

## Jacob A. Tennesen

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### Education

Ph.D. in Zoology, Oregon State University 2009. GPA: 4.0. Dissertation: “Adaptive diversity and divergence at frog antimicrobial peptide loci.”

B.S. in Biological Sciences (Concentration: Ecology and Evolutionary Biology), Magna Cum Laude, Cornell University 2002. GPA: 3.978.

### Publications

Blouin MS, Bollmann SR, Tennesen JA (2022) *PTC2* region genotypes counteract *Biomphalaria glabrata* population differences between M-line and BS90 in resistance to infection by *Schistosoma mansoni*. *PeerJ* 10:e13971

Elsworth B, Keroack CD, Rezvani Y, Tennesen JA, Sack SA, Paul AS, Moreira CK, Gubbels M-J, Zarringhalam K, Duraisingh MT (2022) *Babesia divergens* egress from host cells is orchestrated by essential and druggable kinases and proteases. bioRxiv 2022.02.17.480550; doi: <https://doi.org/10.1101/2022.02.17.480550>

Tennesen JA, Ingham VA, Toé KH, Guelbéogo WM, Sagnon N, Kuzma R, Ranson H, Neafsey DE (2021) A population genomic unveiling of a new cryptic mosquito taxon within the malaria-transmitting *Anopheles gambiae* complex. *Molecular Ecology* 30:775-790

VA Ingham, Tennesen JA, Lucas ER, Elg S, Carrington Yates H, Carson J, Guelbeogo WM, Sagnon N, Hughes G, Heinz E, Neafsey DE, Ranson H (2021) Integration of whole genome sequencing and transcriptomics reveals a complex picture of the reestablishment of insecticide resistance in the major malaria vector *Anopheles coluzzii*. *PLoS Genetics* 17:e1009970

Tennesen JA, Duraisingh MT (2021) Three signatures of adaptive polymorphism exemplified by malaria-associated genes. *Molecular Biology and Evolution* 38:1356-1371

Tennesen JA, Bollmann SR, Peremyslova E, Kronmiller BA, Sergi C, Hamali B, Blouin MS (2020) Clusters of polymorphic transmembrane genes control resistance to schistosomes in snail vectors. *eLife* 9:e59395

Liston A, Wei N, Tennesen JA, Li J, Dong M, Ashman TL (2020) Revisiting the origin of octoploid strawberry. *Nature Genetics* 52:2-4

Allan ERO, Yang L, Tennesen JA, Blouin MS (2019) Allelic variation in a single genomic region alters the hemolymph proteome in the snail *Biomphalaria glabrata*. *Fish & Shellfish Immunology* 88:301-307

Tennessen JA, Wei N, Straub SCK, Govindarajulu R, Liston A, Ashman T-L (2018) Repeated translocation of a gene cassette drives sex chromosome turnover in strawberries. *PLoS Biology* 16:e2006062

Tennessen JA (2018) Gene buddies: Linked balanced polymorphisms reinforce each other even in the absence of epistasis. *PeerJ* 6:e5110

Willoughby JR, Harder AM, Tennessen JA, Scribner KT, Christie MR (2018) Rapid genetic adaptation to a novel environment despite a genome-wide reduction in genetic diversity. *Molecular Ecology* 27:4041-4051

Allan EAO, Tennessen JA, Sharpton TJ, Blouin MS (2018) Allelic variation in a single genomic region alters the microbiome of the snail *Biomphalaria glabrata*. *Journal of Heredity* 109:604-609

Dillenberger MS, Wei N, Tennessen JA, Ashman T-L, Liston A (2018) Plastid genomes reveal recurrent formation of allopolyploid *Fragaria*. *American Journal of Botany* 105:862-874

Tennessen JA, Bollmann SR, Blouin MS (2017) A targeted capture linkage map anchors the genome of the schistosomiasis vector snail, *Biomphalaria glabrata*. *G3: Genes, Genomes, Genetics* 7:2353-2361

Wei N, Tennessen JA, Liston A, Ashman T-L (2017) Present-day sympatry belies the evolutionary origin of a high-order polyploid. *New Phytologist* 216:279-290

