Michael Turchin

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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

2017–*	Postdoctoral Research – Dr. Sohini Ramachandran, Brown University
2012–17	Graduate Research – Dr. Matthew Stephens, University of Chicago
2012–13	Graduate Research – Dr. Jonathan Pritchard, University of Chicago
2009–11	Research Assistant – Dr. Joel Hirschhorn, Children's Hospital Boston / The Broad Institute
2006–09	Undergraduate Research – Dr. Charles Aquadro, Cornell University
2004	Summer Internship – Dr. John True, SUNY Stony Brook

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)
2013–15	Student Representative, Department of Human Genetics (UChicago)
2013–15	Novembre-He-Stephens Lab Meeting Coordinator (UChicago)
2015-19	American Society of Human Genetics DNA Day Essay Contest (Judge)
2014-15,17	Chicago Area Undergraduate Research Symposium (Judge)
2019	Rhode Island Science and Engineering Fair (Judge)
2019	Doctoral Dissertation Enhancement Grant (DDEG) Evaluation Panel, Department of Ecology and Evolutionary Biology, Brown University (Panelist)
Reviewer	Grants: *Ad hoc* NSF Journals: *Genetics, Human Molecular Genetics, Nature Communications, PLOS Genetics, Scientific Reports*

Selected Awards, Grants, and Fellowships

2018,19	BioMed Postdoc Travel Award (Brown)
2016–17	NIH/NIAID F31 NRSA Predoctoral Training Fellowship (UChicago)
2015–16	ITM/NIH 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

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)

Publications

Turchin MC, Tung I, Crawford L, and Ramachandran S. 2019. Differential complex trait architecture across humans: epistasis identified in non-European populations at multiple genomic scales. *In Preparation.*

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