

STEVEN C. MUNGER, Ph.D.

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PROFILE

I explore natural genetic variation segregating in populations to discover how mutations that assert subtle individual effects can, in combination, disrupt gene regulatory networks and confer genetic susceptibility to developmental anomalies, adult disorder, and disease. My research integrates *in vivo* and *in vitro* experimental assays and computational methods with advanced mapping populations – an emerging multidisciplinary field called Systems Genetics - to identify causal genetic variants and network interactions that underlie phenotypic variability in 1) transcript abundance, protein expression, and organ function in adult tissues and 2) disease etiology and severity in a mouse model of Cornelia de Lange Syndrome. I have extensive training in developmental biology, complex trait genetics, genomics, and bioinformatics. I value collaborative science, and seek to apply my computational expertise and the analytical methods I have developed to empower other researchers working with high throughput sequencing data from genetically diverse cohorts.

I have extensive experience in all aspects of RNA sequencing (RNA-seq), from robust statistical design to data analysis and algorithm development. I developed the Seqnature software package to incorporate genetic diversity in RNA-seq analysis to improve gene- and allele-level estimates, and incorporated it with existing tools to identify differentially expressed and co-expressed genes. More recently, I developed methods to integrate liver transcriptomic and proteomic datasets, and in the process discovered a common post-translational mechanism (stoichiometric buffering) by which transcriptional variation in the liver is buffered at the protein level. Finally, I have optimized and conducted *in vitro* shRNA assays to validate gene candidates from transcriptomic screens.

EDUCATION & TRAINING

2011-2015

The Jackson Laboratory, Bar Harbor, ME
Postdoctoral Training, Center for Genome Dynamics
Advisor: Gary Churchill, Ph.D.

Led an interdisciplinary team of post-docs and software engineers to develop advanced analytical methods and computational tools for analyzing RNA-seq data derived from genetically diverse mice. Developed Seqnature software to impute and construct individualized diploid genome sequences for RNA-seq read alignment. Demonstrated that the individualized alignment strategy increases read mapping accuracy, improves estimates of transcript abundance, yields direct estimates of allele-specific expression, reduces spurious expression quantitative trait locus (eQTL) associations, and unmask thousands of real eQTL confounded by the common reference alignment strategy. Implemented novel pipelines to integrate liver eQTL and ENCODE datasets to systematically predict causative strain variants underlying cis- and trans-eQTL.

Designed and conducted a comprehensive sensitized RNA-seq eQTL screen of the gonad transcriptome during sex determination that employs these same analytical methods.

2010-2011 Duke University, Durham, NC
Postdoctoral Training
Advisor: Blanche Capel, Ph.D.
Developed a gonad primary cell assay and optimized a lentiviral-mediated RNAi knockdown method to experimentally validate genetic interactions predicted from the temporal expression and eQTL data.

2010 Duke University, Durham, NC
Ph.D. Genetics
Advisor: Blanche Capel, Ph.D.
A systems-level view of mammalian sex determination.
Designed and conducted the first eQTL study in a developing vertebrate organ, the embryonic mouse gonad at the critical time point of sex determination. Characterized the fine temporal patterns of gene activation and repression in the critical 24-hour window of sex determination, and showed that sensitivity to sex reversal in the C57BL/6J strain background stems from delayed activation of the testis pathway and delayed repression of the ovarian pathway.

1999 The University of Michigan, Ann Arbor, MI
B.S. Biology

ADDITIONAL TRAINING

2014 The Jackson Laboratory, Bar Harbor, ME
The Whole Scientist Course (one-week course)

2012-2014 The Jackson Laboratory, Bar Harbor, ME
Short Course on Medical and Experimental Mammalian Genetics (two-week course)

2011-2013 The Jackson Laboratory, Bar Harbor, ME
Short Course on Systems Genetics (one-week course)

2000-2003 Dow Chemical Company, Midland, MI
Research & Development Technologist
Advisor: Mark Bernius, Ph.D.
Developed flexible flat panel displays to test new light-emitting polymers.