Allan ER, Tennessen JA, Bollmann SR, Hanington PC, Bayne CJ, Blouin MS (2017) Schistosome infectivity in the snail, *Biomphalaria glabrata*, is partially dependent on the expression of Grctm6, a Guadeloupe Resistance Complex protein. *PLoS Neglected Tropical Diseases* 11:e0005362

Wei N, Govindarajulu R, Tennessen JA, Liston A, Ashman T-L (2017) Genetic mapping and phylogenetic analysis reveal intraspecific variation in sex chromosomes of the Virginian strawberry. *Journal of Heredity* 108:731-739

Vining KJ, Salinas N, Tennessen JA, Zurn JD, Sargent DJ, Hancock J, Bassil NV (2017) Genotyping-by-sequencing enables linkage mapping in three octoploid cultivated strawberry families. *PeerJ* 5:e3731

Rabelo ÉM, Miranda RR, Furtado LF, Redondo RA, Tennessen JA, Blouin MS (2017) Development of new microsatellites for the hookworm *Ancylostoma caninum* and analysis of genetic diversity in Brazilian populations. *Infection, Genetics and Evolution* 51:24-27

Denoyes B, Amaya I, Liston A, Tennessen J, Ashman T-L, Whitaker V, Hytönen T, Van De Weg E, Osorio S, Folta K (2017) Genomics tools available for unravelling mechanisms underlying agronomical traits in strawberry with more to come. *Acta Horticulturae* 1156:13-24

Adema CM, Hillier LW, Jones CS, Loker ES, Knight M, Minx P, Oliveira G, Raghavan N, Shedlock A, do Amaral LR, Arican-Goktas HD, Assis JG, Baba EH, Baron OL, Bayne CJ, Bickham-Wright U, Biggar KK, Blouin M, Bonning BC, Botka C, Bridger JM, Buckley KM, Buddenborg SK, Lima Caldeira R, Carleton J, Carvalho OS, Castillo MG, Chalmers IW, Christensens M, Clifton S, Cosseau C, Coustau C, Cripps RM, Cuesta-Astroz Y, Cummins SF, di Stephano L, Dinguirard N, Duval D, Emrich S, Feschotte C, Feyereisen R, FitzGerald P, Fronick C, Fulton L, Galinier R, Gava SG, Geusz M, Geyer KK, Giraldo-Calderón GI, de Souza Gomes M, Gordy MA, Gourbal B, Grunau C, Hanington PC, Hoffmann KF, Hughes D, Humphries J, Jackson DJ, Jannotti-Passos LK, de Jesus Jeremias W, Jobling S, Kamel B, Kapusta A, Kaur S, Koene JM, Kohn AB, Lawson D, Lawton SP, Liang D, Limpanont Y, Liu S, Lockyer AE, Lovato TL, Ludolf F, Magrini V, McManus DP, Medina M, Misra M, Mitta G, Mkoji GM, Montague MJ, Montelongo C, Moroz LL, Munoz-Torres MC, Niazi U, Noble LR, Oliveira

FS, Pais FS, Papenfuss AT, Peace R, Pena JJ, Pila EA, Quelais T, Raney BJ, Rast JP, Rollinson D, Rosse IC, Rotgans B, Routledge EJ, Ryan KM, Scholte LLS, Storey KB, Swain M, Tennessen JA, Tomlinson C, Trujillo DL, Volpi EV, Walker AJ, Wang T, Wannaporn I, Warren WC, Wu XJ, Yoshino TP, Yusuf M, Zhang SM, Zhao M, Wilson RK (2017) Whole genome analysis of a schistosomiasis-transmitting freshwater snail. *Nature Communications* 8:15451

Tennessen JA, Govindarajulu R, Liston A, Ashman TL (2016) Homomorphic ZW chromosomes in a wild strawberry show distinctive recombination heterogeneity but a small sex-determining region. *New Phytologist* 211:1412-1423

Syring JV, Tennessen JA, Jennings TN, Wegrzyn J, Scelfo-Dalbey C, Cronn R (2016) Targeted capture sequencing in whitebark pine reveals range-wide demographic and adaptive patterns despite challenges of a large, repetitive genome. *Frontiers in Plant Science* 7:484

