Y., He C., Wang L., Jiang Y., Han J.-L., Chen Y., Zhou P., Pausch H., Wang X. 2024. Multi-omic Analyses Shed Light on The Genetic Control of High-altitude Adaptation in Sheep. ***Genomics, Proteomics & Bioinformatics***. 22(2):qzae030. doi:10.1093/gpbjnl/qzae030

5). Riccieri A., Spagoni L., **Li M.**, Franchini P., Rossi M.N., Fratini E., Cervelli M., Bologna M.A., Mancini E. 2024. Comparative genomics provides insights into molecular adaptation to hypermetamorphosis and cantharidin metabolism in blister beetles (Coleoptera: Meloidae). ***Integrative Zoology***. 19(5):975-988. doi:10.1111/1749-4877.12819

6). Yu S., Liu Z., **Li M.**, Zhou D., Hua P., Cheng H., Fan W., Xu Y., Liu D., Liang S., Zhang Y., Xie M., Tang J., Jiang Y., Hou S., Zhou Z. 2023. Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. ***Gigascience***. 12 doi: 10.1093/gigascience/giad016.

7). Cheng H., Zhang Z., Wen J., Lenstra J.A., Heller R., Cai Y., Guo Y., **Li M.**, Li R., Li W., He S., Wang J., Shao J., Song Y., Zhang L., Billah M., Wang X., Liu M., Jiang Y. 2023. Long divergent haplotypes introgressed from wild sheep are associated with distinct morphological and adaptive characteristics in domestic sheep. ***PLoS Genet***. 19(2):e1010615 doi: 10.1371/journal.pgen.1010615.

8). Li C.#, Wu Y.-J.#, Chen B.-C.#, Cai Y.-D.#, Guo J.-Z.#, Leonard A.S., Kalds P., Zhou S.-W., Zhang J.-C., Zhou P., Gan S.-Q., Jia T., Pu T.-C., Suo L.-D., Li Y., Zhang K., Li L., Purevdorj M., Wang X.-H., **Li M.**, Wang Y., Liu Y., Huang S.-H., Sonstegard T., Wang M.-S., Kemp S., Pausch H., Chen Y.-L., Han J.-L.*, Jiang Y.*, Wang X.-L.* 2022. Markhor-derived Introgression of a Genomic Region Encompassing PAPSS2 Confers High-altitude Adaptability in Tibetan Goats. ***Molecular Biology and Evolution***. 39(12):msac253 doi: 10.1093/molbev/msac253.

9). Xu N.-Y., Liu Z.-Y., Yang Q.-M., Bian P.-P., **Li M.**, Zhao X.* 2022. Genomic Analyses for Selective Signatures and Genes Involved in Hot Adaptation Among Indigenous Chickens From Different Tropical Climate Regions. ***Frontiers in Genetics***. 13:906447 doi: 10.3389/fgene.2022.906447.

10). Yang Z.-R.#, Li J.-X.#, Zheng Z.-Q., Zhao C., Wang Y., **Li M.**, Nanaei H.A., Dai X.-L., Li Y.-J., Li R., Cao C.-N., Li M., Jiang Y.*, Zheng W.-X.*, Wang X.-H.* 2022. Allele-specific expression analyses reveal immune divergences between ibex and goat species. ***Zoological Research***. 43(4):671-674 doi: 10.24272/j.issn.2095-8137.2022.003.

11). Xu N.-Y., Si W., **Li M.**, Gong M., Lariviere J.-M., Nanaei H.-A., Bian P.-P., Jiang Y.*, Zhao X.* Genome-wide scan for selective footprints and genes related to cold tolerance in Chantecler chickens. ***ZOOLOGICAL RESEARCH*** (2021) doi: 10.24272/j.issn.2095-8137.2021.189

12). Pan X.-Y.#, Cai Y.-D.#, Li Z.-J.#, Chen X.-Q.#, Heller R.#, Wang N.-N.#, Wang Y., Zhao C., Wang Y., Xu H., Li S.-H., **Li M.**, Li C.-Y., Hu S.-W., Li H., Wang K., Chen L., Wei B., Zheng Z.-Q., Fu W.-W., Yang Y., Zhang T.-T., Hou Z.-T., Yan Y.-Y., Lv X.-Y., Sun W., Li X.-Y., Huang S.-S., Liu L.-X., Mao S.-Y., Liu W.-Q., Hua J.-L., Li Z.-P., Zhang G.-J., Chen Y.-L., Wang X.-H., Qiu Q.,

Dalrymple B.-P., Wang W.*, Jiang Y.* Modes of genetic adaptations underlying functional innovations in the rumen. ***SCIENCE CHINA Life Sciences*** (2020) doi: 10.1007/s11427-020-1828-8 (cover story)

13). Li R.#, Tian X.-M.#, Yang P., Fan Y.-Z., **Li M.**, Zheng H.-X., Wang X.-H., Jiang Y.* Recovery of non-reference sequences missing from the human reference genome. ***BMC Genomics*** (2019) doi: 10.1186/s12864-019-6107-1

