Matthew D. MacManes, PhD

189 Rudman Hall Durham, NH 03824 (603) 862 4052 | ⊠ matthew.macmanes@unh.edu " www.genomebio.org | @PeroMHC

Employment

- 2013–current Assistant Professor The University of New Hampshire. Department of Molecular, Cellular & Biomedical Sciences.
 - 2011–2013 **Postdoctoral Training.** The University of California, Berkeley. California Institute for Quantitative Biosciences PI: Michael Eisen

Affiliation

2013-current Hubbard Center for Genome Studies Faculty Affiliate

- 2013–current Molecular and Evolutionary Systems Biology Graduate group
- 2013–current Genetics Graduate group

Publications

- 2014 M. D. MacManes and M.B. Eisen. Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse *Peromyscus eremicus* PeerJ http://dx.doi.org/10.7717/peerj.642.
- 2014 M. D. MacManes On optimal trimming of high-throughput sequence data. Frontiers in Genetics http://journal.frontiersin.org/Journal/10.3389/fgene.2014.00013.
- 2013 Haas, B., A. Papanicolaou, M.,Yassour, M. Grabherr, P. Blood, J. Bowden, M.B. Couger, D. Eccles, B. Li, M. Lieber, M. D. MacManes, M. Ott, J. Orvis, N. Pochet, F. Strozzi, N. Weeks, R. Westerman, T. William, C. Dewey, R. Henschel, R. LeDuc, N. Friedman, A. Regev. *De novo* transcript sequence reconstruction from RNA-Seq: reference generation and analysis with Trinity. Nature Protocols 8, 1494–1512 http://dx.doi.org/10.1038/ nprot.2013.084.
- 2013 M. D. MacManes and M.B. Eisen. Improving transcriptome assembly through error correction of high-throughput sequence reads. PeerJ 1:e113 http://dx.doi.org/10.7717/ peerj.113.
- 2013 Korf, I., K. Bradham, M. D. MacManes and 89 others. Assemblathon 2: genome assembly in three vertebrate species. GigaScience, 2:10 http://dx.doi.org/10.1186/ 2047-217X-2-10.
- 2013 M. D. MacManes On the accurate description of social and genetic mating systems. In review. Animal Behavior [PeerJ Preprint].
- 2012 M. D. MacManes and Eileen A. Lacey. The social brain: Transcriptome assembly and characterization of the hippocampus from a social subterranean rodent, the tuco-tuco (*Ctenomys sociabilis*). PLOS ONE 7(9): e45524 http://dx.plos.org/10.1371/journal.pone.0045524.

- 2012 M. D. MacManes and Eileen A. Lacey. Is promiscuity associated with enhanced selection on MHC-DQα in mice (genus *Peromyscus*)? PLOS ONE 7(5): e37562. http://goo.gl/ S6ySm.
- 2011 M. D. MacManes Promiscuity in mice is associated with increased vaginal bacterial diversity. Naturwissenschaften 98: 951–960. http://dx.doi.org/10.1007/s00114-011-0848-2 [PDF].
- 2011 Rowe, K., S. Singhal, M. D. MacManes , J. Ayroles, T.L. Morelli, E.M. Rubridge, K. Bi, and C.C. Moritz Museum genomics: Low cost and high accuracy genetic data from historical specimens. Molecular Ecology Notes 11: 1082–1092. http://dx.doi.org/10.1111/j.1755-0998.2011.03052.x [PDF].
- 2010 Benedict, L M. D. MacManes , J. Fuchs and R. C. K. Bowie When non-coding is non-neutral: the role of CHD1 gene polymorphism in sexing, in phylogenetics and as a correlate of fitness in birds. Ibis 152(2). 1–3. http://dx.doi.org/10.1111/j.1474-919X.2010.01015.x [PDF].
- 2009 Quan, P M. D. MacManes , L. A. Ebensperger, E. A. Lacey and L. D. Hayes Isolation and characterization of polymorphic microsatellite loci from *Octodon degus*. Molecular Ecology Resources 9(3). 999–1001 http://dx.doi.org/10.1111/j.1755-0998.2009.02536.x [PDF].