Tennessen JA, Bonner KM, Bollmann SR, Johnstun JA, Yeh J-Y, Marine M, Tavalire HF, Bayne CJ, Blouin MS (2015) Genome-wide scan and test of candidate genes in the snail *Biomphalaria glabrata* reveal new locus influencing resistance to *Schistosoma mansoni*. *PLoS Neglected Tropical Diseases* 9:e0004077

Ashman TL, Tennessen JA, Dalton R, Govindarajulu R, Koski M, Liston A (2015) Multilocus sex determination revealed in two populations of gynodioecious wild strawberry, *Fragaria vesca* subsp. *bracteata*. *G3: Genes, Genomes, Genetics* 5:2759-2773

Tennessen JA, Théron A, Marine M, Yeh JY, Rognon A, Blouin MS (2015) Hyperdiverse gene cluster in snail host conveys resistance to human schistosome parasites. *PLoS Genetics* 11:e1005067

Govindarajulu R, Parks M, Tennessen JA, Liston AL, Ashman TL (2015) Comparison of nuclear, plastid, and mitochondrial phylogenies and the origin of wild octoploid strawberry species. *American Journal of Botany* 102:544-554

Tennessen JA, Govindarajulu R, Ashman TL, Liston A (2014) Evolutionary origins and dynamics of octoploid strawberry subgenomes revealed by dense targeted capture linkage maps. *Genome Biology and Evolution* 6:3295-3313

Tennessen JA, Govindarajulu R, Liston A, Ashman TL (2013) Targeted sequence capture provides insight into genome structure and genetics of male sterility in a gynodioecious diploid strawberry, *Fragaria vesca* ssp. *bracteata* (Rosaceae). *G3: Genes, Genomes, Genetics* 3:1341-1351

Christie MR, Tennessen JA, Blouin MS (2013) Bayesian parentage analysis with systematic accountability of genotyping error, missing data, and false matching. *Bioinformatics* 29:725-732

Tennessen JA\*, Bigham AW\*, O'Connor TD\*, Fu W, Kenny EE, Gravel S, McGee S, Do R, Liu X, Jun G, Kang HM, Jordan D, Leal SM, Gabriel S, Rieder MJ, Abecasis G, Altshuler D, Nickerson DA, Boerwinkle E, Sunyaev S, Bustamante CD, Bamshad MJ, Akey JM, Broad GO, Seattle GO, NHLBI Exome Sequencing Project (2012) Evolution and functional impact of rare coding variation from deep sequencing of human exomes. *Science* 337:64-69

Tennessen JA, O'Connor TD, Bamshad MJ, Akey JM (2011) The promise and limitations of population exomics for human evolution studies. *Genome Biology* 12:127

Tennessen JA, Akey JM (2011) Parallel adaptive divergence among geographically diverse human populations. *PLoS Genetics* 7:e1002127

Tennessen JA, Madeoy J, Akey JM (2010) Signatures of positive selection apparent in a small sample of human exomes. *Genome Research* 20:1327-1334

Tennessen JA, Blouin MS (2010) A revised leopard frog phylogeny allows a more detailed examination of adaptive evolution at ranatuerin-2 antimicrobial peptide loci. *Immunogenetics* 62:333-343

Tennessen JA, Woodhams DC, Chaurand P, Reinert LK, Billheimer D, Shyr Y, Caprioli RM, Blouin MS, Rollins-Smith LA (2009) Variations in the expressed antimicrobial peptide repertoire of northern leopard frog (*Rana pipiens*) populations suggest intraspecies differences in resistance to pathogens. *Developmental and Comparative Immunology* 33:1247-1257

Tennessen JA, Blouin MS (2008) Balancing selection at a frog antimicrobial peptide locus: fluctuating immune effector alleles? *Molecular Biology and Evolution* 25:2669-2680

Tennessen JA (2008) Positive selection drives a correlation between non-synonymous/synonymous divergence and functional divergence. *Bioinformatics* 24:1421-1425

