

Martine Zilversmit

American Museum of Natural History / Sackler Institute of Comparative Genomics and Richard Gilder Graduate School / Central Park West @ 79th Street / New York, NY 10024 / mzilversmit@amnh.org

-CURRICULUM VITAE-

Education

- 2007 PhD, Biology, Harvard University (with Daniel Hartl)
“Recombination and Genome Evolution in *Plasmodium falciparum*”
- 2002 MS, Biology, American Museum of Natural History/New York University (with Rob DeSalle)
“High Throughput Sequencing for Comparative Genomics: Studies in Phylogenetics and Molecular Evolution”
- 1995 AB, Anthropology (Biology Concentration), Oberlin College

Professional Experience

- 2015 – Present Gerstner Scholar of Bioinformatics and Computational Biology, American Museum of Natural History
- 2013 - 2015 Mentor, National Institutes of Health Summer Internship Program
- 2012 - 2015 Faculty Member, Department of Bioinformatics, Foundation for Advanced Education in the Sciences, National Institutes of Health
- 2012 - 2015 Postdoctoral Fellow IRTA, National Institutes of Health, National Institute of Allergy and Infectious Disease, Supervisor: Xin-zhuan Su
- 2011 Visiting Researcher, Wellcome Trust Sanger Institute, Malaria Genomics Team
Supervisor: Matt Berriman
- 2008 - 2011 Postdoctoral Fellow, University of Montreal, Sainte-Justine Research Centre
Supervisor: Philip Awadalla
- 2007 - 2008 Royal Society North American Fellow, University of Oxford
Department of Statistics, Sponsor: Gil McVean
- 2007 - 2008 Postdoctoral Fellow, New York University School of Medicine
Department of Medical Parasitology, Supervisors: Karen Day and Jane Carlton
- 2000 - 2001 Research Assistant, Comparative Genomics, American Museum of Natural History
Molecular Systematics Laboratory, Supervisor: Rob DeSalle
- 2000 Researcher, Human Genetics, American Museum of Natural History
Department of Anthropology, Supervisor: Martha Graham
- 1998 - 2000 Laboratory Assistant, Mammal Paleontology, American Museum of Natural History
Department of Vertebrate Paleontology, Supervisor: Malcolm McKenna
- 1995 - 1999 Cultural Resources Assistant, Biological Anthropology, American Museum of Natural History, Department of Anthropology, Supervisor: Martha Graham

Grants

- 2010 National Institutes of Health, USA. Author and Collaborator (PI: Karen P. Day).
(2010-2015, R01 A1 084156-01, \$1,250,000 USD)
- 2009 Operating Grant, Canadian Institute of Health Research, Canada (Co-PI with Philip Awadalla). “The global genomics of human malaria parasites: deep resequencing to identify genetic control points of transmission, drug resistance and immune evasion in *Plasmodium falciparum*.” (9/1/2009-8/32/2013, Grant number: 200183, \$514,916 CAD)

2002 National Science Foundation, USA. Author and Student (co-PIs: Rob DeSalle and Patrick O’Grady) High Throughput Genome Sequencing in Drosophilidae. (2002-2004, DEB 01-29105, \$385,000 USD)

Programming and Software Skills

Genetics and Phylogenetics: BLAST+, SMART (protein domain prediction), Clustal (W and X), Muscle, Mesquite, PhyUtility, PhyML, PHYLIP, Sequencher

Genomics: BWA (using BWA and BWA-MEM alignment methods), SAMtools (using BAQ and extended BAQ algorithms), SNPeff, VCFtools, BEDtools, Velvet, SSPACE, QUAST, Artemis, IGV, GATK, Trinity, BUSCO, Augustus

Programming languages and mathematical programs: Python, BASH scripting, UNIX (including sed and awk scripting), R, Mathematica

Sequencing Platforms

Illumina HiSeq, Illumina MiSeq, ABI SOLiD, ABI 3730

Wet bench skills

PCR, dye-terminator sequencing, plasmid construct cloning, gel electrophoresis, whole-genome library construction, *in vitro* cell culture, electroporation cell transfection, light microscopy