Book Chapters

2014 M. D. MacManes E. A. Lacey and E.P. Lessa. Genetics, genomics, and evolutionary themes in caviomorph rodents In: Biología de los roedores Caviomorfos: diversidad y evolución (D. Antenucci and A.I. Vassallo, eds). Sociedad Argentina para el Estudio de los Mamiferos..

Publications In Prep

2014 M. D. MacManes, Anna Geraghty, Julie Woodruff, and E. A. Lacey. Behavioral Genomics: Towards a molecular characterization of individual variation in mammalian social behavior. Molecular Ecology.

Software and Code

- 2013 **TAMrS** Transcriptome Assembly Made (really) Simple https://sourceforge.net/ projects/tamrs/. This software takes fastQ input, trims, optionally merges, assembles, and quantitates..
- 2013 QC_Pro https://sourceforge.net/projects/qcpro/. This software implements best QC practices for Illumina sequence data..

Grants & Fellowships

- 2013 XSEDE SUPERCOMPUTING GRANT MCB110134 (Renewal): Using genomics to understand physiologic water conservation in desert rodents (450,000 hours)
- 2012 XSEDE SUPERCOMPUTING GRANT MCB110134 (Renewal): Using genomics to understand physiologic water conservation in desert rodents (300,000 hours)
- 2011 NIH NRSA POSTDOCTORAL FELLOWSHIP 1F32DK093227-01 Using genomics to understand physiologic water conservation in desert rodents (\$144,000)

- 2011 XSEDE SUPERCOMPUTING GRANT MCB110134: Using genomics to understand physiologic water conservation in desert rodents (388,000 hours)
- 2010 TERAGRID SUPERCOMPUTING GRANT IBN100014: Analysis of next generation sequence data to advance evolutionary insights (575,000 hours)
- 2010 JOSEPH MAILLARD FELLOWSHIP (\$26,161). Tuition, fees, and stipend during last year of graduate training
- 2009 TERAGRID SUPERCOMPUTING GRANT MCB100004: Next Generation Sequencing of Non-Model Organisms (200,000 hours)
- 2008 NSF DOCTORAL DISSERTATION IMPROVEMENT GRANT 0909798 : MHC and Mating Systems: Is sexual behavior related to selection on MHC genes? (\$14,134)
- 2007 UC NRS MILDRED MATHIAS RESEARCH AWARD: For research conducted at Boyd Deep Canyon Desert Research Center. (\$2,000)
- 2007 NSF GRADUATE RESEARCH FELLOWSHIP: Sexually transmitted disease as a driver of phenotypic and genotypic variability across the monogamy-promiscuity continuum in the genus *Peromyscus* (\$161,750)
- 2006 MVZ MARTENS RESEARCH AWARD: For research conducted at Boyd Deep Canyon Desert Research Center. (\$5,000)
- 2006 CALIFORNIA DESERT RESEARCH FUND AWARD: For research conducted at Boyd Deep Canyon Desert Research Center. (\$4,000)
- 2005 UC BERKELEY CHANCELLORS FELLOWSHIP: Tuition, fees, and stipend for first 2 years of graduate training (\$70,400)

