

# Xin Zhao (David)

## Laboratory Scientist

davidzhao1015@gmail.com

[LinkedIn](#)

[GitHub](#)

### EDUCATION

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#### **University of Alberta** - Doctorate, Food Science and Technology

September 2013 - November 2018

Edmonton, AB

#### **Jiangnan University** - Master's, Food Science and Technology

September 2009 - July 2012

Jiangsu, China

#### **Wuhan University of Science and Engineering** - Bachelor's, Bioengineering

September 2005 - July 2009

Hubei, China

### WORK EXPERIENCE

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#### **SyMBIOTA Lab, Dept of Pediatrics, University of Alberta** -

##### Microbiome Epidemiology Researcher

August 2020 - November 2021

Edmonton AB

- Developed a computational pipeline with R to build predictive models for childhood obesity risk on microbiome data with an accuracy of 80% AUC
- Integrated microbiome profile data and clinical variables from multiple centers in the CHILD cohort, generating a unified format for statistical model analysis
- Cooperated with two biostatisticians on a cohort study, primarily solving coding and statistical problems, leading to one publication that gained 1000+ views within eight months
- Authored two conference posters and three paper manuscripts, creating engaging data visualization on the statistical analysis of microbiome and metabolomics data with R
- Supported the supervisor in counseling three graduate students on biostatistics methodology and R programming

#### **Microbiology Lab, Dept of Agri., Food & Nutrition, University of Alberta** -

##### Food Microbiology Researcher

August 2013 - May 2018

Edmonton AB

- Developed a bioinformatics pipeline for the genome-wide annotation of sugar transporters' genes with online servers (NCBI, KEGG, TCDB, and CAZymes)
- Cooperated with a senior bioinformatician in genome sequencing, comparative genomics analysis, and phylogenetic tree interpretation of 16 *Limosilactobacillus reuteri* strains
- Identified taxonomy of a collection of bacteria commensal to humans, swine, and poultry with 16S rRNA PCR sequencing and bioinformatics database (RDP Taxonomy) and software (BLAST and MEGA 5)
- Conducted a piglet trial, with fermenting feed with probiotic strains mix, collecting intestinal bio-samples, and analyzing qPCR-based data
- Mentored two graduate students in instrument operations and data reporting in the Biosafety Level 2 food microbiology laboratory

## PROJECTS

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### Comparative genomics of gut and sourdough lactobacilli

- Conducted gap-closing by PCR amplification and Sanger sequencing to obtain 12 complete genomes
- Analyzed phylogenetic trees based on core genomes to validate host-specific lineages
- Identified positively-selected genes and accessory genes to elucidate biological forces driving the diversification of the lactobacilli population
- Identified genetic variations in sugar metabolism by multiple genomes alignment in standalone BLAST+ and re-annotation in the CAZymes analysis toolkit
- Reconstructed and visualized global sugar metabolism pathways with KEGG automatic annotation server

### **Toxin genotyping of foodborne pathogen**

- Prepared culture media and chemical agents for *C. perfringens* sampling from poultry meat and feces
- Developed culture- and molecular-based methodology and drafted experimental protocols from sampling to genotyping to computational analysis of *C. perfringens* toxins

### Machine learning prediction of childhood obesity

- Developed machine learning models with R modules to predict childhood obesity based on microbiome profiles and health data in a large-scale birth cohort study
- Recognized and solved technical problems in the workflow of machine learning modeling
- Demonstrated outcome of statistical analysis in a presentation-ready format for academic audience

### Risk factors evaluation for infant microbiome development

- Investigated association between antibiotics, breastfeeding, vitamin D use, and infant microbiome with multivariate models and non-parameter hypothesis testing on multi-omics data
- Conducted ordination analysis on 16S sequence microbiota data and environmental variables
- Identified confounding variables before modeling by literature review and Directed Acyclic Graphs

### Use of probiotics as antibiotics alternative for piglets

- Designed and implemented the daily feeding regime for the piglet experiment
- Detected fecal microbiota changes by weaning time and probiotic administration using 16S sequencing and in-house qPCR primers

### Biochemical assay of antibiotics-utilizing human commensal microbiota

- Measured antimicrobial resistance of gut bacteria on 14 antibiotics using the disk diffusion method
- Investigated biochemical factors affecting antibiotics metabolism by bacteria with culture technique
- Validated hypothesized metabolism pathways with HPLC-MS spectra and literature review