POSITIONS HELD

2015-Present The Jackson Laboratory, Bar Harbor, ME
Assistant Professor

2011-2015 The Jackson Laboratory, Bar Harbor, ME
Postdoctoral Research Fellow

2010-2011 Duke University Medical Center, Durham, NC
Postdoctoral Associate

2003-2004	Dow Chemical Company, Midland, MI <i>Quality Control Technologist</i>
2000-2003	Dow Chemical Company, Midland, MI <i>Research & Development Technologist</i>
1999-2000	Waterford Kettering High School, Waterford, MI <i>Substitute 9-12 Grade Science Teacher</i>

HONORS & AWARDS

2017	Alfond Leaders Award, The Harold Alfond Foundation
2016	Reviewer's Choice Abstract Award <i>American Society of Human Genetics Meeting</i>
2015-2017 term	Elected to Secretariat of the International Mammalian Genome Society
2013-2015	Ruth L. Kirschstein National Research Service Award <i>Individual postdoctoral fellowship</i>
2011-2013	The Jackson Laboratory Fellowship <i>Institution-awarded fellowship</i>
2013	Chicago Prize for Outstanding Oral Presentation <i>12th Annual Meeting of the Complex Trait Community</i>
2012	Best Oral Presentation by a Post-Doctoral Fellow <i>11th Annual Meeting of the Complex Trait Community</i>
2011	Verne Chapman Memorial Young Scientist Award <i>International Mammalian Genome Society</i>
2008	Best Oral Presentation by a Graduate Student <i>7th Annual Meeting of the Complex Trait Consortium</i>
2004-2006	NIH Predoctoral Training Grant <i>Institution-awarded fellowship</i>

PUBLICATIONS

Google Scholar page: <http://scholar.google.com/citations?user=j6C32yAAAAAJ&hl=en>

Peer-reviewed Primary Research

11. Tyler AL, Ji B, **Munger SC**, Churchill GA, Svenson KL, and Carter GW. Epistatic networks jointly influence phenotypes related to Metabolic Disease and gene expression in Diversity Outbred mice. *GENETICS* 2017, 206(2): 621-639.
10. Chick JM*, **Munger SC***, Simecek P, Huttlin EL, Choi KB, Gatti DM, Raghupathy N, Svenson KL, Churchill GA[§], and Gygi SP[§]. Defining the consequences of genetic variation on a proteome-wide scale. *Nature* 2016, 534: 500-505. *Equal contributors. [§]Corresponding authors.
9. Morton NM, Beltram J, Carter RE, Michailidou Z, Gorjanc G, McFadden C, Barrios-Llerena M, Rodriguez-Cuenca S, Gibbins M, Aird R, Moreno-Navarrete JM, **Munger SC**, Svenson KL, Gastaldello A,

Ramage L, Naredo, G, Zeyda M, Wang ZV, Howie AF, Saari A, Sipila P, Stulnig TM, Gudnasson V, Kenyon CJ, Seckl JR, Walker BR, Webster SP, Dunbar DR, Churchill GA, Vidal-Puig A, Fernandez-Real JM, Emilsson V, and Horvat S. Genetic identification of an adipocyte expressed anti-diabetic target in mice selected for resistance to diet-induced obesity. *Nature Medicine* 2016, 22: 771-779.

8. French JE, Gatti DM, Morgan DL, Kissling GE, Shockley KR, Knudsen GA, Shepard KG, Price HC, King D, Witt KL, Pedersen LC, **Munger SC**, Svenson KL, and Churchill GA. Diversity Outbred mice identify population-based exposure thresholds and genetic factors that influence benzene-induced genotoxicity. *Environmental Health Perspectives* 2014, DOI:10.1289/ehp.1408202.
7. **Munger SC**, Raghupathy N, Choi K, Simons AK, Gatti DM, Hinerfeld DA, Svenson KL, Keller MP, Attie AD, Hibbs MA, Graber JH, Chesler EJ, and Churchill GA. RNA-seq alignment to individualized genomes improves transcript abundance estimates in multiparent populations. *Genetics* 2014, 198(1): 59-73.
6. **Munger SC***, Natarajan A*, Looger LL, Ohler U, and Capel B. Fine timecourse expression analysis reveals cascades of activation and repression and maps a regulator of mammalian sex determination. *PLoS Genetics* 2013, 9(7): e1003630. * Equal contributors.
5. Churchill GA, Gatti DM, **Munger SC**, and Svenson KL. The diversity outbred mouse population. *Mammalian Genome* 2012, 23(9-10): 713-718.
4. Jameson SA, Natarajan A, Maatouk DM, DeFalco T, Cool J, Mork L, **Munger SC**, and Capel B. Temporal transcriptional profiling of somatic and germ cells reveals lineage priming of sexual fate in the fetal mouse gonad. *PLoS Genetics* 2012, 8 (3): e1002575.
3. Cook MS, **Munger SC**, Nadeau JH, and Capel B. (2011) Regulation of male germ cell cycle arrest and differentiation by DND1 is modulated by genetic background. *Development* 2011, 138 (1): 23-32.
2. **Munger SC**, Aylor DL, Syed HA, Magwene PM, Threadgill DW, and Capel B. Elucidation of the transcription network governing mammalian sex determination by exploiting strain-specific susceptibility to sex reversal. *Genes & Development* 2009, 23: 2521-2536.
1. Ross A, **Munger SC**, and Capel B. Bmp7 regulates germ cell proliferation in mouse fetal gonads. *Sexual Development* 2007, 1 (2): 127-137.

