

Curriculum Vitae

Ming Li, Ph.D.

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

POSITIONS HELD TO DATE

15/09/2021-present: Postdoctoral Research Fellow, University of Konstanz, Germany.

RESEARCH EXPERIENCES

Linking genomic variation and phenotypic diversity has always been a key challenge in evolutionary and genetic studies. My research mainly focuses on identifying genomic variation of different animals through the analysis of large-scale genomic data, and inferring the evolutionary process and genetic basis of key economic/ecological traits through pangenome analysis, genome selection analysis, genome-wide association analysis, and other omics methods including RNA-seq, Hi-C, ChIP-seq, ATAC-seq, etc. My previous projects were 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. As a bioinformatics analyst with ten years of experience, I also collaborated extensively with other researchers on many genomics-related projects.

My previous key research projects include:

- 1). Identifying comprehensive genomic variants through pan-genome analysis in chicken, pig, and human.
- 2). The genetic basis underlying the domestication of duck, chicken and goat.
- 3). Genetic variation underlying phenotypic trait changes in duck (body size and plumage color) and sheep (thoracic vertebrae number).
- 4). Identifying the source and direction of introgression from closely related species to facilitate local adaptations.

TECHNIQUES & SKILLS

Re-sequencing and population genetics analysis.

De novo genome assembly.

Comparative genomic analysis

3D genome analysis (Hi-C).

Transcriptome analysis with RNA-seq.

ChIP-seq and ATAC-seq analysis.

Statistical analysis.

Linux, Python, and R script skills and experience in working with super computer (cluster server).

PEER-REVIEWED PUBLICATIONS

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

- 1). **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>
- 2). 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-Koopae 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> (**mainly contributed to genetic load analysis**)
- 3). 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 (**mainly contributed to the population structure analysis of Y chromosome**)
- 4). 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) (**mainly contributed to genome selection and introgression analysis**)
- 5). 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-Koopae 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., Senasig 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) (**mainly contributed to genome selection, mitochondria, and W chromosome analysis**)
- 6). 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 (**mainly contributed to genome selection analysis**)
- 7). 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 (**mainly contributed to population structure, genome selection, and the detailed analysis of the genetic basis of body size**)

Other papers

- 1). 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
- 2). 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)

- 3). 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
- 4). 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)
- 5). 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
- 6). 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
- 7). 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)
- 8). 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). 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). 19/11/2019: "Genome-wide association study analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University
- 2). 08/10/2018: "Adaptive evolution analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University
- 3). 17/10/2017: "Genome-wide association study analysis (Experiment)" course on "Bioinformatics" at Northwest A&F University