Sophia B. Gibson

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Education

PhD in Genome Sciences 2022-Present
University of Washington, Seattle, WA
Advisors: Dr. Lea Starita and Dr. Danny Miller

B.A. in Biochemistry and Molecular Biology, *magna cum laude* with honors 2016-2020
Bryn Mawr College, Bryn Mawr, PA
Advisor: Dr. Tamara Davis
Honors Thesis: Identifying 5-Hydroxymethylcytosine Enrichment at Secondary DMRs

Research Experience

Graduate Research Assistant, University of Washington, Department of Genome Sciences 2022-Present
Advisors: Dr. Lea Starita and Dr. Danny Miller

- Developing custom pipelines and web applications for analyzing methylation patterns and repeat expansion sizes for 1000 Genomes ONT Sequencing Consortium data.
- Evaluating the potential of long-read data for explaining X-linked disorder phenotypes in 46,XX individuals.
- Computational languages: R, python, command line utilities

Research Technician, Northwestern University, Department of Molecular Biosciences 2020-2022
Advisor: Dr. Erik Andersen

- Generation of transgenic nematodes using microinjection and high-throughput assays to assess quantitative benzimidazole resistance.
- Data curation for the new Variant Browser tool on the *Caenorhabditis* Natural Diversity Resource (CeaNDR).
- Illumina MiSeq sequencing and data curation for *Caenorhabditis briggsae* recombinant inbred lines.
- Replacement of *Saccharomyces cerevisiae* beta-tubulin genes with nematode versions to obtain protein for crystal structures to understand mechanisms of benzimidazole resistance in parasitic nematodes.
- Computational languages: R, python, command line utilities, nextflow

Undergraduate Research Assistant, Bryn Mawr College, Department of Biology 2018-2020
Advisors: Dr. Joshua Shapiro (2018-2019) and Dr. Tamara Davis (2019-2020)

- Davis Lab: Investigated how secondary differentially methylated regions (DMRs) on imprinted genes become hemimethylated by identifying the presence of hydroxymethylated cytosine.
- Shapiro Lab: Surveyed yeast species identified on Bryn Mawr College trees, *de novo* whole-genome assembly for *Cyberlindnera saturnus*.
- Computational languages: R, python, command line utilities, Galaxy platform

Intern, The Field Museum, Pritzker Laboratory for Molecular Systematics and Evolution 2016
Supervisors: Erica Zahnle and Dr. Shannon Hackett

- Field Museum Women In Science Internship
- Investigated evolutionary genetics of Toll-like receptors in corvid family bird species.

Honors and Awards

NHGRI Genome Training Grant 2023-2024
NSF GRFP - Honorable Mention 2022
Bryn Mawr College Summer Science Fellowship 2018

Publications

Preprints

LaFlamme, C. W., Rastin, C., Sengupta, S., Pennington, H. E., Russ-Hall, S. J., Schneider, A. L., Bonkowski, E. S., Almanza Fuerte, E. P., Galey, M., Goffena, J., **Gibson, S. B**., Allan, T. J., Nyaga, D. M., Lieffering, N., Hebbar, M., Walker, E. V., Darnell, D., Olsen, S. R., Kolekar, P., … Mefford, H. C. (2023).

Diagnostic Utility of Genome-wide DNA Methylation Analysis in Genetically Unsolved Developmental and Epileptic Encephalopathies and Refinement of a CHD2 Episignature. *medRxiv : The Preprint Server for Health Sciences*. https://doi.org/10.1101/2023.10.11.23296741

Peer Reviewed

Crombie, T. A., McKeown, R., Moya, N. D., Evans, K. S., Widmayer, S. J., LaGrassa, V., Roman, N., Tursunova, O., Zhang, G., **Gibson, S. B.**, Buchanan, C. M., Roberto, N. M., Vieira, R., Tanny, R. E., & Andersen, E. C. (2023).

CaeNDR, the Caenorhabditis Natural Diversity Resource. *Nucleic Acids Research*. https://doi.org/10.1093/nar/gkad887

Gibson, S. B., Ness-Cohn, E., & Andersen, E. C. (2022).

Benzimidazoles cause lethality by inhibiting the function of Caenorhabditis elegans neuronal beta-tubulin. *International Journal for Parasitology, Drugs and Drug Resistance*, *20*, 89–96.

Stevens, L., Moya, N. D., Tanny, R. E., **Gibson, S. B.**, Tracey, A., Na, H., Chitrakar, R., Dekker, J., Walhout, A. J. M., Baugh, L. R., & Andersen, E. C. (2022).

Chromosome-Level Reference Genomes for Two Strains of Caenorhabditis briggsae: An Improved Platform for Comparative Genomics. *Genome Biology and Evolution*, *14*(4), evac042.

Gibson, S. B., Harper, C. S., Lackner, L. L., & Andersen, E. C. (2021).

The Caenorhabditis elegans and Haemonchus contortus beta-tubulin genes cannot substitute for loss of the Saccharomyces cerevisiae beta-tubulin gene. *microPublication Biology*, *2021*. https://doi.org/10.17912/micropub.biology.000411

Talks (* = presenter)

S.B Gibson* *et. al*. Haplotype-resolved characterization of repeat expansions and patterns of methylation from 1000 Genomes ONT Consortium data. Genome Informatics, Cold Spring Harbor Laboratory, NY — 2023

S.B Gibson* *et. al*. Haplotype-resolved characterization of repeat expansions and patterns of methylation from 1000 Genomes ONT Consortium data. UW Computational Molecular Biology Symposium, Seattle, WA — 2023

S.B. Gibson* and E.C. Andersen. Benzimidazoles cause lethality by inhibiting the function of neuronal beta-tubulin. Anti-Helmintics V, Worcester, MA — 2022

S.B. Gibson* and E.C. Andersen. Identifying Tissue-specific Susceptibility of *ben-1* to Benzimidazoles. 3rd Chicago Area Worm Meeting, Online — 2021

Poster Presentations (* = presenter)

S.B Gibson* *et. al.* Haplotype-resolved characterization of repeat expansions and patterns of methylation from 1000 Genomes ONT Consortium data. 2023 GREGoR Annual Meeting, St. Louis, MO — 2023

S.B. Gibson*, R.J. McKeown*, and E.C. Andersen. Updating the *Caenorhabditis elegans* Natural Diversity Resource Variant Browser. 23nd International *C. elegans* Conference, Online. 2021

S.B. Gibson* and J.A. Shapiro. Identification and Genome Sequencing of Wild Yeast at Bryn Mawr College. Bryn Mawr College Summer Science Research Symposium**,** Bryn Mawr, PA. 2018

Teaching

Computational Genomics, Teaching Assistant, Cold Spring Harbor Laboratory, November 29-December 6 2023