

CURRICULUM VITAE

Given name: Zhongying **Last name:** Zhao

Chinese name: 趙中應

Research interests: Functional and comparative genomics, bioinformatics, systems biology, developmental biology, evolutionary genetics,

Summary of research profile

Research in my laboratory can be broadly classified into the following two categories

Mechanism of postzygotic hybrid incompatibilities between nematode species

Hybrid incompatibility (HI), including sterility and lethality between closely related species has been noticed over a century ago, but only recently is it possible to decipher the molecular basis of speciation. However, *C. elegans* has not been explored for such research because there is no sister species found with which it mates and produce hybrid viable progeny. *C. briggsae* is the closest living relative of *C. elegans*. We are trying to develop new tools and resources to make *C. briggsae* and its newly isolated sister species, *C. nigoni*, as an attractive model system for research into molecular mechanisms of hybrid incompatibility.

Gene regulatory networks underlying cell fate determination during nematode embryogenesis

During *C. elegans* embryogenesis, the developmental potential of the fertilized egg is restricted in a stepwise manner following each cell division by differentially expressing a cohort of regulatory proteins. Together with the genetic and genomic tools, especially CHIP-Seq, we have been using automatic lineaging to dissect the gene regulatory network underlying the tissue/organ formation.

Academic qualifications

- 06/2005 – 09/2010, Senior Research Fellow, Department of Genome Sciences, University of Washington, Seattle, WA, USA
- 05/2000 – 05/2005, Ph.D., Department of Molecular Biology and Biochemistry, Simon Fraser University, BC, Canada
- 09/1993 – 07/1996, MSc., Department of Biology, Beijing Normal University, Beijing, China
- 09/1989 – 07/1993, BSc., Department of Biology, Anhui Normal University, Wuhu, China

Previous academic positions

- 10/2010 – 08/2015: Assistant professor, Department of Biology, Hong Kong Baptist University, Hong Kong

- 09/2015 – 08/2018: Associate professor, Department of Biology, Hong Kong Baptist University, Hong Kong

Current academic position

- 09/2018 – Present: Professor, Department of Biology, Hong Kong Baptist University, Hong Kong

Professional experiences/services

- RAE 2020 academic leader, Department of Biology, Hong Kong Baptist University
- 02/2013 – 01/2019/, panel member of Hong Kong RGC, Biology and Medicine Panel, Hong Kong RGC and NSF China joint Scheme
- Associate Editor of *Scientific Reports*
- Associate Editor of *Frontiers in Physiology*
- Grant reviewer for NSF, USA, 01-2019 - present
- Grant reviewer for NSERC, Canada, 10-2018 – present
- Journal reviewer, Genetics, Genome Biology, Genome Research, PLoS Genetics, Nucleic Acid Research.

Selected talks at major international conferences

- June 2021, 23rd International *C. elegans* Conference, UCLA, Los Angeles, CA, USA. Invited talk.
- June, 2019, Direct full-length RNA sequencing reveals unexpected transcriptome complexity during *C. elegans* development, 22nd International *C. elegans* Conference, UCLA, Los Angeles, CA, USA. Invited talk.
- June, 2019, Gap phase introduction in every cell cycle of *C. elegans* embryogenesis, 22nd International *C. elegans* Conference, UCLA, Los Angeles, CA, USA. Invited talk.
- June, 2018, *C. elegans* Development, Cell biology and Gene Expression Meeting, Barcelona, Spain. Invited talk.
- March, 2016, Evolutionary Biology of *Caenorhabditis* and Other Nematodes, Cold Spring Harbor Laboratory, NY, USA. Invited speaker and session chair.
- June, 2016, *C. elegans* Development, Cell Biology & Gene Expression Meeting / 7th Asia-Pacific *C. elegans* Meeting, Beijing, China. Invited talk.

- July, 2014, *C. elegans* Development, Cell Biology & Gene Expression Meeting / 6th Asia-Pacific *C. elegans* Meeting, Nara, Japan. Invited talk.

