

Yang I Li

CONTACT INFORMATION

E-mail: yangili1@uchicago.edu

CITIZENSHIP

Canada

RESEARCH INTERESTS

Population genomics, gene regulation, disease.

RESEARCH POSITIONS

University of Chicago, Chicago, IL, USA

Assistant Professor of Genetic Medicine (Primary), 2017 –

Assistant Professor of Human Genetics (Secondary), 2017 –

Stanford University, Stanford, CA, USA

Postdoctoral fellow (Prof. Jonathan Pritchard), 2014 – 2017

EDUCATION

University of Oxford, Oxford, Oxfordshire, United Kingdom

D.Phil., Evolutionary genomics (Prof. Chris Ponting), 2014

University of Liverpool, Liverpool, Merseyside, United Kingdom

M.Phil., Biological Sciences (Dr. João Pedro de Magalhães), 2010

McGill University, Montreal, Qc, Canada

B.Sc., Joint Honours Math & Computer Science, 2009

AWARDS

Research awards/Fellowships:

- Stanford CEHG postdoctoral fellowship (2015-2016)
- St Cross College Ralph A lewin prize (2012)
- University of Oxford NDM Prize Studentship (2010-2014)
- FQRNT Bourses de maîtrise en recherche (2010-2011)
- Gates Cambridge Scholarship (2010-2014, declined)
- NSERC Postgraduate scholarship PGS-M (2009-2010)
- NSERC Undergraduate Summer Research Award (2007 and 2009)
- ISM Undergraduate Summer Scholarship (2008)

PUBLICATIONS

Most updated list available on [google scholar](#).

Note: * denotes equal contribution.

28. Mu Z, Wei W, Fair BJ, Miao J, Zhu P, Li YI. (2020). Impact of cell-type and context-dependent regulatory variants on human immune traits. *bioRxiv* 212753.
27. Mittleman BE, Pott S, Warland S, Zheng T, Laur M, Gilad Y, Li YI. (2020) Alternative polyadenylation mediates genetic regulation of gene expression. *eLife* e57492.
26. Chen M, Zhan Q, Mu Z, Wang L, Zheng Z, Miao J, Zhu P, Li YI. (2020) Alignment of single-cell RNA-seq samples without over-correction using kernel density matching. *bioRxiv* 895136.
25. Sarkar A et al. (2019) Discovery and characterization of variance QTLs in human induced pluripotent stem cells. *PLoS Genetics* 15 (4), e1008045.
24. Liu X*, Li YI*, Pritchard JK*. (2019) Trans effects on gene expression can drive omnigenic inheritance. *Cell* (4), 1022-1034.
23. Li YI, Wong G, Humphrey J, Raj T. (*in press*) Prioritizing Parkinson's Disease genes using population-scale transcriptomic data. *Nature Communications* 10 (1), 994.
22. Audano P et al., (2019) Characterizing the major structural variant alleles of the human genome. *Cell*. Pages 663-675.e19
21. Jaganathan K et al., (2019) Predicting splicing from primary sequence with deep learning. *Cell*. Pages 535-548.e24
20. Raj T, Li YI, Wong G, et al. (2018) Integrative analyses of splicing in the aging brain: role in susceptibility to Alzheimer. *Nature Genetics*, 50, 1584–1592 .
19. Banovich NE*, Li YI*, Raj A*, et al. (2018) Impact of regulatory variation across human iPSCs and differentiated cells. *Genome Research* doi:10.1101/gr.224436.117.
18. Li YI*, Knowles DA*, Humphrey J, Barbeira AN, Dickinson SP, Im HK, Pritchard JK. (2018) Annotation-free quantification of RNA splicing using LeafCutter. *Nature Genetics* doi:10.1038/s41588-017-0004-9.
17. Boyle EA*, Li YI*, Pritchard JK*. (2017) An expanded view of complex traits: from polygenic to omnigenic. *Cell* 169 (7), 1177-1186. (Citations: >390)
16. Li YI, van de Geijn B, Raj A, Knowles DA, Petti A, Golan D, Gilad Y, Pritchard JK. (2016) RNA splicing is a primary link between genetic variation and disease. *Science* 352 (6285), 600-604. (Citations: >150)
15. Raj A, Wang S, Shim H, Harpak A, Li YI, Englemann B, Stephens M, Gilad Y, Pritchard JK. (2016) Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. *eLife* 5, e13328.
14. Jore MM, Sheppard D, Barber NM, Johnson S, Li YI, Nunn MA, Elmlund H, Lea SM (2016) Structural basis for therapeutic inhibition of complement C5. *Nature Structural & Molecular Biology* 23 (5), 378-386.
13. Macaulay I, Haerty W, Kumar P, Li YI, et al. (2015) G&T-seq: Separation and parallel sequencing of the genomes and transcriptomes of single cells. *Nature methods* 12 (6), 519-522.

