Bryan P. Brown

Postdoctoral Fellow, Center for Global Infectious Disease Research, Seattle Children's bryan.brown@seattlechildrens.org | itsmisterbrown.github.io 330.933.2112

EDUCATION

2017 Doctor of Philosophy, Duke University, Durham, NC

Center for Genomic and Computational Biology; Nicholas School of the Environment

Dissertation: Ecological and Evolutionary Factors Shaping Animal-Bacterial Symbioses: Insights

from Insects & Gut Symbionts
Advisor: Jennifer J. Wernegreen, PhD

2011 Bachelor of Science, The University of Akron, Akron, OH

Majors: Biochemistry, Biology; Minor: Spanish

Advisors: Stephen C. Weeks, PhD and John M. Senko, PhD

RESEARCH EXPERIENCE AND FELLOWSHIPS

Research experience

2017 - Present Postdoctoral Fellow, Seattle Children's

Seattle Children's Research Institute, Center for Global Infectious Disease Research, Seattle, WA (PIs: Heather Jaspan, MD, PhD; Michael Gale Jr., PhD)

- Used 16S rRNA gene sequencing and polychromatic flow cytometry to asses shifts in vaginal microbiota and immune activation associated with contraceptive initiation in a cohort of African women. Conducted as part of the ECHO trial.
- Performed viral and bacterial metagenome sequencing and analysis on maternal and infant stool samples to assess the effects of maternal HIV infection on the enteric microbiota of mothers and related infants.
- Developed two R packages to enable robust statistical analysis of marker gene datasets.
- Employed various supervised and unsupervised learning approaches to interrogate shifts in microbial communities associated with HIV infection.
- Resulted in two first-author publications, one first-author manuscript in revision, and several co-author publications.

2012 - 2017 Predoctoral Fellow, Duke University

Nicholas School of the Environment, Durham, NC (PI: Jennifer Wernegreen, PhD)

- Discovered novel, gut-associated species of Acetobacteraceae bacteria and characterized their genomes using isolate culturing and PacBio sequencing.
- Performed bacterial metagenome sequencing on an Illumina platform to identify sources of horizontal gene transfer in specific strains of gut bacteria.
- Employed phylogenomics to reconstruct evolutionary histories of various gut associated bacteria.
- Resulted in two first-author publications with two additional first-author manuscripts in revision/preparation.

2009 – 2011 Research Assistant, The University of Akron

Department of Biology, Akron, OH

- Modeled crustacean development using geometric morphometric analyses.
- Employed various unsupervised learning approaches to infer population gender ratios and sexual system evolution through deep time via the fossil record.
- Resulted in one first-author publication and a co-author publication

2010 – 2011 Research Assistant, The University of Akron

Department of Geosciences, Akron, OH

- Performed 16S rRNA gene pyrosequencing to identify bacterial communities with high corrosive potential in engineered environments.
- Resulted in one first-author publication

2009 Visiting Researcher, Australian Museum

Sydney, Australia

• Developed a workflow for the identification and analysis of fossilized crustacean specimens using a combination of geometric morphometrics and unsupervised learning approaches.

Fellowships

2013 - 2017	Graduate Research Fellow, National Science Foundation
	Duke University, Durham, NC

2015 - 2016 Research and Innovation Fellow, United States Agency for International Development Duke University, Durham, NC, and University of Cape Town, Cape Town, South Africa

AWARDS AND HONORS

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RESEARCH SUPPORT

Completed Research Support

DUNSOE0789 1/1/2016 – 5/1/2017

Duke University PI: Wernegreen

SEED grant, Duke University Nicholas School of the Environment

Title: Evolutionary dynamics across the genomes of persistent gut bacterial associates

Description: This project aims to characterize the genomes of persistent gut bacteria and to identify selective pressures acting on these associates via adaptation to the gastrointestinal tract. Role: Co-Investigator.

