BIOGRAPHICAL SKETCH

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NAME: Xuegeng Wang

eRA COMMONS USER NAME:

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	Biosciences
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, Environmental Epigenetics

A. Personal Statement

My long-standing interest has been in developmental biology, epigenetics, and 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. program, I focused on the mechanisms underlying epigenetic reprogramming embryos generated by somatic cell nuclear transfer (SCNT) using zebrafish as an organismal model. My skills include methods in molecular biology (gene expression and next generation sequencing) and genetic manipulation (CRISPR-Cas9, CRISPR-dCas9, TALEN, and RNAi). I have extensive experience in fish embryo manipulation. I am capable of library preparation for whole genome sequencing and high throughput sequence data analysis using bioinformatic tools/languages that are publicly available. In addition, I have 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 field of science that will allow me to address additional questions regarding the mechanism of epigenetic inheritance of phenotypic traits, health, and diseases. My current research focus at the Bhandari Laboratory is to dissect mechanisms underlying environmentally induced phenotypes and their genome-wide epigenetic association using medaka fish as an organismal model. Recently, I have successfully developed a Crispr-dCas9 method to introduce DNA methylation into a genomic locus using Crispr-dCas9-mdDnmt3aa system. Following are relevant publications, which are being revised or in preparation.

1. 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.
2. 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)
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. (Submitted, * 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. (Submitted, * co-first author).
5. Wang, X. Bhandari, R.K. (2019). Incorporation of DNA methylation into hypomethylated genomic locus by Crispr-dCas9. (In preparation)

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, USA.

Honors

2015- Excellent Reporting Award, The 4th 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.
   a) Wang, X.; Bhandari, R.K. (2019). DNA methylation Dynamics during epigenetic reprogramming in medaka embryos. *Epigenetics*. 14(6):611-622.
   b) Wang, X., *Hill, D., Tillitt, D.E., Bhandari, R.K (2019). Bisphenol A and 17alpha-ethinylestradiol induced transgenerational differences in expression of osmoregulatory genes in the gill of medaka (Oryzias latipes). Aquatic Toxicology. 211: 227-234.
   c) Wang, X., Bhandari, R.K. The Dynamics of DNA Methylation during Epigenetic Reprogramming of Primordial Germ Cells in Medaka (*Oryzias latipes*), *In review*
   d) Thayil, A.J., Wang, X., Bhandari, P., vom Saal, F.S., Tillitt, D.E., Bhandari, R.K. Bisphenol A and 17 alpha-ethinylestradiol-induced Transgenerational Gene Expression Differences in the Brain-Pituitary-Testis Axis of Medaka, Oryzias latipes. In review.
   e) Song, X., Wang, X., Bhandari, R.K. Developmental abnormalities and epigenetic effects in medaka (Oryzias latipes) embryo induced by triclosan exposure. In review.
   f) Bhandari, R.K., Wang, X., vom Saal, F.S., Tillitt, D.E. Transcriptome analysis of testis reveals the effects of developmental exposure to bisphenol A or 17α-ethinylestradiol in medaka. *In review*

Additional Information: Research Support and/or Scholastic Performance
N/A