Awards and Fellowships

2010 Society for the Study of Evolution International Young Investigator Award
2010 Workshop on the Ecology and Evolution of Infectious Disease Scholarship
2007 Royal Society Visiting Researcher Fellowship, UK. “Recombination dynamics in the *var* gene family of *Plasmodium falciparum*.” (9/1/2007 - 6/30/2008, £4,000 GBP)
2006 Summer Institute for Statistical Genetics Scholarship

Teaching and Mentoring

2013-Present Instructor, Foundation for Advanced Education in the Sciences, National Institutes of Health, Next-Generation Sequencing (BIOF521)
2012-2014 Instructor, Bio-Trac, National Institutes of Health, Bioinformatic Analysis of Next Generation Sequencing Data
2012 Instructor, Foundation for Advanced Education in the Sciences, National Institutes of Health, Evolutionary Genomics (BIOF508)
2006 Course Coordinator (with John Wakeley), Harvard University, Evolutionary Genetics Seminar (OEB 253r)
2005 - 2006 Graduate Student Director, Harvard College Science Mentoring Program
2005 Teaching Fellow, Harvard University, Systematics (OEB 181)
2004 Teaching Fellow, Harvard University, Genetics and Genomics (BS 50)
2002 - 2005 Mentor, Harvard College Science Mentoring Program
2002 Project Coordinator/Mentor, Woodrow Wilson National Fellowship Foundation
1997 - 1999 Director, Graduate/Undergraduate Intern Program, Cultural Resources Division, American Museum of Natural History

Publications

Nair, S.C., Pattaradilokrat, S., Wu, J., Qi, Y., **Zilversmit, M.M.**, Nagarajan, V., Eastman, R., Orandale, M., Tan, J., Myers, T.G., Long, C.A., Su, X-Z, A malaria HECT-like ubiquitin ligase linked to virulence and host mortality. *In review*

Molina-Cruz A., **Zilversmit, M.M.**, Neafsey, D.E., Hartl, D.L., Barillas-Mury. Mosquito Vectors and the Globalization of *Plasmodium falciparum* Malaria. *Annual Review of Genetics*. *In press*

Zilversmit, M.M., Pattaradilokrat, S., Su, X-Z. Parasite Genomics. In “*Advances in Malaria Research*” (V.S. Chauhan, C. Chitnis, D. Gaur eds). Wiley-IUBMB Publishing. *In press*.

Qi, Y., Feng, Z., Eastman, R.T., Fu, Y., **Zilversmit, M.**, Pattaradilokrat, S., Hong, L., Liu, S., McCutchan, T., Wenyue, X., Li, J., Huang, F., Su, X-Z. A Sexual Stage-Specific Ribosomal RNA Essential for *Plasmodium yoelii* Oocyst Maturation. *MBio*. 10(6):2

Nair, S.C.,* Pattaradilokrat, S.,* **Zilversmit, M.M.**,* Nagarajan M., Stephens M.T., Xiao W., Tan J.C., Su X-Z. (2014) Genome-wide polymorphisms and development of a microarray platform to detect genetic variations in *Plasmodium yoelii*. *Molecular and Biochemical Parasitology*. 194(1)9-15. *Authors contributed equally

Pattaradilokrat, S., Li, J., Wu, J., Qi, Y., Eastman, R.T., **Zilversmit, M.**, Nair, S., Huaman, M.C., Quinones, M., Jiang, H., Li, N., Zhug, J., Zhaog, K., Kanekoh, O., Long, C.C., Xiaoi, W., Su, X-Z. (2014) *Plasmodium* genetic loci modulating strain-specific innate immune response and virulence. *Genes and Immunity*. 15(3):145-152.

Zilversmit, M.M., Chase, E.K., Chen, D., Awadalla, P., Day, K.P., McVean, G. (2013) Hypervariable antigen genes in malaria have ancient roots. *BMC Evolutionary Biology*. 13:110-110. (Corresponding author)

- Highlighted on the *Malaria Research Communication Network* and in *Malaria World*
- #1 “Most Viewed” and “Most Emailed” article for assessment period (30 days post-publication)
- “Highly Accessed”

Conrad, D.F., Keebler, J., DePristo, M., Lindsay, S.J., Zhang, Y., Casals, F., Idaghdour, Y., Torroja, C., Hartl, C., Garimella, K., **Zilversmit, M.M.**, Cartwright, R., Rouleau, G., Daly, M., Stone, E.A., Hurles, M.E., Awadalla, P on behalf of the 1000 Genomes Project. (2011) Variation in genome-wide mutation rates within and between human families. *Nature Genetics*. 43(7):712-4.