Peer-reviewed Review Articles/ Meeting Reports

2. Musser MA*, **Munger SC***, and Gunn TM. Meeting report of the 26th International Mammalian Genome Conference. *Mammalian Genome* 2013, 24(5-6): 179-89. Meeting Report.
* Equal contributors.
1. **Munger SC** and Capel B. Sex and the circuitry: Progress toward a systems-level understanding of vertebrate sex determination. *Wiley Interdisciplinary Reviews – Systems Biology and Medicine* 2012, doi: 10.1002/wsbm. 1172. Review article.

INVITED PRESENTATIONS

“Harnessing genetic diversity to discover protein regulatory networks.”
Invited Guest Lecture, Next Generation Sequencing Analysis Course
Wellcome Trust Sanger Institute, Genome Campus, Hinxton, UK
October 5, 2017

“Harnessing genetic diversity to discover protein regulatory networks.”
3rd Annual JAX-EWHA Scientific Symposium
EWHA Women’s University, Seoul, South Korea
August 30, 2017

“Harnessing genetic diversity to discover protein regulatory networks.”
Applied Bioinformatics Course
Mount Desert Biological Laboratory, Salisbury Cove, ME
July 13, 2017

“Harnessing genetic diversity to discover protein regulatory networks.”
Vanderbilt Genetics Institute
Vanderbilt University, Nashville, TN
May 21, 2017

“Death by a Thousand (genetic) Cuts.”
Maine Science Festival, Invited “5-Minute Genius” Talk
Link: <https://www.youtube.com/watch?v=GRbWtyJ2n9I>
March 19, 2017

“Harnessing genetic diversity to discover protein regulatory networks.”
School of Biology and Ecology Seminar
University of Maine, Orono, ME
March 3, 2017

“Harnessing genetic diversity to discover protein regulatory networks.”
Department of Genetics Invited Seminar
Tufts University Sackler Medical School, Boston, MA
September 14, 2016

“Defining the consequences of genetic variation on a proteome-wide scale.”
43rd Maine Biological and Medical Sciences Symposium
Mount Desert Biological Laboratory, Hulls Cove, ME
April 29, 2016

“Systems genetic approaches to understanding normal development, disorder, and disease.”
Genome Science Seminar Series, Host: Charles Farber
University of Virginia, Charlottesville, VA
November 19, 2014

“Exploring the genetics of transcript and protein abundance in the murine liver.”
Invited Seminar, Host: Steven Gygi, Harvard Medical School, Boston, MA
October 10, 2014

“RNA-seq alignment to individualized genomes.”
Environmental Genomics Short Course, Mount Desert Island Biological Laboratory, Salisbury Cove, ME
August 6, 2014

“RNA-seq alignment to individualized genomes.”
Invited Seminar, Host: Darren Logan, Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, UK
May 23, 2014

“Finding sex in the circuitry: Toward a predictive network model of mammalian sex determination.”
Behavior, Ecology, Evolution, and Systematics Invited Seminar, Host: Thomas Kocher
University of Maryland, College Park, MD
March 24, 2014

“A systems genetic analysis of the dynamic transcription network governing primary sex determination.”
Invited Seminar, Host: April Binder, National Institute of Environmental Health Sciences, Triangle Park, NC
August 22, 2011

PRESENTATIONS & POSTERS

“Lessons from combined transcriptomic and proteomic studies in genetically diverse mice.”
(oral platform presentation selected from submitted abstract)
Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications
EMBL-Heidelberg, Germany 2017

“Conserved and tissue-specific effects of natural genetic variation on transcript and protein abundance.”
(poster talk and Reviewer’s Choice Abstract Award)
American Society of Human Genetics 2016, Vancouver, BC

“Conserved and tissue-specific effects of natural genetic variation on transcript and protein abundance.”
(oral platform presentation selected from submitted abstract)
The Allied Genetics Conference 2016, Orlando, FL