12. Keane M*, Semeiks J*, Webb AE*, Li YI*, Quesada V* et al. (2015) Insights into the evolution of longevity from the bowhead whale genome. *Cell Reports* 10, 112-122. (Citations: >90)
11. Li YI, Sanchez-Pulido L, Haerty W, Ponting CP. (2015) RBFOX and PTBP1 proteins regulate the alternative splicing of micro-exons in human brain transcripts. *Genome Research* 25 (1), 1-13. (Citations: >60)
10. Brawand D*, Wagner C*, Li YI*, et al. (2014), The genomic substrate for adaptive radiation in African cichlid fish. *Nature* 513, 375-381. (Citations: >410)
9. Li YI, Kong L, Ponting CP, Haerty W. (2013) Rapid evolution of beta-keratin genes contribute to phenotypic differences that distinguish turtles and birds from other reptiles. *Genome biology and evolution* 5 (5), 923-933.
8. Schaffer HB et al. (2013) The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. *Genome Biology* 14 (3), R28.
7. Li YI, Copley RR. (2013) Scaffolding low quality genomes using orthologous protein sequences. *Bioinformatics* 29(2):160-5.
6. Wood HS, Craig T, Li Y, Merry B, de Magalhães JP. (2012) Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. *Age (Dordr)*, 1-14.
5. Wuttke D, Connor R, Vora C, Craig T, Li Y, Wood S, Vasieva O, Tang F, de Magalhães JP. (2012) Dissecting the Gene Network of Dietary Restriction to Identify Evolutionary Conserved Pathways and New Functional Genes. *PLoS Genetics* 8 (8), e1002834.
4. Li Y, de Magalhães JP. (2011) Accelerated protein evolution analysis reveals genes and pathways associated with the evolution of mammalian longevity. *Age (Dordr)*, 1-14.
3. Yu C*, Li Y*, Holmes A, Szafranski K, Faulkes CG, Coen CW, Buffenstein R, Platzer M, de Magalhães JP, Church GM (2011) RNA Sequencing Reveals Differential Expression of Mitochondrial and Oxidation Reduction Genes in the Long-Lived Naked Mole-Rat When Compared to Mice. *PLoS ONE* 6(11): e26729.
2. Aledo JC, Li Y, de Magalhães JP, Ruiz-Camacho M, Perez-Claros JA. (2011) Mitochondrially encoded methionine is inversely related to longevity in mammals. *Aging Cell* 10:198-207.
1. de Magalhães JP, Budovsky A, Lehmann G, Costa J, Li Y, Fraifeld V, Church GM. (2009) The Human Ageing Genomic Resources: online databases and tools for biogerontologists. *Aging Cell* 8(1):65-72.

INVITED AND
SUBMITTED TALKS

1. UC Berkeley CTEG Seminar. 11 Dec 2020, UC Berkeley via Zoom. The Regulatory Links Between Genetics Variation and Complex Traits. (Invited Speaker)
2. McGill Genome Science Seminar. 3 Dec 2020, McGill University via Zoom. The Regulatory Links Between Genetics Variation and Complex Traits. (Invited Speaker)
3. 37th Conference of the International Society for Animal Genetics. 7-12 July 2019 Lleida, Spain. The Omnigenic model for complex traits and disease. (Invited plenary speaker)

4. SMBE satellite meeting 'Towards an integrated concept of adaptation: uniting molecular population genetics and quantitative genetics' 11-14 February 2019 in Vienna, Austria. The Omnigenic model for complex traits and disease. (Invited speaker)
5. Canadian Human and Statistical Genetics, Harrison Spring, Canada, June 2018. The Omnigenic model for complex traits and disease. (Invited speaker)
6. The 3rd GENMED Workshop on Medical Genomics, Paris, France, May 2018. An expanded view of complex traits: from polygenic to omnigenic. (Invited speaker)
7. Departmental seminar. University of Carolina Charlotte, Charlotte, NC, February 2018. Understanding the regulatory links between genetic variation and complex traits. (Invited speaker)
8. Department of Medicine Grand Rounds. University of Chicago. Chicago, IL, January 2018. Understanding the regulatory links between genetic variation and complex traits.
9. American Society of Human Genetics, Orlando, 2017. An expanded view of complex traits: from polygenic to omnigenic. (Abstract selected speaker)

GRANTS

- **NIH R01 GM130738 (PI) 2019-2014:** "Investigating the co-transcriptional impact of genetic variation on gene regulation and disease", 1.45M USD
- **NIH R01 HG011067 (MPI) 2020-2024:** "Novel methods to detect and interpret splicing quantitative trait loci", 2.63M USD.
- **NIH R01 CA242929 (co-I) 2019-2023:** "Transcriptome-wide association studies and genetic risk prediction for breast cancer integrating RNA splicing and gene expression from multiple tissues.
- **Cancer Research Foundation (PI) 2018-2020:** "Using Recurrent Aberrant mRNA Isoforms for Early Cancer Detection", 75K USD.

SERVICE AND ACHIEVEMENTS

Ad-hoc reviewer, 2012-

- Manuscript reviews for *PLoS Genetics*, *Genome Research*, *Bioinformatics*, *BMC Evolutionary Biology*, *PLoS One*, *Nature Genetics*, *Science*, *Cell*, *Communications Biology*, *Nature Communications*, *Frontiers in Genetics*, *Nucleic Acids Research*, *eLife*, *Genome Biology and Evolution*.

ACM ICPC World Finalist, Sweden 2009

- McGill ACM International Collegiate Programming Contest team.