

Dr. Michael Turchin

Institute for Genomic Health, Icahn School of Medicine at Mount Sinai
1_Gustave_L_Levy_Place_New_York_NY_10029 • Michael.turchin@mssm.edu

Education

- 2017 PhD – University of Chicago
Human Genetics (Advisor: Matthew Stephens)
- 2009 BS (Dual; *Magna Cum Laude*) – Cornell University
Biological Sciences (Genetics) and Animal Science

Professional Experience

- 2020-* Postdoctoral Fellow – Dr. Eimear Kenny, Icahn School of Medicine at Mount Sinai
- 2017–20 Postdoctoral Research Associate – Dr. Sohini Ramachandran, Brown University
- 2012–17 Graduate Researcher – Dr. Matthew Stephens, University of Chicago
- 2012–13 Graduate Researcher – Dr. Jonathan Pritchard, University of Chicago
- 2009–11 Research Assistant – Dr. Joel Hirschhorn, Children’s Hospital Boston /
The Broad Institute
- 2006–09 Undergraduate Researcher – Dr. Charles Aquadro, Cornell University
- 2004 Summer Internship – Dr. John True, SUNY Stony Brook

Selected Awards, Grants, and Fellowships

- 2018–19 BioMed Postdoc Travel Award (Brown)
- 2016–17 NIH/NIAID F31 NRSA Predoctoral Training Fellowship (UChicago)
- 2015–16 NIH/ITM CTSA TL1 Training Grant (UChicago)
- 2013 NSF Graduate Research Fellowship Program – Honorable Mention (UChicago)
- 2011–14 NIH T32 Genetics and Regulation Training Grant (UChicago)
- 2011 Pauley Fellowship (UCLA; Declined)
- 2008 S. Ann and Robert R. Morley Student Research Grant (Cornell)
- 2007 Howard Hughes Summer Research Program in Biology (Cornell)

Selected Conference and Meeting Presentations

- 2020 International Conference of Quantitative Genetics 6 (Talk; virtual due to COVID-19)
- 2020 Center for Computational Molecular Biology, Brown University (Seminar)
- 2019 Probabilistic Modeling in Genomics – Aussois (Talk)
- 2017 Department of Computer Science, Princeton University (Seminar)
- 2017 Big Data Institute, Oxford University (Seminar)
- 2017 Department of Genetics, Perelman School of Medicine, University of Pennsylvania (Seminar)

2017 Gordon Research Seminar – Quantitative Genetics and Genomics (Talk)
2016 Probabilistic Modeling in Genomics – Oxford University (Talk)
2011 The Broad Institute: Program in Medical and Population Genetics (Seminar)
2011 Cold Spring Harbor Labs – Biology of Genomes (Talk)

Teaching and Academic Services

2014 Winter ECEV 3560 – Principles of Population Genetics I (TA)
2013 Fall HGEN 4700 – Human Genetics I (TA)
2013 Winter ECEV 3560 – Principles of Population Genetics I (TA)
2012 Fall MGCB/HGEN 3140 – Genetic Analysis of Model Organisms (TA)

2019 Rhode Island Science and Engineering Fair (Judge)
2018-19 Doctoral Dissertation Enhancement Grant (DDEG) Evaluation Panel,
Department of Ecology and Evolutionary Biology, Brown University (Panelist)
2015-20 American Society of Human Genetics DNA Day Essay Contest (Judge)
2014-15,17 Chicago Area Undergraduate Research Symposium (Judge)

Reviewer Grants: *Ad hoc* CIBR NSF
Journals: *Bioinformatics*, *eLife*, *Genetics*, *Heredity*, *Human Molecular Genetics*,
Nature Communications, *PLOS Genetics*, *Scientific Reports*

Publications

Turchin MC, Darnell G, Crawford L, and Ramachandran S. 2020. Pathway analysis within multiple human ancestries reveals novel signals for epistasis in complex traits. *bioRxiv*. <https://doi.org/10.1101/2020.09.24.312421>

Turchin MC and Stephens M. 2019. Bayesian multivariate reanalysis of large genetic studies identifies many novel associations. *PLOS Genetics*. 15(10): e1008431

Sohail M*, Maier RM*, Ganna A, Bloemendal A, Martin AR, **Turchin MC**, Chiang CWK, Hirschhorn JN, Daly M, Patterson N, Neale B, Mathieson I, Reich D, and Sunyaev SR. 2019. Signals of polygenic adaptation on height have been overestimated due to uncorrected population structure in genome-wide association studies. *eLife*. 8, e39702

Simons YB*, **Turchin MC***, Pritchard JK, and Sella G. 2014. The deleterious mutation load is insensitive to recent population history. *Nature Genetics*. 46(3): 220-224

Turchin MC*, Chiang CWK*, Palmer CD, Sankararaman S, Reich D, GIANT Consortium, and Hirschhorn JN. 2012. Evidence of widespread selection on standing variation in Europe at height-associated SNPs. *Nature Genetics*. 44(9): 1015-9

Turchin MC and Hirschhorn JN. 2012. Gencrypt: One-way cryptographic hashes to identify overlapping individuals. *Bioinformatics*. 28(6): 886-8

Wong AW, **Turchin MC**, Wolfner MF, and Aquadro CF. 2012. Temporally variable selection on proteolysis-related reproductive tract proteins in *Drosophila*. *Molecular Biology and Evolution*. 29(1): 229–38

Dauber A*, Yongguo L*, **Turchin MC**, Chiang CWK, Meng YA, Demerath EW, Patel SR, Rich SS, Rotter JI, Schreiner PJ, Wilson JG, Yiping S, Wu B, and Hirschhorn JN. 2011. Genome-wide association of copy number variation reveals an association between short stature and the presence of low frequency genomic deletions. *American Journal of Human Genetics*. 89(6): 751-9

Lango AH, Estrada K, Lettre G, Berndt SI, Weedon MN, Rivadeneira F, Willer CJ, et al. 2010. Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*. 467(7317): 832-8

Wong AW, **Turchin MC**, Wolfner MF, and Aquadro CF. 2008. Evidence for positive selection on *Drosophila melanogaster* seminal fluid protease homologs. *Molecular Biology and Evolution*. 25(3): 497–506

* indicates these authors have contributed equally