Presentations

- Fall 2014 **Invited Seminar**: High Performance Computing Meets the Biological Sciences Illustrated by ongoing work on adaptive genomics University of New Hampshire Dept. of Computer Science
- Summer 2014 **Contributed Talk**: Understanding Adaptation to Deserts in a Novel Model Organism, *Peromyscus eremicus* Evolution 2014, Raleigh, NC
- Summer 2014 **Contributed Talk**: On the optimal trimming of high-throughput mRNA sequence data Evolution 2014, Raleigh, NC
- Summer 2014 **Contributed Talk**: Linking phenotype to expression: A comparative approach to understanding the effects of mating system on immune system processes Evolution 2014, Raleigh, NC (presented by Jeremy Crawford)
- Summer 2014 Contributed Poster: Comparative Genomics of Desert Adaptation Among Mice in the Genus *Peromyscus* Evolution 2014, Raleigh, NC (presented by Lauren Kordonowy)
- Summer 2014 **Contributed Poster**: Identification of genomic underpinnings of spot polymorphism in *Harmonia axyridis* Evolution 2014, Raleigh, NC (presented by Lindsay Havens)
 - Fall 2013 Contributed Talk: Expression genica y socialidad en tuco-tucos XXVI Jornadas Argentinas de Mastozoologia 2013, Mar del Plata, Argentina (presented by Eileen Lacey)
- Summer 2013 Contributed Talk: Brains aren't everything: Gene expression and sociality in tuco-tucos IMC 2013, Belfast, Ireland (presented by Eileen Lacey)

Contributed Talk: A new genome-wide method for annotation and gene expression measurement Evolution 2013, Snowbird, UT (presented by Mathilde Paris)

- Spring 2013 Invited Talk: No water, no pee, no problem. Using genomics to understand adaptation in desert rodents. University of New Hampshire. College of Life Sciences and Agriculture Contributed Talk: Physical Access to a mate regulates follicle maturation: Endocrine and Molecular Correlates. North American Society for Comparative Endocrinology. Queretaro, MX (Presented by Nicole Perfito)
- Winter 2013 Invited Talk: No water, no pee, no problem. Using genomics to understand physiologic adaptation in desert rodents. University of Washington. Biology Department
 - Fall 2012 Invited Talk: Using genomics to understand adaptation in *Peromyscus eremicus*. Computational Genomics Resource Laboratory. UC Berkeley
- Summer 2012 **Contributed Talk**: Parentesco e estrutura social do rabo-de-facho, *Trinomys yonenagae* (Echimyidae) nas dunas do rio São Francisco, BA Congresso Brasileiro de Mastozoologia 2012. (Presented by Wly dos Santos)

Contributed Talk: No water, no pee, no problem! Using genomics to understand adaptation to desert life in *Peromyscus eremicus* Evolution 2012. Ottawa, Ontario. Canada

Winter 2012 Invited Talk: Conquer Data-Intensive Biosciences Problems SGI, Fremont, CA. Link to webinar (registration required): http://info.sgi.com/genomics/webinar.aspx
Invited Talk: Behavioral Genomics: Using Transcriptome Sequencing to Identify Genes

Influencing Social Behavior. UC Berkeley, Museum of Vert. Zoology. Link to video: http://youtu.be/0eIN5j-SWQY

Summer 2011 **Contributed Talk**: Understanding the relationship between sexual behavior, selection on immunogenes, and vaginal bacteria in Peromyscine rodents. Evolution Conference. Norman, OK

Contributed Talk: Behavioral genomics: Using transcriptome sequencing to identify genes influencing social behavior. Mammalogy Conference. Portland, OR

- Summer 2010 **Contributed Talk**: Scale matters: sex and selection on MHC genes in the genus *Peromyscus*. Evolution Conference. Portland, OR
 - Fall 2009 Contributed Talk: Mating systems are continuous variables. Animal Behavior Lunch Seminar Series, UC Berkeley
- Summer 2009 Contributed Talk: MHC and mating systems: Is sexual behavior related to selection on MHC genes? Evolution Conference. Moscow, ID
- Summer 2008 Contributed Poster: MHC and mating systems: Is sexual behavior related to selection on MHC genes? International Society for Behavioral Ecology. Ithaca, NY
- Spring 2008 Contributed Talk: The genetic mating system of *Peromyscus eremicus*. Animal Behavior Lunch Seminar Series, UC Berkeley