DUSOM1075 2/1/2016 – 2/1/2017

Duke University PI: Wernegreen

Research Grant. Duke University School of Medicine

Title: A world within: Diversity and dynamics of bacterial communities inhabiting ants

Description: The purpose of this study is to identify mechanisms and dynamics of bacterial transmission between interacting hosts and across developmental stages. Role: Co-Investigator

NSF1106401 8/1/2015 – 5/1/2016

National Science Foundation, United States Agency for International Development

PI: Brown

NSF Graduate Research Opportunities Worldwide, and USAID Research and Innovation Fellowship Title: Structural and functional dynamics of vaginal microbiota associated with altered HIV susceptibility Description: The goal of this study is to identify shifts in vaginal bacterial microbiota that are associated with elevated HIV susceptibility in adolescent South African women. Role: Principal Investigator

PUBLICATIONS

Articles in Peer-Reviewed Journals

- Brown BP, Jaspan HB. Compositional analyses reveal correlations between taxon-level gut bacterial abundance and peripheral T cell marker expression in African infants. Gut microbes. 2019 Jul 28:1-8. PMID31347944
- 2. **Brown BP**, Wernegreen JJ. Genomic erosion and extensive horizontal gene transfer in gut-associated Acetobacteraceae. BMC genomics. 2019 Dec;20(1):472. PMID31182035.
- 3. Wood LF*, **Brown BP***, Lennard K, Karaoz U, Passmore JS, Hesseling AC, Edlefson PT, Mulder N, Brodie EL, Sodora DL, Jaspan HB. Feeding related gut microbial composition associates with peripheral T cell activation and mucosal gene expression in African infants. Clin Infect Dis 2018 Sep 28;67(8):1237-1246. PMID29659737. *co-first authors.
- 4. Nyangahu D, Lennard KS, **Brown BP**, Darby MG, Wendoh JM, Havyarimana H, Smith P, Butcher J, Stintzi A, Mulder N, Horsnell W, Jaspan HB. Disruption of maternal gut microbiota during gestation alters offspring immunity. Microbiome 2018 Jul 7;6(1):124. PMID29981583. PMC6035804.
- 5. Ho NT, Li F, Lee-Sarwar KA, Tun HM, **Brown BP**, Pannaraj PS, Bender JM, Azad MB, Thompson AL, Weiss ST, Azcarate-Peril MA, Litonjua AA, Kozyrskyj AL, Jaspan HB, Aldrovandi GM, Kuhn L. Meta-analysis of effects of exclusive breastfeeding on infant gut microbiota across populations. Nat Commun 2018 Oct 9;9(1):4169. PMID30301893. PMC6177445.
- 6. **Brown BP** and Wernegreen JJ. Deep divergence and rapid evolutionary rates in gut-associated Acetobacteraceae of ants. BMC Microbiol 2016 Jul 11;16(1):140. PMID27400652. PMC4939635.
- 7. **Brown BP**, Astrop TI, Weeks SC. Post-larval developmental dynamics of the Spinicaudatan (Branchiopoda: Diplostraca) carapace. Journal of Crustacean Biology 2014 34 (5), 611-617.
- 8. Astrop, TI, Park, LE, **Brown, BP**, and Weeks, SC. Sexual discrimination at work: Spinicaudatan 'Clam Shrimp' (Crustacea: Branchiopoda) as a model organism for the study of sexual system evolution. Palaeontologia Electronica 2012 Vol. 15, Issue 2;20A,15p.
- 9. **Brown BP**, Brown SR and Senko JM. Microbial communities associated with wet flue gas desulfurization systems. Front Microbiol 2012 3:412. PMID23226147. PMC3510643.

Preprints

1. **Brown BP**, Wendoh J, Chopera D, Havyarimana E, Jaumdally SZ, Nyangahu DD, Gray C, Martin DP, Varsani A, Jaspan HB. crAssphage abundance and genomic selective pressure correlate with altered bacterial abundance in the fecal microbiota of South African mother-infant dyads. bioRxiv. 2019 Jan 1:582015.

