

Curriculum Vitae

Rajiv C. McCoy

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Foege Hall
Box 355065
1705 NE Pacific St.
Seattle, WA 98195 USA

Fax: 206-685-7301
Email: rcmccoy@uw.edu
URL: <http://rajivmccoy.wordpress.com>

Education

- 2015 PHD in Biology, Stanford University
- 2010 BS in Biology; Ecosystem Science & Policy, *summa cum laude*, University of Miami

Professional experience

- 2015–Present Postdoctoral Fellow, Department of Genome Sciences, University of Washington
Advisor: Joshua Akey
- 2010–2015 Graduate Researcher, Department of Biology, Stanford University
Advisors: Dmitri Petrov & Carol Boggs
- 2009–2010 Undergraduate Researcher, Department of Biology, University of Miami
Advisor: Barbara Whitlock
- 2008–2009 Undergraduate Researcher, Department of Environmental Sciences, University of Toledo
Advisor: Daryl Dwyer

Grants, honors, & awards

- 2015–2017 Genome Training Grant (NIH/NHGRI T32), U. of Washington, Dept. of Genome Sciences
- 2015 Epstein Trainee Award for Excellence in Human Genetics Research – Finalist, ASHG
- 2014 Office of Graduate Education Travel Award, Stanford University
- 2013 & 2012 Excellence in Teaching Award, Stanford University, Department of Biology
- 2012 Rosemary Grant Award, Society for the Study of Evolution
- 2012 Arthropod Genomics Consortium i5K Workshop Fellowship Award

2010–2013 Stanford University Graduate Fellowship
2010 Phi Beta Kappa Society
2010 Abess Center for Ecosystem Science and Policy Award, University of Miami

Publications & presentations

RESEARCH AND REVIEW ARTICLES (PEER REVIEWED)

- 2017 **McCoy, R. C.** (2017). Mosaicism in preimplantation human embryos: when chromosomal abnormalities are the norm. *Trends in Genetics*, 33(7): 448–463. DOI: [10.1016/j.tig.2017.04.001](https://doi.org/10.1016/j.tig.2017.04.001)
- 2017 **McCoy, R. C.**, Wakefield, J., Akey, J. M. (2017), Impacts of Neanderthal-Introgressed Sequences on the Landscape of Human Gene Expression. *Cell*, 168(5): 916–927.e12. DOI: [10.1016/j.cell.2017.01.038](https://doi.org/10.1016/j.cell.2017.01.038)
- 2016 Vernot, B., Tucci, S., Kelso, J., Schraiber, J. G., Wolf, A. B., Gittelman, R. M., Dannemann, M., Grote, S., **McCoy, R. C.**, Norton, H., Scheinfeldt, L. B., Merriwether, D. A., Koki, G., Friedlaender, J. S., Wakefield, J., Pääbo, S., Akey, J. M. (2016), Excavating Neanderthal and Denisovan DNA from the genomes of Melanesian individuals. *Science*, 352(6282): 235–239. DOI: [10.1126/science.aad9416](https://doi.org/10.1126/science.aad9416)
- 2016 Demko, Z. P., Simon, A. L., **McCoy, R. C.**, Petrov, D. A., Rabinowitz, M. (2016), Effects of maternal age on euploidy in a large cohort of embryos analyzed with 24 chromosome single nucleotide polymorphism-based preimplantation genetic screening. *Fertility & Sterility*, 105(5): 1307–1313. DOI: [10.1016/j.fertnstert.2016.01.025](https://doi.org/10.1016/j.fertnstert.2016.01.025)
- 2015 **McCoy, R. C.**, Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Petrov, D. A. (2015), Evidence of selection against complex mitotic-origin aneuploidy during preimplantation development. *PLoS Genetics*, 11(10): e1005601. DOI: [10.1371/journal.pgen.1005601](https://doi.org/10.1371/journal.pgen.1005601)
- 2015 **McCoy, R. C.**, Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Fraser, H. B., Petrov, D. A. (2015), Common variants spanning *PLK4* are associated with mitotic-origin aneuploidy in human embryos. *Science*, 348(6231): 235–238. DOI: [10.1126/science.aaa3337](https://doi.org/10.1126/science.aaa3337)
- 2014 Ahola, V., Lehtonen, R., Somervou, P., ..., **McCoy, R. C.** (18/45) , ..., Hanski, I. (2014), The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. *Nature Communications*, 5. DOI: [10.1038/ncomms5737](https://doi.org/10.1038/ncomms5737)
- 2014 **McCoy, R. C.**, Taylor, R., Blauwkamp, T. A., Kelley, J. L., Kertesz, M., Pushkarev, D., Petrov, D. A., Fiston-Lavier, A. S. (2014), Illumina TruSeq synthetic long reads empower *de novo* assembly and resolve complex, highly repetitive transposable elements. *PLoS ONE*, 9(9): e106689. DOI: [10.1371/journal.pone.0106689](https://doi.org/10.1371/journal.pone.0106689)
- 2014 **McCoy, R. C.**, Garud, N. R., Kelley, J. L., Boggs, C. L., Petrov, D. A. (2014), Genomic inference accurately predicts the timing and severity of a recent bottleneck in a non-model insect population. *Molecular Ecology*, 23(1): 136–150. DOI: [10.1111/mec.12591](https://doi.org/10.1111/mec.12591)