Tennessen JA, Zamudio KR (2008) Genetic differentiation among mountain island populations of the striped plateau lizard, *Sceloporus virgatus* (Squamata: Phrynosomatidae). *Copeia* 2008:558-564

Miranda RR, Tennessen JA, Blouin MS, Rabelo EM (2008) Mitochondrial DNA variation of the dog hookworm *Ancylostoma caninum* in Brazilian populations. *Veterinary Parasitology* 151:61-67

Tennessen JA, Blouin MS (2007) Selection for antimicrobial peptide diversity in frogs leads to gene duplication and low allelic variation. *Journal of Molecular Evolution* 65:605-615

Tennessen JA (2005) Molecular evolution of animal antimicrobial peptides: widespread moderate positive selection. *Journal of Evolutionary Biology* 18:1387-1394

Tennessen JA (2005) Enhanced synonymous site divergence in positively selected vertebrate antimicrobial peptide genes. *Journal of Molecular Evolution* 61:445-455

Tennessen JA, Zamudio KR (2003) Early-male reproductive advantage, multiple paternity, and sperm storage in an amphibian aggregate breeder. *Molecular Ecology* 12:1567-1576

## **Employment and Affiliations**

May 2021 – present: Research Scientist, Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health.

June 2021 – present: Research Scholar, Ronin Institute for Independent Scholarship

August 2018 – present: Associated Scientist, Infectious Disease and Microbiome Program, The Broad Institute.

August 2018 – May 2021: Research Associate, Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health.

July 2015 – August 2018: Assistant Professor (Senior Research), Department of Integrative Biology, Oregon State University

July 2011 – June 2015: Postdoctoral Scholar / Research Associate, Department of Integrative Biology, Oregon State University.

June 2009 – June 2011: Postdoctoral Fellow, Department of Genome Sciences, University of Washington.

September 2003 – June 2009: Graduate student, Department of Zoology, Oregon State University. Advisor: Michael Blouin

August 2002 – June 2003: 10<sup>th</sup> grade biology teacher, Bread and Roses High School, New York, NY

## Funding

### *Senior role*

Subaward PI, NIH R01 Subaward, “Identifying schistosomiasis resistance genes of snail vectors in hotspot transmission zones: Translating from laboratory models to the field” (Pass-through entity PI Michelle Steinauer), \$30,815/year. NIH R01-AI141862-01. December 2018 – November 2023.

Co-investigator, NIH R01, “Latitudinal landscape genomics and ecology of *Anopheles darlingi*” (PI Jan Conn), \$733,700/year. NIH R01-AI110112-06A1. September 2020 – August 2025.

Co-investigator, NIH R01, “Genetic mechanisms of snail/schistosome compatibility” (PI Michael Blouin), \$250,000/year. NIH R01AI143991-01. January 2019 – December 2022.

Named Consultant, NSF Collaborative Proposal, “Testing mechanisms and consequences of W chromosome turnover in a dynamic plant system” (PIs Aaron Liston and Tia-Lynn Ashman), \$790,000/year, my fees \$2000/year. NSF 1912180. July 2019 – June 2022.

Co-investigator, NIH R21, “High-density linkage map to find snail genes that block schistosome transmission” (PI Michael Blouin), \$100,000/year. NIH R21AI111201. November 2014 – October 2017.

PI, Environmental Protection Agency Science to Achieve Results (STAR) Fellowship, \$37,000/year. EPA-F2006-STAR-D1. September 2006 – June 2009.

PI, National Science Foundation Graduate Research Fellowship, \$42,000/year. NSF 0305342. September 2003 – August 2006.

### *Other named role, with substantial contribution to proposal development*

Post-doc, NIH R01, “A new genetic mechanism in snails that controls transmission of schistosomes” (PI Michael Blouin), \$250,000/year. NIH R01-AI109134-01. August 2014 – July 2017.

Post-doc, NSF Collaborative Research, “An integrated understanding of how polyploidy generates biodiversity” (PIs Aaron Liston, Rich Cronn, and Tia-Lynn Ashman), \$931,466/year. NSF 1241217. January 2013 – September 2018.