Jiang, H., Li N., Gopalan V., **Zilversmit M.M.**, Varma, S., Nagarajan, V., Li J., Mu J., Hayton K., Henschen G., Yi M., Stephens R, McVean G, Awadalla P., Wellems T. E., Su X-Z. (2011) High chromosome recombination rates and hotspots from a *Plasmodium falciparum* genetic cross. *Genome Biology* 12:R33.

Zilversmit, M.M., Awadalla P. (2011) The Importance of the Natural History of Malaria. *Science* (E-Letter, 14 February). <http://www.sciencemag.org/content/329/5999/1586/reply>.

Myers, R.A., Casals, F., Gaultier, J., Keebler, J., Boyko, A.R., Bustamante, C.D., Piton, A.M., Speigelman, D., Henrion, E., **Zilversmit, M.M.**, Hussin, J., Quinlan, J., Yang, Y., Lafreniere, R., Griffing, A.R. Stone, E.A., Rouleau, G.A., Awadalla, P. (2010) A Population Genetic Approach to Mapping Neurological Disorder Genes Using Deep Resequencing. *PLoS Genetics* 7:e1001318.

Zilversmit, M.M., Volkman, S.K., Wirth, D.F., Awadalla, P., Hartl D.L. (2010) Low-Complexity Regions in *Plasmodium falciparum*: Missing Links in the Evolution of an Extreme Genome. *Molecular Biology and Evolution*. 27(9):2198-2209. (Corresponding author)

1000 Genomes Project Consortium (2010) A map of human genome variation from population scale sequencing. *Nature*. 467(7319)1061–1073

Awadalla, P., Gauthier, J., Myers R., Casals, F., Griffin, A., Hamdan, F., Spiegelman, D., Henrion, E., Lafreniere, R., Boyko, A., Bustamante, C., Yang Y, Rapoport, J.L., DeLisi, L.E., Krebs, M-O., Joobor, R., Mouaffak, F., Fombonne, E., Mottron, L., **Zilversmit, M.M.**, Keebler J., Marineau, C., Forget-Dubois, N., Boivin, M., Roy-Gagnon, M-H., Dube, M-P., Stone, E., Rouleau, G.A. (2010) Direct Estimates of De novo Mutation Rates and Constraints in Autism and Schizophrenia. *American Journal of Human Genetics* 87:1-9.

Zilversmit, M.M., Perkins SL. (2008) *Plasmodium*. Apicomplexa. <http://www.tolweb.org/Plasmodium>. In The Tree of Life Web Project.

Ferreira, M.U., **Zilversmit, M.**, Wunderlich, G. (2007) Origins and Evolution of Antigenic Diversity in Malaria Parasites. *Current Molecular Medicine* 7:588-602.

Jennings, C.*, Ahouidi, A*., **Zilversmit, M.M.**, Bei, A., Saar, O., Ndir, O., Mboup, S., Wirth, D., Duraisingh, M. (2007) Sequence polymorphism and protein expression in members of the *Plasmodium falciparum* Reticulocyte Binding Protein homolog family in field isolates from Senegal. *Infection and Immunity* 75:3531-3538. *Authors contributed equally

Bethke, L.L., **Zilversmit, M.M.**, Daily, J., Volkman, S. K., Ndiaye, D., Lozovsky, E.R., Hartl, D.L., Wirth, D.F. (2006) Creation of a new acyl-CoA synthetase gene by a double gene conversion event in the subtelomeric chromosomal regions of *P. falciparum*. *Molecular and Biochemical Parasitology* 150:10-24.

DePristo, M.A.* , **Zilversmit, M.M.***, Hartl, D.L. (2006) On the function and evolution of low-complexity regions in proteins. *Gene* 378:19-30. *Authors contributed equally.