External grants awarded in the past 8 years

1. Principle coordinator (PC) of Collaborative Research Fund awarded by Hong Kong Research Grant Council (RGC) (5.75 million HKD), 2012-2015
2. PI of General Research Fund (GRF) funded by Hong Kong RGC (1.16 million HKD), 2021-2023
3. PI of RGC-NSFC Joint Scheme, Biology and Medicine (1.16 million HKD), 2019-2022
4. PI of General Research Fund (GRF) funded by Hong Kong RGC (0.86 million HKD), 2018-2021
5. PI of General Research Fund (GRF) funded by Hong Kong RGC (0.65 million HKD), 2017-2020
6. PI of General Research Fund (GRF) funded by Hong Kong RGC (1.26 million HKD), 2016-2019
7. Co-Principle Investigator (Co-PI) of Collaborative Research Fund awarded by Hong Kong Research Grant Council (6.8 million HKD), 2015-2017
8. PI of General Research Fund (GRF) funded by Hong Kong RGC (0.66 million HKD), 2014-2017
9. Co-PI of NSFC Young Scientist Fund by China NSF (200,000 RMB), 2013-2015
10. PI of Early Career Scheme (ECS) Award funded by Hong Kong RGC (1.94 million HKD), 2012-2016

Representative publications in the past seven years as a corresponding author after becoming a PI in Hong Kong

1. Dongying Xie^{1, #}, Hin Chu^{2, #}, Dong Yang^{2, #}, Qiutao Ding¹, Gefei Huang^{3,6}, Luo Chen¹, Zongwei Cai^{3,6*}, Jiandong Huang^{4,5*}, and **Zhongying Zhao**^{1,6*}. 2021 A stark difference in the profiles of defective viral transcripts between SARS-CoV-2 and SARS-CoV. *Journal of infection*. 2021 Sep;83(3):381-412
2. Zhongyang Lin, Yichun Xie, Wenyan Nong, Xiaoliang Ren, Runsheng Li, **Zhongying Zhao**, Jerome Ho Lam Hui, Karen Wing Yee Yuen* Formation of artificial chromosomes in *Caenorhabditis elegans* and analyses of their segregation in mitosis, DNA sequence composition and holocentromere organization. *Nucleic Acids Res*. 2021, 49(16):9174-9193 PMID: 34417622. DOI: 10.1038/s41467-020-19863-x.
3. Jianfeng Cao, Guoye Guan, Vincy Wing Sze Ho, Ming-Kin Wong, Lu-Yan Chan, Chao Tang*, **Zhongying Zhao*** & Hong Yan* Establishment of morphological atlas of *Caenorhabditis elegans* embryo using deep-learning-based 4D segmentation. *Nature Communications*. 2020. DOI: 10.1038/s41467-020-19863-x.
4. Shoudong Zhang, Runsheng Li, Li Zhang, Shengjie Chen, Min Xie, Liu Yang, Yiji Xia, Christine H. Foyer, **Zhongying Zhao***, Hon-Ming Lam* New insights of *Arabidopsis*

transcriptome complexity revealed by direct sequencing of native RNAs. *Nucleic Acids Research*. 2020, <https://doi.org/10.1093/nar/gkaa588>.