RESEARCH ARTICLES UNDER REVIEW

Press, M. O., **McCoy, R. C.**, Hall, A. N., Akey, J. M., Queitsch, C. Short tandem repeats with massive variation and functional consequences across strains of *Arabidopsis thaliana*. DOI: [10.1101/145128](https://doi.org/10.1101/145128)

EDITORIALS AND COMMENTARIES

- 2017 **McCoy, R. C.**, Akey, J. M. (2017). Selection plays the hand it was dealt: evidence that human adaptation commonly targets standing genetic variation. *Genome Biology*, 18: 139. DOI: [10.1186/s13059-017-1280-5](https://doi.org/10.1186/s13059-017-1280-5)
- 2017 Adashi, E. Y., **McCoy, R. C.** (2017). Technology versus biology: the limits of pre-implantation genetic screening. *EMBO Reports*: e201743941. DOI: [10.15252/embr.201743941](https://doi.org/10.15252/embr.201743941)
- 2016 **McCoy, R. C.**, Akey, J. M. (2016), Patterns of deleterious variation between human populations reveal an unbalanced load. *Proceedings of the National Academy of Sciences*, 113(4): 809–811. DOI: [10.1073/pnas.1524016113](https://doi.org/10.1073/pnas.1524016113)

NON-ACADEMIC ARTICLES

- 2015 **McCoy, R. C.**, Petrov, D. A. (April 15, 2015), Chromosome errors cause many pregnancies to end before they are even detected., *The Conversation*, URL: <http://goo.gl/RBCdYv>
- 2013 **McCoy, R. C.** (November 26, 2013), Genomic analyses of ancestry of Caribbean populations., *CEHG Blog*, URL: <http://goo.gl/8ALT8P>

ORAL PRESENTATIONS

- 2017 “Gone but not forgotten: excavating archaic hominin sequences from modern human genomes”, 27th Marabou Symposium on Nutrition and Human Development, Stockholm, Sweden
- 2017 “Impacts of Neanderthal-introgressed sequences on the landscape of human gene expression”, Genome Sciences / Computational Molecular Biology Combi Seminar, University of Washington, Seattle, USA
- 2017 “Common variants associated with mitotic-origin of aneuploidy in human embryos”, 16th Annual International Conference on Preimplantation Genetics, Valencia, Spain
- 2016 “Impacts of Neanderthal-introgressed sequences on the landscape of human gene expression”, Genotype-Tissue Expression (GTEx) Project Community Meeting, Stanford, USA
- 2015 “Complex mitotic-origin aneuploidy in human embryos: genetic risk factors and fertility consequences”, 65th Annual Meeting of the American Society for Human Genetics, Baltimore, USA
- 2014 “Causes and consequences of aneuploidy in human embryos”, Bay Area Population Genomics Meeting, University of California, Davis, USA

- 2014 “*De novo* genome assembly and accurate reconstruction of *Drosophila melanogaster* transposable elements using synthetic long-reads”, Illumina Long-Reads Applications Symposium, University of California, Davis, USA
- 2014 “*De novo* genome assembly and accurate reconstruction of *Drosophila melanogaster* transposable elements using synthetic long-reads”, Ecology and Evolution Lunch Seminar, Stanford, USA
- 2014 “Patterns, rates, and mechanisms of aneuploidy in preimplantation human embryos”, Presentation to Management Team at Natera, Inc., San Carlos, USA

