MATTHEW J. MCCOY, PHD

Department of Pathology, Stanford University School of Medicine, Stanford, CA
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EDUCATION

Ph.D. in Molecular Genetics & Genomics 2018
Washington University in St. Louis, St. Louis, MO

B.A. in Biology, Chemistry Minor 2011
University of Utah, Salt Lake City, UT 2008 – 2011
University of Hawaii at Manoa, Honolulu, HI 2005 – 2008

RESEARCH EXPERIENCE

Postdoctoral Research Fellow 2018 – Present
Department of Pathology, Stanford University School of Medicine, Stanford, CA
Advisor: Andrew Z. Fire, Ph.D.
Project: Investigating the causes and consequences of gene size expansion during nervous system evolution.

Graduate Student 2012 – 2018
Department of Developmental Biology, Washington University in St. Louis, St. Louis, MO
Advisor: Andrew S. Yoo, Ph.D.
Project: Defining neuronal identity using microRNA-mediated reprogramming of human skin cells to neurons.

Laboratory Technician 2008 – 2012
Department of Pediatrics, Division of Neonatology, University of Utah, Salt Lake City, UT
PI: Kurt Albertine, Ph.D.
Project: Characterizing molecular morphologies of acute and chronic lung injury in a sheep (*Ovis aries*) model.

Undergraduate Research 2007 – 2008
Department of Zoology, University of Hawaii at Manoa, Honolulu, HI
PI: Steve Robinow, Ph.D.
Project: Characterizing neuronal nuclear hormone receptor (*DHR51*) in *Drosophila melanogaster*.

FELLOWSHIPS

Whitman Early Career Award Summer 2023
Marine Biological Laboratory, Woods Hole, MA

Wu Tsai Interdisciplinary Scholar 2021 – 2022
Stanford University, Stanford, CA

Whitman Early Career Award Summer 2019
Marine Biological Laboratory, Woods Hole, MA

Stanford Genome Training Grant Post-Doctoral Fellowship 2018 – 2019
Institutional National Research Service Award (T32HG000044; Snyder, PI)

Grass Fellowship in Neuroscience Summer 2018
Marine Biological Laboratory, Woods Hole, MA

Interface of Psychology, Neuroscience & Genetics Pre-Doctoral Fellowship 2014 – 2015
Institutional National Research Service Award (T32GM081739; Barch, PI)

PUBLICATIONS

1 **McCoy MJ**, Fire AZ. Ancient origins of complex neuronal genes. *BioRxiv* (2023). DOI: 10.1101/2023.03.28.534655

2 Baden T, Briseño J, Coffing G, Cohen-Bodénès S, Courtney A, Dickerson D, Dölen G, Fiorito G, Gestal C, Gustafson T, Heath-Heckman E, Hua Q, Imperadore P, Kimbara R, Król M, Lajbner Z, Lichilín N, Macchi F, **McCoy MJ**, Nishiguchi M K, Nyholm S V, Otjacques E, Pérez-Ferrer P A, Ponte G, Pungor J R, Rogers T F, Rosenthal J J C, Rouressol L, Rubas N, Sanchez G, Pereira C, Schultz D T, Seuntjens E, Songco-Casey J O, Stewart I E, Styfhals R, Tuanapaya S, Vijayan N, Weissenbacher A, Zifcakova L, Schulz G, Weertman W, Simakov O, Albertin C. Cephalopod-omics: emerging fields and technologies in cephalopod molecular biology and evolution. *Under Review*.

3 Lu YL, Liu Y, **McCoy MJ**, and Yoo AS. MiR-124 synergism with ELAVL3 enhances target gene expression to promote neuronal maturity. *Proceedings of the National Academy of Sciences 118(22)*:e2015454118 (2021). DOI: 10.1073/pnas.2015454118

4 Cates K*, **McCoy MJ***, Kwon JS*, Liu Y*, Abernathy DG, Zhang B, Liu S, Gontarz P, Kim WK, Chen S, Kong W, Ho JN, Burbach KF, Gabel HW, Morris SA, and Yoo AS. Deconstructing stepwise fate conversion of human fibroblasts to neurons by MicroRNAs. *Cell Stem Cell 28*, 127-140, e9 (2020). *Co-first author. DOI: 10.1016/j.stem.2020.08.015

5 **McCoy MJ** and Fire AZ. Intron and gene size expansion during nervous system evolution. *BMC Genomics 21*, 360 (2020). DOI: 10.1186/s12864-020-6760-4