## CERTIFICATIONS

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- Ethical Conduct for Research Involving Humans (TCPS 2: CORE 2022) (Panel on Research Ethics)
- Workplace Hazardous Materials Information System (WHMIS) (University of Alberta)
- R Programming ([Coursera](#), Credential ID 9V7ATEJB7HUR)
- Epidemiology for Public Health Specialization ([Coursera](#), Credential ID 7ZH2XA38AFQJ)

## SKILLS

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### Language

R (R Studio); SQL

### Computational Skills

Multivariate Statistics; Correlation and Regression; Hypothesis Testing; Supervised Learning; Unsupervised Learning; Data Exploratory Analysis; Data Visualization; Bioinformatics (standalone BLAST toolkit, MEGA 5, MAUVE, Geneious and KEGG server); GitHub

### Domain Knowledge

Food Microbiology; Molecular Microbiology; Biostatistics; Microbiome Epidemiology; Applied Machine Learning

### Laboratory Techniques

Biosafety Level II Laboratory Practice; qPCR; Primer Design; Bacterial Identification; Comparative Genomics; Phylogenetics; Gel Electrophoresis; RNA Expression; Experiment Design

## CONFERENCE PRESENTATIONS (PRESENTING AUTHOR IS UNDERLINED)

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- Xin Zhao, Kelsea M Drall, Sarah Bridgman, Mandal Rupasri, Allan B Becker, Piush J Mandhane, Theo J Moraes, Malcolm R Sears, Stuart E Turvey, Padmaja Subbarao, James A Scott, and Anita L Kozyskyj. Effect of infant vitamin D drops on fecal glycerol, propylene glycol, and microbiota at 3 months of age, **Slide show**, at Having IMPACTT: Advancing Microbiome Research, Virtual Symposium, June 2021.
- Xin Zhao, and Michael G. Gänzle. Genetic and phenotypic analysis of carbohydrate metabolism and transport in *Lactobacillus reuteri*. **Poster presentation**, at 12th International Symposium on Lactic Acid Bacteria, in Egmond aan Zee, the Netherlands, August 2017.
- Xin Zhao, Jingshui Zheng, Xiaoxi B. Lin, and Michael G. Gänzle. Comparative genomics *Lactobacillus reuteri* from sourdough reveals adaptation of an intestinal symbiont to food fermentations, **Oral presentation**, at VIth Sourdough Symposium, in Nantes, France, October 2015.

## PUBLICATIONS

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- Yuanyao Chen, Xin Zhao, Wolfgang Moeder, Hein M. Tun, Elinor Simons, Piushkumar J. Mandhane, Theo J. Moraes et al. "Impact of Maternal Intrapartum Antibiotics, and Caesarean Section with and without Labour on Bifidobacterium and Other Infant Gut Microbiota." [\*Microorganisms\* 9, no. 9 \(2021\): 1847](#)
- Xin Zhao, Weilan Wang, A. Blaine, S. T. Kane, R. T. Zijlstra, and M. G. Gänzle. "Impact of probiotic *Lactobacillus* sp. on autochthonous lactobacilli in weaned piglets." [\*Journal of Applied Microbiology\* 126, no. 1 \(2019\): 242-254](#)
- Xin Zhao, and Michael G. Gänzle. "Genetic and phenotypic analysis of carbohydrate metabolism and transport in *Lactobacillus reuteri*." [\*International Journal of Food Microbiology\* 272 \(2018\): 12-21](#)
- Yan Yang, Xin Zhao, Minh HA Le, Ruurd T. Zijlstra, and Michael G. Gänzle. "Reutericyclin producing *Lactobacillus reuteri* modulates development of fecal microbiota in weanling pigs" [\*Frontiers in Microbiology\* 6 \(2015\): 762](#)
- Jinshui Zheng, Xin Zhao (co-first author), Xiaoxi B. Lin, and Michael Gänzle. "Comparative genomics *Lactobacillus reuteri* from sourdough reveals adaptation of an intestinal symbiont to food fermentations" [\*Scientific Reports\* 5, no. 1 \(2015\): 1-11](#)
- Xin Zhao, Tian Fengwei, Wang Gang, Liu Xiaoming, Zhang Qiuxiang, Zhang Hao, and Chen Wei. "Isolation, identification and characterization of human intestinal bacteria with the ability to utilize chloramphenicol as the sole source of carbon and energy." [\*FEMS Microbiology Ecology\* 82, no. 3 \(2012\): 703-712](#)