5. Runsheng Li#, Xiaoliang Ren#, Qiutao Ding, Yu Bi, Dongying Xie, **Z Zhao***. Direct full-length RNA sequencing reveals unexpected transcriptome complexity during *C. elegans* development. *Genome Research*. 2020 Feb;30(2):287-298.
6. Bi Y, Ren X, Li R, Ding Q, Xie D, **Zhao Z***. Specific Interactions between Autosome and X Chromosomes Cause Hybrid Male Sterility in *Caenorhabditis* Species. *Genetics*. 2019 Jul;212(3):801-813.
7. Ren X, Li R, Wei X, Bi Y, Ho VW, Ding Qiu, Zhang Z, Hsieh C, Young A, Zeng J, Liu X, **Zhao Z***. Genomic bases of recombination suppression in the hybrid between hermaphroditic *Caenorhabditis briggsae* and gonochoristic *C. nigoni*. *Nucleic Acids Res*. 2018 Feb 16;46(3):1295-1307.
8. Chen L, Ho VW, Wong MK, Huang X, Chan L, Ng HC, Ren X, Yan H & **Zhao Z***. Establishment of Signaling Interactions with Cellular Resolution for Every Cell Cycle of Embryogenesis. *Genetics* (**highlighted**). 2018 May;209(1):37-49. doi: 10.1534/genetics.118.300820.
9. Li R, Ren X, Bi Y, Ding Q, Ho VWS, **Zhao Z***. Comparative mitochondrial genomics reveals a possible role of a recent duplication of NADH dehydrogenase subunit 5 in gene regulation. *DNA Res*. 2018 Dec 1;25(6):577-586.
10. An X, Shao J, Zhang H, Ren X, Ho VWS, Li R, Wong MK, **Zhao Z***. Comparative proteome analysis between *C. briggsae* embryos and larvae reveals a role of chromatin modification proteins in embryonic cell division. *Sci Rep*. 2017 Jun 27;7(1):4296. doi: 10.1038/s41598-017-04533-8.
11. Li R, Ren X, Bi Y, Ho VW, Hsieh CL, Young A, Zhang Z, Lin T, Zhao Y, Miao L, Sarkies P*, **Zhao Z***. Specific Downregulation of Spermatogenesis Genes Targeted by 22G RNAs in Hybrid Sterile Males Associated with an X-Chromosome Introgression. *Genome Research*. 2016, 26(9):1219-32
12. Ho VW#, Wong MK#, An X#, Guan D#, Shao J, Ng HC, Ren X, He K, Liao J, Ang Y, Chen L, Huang X, Yan B, Xia Y, Chan LL, Chow KL, Yan H, **Zhao Z***. Systems-level quantification of division timing reveals a common genetic architecture controlling asynchrony and fate asymmetry. *Molecular Systems Biology*. 2015, 11(6):814.
13. Yu Bi#, Xiaoliang Ren#, Cheung Yan, Jiaofang Shao, Dongying Xie and **Zhongying Zhao***. Genome-Wide Introgression Revealed Pervasive Hybrid Incompatibilities (HI) between *Caenorhabditis* species. *PLoS Genetics*. 2015, 11(2):e1004993. **Faculty of 1000 recommended.**

14. Wong MK, Guan D, Ng KH, Ho VW, An X, Li R, Ren X, **Zhao Z***. Timing of Tissue-specific Cell Division Requires a Differential Onset of Zygotic Transcription during Metazoan Embryogenesis. *Journal of Biological Chemistry*. 2016 291(24):12501-13.
15. Runsheng Li, Chia-Ling Hsieh, Amanda Young, Zhihong Zhang, Xiaoliang Ren and **Zhongying Zhao*** Illumina Synthetic Long Read Sequencing Allows Recovery of Missing Sequences even in the "Finished" *C. elegans* Genome. *Scientific Reports*. 2015, 5:10814.
16. Huang RE, Ye W, Ren X, **Zhao Z***. Morphological and Molecular Characterization of *Phasmarhabditis huizhouensis* sp. nov. (Nematoda: Rhabditidae), a New Rhabditid Nematode from South China. *PLoS One*. 2015 Dec 16;10(12):e0144386.
17. Jiaofang Shao#, Kan He#, Hao Wang#, Wing Sze Ho, Xiaoliang Ren, Xiaomeng An, Ming Kin Wong, Bin Yan, Dongying Xie, John Stamatoyannopoulos* and **Zhongying Zhao***. Collaborative Regulation of Development but Independent Control of Metabolism by Two Epidermis Specific Transcription Factors in *C. elegans*. *Journal Biological Chemistry*. 2013, 15;288(46):33411-26.
18. Huang RE, Ren X, Qiu Y, **Zhao Z***. Description of *Caenorhabditis sinica* sp. n. (Nematoda: Rhabditidae), a nematode species used in comparative biology for *C. elegans*. *PLoS One*. 2014 Nov 6;9(11):e110957.
19. Yan C, Bi Y, Yin D, **Zhao Z***. A method for rapid and simultaneous mapping of genetic loci and introgression sizes in nematode species. *PLoS One*. 2012;7(8):e43770.