Synergistic Activities

- 2005–current **Peer Reviewer**: NSF DEB panel and NSF DEB & IOS *ad hoc*, National Science Centre (Poland), American Naturalist, Conservation Biology, Molecular Biology and Evolution, PLOS One, J. Mammalogy, Behavioral Ecology, Southeastern Naturalist, Evolutionary Ecology, American Journal of Primatology, Proceedings of the Royal Society B, Behaviour., Frontiers in Genetics, BMC Genomics, Nucleic Acids Research, Bioinformatics, PeerJ, International Journal of Molecular Sciences
- 2005–current Society membership: SACNAS, SSE, ISBE, ASM, Sigma Xi

- 2012–2013 **Curriculum Development**: Active member of Albany High School Instructional Improvement Committee (IIC). Approve new classes, assess quality of current classes, multi-year curriculum planning.
- 2005–2013 Mentored Undergraduate Students: Mentored UC Berkeley undergraduates in lab and field techniques: Robert Beck (2006), Manpuneet Samra (2006), Katharine Lovett (2007), Quang Nguyen (2008), Soo Ro (Honors Thesis student, 2010) in lab techniques, and Jon Epperson in bioinformatics (2012)
- 2011-2013 **Career Day**: Led classroom discussion with high school juniors and seniors interested in a career in the biological sciences.
- 2006-2011 **Childhood Education**: Organized educational program (four events) that brought children to the Museum of Vertebrate Zoology to learn about evolution, biodiversity, conservation, and vertebrate zoology
- 2008-2010 **Behavior Lunch Seminar Series**: Coordinated speakers, schedules, and attendance for UC Berkeley Behavior Seminar Series
- 2008-2010 Graduate Admissions Committee Member: Served as graduate student representative on admissions committee. Evaluated applications, with specific attention to increasing minority representation
- 2005-2010 **Minority Retention and Recruitment**: Participation in the Berkeley EDGE, a NSF funded program with aims of increasing minority recruitment, retention, and advancement in science and engineering

Press and Research Coverage

- 2013 Assemblathon 2 review, round 1, parts thereof. (written by C. Titus Brown) On assembly uncertainty (inspired by the Assemblathon 2 debate). (written by Lex Nederbragt)
- 2012 Behavioral Genomics: Alone Time for Tucos. (written by Michael Schneider) Monogamy and the Immune System. Texas Advanced Computing Center.

Monogamy and the Immune System: Differences in Sexual Behavior Impact Bacteria Hosted and Genes That Control Immunity. Science Daily

Promiscuity Boosts Immune Systems in Mice. LiveScience

White Paper: Blacklight at Pittsburgh Supercomputing Center Shines Light on Life Sciences Research

2006 Pursuing the mystery of the monogamous mouse. Transect. 25:1 pp 14-15

Active Research

Core Projects Genomics of functional anuria in desert adapted rodents

Host-Parasite biology of mutually exclusive relationship between an unknown Laelapid mite and ${\it C.\ spinatus}$

Social genomics of tuco tucos

Collaborations Investigating the genomics of the winner effect in spiders (D. Elias, M. Kasumovic) Tuco tuco genome project (with Broad Institute)

Historical demographics of the tuco-tuco (E. Lacey, L. Hadley)

Happy face spider (Theridion grallator) genome project (R. Gillespie, P. Croucher)

Poison Dart Frog (*Oophaga pumilio*) genome project (C. Richards-Zawacki, M. Eisen, R. Nielsen, BGI)

Genetics of extreme color polymorphism in Dentrobatid frogs (K. Summers, M. Eisen, R. Nielsen)

Speciation and the sage-sparrow (R. Bowie, C. Cicero)

Speciation in the Pacific Slope and Cordilleran Flycatchers (R. Bowie, A. Rush)

Education

- 2005–2011 **Doctor of Philosophy.** The University of California–Berkeley. Integrative Biology. PI: Eileen Lacey
- 2002–2005 **Bachelor of Science.** The University of Michigan–Ann Arbor. Major: Natural Resources Minor: Ecology and Evolutionary Biology
- 1996–1999 Associate of Science. Broome Community College. Binghamton, NY. Major: Nursing