

**BIOGRAPHICAL SKETCH**

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NAME: Xuegeng Wang

eRA COMMONS USER NAME (credential, e.g., agency login): WANGXUEGENG

POSITION TITLE: Postdoctoral Researcher

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Nankai University, Tianjin	B. S	09/2006	07/2010	Bioscience
Peking University, Beijing	Ph.D.	09/2010	01/2017	Cell/Developmental Biology
The University of North Carolina at Greensboro, Greensboro	Postdoctoral	05/2017	present	Developmental Biology

**A. Personal Statement**

I have the expertise, training, and motivation necessary to successfully carry out the proposed research project. My long-standing interest has been in developmental biology and epigenetics, and I have developed a great appreciation for the mechanisms of epigenetic inheritance. My academic training and research experience have provided me with an excellent background in multiple biological disciplines including molecular biology, genetics, developmental biology and bioinformatics. During my Ph.D. studies, I focused on the mechanisms of development and reprogramming of somatic cell nuclear transfer (SCNT) embryos using zebrafish model. Two manuscripts are under preparation to submit right now. I am skilled in molecular and genetic approaches and have lot of experience in fish embryonic manipulation. I also accumulated a lot of experience in bioinformatics and high-through sequencing library preparation during the past years. In addition, I successfully participated in the projects collaborated with other researchers. As a result of these previous experiences, I am aware of the importance of frequent communication among project members and of constructing a realistic research plan. For my postdoctoral training, I will continue to build on my previous training in epigenetic inheritance by moving into a transgenerational inheritance system that will allow me to address additional questions regarding the mechanism of epigenetic inheritance. My research focus is to dissect phenotypes and their genome wide epigenetic association in medaka fish exposed to environmental stressors.

1. **Xuegeng Wang**, Zuoyan Zhu, Yonghua Sun, Jue Zhao. 2013. Nuclear transfer and reprogramming in fish. *Hereditas(Beijing)*, 35(4), 433-440.(Review, written in Chinese)
2. Lan Jiang, Jing Zhang, Jing-Jing Wang, Lu Wang, Li Zhang, Guoqiang Li, Xiaodan Yang, Xin Ma, Xin Sun, Jun Cai, Jun Zhang, Xingxu Huang, Miao Yu, **Xuegeng Wang**, Feng Liu, Chung-I Wu, Chuan He, Bo Zhang, Weimin Ci, Jiang Liu. 2013. Sperm, but Not Oocyte, DNA methylome is inherited by zebrafish early embryos. *Cell*, 153:773-784.
3. **Xuegeng Wang\***, Yi Zhao\*, Tian Tian, Zuoyan Zhu, Jingchu Luo, Jue Zhao. Genome-wide DNA methylation analysis of somatic cell nuclear transfer(SCNT) zebrafish embryos. (In preparation, \* co-first author).
4. Yi Zhao\*, **Xuegeng Wang\***, Zuoyan Zhu, Jingchu Luo, Jue Zhao. The DNA methylation landscape of zebrafish embryos during blastula gastrulation transition. (In preparation, \* co-first author).

## B. Positions and Honors

### Positions and Employment

2017- Postdoctoral Fellow with Dr. Ramji Bhandari, Department of biology, The University of North Carolina at Greensboro, NC

### Honors

2015- Excellent Reporting Award, The 4<sup>th</sup> Chinese Zebrafish Conference

2015- Zeiss-Zebrafish Scientific Research Award

## C. Contributions to Science

1. I analyzed DNA methylation patterns during embryonic development of SCNT zebrafish embryos and generated a series of single-base resolution DNA methylomes. I compared DNA methylation patterns of SCNT embryos with normal embryos and studied the dynamics of genomic elements. I further analyzed the differentially methylated sites, differentially methylated regions and differentially methylated promoters between SCNT embryos and normal embryos.
  - a) **Wang\***, X.; Zhao\*, Y.; Tian, T.; Zhu, Z.; Luo, J.; Zhao, J. (2018). Genome-wide DNA methylation analysis of somatic cell nuclear transfer (SCNT) in zebrafish embryos. (*In preparation*, \* co-first author).
  - b) Zhao\*, Y.; **Wang\***, X., Zhu, Z.; Luo, J.; Zhao, J. (2018). The DNA methylation landscape of zebrafish embryos during blastula gastrulation transition. (*In preparation*, \* co-first author).
2. I studied the roles of transcription factors in embryonic development of SCNT embryos by examining the expression patterns of these factors. I genetically manipulated expression of genes to maximize success of SCNT embryos.
3. Past exposures to environmental chemicals can result in disease in future generations. This process is believed to be mediated by epigenetic mechanisms. Currently, together with Dr. Bhandari, I am examining what epigenetic marks are established on the genome in response to bisphenol A exposure and in what form they are being transmitted and what is their relationship with diseases in future generations. I am developing CRISPR-dCas9 system to edit epigenetic alterations *in vivo* with an aim to restore normal health from transgenerational defects.
  - c) Bhandari, R.K.; **Wang**, X.; Jandegian, C.; vom Saal, F.S.; Tillitt D.E.. Transcriptome analysis of testis reveals the effects of developmental exposure to bisphenol A or 17 $\alpha$ -ethinylestradiol in medaka. (Submitted, \* co-first author).
  - d) **Wang**, X.; Bhandari, R.K. Global genome methylation changes during early embryonic development in medaka, *Oryzias latipes*. (*Submitted*).
  - e) **Wang**, X., Hill, D.; Bouttier, M.; Bhandari; R.K. Gene expression profile reveal transgenerational osmoregulatory stress in medaka gills induced by past embryonic exposure to bisphenol A and 17 $\alpha$ -ethinylestradiol. (*Submitted*).

## D. Additional Information: Research Support and/or Scholastic Performance

N/A