Other representative publications in the past seven years as a corresponding author after becoming a PI in Hong Kong

1. Sun J, Mu H, Ip JCH, Li R, Xu T, Accorsi A, Sánchez Alvarado A, Ross E, Lan Y, Sun Y, Castro-Vazquez A, Vega IA, Heras H, Ituarte S, Van Bocxlaer B, Hayes KA, Cowie RH, **Zhao Z**, Zhang Y, Qian PY, Qiu JW. Signatures of Divergence, Invasiveness, and Terrestrialization Revealed by Four Apple Snail Genomes. *Mol Biol Evol*. 2019 Jul 1;36(7):1507-1520.
2. Liang W, Yang Y, Fang Y, **Zhao Z**, Hu J. Bayesian Detection of Abnormal Asynchrony of Division Between Sister Cells in Mutant *Caenorhabditis elegans* Embryos. *J Comput Biol*. 2019 May;26(5):495-505.
3. Cao J, Wong MK, **Zhao Z**, Yan H. 3DMMS: robust 3D Membrane Morphological Segmentation of *C. elegans* embryo. *BMC Bioinformatics*. 2019 Apr 8;20(1):176.

4. Huang XT, Zhu Y, Chan LHL, **Zhao Z**, Yan H. Inference of cellular level signaling networks using single-cell gene expression data in *Caenorhabditis elegans* reveals mechanisms of cell fate specification. *Bioinformatics*. 2017 May 15;33(10):1528-1535.
5. Guan D, Yan B, Thieme C, Hua J, Zhu H, Boheler KR, **Zhao Z**, Kragler F, Xia Y, Zhang S*. PlaMoM: a comprehensive database compiles plant mobile macromolecules. *Nucleic Acids Res*. 2017 Jan 4;45(D1):D1021-D1028.
6. Guan D, Shao J, **Zhao Z**, Wang P, Qin J, Deng Y, Boheler KR, Wang J, Yan B*. 2014 PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. *Nucleic Acids Research*. 2014, 42: W130-6.
7. Guan D, Shao J, Deng Y, Wang P, **Zhao Z**, Liang Y, Wang J, Yan B. CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. *Bioinformatics*. 2014 Jan 21.
8. Yalamanchili HK, Yan B, Li MJ, Qin J, **Zhao Z**, Chin FY, Wang J. DDGni: dynamic delay gene-network inference from high-temporal data using gapped local alignment. *Bioinformatics*. 2014 Feb 1;30(3):377-83.
9. Chen L, Chan LL, **Zhao Z**, Yan H. A novel cell nuclei segmentation method for 3D *C. elegans* embryonic time-lapse images. *BMC Bioinformatics*. 2013;14:328. doi: 10.1186/1471-2105-14-328.
10. Huang X, Chen L, Chim H, Chan LL, **Zhao Z***, Yan H. Boolean genetic network model for the control of *C. elegans* early embryonic cell cycles. *Biomed Eng Online*. 2013;12

For all publications, see <https://www.ncbi.nlm.nih.gov/pubmed/?term=Zhongying+Zhao>

Equal contributor, * Corresponding author

Patents

1. US patent, 10,255,692 B2

Title: Method for tracking an object in an image sequence

Inventers: Long Chen, Zhongying Zhao, Hong Yan

Approved date: April 9, 2019

2. US Patent, 2021/0139977A1

Title: Method for identifying RNA isoforms in transcriptome using Nanopore RNA reads.

Inventors: ZHAO Zhongying & LI Runsheng,

Approved Date: May 13, 2021

3. US provisional patent: 63/230,171

Title: Highly effective antisense oligoes (ASOs) that target the negative strand of SARS-CoV-2 RNA genome.

Applicant: ZHAO Zhongying.

Filing date: August 6th, 2021. Application No: 63/230,171

Courses taught:

- Genetics (undergraduate)
- Developmental Biology (undergraduate and Rpg)
- Molecular Biology (undergraduate and Rpg)
- Advanced topics (Rpg)

Contact

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