## Academic Presentations

### *Invited talks*

MalariaGEN / Pan-African Mosquito Control Association (PAMCA), Summer 2022: “A population genomic unveiling of a new cryptic mosquito taxon within the malaria-transmitting *Anopheles gambiae* complex” (via Zoom)

German Center for Infection Research (DZIF) Seminar, Heidelberg University, Fall 2021: “Population genomics of South American malaria vectors” (via Zoom)

Boston Evolutionary Genomics Supergroup Seminar Series, Fall 2020: “Three signatures of adaptive polymorphism exemplified by malaria-associated genes” (via Zoom)

Center for Theoretical Evolutionary Genomics (CTEG) Seminar Series, University of California, Berkeley, Spring 2020: “Three hallmarks of malaria-induced selection in human genomes” (via Zoom)

Lester Newman Seminar Series, Biology Department, Portland State University, Fall 2014: “Extra sexes, extra genomes: Evolution of dioecy and polyploidy in strawberries”

Environmental Systems Seminar, University of California Merced, Winter 2013: “How infectious disease maintains adaptive genetic diversity”

Application of Genomics to Anthropological Research Workshop, Texas Biomedical Research Institute, Winter 2013: “Detecting natural selection in human genomic data”

Department of Animal Science, University of California Davis, Spring 2012: “Darwinian prospecting: evolutionary approaches to finding functionally important genetic variants”

#### *Other*

American Society of Tropical Medicine and Hygiene Annual Meeting, Seattle, WA, Fall 2022 (poster)

American Society of Tropical Medicine and Hygiene Annual Meeting, National Harbor, MD, Fall 2019 (talk)

Annual Meeting for the Society for Molecular Biology and Evolution, Manchester UK, Summer 2019 (talk)

Evolution 2017, Portland, OR, Summer 2017 (talk)

International Plant & Animal Genome (PAG) XXIII, San Diego, CA, Winter 2017 (talk)

International Plant & Animal Genome (PAG) XXIII, San Diego, CA, Winter 2015 (talk)

International Plant & Animal Genome (PAG) XXI, San Diego, CA, Winter 2013 (talk)

Center for Genome Research and Biocomputing Fall Conference, Oregon State University, Fall 2012 (talk)

Northwest Institute of Genetic Medicine Annual Retreat, University of Washington, Spring 2011 (talk)

Evolution 2010, Portland, OR, Summer 2010 (talk)

Evolution 2008, University of Minnesota, Summer 2008 (talk)

Evolution Washington/Idaho/British Columbia/Oregon (EVO-WIBO), Port Townsend, WA, Spring 2008 (poster)

Annual Meeting for the Society for Molecular Biology and Evolution, Dalhousie University, Summer 2007 (poster)

Peter Yodzis Colloquium in Fundamental Ecology, University of Guelph, Spring 2007 (poster)

EPA STAR Conference, Washington, D.C., Fall 2006 (poster)

Annual Meeting for the Society for Molecular Biology and Evolution, Arizona State University, Spring 2006 (talk)

Evolution Washington/Idaho/British Columbia/Oregon (EVO-WIBO), Port Townsend, WA, Spring 2006 (talk)

Biology Graduate Student Symposium, Oregon State University, Winter 2006 (talk)

Biology Graduate Student Symposium, Oregon State University, Winter 2005 (talk)

Evolution Washington/Idaho/British Columbia/Oregon (EVO-WIBO), Port Townsend, WA, Spring 2004 (poster)

## Software

Perl scripts for analyzing DNA sequence data (POLiMAPS, HOLDRS, MiSCVARS, GOPOPS, GeneBuddies, MalariaHallmarks)

<https://github.com/jacobtennessen/>

SOLOMON, Parentage analysis using Bayes' theorem (collaborator; Mark Christie is first author)

<http://cran.r-project.org/web/packages/SOLOMON/>

## Bioinformatics Skills

Scripting expertise with published tools (see above) in Perl and R

Other scripting expertise in Bash (Linux shell), Python, and Windows Cmd

Software expertise with numerous bioinformatic packages and tools

## Peer Review

### *Editorial positions*

Associate Editor for Evolutionary and Population Genetics, Frontiers (Frontiers in Genetics / Frontiers in Ecology and Evolution): see <https://loop.frontiersin.org/people/30271/overview>