6 Wahba L*, Jain N*, Fire AZ*, Shoura MJ*, Artiles KL*, **McCoy MJ*** and Jeong DE*. An Extensive Meta-Metagenomic search identifies SARS-CoV-2-homologous sequences in pangolin lung viromes. *mSphere 5(3)*:e00160-20 (2020). *All authors contributed equally and author order was chosen randomly. DOI: 10.1128/mSphere.00160-20

7 **McCoy MJ***, Paul AJ*, Victor MB, Richner M, Gabel HW, Gong H, Yoo AS & Ahn T. LONGO: an R package for interactive gene length dependent analysis for neuronal identity. *Bioinformatics 34.13*, i422-i428. (2018). *Co-first author. DOI: 10.1093/bioinformatics/bty243

8 Abernathy DG*, Kim W*, **McCoy MJ***, Lake A, Ouwenga R, Xing X, Li D, Lee HJ, Heuckeroth RO, Dougherty JD, Wang T, Yoo AS. MicroRNAs induce a permissive chromatin environment that enables neuronal subtype-specific reprogramming of adult human fibroblasts**.** *Cell Stem Cell 21.3*, 332-348 e339 (2017). *Co-first author. DOI: 10.1016/j.stem.2017.08.002

HONORS & AWARDS

Best Poster Award, Bay Area RNA Club, UCSF 2023

Best Poster Award, Department of Pathology Retreat, Stanford University 2022

Outstanding Presentation Award, IPNG Research Day, Washington University in St. Louis 2015

Best Poster Award, Genetics & Computational Biology Retreat, Washington University in St. Louis 2014

Outstanding Presentation Award, IPNG Research Day, Washington University in St. Louis 2013

Undergraduate Research Scholar, University of Utah 2011

TEACHING EXPERIENCE

Adjunct Faculty in Biology; BIOL 12 Genomics Data Sciences — Summer 2022
Clovis Community College, Fresno, CA
Co-taught with Prof. Rosa Alcazar and Dr. Lindsay Hayes

Teaching Assistant/Mentor; BIOL 12 Genomics Data Sciences — Spring 2022
Clovis Community College, Fresno, CA
Professor Rosa Alcazar

Mentor to Lorenzo Angcanan Del Rosario, Stanford undergraduate student — Summer 2021
Stanford Bio-X
Stanford University, Stanford, CA

Teaching Assistant; Principles of the Nervous System — Fall 2014
Washington University in St. Louis, St. Louis, MO
Professors Larry Salkoff and Thomas Woolsey

SERVICE & OUTREACH

Video Interview, 90 Seconds w/ Lisa Kim, Stanford University — 2023
"What can octopus teach us about human brains?" Lisa Kim.
Link: https://www.youtube.com/watch?v=n3gRRo95Fxs

Podcast Interview, From Our Neurons to Yours, Stanford University — 2023
"The Octopus Brain." Nick Weiler.
Link: https://open.spotify.com/episode/3TQGAcEBgskUjgtztSD50x?si=2e70159aa4804450

Podcast Interview, The Synapse by Simply Neuroscience, a student-run podcast series — In Production
"The College Neuroscience Network: Stanford University from a Postdoctoral Researcher."
Tony Zhang.

Printed Interview, Wu Tsai Neurosciences Institute, Stanford University — 2022
"Q&A: Evolution of octopus and squid brains could shed light on origins of intelligence."
Rachel Grant.
Link: https://neuroscience.stanford.edu/news/qa-evolution-octopus-and-squid-brains-could-shed-light-origins-intelligence

Invited Grass Fellowship Technical Reviewer — 2022
Grass Foundation, Woods Hole, MA

Invited Grass Fellowship Technical Reviewer — 2021
Grass Foundation, Woods Hole, MA

Co-Organizer of Superworm (Stanford *C. elegans* community seminars) — 2020 – Present
Stanford University, Stanford, CA

Invited Grass Fellowship Technical Reviewer — 2020
Grass Foundation, Woods Hole, MA

Graduate Student Senate — 2013 – 2014
Washington University in St. Louis, St. Louis, MO

Health Professional Student Leadership Council — 2013 – 2014
Washington University in St. Louis, St. Louis, MO

Student Advisory Committee 2013 – 2014
Washington University in St. Louis, St. Louis, MO

University Undergraduate Research Association 2009 – 2011
Co-Founder and Vice President
University of Utah, Salt Lake City, UT

PRESENTATIONS

Oral Presentations

Cephalopod International Advisory Committee (CIAC), Sesimbra, Portugal 2022
"Intron and gene size expansion during cephalopod nervous system evolution."