14). Wang Y., Gao S., Zhao Y., Chen W.-H., Shao J.-J., Wang N.-N., **Li M.**, Zhou G.-X., Wang L., Shen W.-J., Xu J.-T., Deng W.-D., Wang W., Chen Y.-L., Jiang Y.* Allele-specific expression and alternative splicing in horse x donkey and cattle x yak hybrids. ***ZOOLOGICAL RESEARCH*** (2019) doi: 10.24272/j.issn.2095-8137.2019.042 (cover story)

15). Cheng H.#, Liu J.#, Wen J.#, Nie X.-J.#, Xu L.-H., Chen N.-B., Li Z.-X., Wang Q.-L., Zheng Z.-Q., **Li M.**, Cui L.-C., Liu Z.-H., Bian J.-X., Wang Z.-H., Xu S.-B., Yang Q., Appels R., Han D.-J., Song W.-N.*, Sun Q.-X.*, Jiang Y.* Frequent intra- and inter-species introgression shapes the landscape of genetic variation in bread wheat. ***Genome Biology*** (2019) doi: 10.1186/s13059-019-1744-x

16). Tian X.-M.#, Li R.#, Fu W.-W.#, Li Y.#, Wang X.-H., **Li M.**, Du D., Tang Q.-Z., Cai Y.-D., Long Y.-M. Zhao Y., Li M.-Z.*, Jiang Y.* Building a sequence map of the pig pan-genome from multiple *de novo* assemblies and Hi-C data. ***SCIENCE CHINA Life Sciences*** (2019) doi: 10.1007/s11427-019-9551-7

17). Wang Y.#, Zhang C.-Z.#, Wang N.-N.#, Li Z.-P.#, Heller R.#, Liu R.#, Zhao Y.#, Han J.-G.#, Pan X.-Y., Zheng Z.-Q., Dai X.-Q., Chen C.-S., Dou M.-L., Peng S.-J., Chen X.-Q., Liu J., **Li M.**, Wang K., Liu C., Lin Z.-S., Chen L., Hao F., Zhu W.-B., Song C.-C., Zhao C., Zheng C.-L., Wang J.-M., Hu S.-W., Li C.-Y., Yang H., Jiang L., Li G.-Y., Liu M.-J., Sonstegard T.-S., Zhang G.-J., Jiang Y.*, Wang W.*, Qiu Q.* Genetic basis of ruminant headgear and rapid antler regeneration. ***Science*** (2019) doi: 10.1126/science.aav6335 (cover story)

18). Fan W.-L., Xu L.-Y., Cheng H., **Li M.**, Liu H.-H., Jiang Y., Guo Y.-M., Zhou Z.-K.*, Hou S.-S.* Characterization of Duck (*Anas platyrhynchos*) Short Tandem Repeat Variation by Population-Scale Genome Resequencing. ***Frontiers in Genetics*** (2018) doi: 10.3389/fgene.2018.00520

INVITED RESEARCH TALKS

1). 21/07/2025: "Evolution and maintenance of a transspecies color polymorphism" Annual Meeting of the Society for Molecular Biology & Evolution, 2025 (Beijing, China)

2). 17/07/2025: "Evolution and maintenance of a transspecies color polymorphism" South China Sea Institute of Oceanology, CAS

3). 02/01/2025: "Time matters: color polymorphism maintenance under strong assortative mating in crater lake cichlid fish" Kunming institute of zoology, CAS.

4). 04/06/2022: "The role of structural variations in parallel sympatric speciation of Midas cichlids" ***Genomics of Convergence Symposium*** *(Konstanz, Germany)*

5). 28/07/2021: "Uncovering abundant missing genes in the chicken reference genome solves the avian gene depletion puzzle" ***ISAG 2021 Virtual Conference***

ABSTRACTS / POSTERS

1). 26/07/2021 – 30/07/2021: **Li M.**, Xu N.-Y., Bian P.-P., Hu X.-X., Jiang Y., Yang N. "Uncovering abundant missing genes in the chicken reference genome solves the avian gene depletion puzzle" ***ISAG 2021 Virtual Conference***

2). 28/06/2020 – 02/07/2020: Wang M.-S., Thakur M., Peng M.-S., Jiang Y., Frantz L., **Li M.**, Shapiro B., Larson G., Han J.-L., Wu D.-D., Zhang Y.-P. "863 genomes reveal the origin and domestication of chicken" ***SMBE 2020*** *(Montréal, Québec, Canada)*

3). 15/07/2019 – 18/07/2019: Xu N.-Y., Si W., **Li M.**, Jiang Y., Zhao X. "Whole-genome resequencing identifies potential genes for cold adaption in the Chantecler chicken breed" ***Poultry Science Association 2019 Annual Meeting*** *(Montréal, Québec, Canada)*

TEACHING EXPERIENCES

1). 2022, 2023 and 2024: Co-instructor: "Molecular Evolutionary Biology" to Bachelor and Master students (VTK program). Course code: BIO-11130. University of Konstanz, Germany.

2). 19/11/2019: "Genome-wide association study analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University

3). 08/10/2018: "Adaptive evolution analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University

4). 17/10/2017: "Genome-wide association study analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University

REVIEWER FOR PEER-REVIEWED JOURNALS

Molecular Biology and Evolution; Molecular Ecology; Review editor of Frontiers in Genetics; Biology; Genes; Diversity.