Guest Editor, PLoS Pathogens

### *Review of journal articles*

American Journal of Botany; Applications in Plant Sciences; Asian Herpetological Research; Biochimie; Bioinformatics; BMC Evolutionary Biology; BMC Genetics; BMC Genomics; Ciência Rural; Communications Biology; Computational Biology and Chemistry; EcoHealth; eLife; Endocrine, Metabolic & Immune Disorders; Endocrinology; Environmental Microbiology; Evolution; Evolutionary Bioinformatics; Frontiers in Ecology and Evolution; Frontiers in Genetics; Frontiers in Immunology; Frontiers in Plant Science; Gene; Genes; Genome Biology and Evolution; GigaScience; Heredity; International Journal of Molecular Sciences; Journal of Avian Biology; Journal of Heredity; Journal of Molecular Evolution; Marine Ecology; Memórias do Instituto Oswaldo Cruz; Molecular & Biochemical

Parasitology; Molecular Biology and Evolution; Molecular Breeding; Molecular Ecology; Molecular Ecology Resources; Molecular Phylogenetics and Evolution; Nature Communications; New Phytologist; One Health & Implementation Research; Open Biology; Parasites & Vectors; Parasitology; Peptides; Physiological and Biochemical Zoology; The Plant Cell; PLoS Genetics; PLoS Neglected Tropical Diseases; PLoS One; PLoS Pathogens; Proceedings of the Royal Society B: Biological Sciences; Scientific Reports; Trends in Parasitology; Tropical Medicine and Infectious Disease; Zoologischer Anzeiger

#### *Review of grant proposals*

National Science Foundation Division of Environmental Biology (DEB) Review Panel (2016); Biotechnology and Biological Sciences Research Council (BBSRC); ETH Zurich Research Commission; Czech Science Foundation

### **University Teaching**

Population Genetics (Co-taught with Michael Blouin), Oregon State University, Winter 2018

Honors Genetics, Oregon State University, Winter 2016

Genomics in Ecology and Evolution (Co-taught with Michael Blouin), Oregon State University, Winter 2012 and Spring 2014

#### Guest lectures:

Computational Biology: Genomes, Networks, Evolution; Boston University, Fall 2018, Fall 2019

Evolution; Linfield College, Fall 2017

Honors Genetics; Oregon State University, Spring 2017, Spring 2018

Genetic Mapping; Oregon State University, Fall 2016

Genetics; Oregon State University, Fall 2014

Population Genetics; Oregon State University, Spring 2004, Spring 2012

Evolution; Oregon State University, Summer 2005, Spring 2012, Fall 2016

Debates in Genetics; University of Washington, Spring 2010, Spring 2011

Evolution; Willamette University, Spring 2008

(Teaching Assistant) Introductory Biology, Cornell University, Fall 2001

### **University Service**

#### *Undergraduate mentoring*

Primary mentor for an undergraduate researcher via Harvard Summer Undergraduate Research in Global Health and Harvard College Research Program, Summer & Fall 2020

Primary mentor for an undergraduate researcher via Harvard Summer Internship in Biological Sciences in Public Health, Summer 2019

Thesis committee for an Oregon State University Honors College student, Spring 2016

*Other*

Equity, Justice, and Inclusion committee, Oregon State University Department of Integrative Biology, 2017 – 2018

Louis Stokes Alliance for Minority Participation Bridge Program, Oregon State University, 2016 – 2017

Search Advocate, Oregon State University, 2016 – 2017

Seminar Committee, Oregon State University Department of Integrative Biology, 2015 – 2016

**Outreach**

Blog: <https://adaptivediversity.wordpress.com>

The Emoji Guide to Human Genetic Diversity: <https://scholar.harvard.edu/jtennessen/emojiguide>

Mastodon: @JacobPhD@scicomm.xyz

Twitter (no longer maintained): @JacobPhD, @biolojical