ACADEMIC PRESENTATIONS

Conference presentations

- 1. **Brown BP**, Wendoh J, Chopera D, Havyarimana E, Jaumdally SZ, Martin DP, Varsani A, Jaspan HB. (2019, July). Maternal HIV infection alters the community composition and dynamics of the enteric microbiome of associated infants. 10th International AIDS Society Conference on HIV Science, Mexico City, Mexico.
- 2. Balle C, Lennard K, Konstantinus I, Jaumdally S, Esra R, Gasper M, **Brown BP**, Karaoz U, Gill K, Myer L. (2018, October). Hormonal Contraception Induced Changes to the Female Genital Microbiota in South African Adolescents: A Randomized, Crossover Trial. HIV Research for Prevention. Madrid, Spain.
- 3. **Brown BP**, Jaspan HB, Study Team I. (2018, October). A compositional transform reveals HIV exposure induced shifts in the fecal microbiota and vaccine responsiveness of Nigerian infants. 4th International Workshop on Microbiome in HIV Pathogenesis, Prevention and Treatment. Washington, DC, USA.
- 4. **Brown BP**, Jaspan HB. (2018, September). A penalized compositional transform reveals shifts in the fecal microbiota of HIV exposed Nigerian infants. Fred Hutchinson Microbiome Research Initiative Biennial Symposium. Seattle, WA, USA.

Conference posters

 Brown BP, Jaspan HB. (2018, October). A compositional transform reveals HIV exposure induced shifts in the fecal microbiota and vaccine responsiveness in Nigerian infants. HIV Research for Prevention. Madrid, Spain.

- 2. **Brown BP**, Varsani A, Jaspan HB. (2018, October). Altered composition and elevated diversity in the enteric virome of HIV exposed uninfected South African infants. HIV Research for Prevention. Madrid. Spain.
- 3. **Brown BP**, Jaspan HB, Study Team I. (2018, April). HIV exposure alters the fecal microbiome and efficacy of oral polio vaccine in Nigerian infants. 25th International HIV Dynamics & Evolution. Leavenworth, WA, USA.
- 4. **Brown BP**, Senko J. (2012, June). Microbial Communities Associated With Flue Gas Desulfurization Systems. American Society for Microbiology: 112th General Meeting. San Francisco, CA, USA.
- 5. **Brown BP**, Weeks S. (2011, June). Morphometrics and Ontogenetics: Evolutionary Dynamics of the Spinicaudatan 'Clam Shrimp'. The Evolution Conference. Norman, OK, USA.

TEACHING AND MENTORING

Courses taught

One Health: Philosophy to Practical Integration of Human, Animal, and Environmental Health

Duke University, Global Health Institute

Role: Teaching Assistant, Co-Instructor

Description: This graduate-level, interdisciplinary course will introduce the concept of One Health as an increasingly important approach to a holistic understanding of the promotion and maintenance of human, animal, and environmental health.

Applied Data Analysis for Environmental Sciences

Duke University, Nicholas School of the Environment

Role: Teaching Assistant, Laboratory Instructor

Description: This graduate-level course provides an introduction to statistical analysis and modeling for applied problems in the environmental sciences. All labs are instructed using the R statistical framework.

Molecular Ecology

Duke University, Department of Biology

Role: Teaching Assistant, Co-Instructor

Description: This graduate-level course explores key questions in molecular ecology, a field that employs molecular tools to investigate ecological processes within natural populations and communities. While genetic techniques are central to this discipline, the course is not a methods class per se. Rather, emphasis is placed on fundamental principles and predictions from ecological and evolutionary theory, as well as historical approaches and precedents.

Genetics and Evolution

Duke University, Department of Biology

Role: Teaching Assistant, Laboratory Instructor

Description: This undergraduate-level course provides an introduction to principles of genetics and evolution. Includes Mendelian and non-Mendelian inheritance, quantitative genetics, genetic mapping, evidence for evolution, natural selection, genetic drift, kin selection, speciation, molecular evolution, and phylogenetic analysis.

Mentoring

Advising: Research

- 1 Master's student
- 7 Undergraduate students

SERVICE AND OUTREACH

Reviewing activities

Journals:

PLOS ONE

Clinical and Translational Medicine

Outreach

2012

Environmental Science Instructor, Lakewood Elementary School, Durham, NC

SOFTWARE

R packages

pico: enables robust statistical analysis and modeling of compositional microbiome datasets by coupling an L1 penalized matrix decomposition to the isometric log ratio transformation.

microfiltR: identifies and corrects for multiple sources of contamination (exogenous and cross) in compositional marker gene surveys. https://github.com/itsmisterbrown/microfiltR