Zilversmit, M., Hartl, D.L. (2005) Evolutionary history and population genetics of human malaria parasites. pp 95-115. In *Molecular Approaches to Malaria* (I.W. Sherman, ed). ASM Press, Washington. (Corresponding author)

O'Grady, P.* , **Zilversmit, M.*** (2004) Phylogenetic Relationships Within the *Drosophila haleakalae* Species Group Inferred by Molecular and Morphological Characters (Diptera: Drosophilidae). *Bishop Museum Bulletin in Entomology* 12:117-134. *Authors contributed equally. (Corresponding author)

Zilversmit, M., O'Grady P., DeSalle, R. (2002) Shallow Genomics, Phylogenetics, and Evolution in the Family Drosophilidae. pp 512-523. In *Pacific Symposium on Biocomputing* (Altman, R., Dunker, A.K., Hunter, L., Lauderdale, K., Klein, T. eds).

Zilversmit, M., O'Grady, P., Russello, M., DeSalle R. (2001) High Throughput Sequencing Protocols for a Survey of Genomic Characters in the Family Drosophilidae. *Drosophila Information Service* 84:199-201.

Bonacum, J., DeSalle, R., O'Grady, P., Olivera, D., Wintermute, J., and **Zilversmit, M.** (2001) New nuclear and mitochondrial primers for systematics and comparative genomics in Drosophilidae. *Drosophila Information Service* 84:201-204.

Published Abstracts

Zilversmit, M.M., Nair, S.C., Quinones, M., Oler, A., Pattaradilokrat, López-Barragánan, M.J., Su, X-Z., (2013) ComPar: A fast and flexible pipeline for analysis of malaria genome variation using next-generation

sequencing data. World Malaria Day. Johns Hopkins University, Baltimore, MD, USA.

Zilversmit M.M., Chase E.K., Day K.P., McVean G., Awadalla, P. (2010) Mosaic recombination in gene families and host-parasite coevolution. *The Biology of Genomes*. Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, USA.

Zilversmit M.M., Chase E. K., Day K.P., McVean G. (2008) Ancient Recombination and the birth and evolution of the *Plasmodium falciparum* var genes. Genomic Epidemiology of Malaria Conference. The Wellcome Trust Sanger Institute, Hinxton, UK.

Zilversmit M.M., DePristo M.A., Hartl D.L. (2006) The Evolution of Low-Complexity Regions in *Plasmodium falciparum* Proteins: A+T Bias, Recombination, and Antigenic Diversity. For Poster Presentation. Keystone Symposium on Malaria, Taos, NM, USA.

Invited Talks

University of Rochester, Department of Biology Seminar Series, 2015: “The Evolutionary Genomics of Malaria: Mutation, Duplication, and Recombination.”

Johns Hopkins Malaria Research Institute, Department Seminar Series, 2014: “Capturing Cryptic Variation in Malaria Parasite Genomes.”

National Institutes of Health, National Institute of Allergy and Infectious Diseases, Twinbrook Seminar, 2011: “Genetic Recombination and Evolution in Malaria Parasites and the Human Host.”

Santa Clara University, Biology Department Seminar Series, 2010: “Human Malaria in an Evolutionary Context.”

University of Pennsylvania, Department of Genetics, 2010: “Mosaic Genetic Recombination and Host-Parasite Coevolution.”

Oberlin College, Biology Department Seminar Series, 2009: “Genome Evolution in Malaria Parasites.”

Courant Institute of Mathematical Sciences of New York University, Biomathematics Seminar Series, 2008: “Host and Parasite Evolution in Malaria Endemic Areas.”

University of Montreal, CHU Sainte-Justine Research Centre, Axes of Infectious Diseases Seminar Series, 2008: “Low-Complexity Regions and Genome Evolution in Malaria Parasites.”

University of Oxford, Mathematical Genetics and Bioinformatics Groups Seminar Series, 2007: “Low-Complexity Regions and Genome Evolution in Malaria Parasites.”