Invited Seminar, Hopkins Marine Station, Stanford University, Stanford, CA 2019
"Intron and gene size expansion during nervous system evolution."

Whitman Fellowship Seminar, Marine Biological Laboratory, Woods Hole, MA 2019
"Intron and gene size expansion during nervous system evolution."

Department Seminar, Department of Genetics, Stanford University, Stanford, CA 2018
"Intron and gene size expansion during nervous system evolution."

Grass Fellowship Symposium, Marine Biological Laboratory, Woods Hole, MA 2018
"Intron and gene size expansion during nervous system evolution."

International Conference on Epigenetics and Bioengineering, Miami, FL 2017
"MicroRNA-mediated reprogramming reveals genomic features underlying neuronal identity."

Developmental, Regenerative and Stem Cell Biology Retreat, WashU, St. Louis, MO 2017
"Long gene expression as a metric for neuronal maturity."

Developmental, Regenerative and Stem Cell Biology Retreat, WashU, St. Louis, MO 2015
"MicroRNA-mediated regulation of DNA and RNA methylation during reprogramming of skin cells to neurons."

IPNG Research Day, WashU, St. Louis, MO 2015
"Epigenetic mechanisms of reprogramming human fibroblasts to neurons."

Genetics and Computational Biology Retreat, WashU, St. Louis, MO 2014
"Direct neuronal reprogramming alters DNA methylation at specific loci."

IPNG Research Day, WashU, St. Louis, MO 2013
"The role of DNA methylation during microRNA-mediated direct reprogramming of human fibroblasts to neurons."

28th Conference on High-Frequency Ventilation of Infants, Children, and Adults, Salt Lake City, UT 2011
"Epigenetic changes in chromatin structure and DNA methylation in the lung of preterm lambs following three days of mechanical ventilation and 10 weeks of recovery."

Western Society for Pediatric Research, Carmel, CA 2010
"Vitamin A therapy reduces IGF-1 promoter 2 mRNA levels in the lungs of chronically ventilated preterm lambs."

27th Conference on High-Frequency Ventilation of Infants, Children, and Adults, Salt Lake City, UT 2010
"Vitamin A therapy reduces IGF-1 promoter 2 mRNA levels in the lungs of chronically ventilated preterm lambs."

National Conference on Undergraduate Research, Bozeman, MO 2010
"Retinoids reduce IGF-1 expression in the lung of mechanically ventilated preterm lambs."

Western Society for Pediatric Research, Carmel, CA 2009
"Ventilation mode affects ovine pulmonary IGF-1 epigenetic characteristics."

Utah Conference on Undergraduate Research, Salt Lake City, UT 2009
"Ventilation mode affects ovine pulmonary IGF-1 epigenetic characteristics."

26th Conference on High-Frequency Ventilation on Infants, Children, and Adults, Salt Lake City, UT 2009
"Ventilation mode affects ovine pulmonary IGF-1 epigenetic characteristics."

National Conference on Undergraduate Research, LaCrosse, WI 2009
"Ventilation mode affects ovine pulmonary IGF-1 epigenetic characteristics."

Poster Presentations

Bay Area RNA Club, UCSF, San Francisco, CA 2023
"Consequences of gene size variation during evolution."

Department of Pathology Retreat, Stanford University, Stanford, CA 2022
"Consequences of gene size variation during evolution."

Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 2022
"Consequences of gene size variation during evolution."

NHGRI Research Training and Career Development Annual Meeting, Saint Louis, MO 2019
"Gene complexity and the evolution of nervous systems."

Department of Pathology Retreat, Stanford University, Stanford, CA 2019
"Gene complexity and the evolution of nervous systems."

Nature Conference on Neurogenetics, New York University, New York, NY 2017
"Long gene expression identifies functional neurons in microRNA-mediated direct reprogramming."

Genetics and Computational Biology Retreat, WashU, St. Louis, MO 2014
"Neuronal reprogramming by microRNAs alters DNA methylation at specific loci."

Midwest Society for Developmental Biology Meeting, WashU, St. Louis, MO 2014
"Neuronal reprogramming by microRNAs alters DNA methylation at specific loci."

Annual Cell & Molecular Biology Mini-Symposium, WashU, St. Louis, MO 2014
"Neuronal reprogramming by microRNAs alters DNA methylation at specific loci."