JUN ZENG

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Durham, NC, USA

Ph.D. Candidate, Molecular Genetics and Microbiology

Molecular microbiologist with 9+ years of experience in next-generation sequencing workflows, microbiome research, clinical cohort studies, and bacterial genetics. Skilled in both experimental and computational approaches with a strong publication record.

EDUCATION

08/2019 – Present	**Ph.D., Molecular Genetics and Microbiology** Advisor: Dr. Lawrence David Expected Graduation: Spring 2026	Duke University, Durham, NC, USA
09/2015 – 06/2019	**B.S., Microbiology, Biology (Double Major)** Graduated *Cum Laude* with a minor in Philosophy	University of Washington, Seattle, WA, USA

RESEARCH

05/2020 – Present **Graduate Research Assistant**

- David Lab, Duke University, Durham, NC, USA
- Advisor: Dr. Lawrence David
- Thesis Project: “Dietary Signatures from Fecal DNA Predict Hematopoietic Stem Cell Transplantation (HCT) Outcomes”
- Executed 14 full amplicon-sequencing workflows—from fecal sample processing through data visualization—on 878 samples collected from two tertiary care centers. Identified key interactions between dietary intake, gut microbiome composition, and post-HCT outcomes. Conducted the first study to use residual diet-derived DNA in clinical stool samples to retrospectively reconstruct dietary patterns otherwise inaccessible after patient discharge.

08/2016 – 06/2019 **Undergraduate Research Assistant**

- Mougous Lab, University of Washington, Seattle, WA, USA (Now at Yale University)
- Mentors: Dr. Joseph Mougous, Dr. Marcos de Moraes, Dr. Brook Peterson
- Research Project: “An Interbacterial Toxin with Novel Gene Editing Activity Promotes Genetic Diversity of Microbial Communities”
- Contributed to the discovery, genetic characterization, and biochemical analysis of the world's first double-stranded DNA deaminase, DddA. Established groundwork for subsequent efforts that achieved the first case of precise editing of mitochondrial DNA using DddA.

SELECTED SKILLS

Experimental
- Molecular Biology
  - Next-Generation Sequencing, Sequencing Library Prep, Molecular Cloning, Bacterial Mutagenesis, Protein Purification, PCR/qPCR, Plasmid Design, Primer Design, DNA extraction.
- Instruments
  - MiniSeq (Illumina), Anaerobic Chamber (Coy), GC-FID (Agilent), HPAE (Agilent), Automatic Liquid Handler (epMotion).

Computational
- Data Analysis
  - R/RStudio, bash, Linear Mixed-Effects Models, Principal Component Analysis, Hierarchical Clustering, Dynamic Time Warping Clustering.
- Packages, Tools, and AI Platforms
  - microbiome, phyloseq, tidyverse, pROC, dtwclust, ggplot2, circlize, BioRender, Geneious, PyMOL, AlphaFold, OpenAI API, Claude Code, VS Code.

MENTORING

06/2022 – 05/2024 **Undergraduate Research Mentor**
- Mentored an undergraduate student to benchmark accuracy of our NGS pipeline.

08/2022 – 05/2023 **Graduate Peer Mentor**
- Mentored first-year doctoral students and led a course on Responsible Conduct for Research.

PRESENTATIONS

10/2022 **CSHL Microbiome**
- Cold Spring Harbor Laboratory, NY, USA
- Presentation Type: oral

09/2022 **Center for Host-Microbial Interactions**
- Duke University, NC, USA
- Presentation Type: oral

SELECTED PUBLICATIONS

Zeng J, García-González AP, Epstein P, Bauer AE, Jiang S, Kirtley MC, Neubert BC, Rivera CN, Bergens MA, Bush AT, Hill L, Gauthier J, McGriff C, Tang H, Andermann TM, Jobin C, Chao NJ, Dahl WJ, Wingard JR, Sung AD, David LA. (2025). Dietary signatures from fecal DNA predict hematopoietic stem cell transplantation outcomes. *Submitted*.

Mok BY, de Moraes MH, **Zeng J**, Bosch DE, Kotrys AV, Raguram A, Hsu F, Radey MC, Peterson SB, Mootha VK, Mougous JD, Liu DR. (2020). A bacterial cytidine deaminase toxin enables CRISPR-free mitochondrial base editing. *Nature*, 583(7817), 631–637.