Harvard University, Program for Evolutionary Dynamics, 2005: “Low-Complexity Regions in Proteins: A+T Bias, Antigenic Diversity, and Implications for Genome Evolution Using *Plasmodium falciparum* as Model.”

The Broad Institute of Harvard and MIT, Infectious Disease Initiative, 2005:” Structure and Evolution of Low-Complexity Regions in Proteins.”

The Broad Institute of Harvard and MIT, Medical and Population Genetics Program, 2004: “The Evolutionary History of Malaria Parasites: New Insights from Genomics and Molecular Biology.”

Oral Conference Presentations:

iEvoBio Meeting, 2014: “ComPar: Next-Generation Sequencing Pipelines for Capturing and Validating Cryptic Variation in Non-model Genomes.”

Annual Meeting of the Society for the Study of Evolution, 2014: “Capturing highly divergent regions in genomes: Next-Gen Sequencing and why “false positives” might be exactly what you are looking for.”

Annual Meeting of the Society for the Study of Evolution, 2011: “Recombination and Evolution in Malaria Parasites and the Human Host.”

Annual Meeting of the Society for the Study of Evolution, 2010: “Recombination, Gene Families, and Host-Parasite Coevolution.”

Montreal Bioinformatics Users Group Symposium (Invited Speaker), 2009: “Using Next-Generation Genome Sequencing Technologies to Examine Genome Change and Virulence in Malaria Parasites.”

Comparative Genomics of Malaria Parasites Symposium (Invited Speaker), 2007: “Low-Complexity Regions in *Plasmodium falciparum*: Missing Links in Genome Evolution.”

Annual Meeting of the Society for Molecular Biology and Evolution, 2007: “Low-Complexity Region Evolution in the Human Malaria Parasite *Plasmodium falciparum*: Missing Links in the Evolution of an Extreme Genome.”

Molecular Parasitology Meeting (Plenary Talk), 2006: “The Evolution of Low-Complexity Regions in Proteins: Genome Evolution, Recombination, and Pathogenesis in Malaria Parasites.”

Annual Meeting of the Society for the Study of Evolution, 2005: “Low-Complexity Regions in Proteins Allow for Genome Structure Change and Adaptation to the Human Host in the Malaria Parasite *Plasmodium falciparum*.”

Leadership Positions

2015 -Present Co-chair Mentoring Circles Program Steering Committee, Women in Natural Sciences
2013 Association for Women in Science Mentoring Circle Leader
2007- Present Basal Eukaryote Branch Coordinator, *Plasmodium*, Tree of Life Web Project
2004-2006 Co-founder and Executive Board Member, Harvard Graduate Women in Science and Engineering
2005-2006 Graduate Student Director, Harvard College Science Mentoring Program
2005 Coordinator, Harvard Malaria Genetics Working Group
2003 Co-coordinator, Genetics and Genomics Training Program Annual Symposium, Harvard University

Graduate and Undergraduate Thesis Students Advised

Edwin Wintermute (New York University, 2000-2002)

Jehee Choi (Harvard University, 2004-2007)

Natalia Tichshenko (University of Montreal, 2009-2010)

Gordon Bullen (Colorado College/National Institutes of Health, 2013)

Lucky Amuza (Institute of Tropical Medicine, Nagasaki University, 2014)

Synergistic Activities

Member, Education Committee, The Society for the Study of Evolution, 2010-Present

Manuscript Reviewer – *Nature. Molecular Biology and Evolution, Genome Biology and Evolution, PLoS Neglected Tropical Diseases, G3: Genes • Genomes • Genetics, PLoS ONE.*

Workshop Participation

Workshop on the Ecology and Evolution of Infectious Disease, Cornell University, Ithaca, NY, June 2010

ApiDB Workshop, University of Georgia, Athens, GA, June 2006

Summer Institute in Statistical Genetics, University of Washington, Seattle, WA, June 2006

Workshop on Molecular Evolution, Marine Biological Laboratory, Woods Hole, MA, August 2003

Professional Societies

American Association for the Advancement of Science

American Association of Tropical Medicine and Hygiene

American Society for Microbiology

Association for Women in Science

Malaria Research Coordination Network

Society for Molecular Biology and Evolution

Society for the Study of Evolution