Jun Zeng

Doctoral Candidate, Molecular Genetics &
Microbiology (expected Spring 2026)
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Curriculum Vitae

SUMMARY

Ph.D. candidate (Spring 2026) with 9+ years of research experience in microbiome science, clinical cohort studies, and bacterial genetics. Skilled in NGS workflows, multi-omics data analysis, and combined wet-lab and computational approaches that support interdisciplinary microbiome research.

EDUCATION

08/2019 – Present **Ph.D., Molecular Genetics and Microbiology**
Duke University, Durham, NC, USA
Advisor: Dr. Lawrence David
Expected Graduation: Spring 2026

09/2015 – 06/2019 **B.S., Microbiology, Biology (Double Major)**
University of Washington, Seattle, WA, USA
Graduated *Cum Laude* with a minor in Philosophy

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"
Research Outcomes:

- Independently executed all experimental and computational steps of 14 in-house amplicon sequencing workflows (plant *trnL*, animal 12S, and bacterial 16S) on 878 fecal samples from 296 patients, enabling retrospective dietary and diet-microbiome analysis in two independent HCT cohorts.
- Explored the interplay between diet, gut microbiome, and clinical outcomes through integrated analyses of data from amplicon sequencing, gas chromatography, and clinical records.
- Identified diet-derived molecular signatures associated with patients' platelet recovery and overall survival following allogeneic HCT.

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"
Research Outcomes:

- Contributed to a project that led to the discovery and biological and biochemical characterization of DddA, the first known double-stranded DNA deaminase.
- Investigated the toxicity and molecular mechanism of DddA as a toxin mediating interbacterial antagonism in *Burkholderia cenocepacia*.
- Assessed the mutagenic activity of DddA and established a foundation for its development as a targeted DNA editing tool.

PUBLICATIONS

1. **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.*

2. Aqeel A, Kay MC, **Zeng J**, Petrone BL, Yang C, Truong T, Brown CB, Jiang S, Carrion VM, Bryant S, Kirtley MC, Neshteruk CD, Armstrong SC, David LA. (2025). Grocery intervention and DNA-based assessment to improve diet quality in pediatric obesity: a pilot randomized controlled study. *Obesity (Silver Spring, Md.)*, 33(2), 331–345.

3. Letourneau J, Carrion VM, **Zeng J**, Jiang S, Osborne OW, Holmes ZC, Fox A, Epstein P, Tan CY, Kirtley M, Surana NK, David LA. (2024). Interplay between particle size and microbial ecology in the gut microbiome. *The ISME journal*, 18(1), wrae168.

4. de Moraes MH, Hsu F, Huang D, Bosch DE, **Zeng J**, Radey MC, Simon N, Ledvina HE, Frick JP, Wiggins PA, Peterson SB, Mougous JD. (2021). An interbacterial DNA deaminase toxin directly mutagenizes surviving target populations. *eLife*, 10, e62967.

5. 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. **Authors contributed equally*

PRESENTATIONS

10/2022 **CSHL Microbiome**

- Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA
- Presentation Type: oral
- Presentation Title: “Dietary Perturbation-Mediated Gut Microbiome Disruption during Hematopoietic Stem Cell Transplant Exacerbates Patient Outcomes”

09/2022 **Center for Host-Microbial Interactions**

- Duke University, Durham, NC, USA
- Presentation Type: oral
- Presentation Title: “Dietary Perturbation-Mediated Gut Microbiome Disruption during Hematopoietic Stem Cell Transplant”

MENTORING

06/2022 – 05/2024 **Mentor for Undergraduate Research**

- David Lab, Duke University
- Mentee: Piper Epstein
- Mentored an undergraduate student on a project that benchmarked the accuracy of our dietary DNA sequencing method on hospital foods.

08/2022 – 05/2023 **Graduate Peer Mentor**

- Office of Biomedical Graduate Education, Duke University
- Provided mentorship to first-year doctoral students to help them acclimate to graduate school. Organized and led sessions for a course on Responsible Conduct for Research.

AWARDS

09/2018	Undergraduate Tuition Exemption, University of Washington
12/2017	Undergraduate Research Scholarship, University of Washington
09/2017	Academic Excellence Award, University of Washington

SKILLS

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