

Benjamin Robert Evans

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Education

Yale University, New Haven, CT (08/2012 – 12/2016)

PhD Ecology and Evolutionary Biology

Thesis Title: "Population Genomics in *Aedes aegypti*", *Advisor:* Jeffrey Powell

Honors/Awards: Ruth L. Kirschstein National Research Service Award,

Dillon and Mary Ripley Graduate Fellowship, Robert W. Carle Scholarship

NIH 5T32AI007404 Training in Parasitology and Vector Biology

Lehigh University, Bethlehem, PA (09/2005 – 05/2009)

BA Biology, minor in Computer Science

Honors/Awards: Dean's List, Phi Eta Sigma, Dean's Scholarship,

Donald & Dorothy Stabler scholarship, Lehigh University Grant, Patricia Battin Scholarship

Related Experience

Data Scientist III, Sema4 Genomics, Stamford, CT (01/2021 – 01/2023)

Production Bioinformatics

- Manage/develop/run HIPAA compliant AWS Cloud native bioinformatics pipelines

- Update and maintain metadata database used to orchestrate pipelines

Sr. Computational Research Support Analyst, Yale University, New Haven, CT (10/2016 - 12/2021)

Yale Center for Research Computing

- Computational research consulting for life & biomedical Sciences: 4 HPC Clusters ~1000 Researchers

- Develop and give workshops and tutorials

- XSEDE Campus Champion: national community engagement

- Researcher collaboration: genomics, phylogenetics, epidemiology models, IoT freezer monitoring

Research Assistant II, Caccione Lab, Yale University, New Haven, CT (08/2009-08/2012)

DNA Analysis Facility On Science Hill

Skills & Abilities

AWS: S3, EC2, Lambda, SQS/SNS, ECR, Batch

SLDC: Agile/Scrum, GitHub&GitHub Actions, Jira, Confluence

Linux/HPC: Coreutils & Linux CLI, Git, Docker/Singularity, Slurm, Lmod, EasyBuild

Languages: Bash, Python, R, SQL

Bioinformatics: Sequence analysis (QC/alignment), variant calling (GATK etc),
pipeline development (NextFlow, custom scripts, etc)

Publications

Kortright KE, Chan BK, Evans BR, Turner PE Arms race and fluctuating selection dynamics in *Pseudomonas aeruginosa* bacteria coevolving with phage OMKO1. *J Evol Biol.* doi:10.1111/jeb.14095 (2022)

Li W, Shen X, Evans BR, Dunn CW, Rokas A Rooting the Animal Tree of Life. *Mol. Biol* doi:10.1093/molbev/msab170 (2021)

Evans BR, Kotsakiozi P, Costa-da-Silva AL, Ioshino RS, Garziera L et al. Transgenic *Aedes aegypti* mosquitoes transfer genes into a natural population. *Sci. Rep.* doi:10.1038/s41598-019-49660-6 (2019)

Quesada V, Freitas-Rodríguez S, Miller J, Pérez-Silva JG, et al. Giant tortoise genomes provide insights into longevity and age-related disease. *Nat Ecol Evol.* doi:10.1038/s41559-018-0733-x (2019)

Publications (continued)