“Post-translational mechanisms buffer protein abundance against transcriptional variation.”
(oral platform presentation selected from submitted abstract)
International Mammalian Genome Conference 2015, Yokohama, Japan

“Post-translational mechanisms buffer protein abundance against transcriptional variation.”
(oral platform presentation selected from submitted abstract)
American Society of Human Genetics Meeting 2015, Baltimore, MD

“Genetic control of transcript and protein abundance in the liver.” (oral presentation)
Meeting of the National Centers for Systems Biology 2015, Albuquerque, NM

“Genetic control of transcript and protein abundance in the liver.”
(oral presentation selected from submitted abstract)
28th International Mammalian Genome Conference 2014, Bar Harbor, Maine

“Allele specific expression and eQTL in diploid genomes.” (poster)
American Society of Human Genetics Meeting 2014, San Diego, CA

“Reconsidering the laboratory mouse.” (oral presentation)
Genomics of Common Diseases 2014 Meeting, Potomac, MD

“Dissection of expression quantitative trait loci in the Diversity Outbred mouse population.”
(oral presentation selected from submitted abstract)
13th Annual Meeting of the Complex Trait Community 2014, Berlin, Germany

“RNA-seq alignment to individualized transcriptomes.” (poster)
American Society of Human Genetics Meeting 2013, Boston, MA

“RNA-seq alignment to individualized diploid transcriptomes reveals extensive local genetic regulation and differential allelic expression in outbred DO mice.” (oral presentation selected from submitted abstract)
27th International Mammalian Genome Conference 2013, Salamanca, Spain

“RNA-seq alignment to individualized genomes.”

(oral presentation selected from submitted abstract)

12th Annual Meeting of the Complex Trait Community 2013, Madison, WI

Chicago Prize for Outstanding Oral Presentation

“RNA-seq alignment to individualized genomes.”

(oral presentation selected from submitted abstract)

40th Maine Biological and Medical Sciences Symposium 2013, Salisbury Cove, ME

“Expression QTL mapping in the Diversity Outbred mouse population.”

(oral presentation selected from submitted abstract)

26th International Mammalian Genome Conference 2012, St. Pete Beach, FL

“Expression QTL mapping in the Diversity Outbred mouse population.” (poster)

Annual Meeting of the National Centers for Systems Biology 2012, Chicago, IL

“Expression QTL mapping in the Diversity Outbred mouse population.”

(oral presentation selected from submitted abstract)

11th Annual Meeting of the Complex Trait Community 2012, Paris, France

Best Oral Presentation by a Post-Doctoral Fellow

“Systems genetic analysis reveals a complex and highly dynamic transcription network governing sex determination.” (oral presentation selected from submitted abstract)

Mouse Genetics 2011, Washington, DC

Awarded the prestigious Verne Chapman Memorial Young Scientist Prize

“Systems genetic analysis of gonadogenesis in mice reveals a dynamic transcription network governing sex determination and testis organogenesis.” (poster)

Duke School of Medicine 1st Annual Basic Science Day 2010, Durham, NC

“Systems genetic analysis of gonadogenesis in mice reveals a dynamic transcription network governing sex determination and testis organogenesis.” (poster)

Annual Meeting of the National Centers for Systems Biology 2009, Bethesda, MD

“Integrating genetics and genomics to elucidate the transcription networks governing sex determination and testis organogenesis in mice.”

(oral presentation selected from submitted abstract)

Symposium on the Biology of Vertebrate Sex Determination 2009, Kona, HI

“Integrating genetics and genomics to elucidate the transcription networks governing sex determination and testis organogenesis in mice.”

3rd Annual Duke Center for Systems Biology Symposium 2008, Durham, NC

“Integrating genetics and genomics to elucidate the transcription networks governing organogenesis.”

(oral presentation selected from submitted abstract)

7th Annual Meeting of the Complex Trait Consortium 2008, Montreal, Quebec

Best Oral Presentation by a Graduate Student

“Whole-genome expression profiling of embryonic male gonads at the time of sex determination reveals significant differences between the C57BL/6J and 129S1/ImJ inbred mouse strains.” (poster)

Society for Developmental Biology Southeast Regional Conference 2007, Chapel Hill, NC

FUNDING

9/2013-6/2015 F32 HD074299-01 \$161,802
NIH/NICHD
Sensitized Screen in the Diversity Outcross Mouse Population.
Individual Ruth L. Kirschstein National Research Service Award Fellowship