POSTER PRESENTATIONS

- 2017 “Evidence of a selective sweep at the FADS locus in the Rampasasa population from Flores, Indonesia”, NHGRI Annual Training and Career Development Meeting, St. Louis, USA
- 2016 “Pervasive *cis*-regulatory impacts of Neanderthal introgression on modern human gene expression”, 66th Annual Meeting of the American Society for Human Genetics, Vancouver, Canada
- 2016 “Pervasive *cis*-regulatory impacts of Neanderthal introgression on modern human gene expression”, NHGRI Annual Training and Career Development Meeting, Bethesda, USA
- 2014 “Characterizing patterns of human aneuploidy in a large sample of IVF patients”, Bay Area Population Genomics Meeting, University of California, Davis, USA
- 2014 “Characterizing patterns of human aneuploidy in a large sample of IVF patients”, Stanford Biosciences Student Association Poster Session, Stanford, USA
- 2014 “Characterizing patterns of human aneuploidy in a large sample of IVF patients”, Society for the Study of Molecular Biology & Evolution, San Juan, Puerto Rico, USA
- 2014 “TruSeq synthetic long-reads empower *de novo* assembly and resolve complex, highly-repetitive transposable elements”, Society for the Study of Molecular Biology & Evolution, San Juan, Puerto Rico, USA
- 2014 “TruSeq synthetic long-reads empower *de novo* assembly and resolve complex, highly-repetitive transposable elements”, Center for Computational, Evolutionary, and Human Genomics Symposium, Palo Alto, USA
- 2013 “TruSeq synthetic long-reads empower *de novo* assembly and resolve complex, highly-repetitive transposable elements”, Bay Area Population Genomics Meeting, Stanford, USA
- 2013 “Evaluating methods of demographic inference and testing for balancing selection using genomic data from the checkerspot butterfly *Euphydryas gillettii*”, Annual Meeting of the Society for Integrative & Comparative Biology, San Francisco, USA
- 2012 “*De novo* transcriptome assembly and SNP discovery in *Euphydryas gillettii* to test for balancing selection”, Arthropod Genomics Symposium, Kansas City, USA
- 2012 “*De novo* transcriptome assembly and SNP discovery in *Euphydryas gillettii* to test for balancing selection”, 1st Joint Congress on Evolutionary Biology, Ottawa, Canada

Teaching

- 2014–2015 Senior Honors Thesis Co-Advisor, Jack McGregor, Stanford University
- 2014 AP Biology E-mentor, Arroyo High School, San Lorenzo, USA
- 2014 Teaching Assistant Mentor, Department of Biology, Stanford University
- 2013 & 2011 Teaching Assistant: Ecology, Evolution, and Plant Biology, Stanford University
- 2013 & 2012 Biocore Explorations Course Instructor, Department of Biology, Stanford University
- 2012 Teaching Assistant: Conservation Biology, Stanford University
- 2010 Undergraduate Workshop Leader: Evolution and Biodiversity, University of Miami
- 2009–2010 Peer Tutor, Camner Academic Resource Center, University of Miami

Academic, community, & university service

- 2013–Present Reviewer/Co-Reviewer, *Nature Communications*, *PLoS Biology*, *PLoS Genetics*, *PLoS ONE*, *Molecular Ecology*, *Journal of Heredity*, *BioData Mining*, *Journal of Biogeography*, *Journal of Ovarian Research*, *Current Urology*
- 2017 Education Outreach Volunteer, University Prep Middle School, Seattle, USA
- 2017 Invited Speaker, Emerald City Rotary, Seattle, USA
- 2016 Volunteer, University of Washington Paws on Science, Pacific Science Center, Seattle, USA
- 2016 Invited Speaker, Open Mic Science, Treehouse Cafe, Bainbridge Island, USA
- 2012–2013 Copy Editor, *Six Degrees: The Stanford Journal of Human Rights*
- 2012 Judge, Synopsys Silicon Valley Science and Technology Championship, San Jose, USA
- 2012 PhD Interview Visit Committee, Department of Biology, Stanford University
- 2011 New PhD Student Orientation Committee, Department of Biology, Stanford University

Technical skills

Programming & statistics: R, Python, MATLAB, Bash, C++ (Stanford CS106B)
Graphics: Adobe Illustrator, Adobe Photoshop, ggplot2 & Shiny
Word processing: L^AT_EX, Microsoft Office
Built and maintain Akey Lab website, URL: <http://akeylab.gs.washington.edu>