- Orr AR, Quagrainie JE, Suwondo P, George S, Harrison LM, et al. Genetic Markers of Benzimidazole Resistance among Human Hookworms (*Necator americanus*) in Kintampo North Municipality, Ghana. *Am J Trop Med Hyg*. doi:10.4269/ajtmh.18-0727 (2019)
- Kotsakiozi P, Evans BR, Gloria-Soria A, Kamgang B, et al. Population structure of a vector of human diseases: *Aedes aegypti* in its ancestral range, Africa. *Ecol Evol*. doi:10.1002/ece3.4278 (2018)
- Matthews BJ, Dudchenko O, Kingan SB, Koren S, Antoshechkin I, et al. Improved reference genome of *Aedes aegypti* informs arbovirus vector control. *Nature*. doi:10.1038/s41586-018-0692-z (2018)
- Pless E, Gloria-Soria A, Evans BR, Kramer V, Bolling BG, et al. Multiple Introductions of the Dengue Vector, *Aedes aegypti*, into California. *PloS NTD*. doi:10.1371/journal.pntd.0005653 (2017)
- Saarman NP, Gloria-Soria A, Anderson EC, Evans BR, Pless E, et al. Effective population sizes of a major vector of human diseases, *Aedes aegypti*. *Evol Appl*. doi:10.1111/eva.12508 (2017)
- Kotsakiozi P, Gloria-Soria A, Caccone A, Evans B, Schama R, et al. Tracking the return of *Aedes aegypti* to Brazil, the major vector of the dengue, chikungunya and Zika viruses. *PloS NTD*. doi:10.1371/journal.pntd.0005653 (2017)
- Saarman NP, Gloria-Soria A, Anderson EC, Evans BR, Pless E, et al. Effective population sizes of a major vector of human diseases, *Aedes aegypti*. *Evol Appl*. doi:10.1111/eva.12508 (2017)
- Powell JR, Evans B. How Much Does Inbreeding Reduce Heterozygosity? Empirical Results from *Aedes aegypti*. *Am J Trop Med Hyg*. doi:10.4269/ajtmh.16-0693 (2017)
- Walter K, Carpi G, Evans B, Caccone A, Diuk-Wasser M. Vectors as Epidemiological Sentinels: Patterns of Within-Tick *Borrelia burgdorferi* Diversity. *PLoS Pathogens*. doi:10.1371/journal.ppat.1005759 (2016)
- Gloria-Soria A, Dunn W, Telleria E, Evans B, Okedi L, et al. Patterns of Genome-Wide Variation in *Glossina fuscipes fuscipes* Tsetse Flies from Uganda. *G3 Genes|Genomes|Genetics*. doi:10.1534/g3.116.027235 (2016)
- Richardson JB, Evans B, Pyana PP, Reet N Van, Sistrom M. Whole genome sequencing shows sleeping sickness relapse is due to parasite regrowth and not reinfection. *Evol Appl*. doi:10.1111/eva.12338 (2016)
- Sistrom M, Evans B, Benoit J, Balmer O, Aksoy S, Caccone A. De Novo Genome Assembly Shows Genome Wide Similarity between *Trypanosoma brucei brucei* and *Trypanosoma brucei rhodesiense*. *PLoS One*. doi:10.1371/journal.pone.0147660 (2016)
- Evans BR, Gloria-Soria A, Hou L, McBride C, Bonizzoni M, Zhao H, et al. A Multipurpose High Throughput SNP Chip for the Dengue and Yellow Fever Mosquito, *Aedes aegypti*. *G3 Genes|Genomes|Genetics*. doi:10.1534/g3.114.016196 (2015)
- Eytan RI, Evans BR, Dornburg A, Lemmon AR, Lemmon EM, Wainwright PC, et al. Are 100 enough? Inferring acanthomorph teleost phylogeny using Anchored Hybrid Enrichment. *BMC Evol Biol*. doi:10.1186/s12862-015-0415-0 (2015)
- Gallant JR, Imhoff VE, Martin A, Savage WK, Chamberlain NL, et al. Ancient homology underlies adaptive mimetic diversity across butterflies. *Nat Commun*. doi:10.1038/ncomms5817 (2014)
- Sistrom M, Evans B, Bjornson R, Gibson W, Balmer O, Mäser P, et al. Comparative genomics reveals multiple genetic backgrounds of human pathogenicity in the *Trypanosoma brucei* complex. *Genome Biol Evol*. doi:10.1093/gbe/evu222 (2014)
- Brown JE, Evans BR, Zheng W, Obas V, Barrera-Martinez L, et al. Human impacts have shaped historical and recent evolution in *Aedes aegypti*, the dengue and yellow fever mosquito. *Evolution*. doi:10.1111/evo.12281 (2013)