TEACHING EXPERIENCE & MENTORING

Spring & Fall 2017 Participated as one of four primary course instructors for The Genome Access Course (Cold Spring Harbor Laboratory, NY)

Summer 2017 Mentored JAX Summer Student Program student Douglas Perkins

Fall 2016 Serving on four graduate student thesis committees (Borikar, Fine, Mundlein, Gans)

Fall 2016 Taught 1-hour systems genetics lecture at The Genome Access Course (Cold Spring Harbor Laboratory, NY)

Fall 2016-Spring 2017 Mentored two MDI high school students on independent research projects

Summer 2015-2017 Annual JAX Short Course on Medical and Experimental Mammalian Genetics
Taught two 1-hour workshops on RNA-seq statistical experimental design and analysis.

Summer 2016 Mentored Tufts rotating graduate student Candice Byers

Spring 2016 Mentored Tufts rotating graduate student Alex Stanton (joined lab Summer 2016).

Fall 2014 Mentored local high school student on senior independent research project.

Summer 2014 &
Summer 2015 Annual JAX Short Course on Experimental Models of Human Cancer
Developed and led a 2-hour problem-driven training session that explored the power of common genome browsers for guiding gene discovery in cancer biology.

Summer 2014 &
Summer 2013 Journal Club – The Jackson Laboratory Summer Student Program
Mentored two groups of talented high school and college students to present and critique recent high-profile genome-wide association and next generation sequencing studies.

Spring 2014 -
Spring 2017 Mammalian Genetics Course - Tufts University/University of Maine
Taught two 2-hour classes on genetic mapping and RNA-seq analysis. Designed data-driven exam questions to test students' comprehension of concepts and applications.

October 2012-2014
Fall 2013 & 2014 Developed and led a 3-hour training session on all aspects of RNA-seq analysis.
Applied Bioinformatics Course – Mount Desert Island Biological Laboratory
Presented a lecture on methods for RNA-seq analysis in diverse populations.

Fall 2013 & 2014 Computational Methods in Biology/Genomics – University of Maine
Presented a one-hour lecture on methods for RNA-seq alignment and quantitation.

May 2013 Workshop on Modern Approaches to High Throughput Sequencing
Presented a one-hour lecture on methods for RNA-seq alignment and quantitation.

Spring 2013, 2016 Genetics Journal Club – Tufts University
Facilitated three journal club sessions focused on genome-wide association studies. Mentored student presenters on experimental design and results.

Spring 2012 RNA-seq Interest Group – The Jackson Laboratory

Initiated a new interest group at the laboratory centered on RNA-seq, and led seven monthly 1-hour sessions covering all aspects of RNA-seq analysis from RNA extraction to expression quantitation and differential expression analysis.

Summer 2011

Summer Fellows Program – Duke IGSP Center for Systems Biology
Mentored a talented undergraduate student from North Carolina State University on an independent systems biology research project.

Spring 2010 &
Spring 2009

Undergraduate Independent Study Program – Duke University
Mentored two Duke undergraduate students on independent research projects.

Spring 2007

Genetics and Molecular Biology – Biology 118, Duke University
Served as a graduate teaching assistant in a large undergraduate genetics course. Led weekly study sections, held office hours, and graded midterm and final exams.

PROFESSIONAL MEMBERSHIPS & SERVICE

Ad hoc reviewer for: *Nature Genetics*
Genome Research
GENETICS
G3: Genes | Genomes | Genetics
Bioinformatics
Circulation: Cardiovascular Genetics
Experimental Cell Research
Frontiers Neuroscience
PLoS Computational Biology
BMC Developmental Biology
NIEHS Environmental Health Perspectives

Guest associate editor: *PLoS Genetics*

Member of: International Mammalian Genome Society (Served on the Secretariat 2011-2013, Elected to the Secretariat for 2015-2017 term)
American Society of Human Genetics
Genetics Society of America
Complex Trait Community

Session Chair: Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications 2017, EMBL, Heidelberg, Germany
44th Maine Biological Medical Sciences Symposium 2017, Bar Harbor, ME
The Allied Genetics Meeting 2016, Orlando, FL
13th Annual Meeting of the Complex Trait Community 2014, Berlin, Germany
27th International Mammalian Genome Conference 2013, Salamanca, Spain
26th International Mammalian Genome Conference 2012, St. Pete Beach, FL
11th Annual Meeting of the Complex Trait Community 2012, Paris, France

External Service: Secretariat of International Mammalian Genome Society 2011-2013, 2015-2017
Organizing committee for Maine Biological Medical Sciences Symposium 2016-2018