Premal Shah

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EDUCATION

2011 Ph. D. Ecology and Evolutionary Biology

University of Tennessee, Knoxville TN Advisor: Dr. Michael A. Gilchrist

2006 B. Tech. Biotechnology

Anna University, Chennai, India Advisor: Dr. Gautam Pennathur

PROFESSIONAL APPOINTMENTS

2016-Current Assistant Professor of Genetics

Rutgers University, New Brunswick NJ

2011-2015 Postdoctoral Fellow

University of Pennsylvania, Philadelphia PA

Advisor: Dr. Joshua B. Plotkin

2009-2011 Graduate Research Assistant

National Institute for Mathematical and Biological Sciences University of Tennessee, Knoxville TN

2006-2009 Graduate Teaching Assistant

Department of Ecology and Evolutionary Biology University of Tennessee, Knoxville TN

2006 Undergraduate Researcher

Institute for Mathematical Sciences, Chennai, India

2004 Summer Research Fellow

Indian Institute of Sciences, Bangalore, India

PUBLICATIONS

Google Scholar

17. Carja, O, Xing T, Plotkin JB, and Shah P. (2017)

riboviz: analysis and visualization of ribosome profiling datasets.

bioRxiv 10.1101/100032

16. McCandlish DM, **Shah P**, and Plotkin JB. (2016)

Epistasis and the dynamics of reversion in molecular evolution.

Genetics 203 (3): 1335-1351

15. Weinberg DE*, **Shah P***, Eichhorn SW, Hussmann JA, Plotkin JB, and Bartel DP. (2016) Improved ribosome-footprint and mRNA measurements provide insights into dynamics and regulation of yeast translation.

Cell Reports 14 (7): 1787-1799 *Equal contribution

14. Kubatko L, **Shah P**, Herbei R, and Gilchrist MA. (2016)

A codon model of nucleotide substitution with selection on synonymous codon usage.

Molecular Phylogenetics and Evolution 94: 290-297

13. Shah P, McCandlish DM, and Plotkin JB. (2015)

Contingency and entrenchment in protein evolution under purifying selection.

Proceedings of the National Academy of Sciences, USA E3226-E3235

12. Gilchrist MA, Chen WC, Shah P, Landerer C, and Zaretzki R. (2015)

Estimating gene expression and codon specific translational efficiencies, mutation biases, and selection coefficients from genomic data alone.

Genome Biology and Evolution 7 (6): 1559-1579

11. Fordyce JA, Shah P, and Fitzpatrick BM. (2014)

iteRates: An R package for implementing a parametric rate comparison on phylogenetic tree.

Evolutionary Bioinformatics (10): 127-130

10. Shah P, Ding Y, Niemczyk M, Kudla G, and Plotkin JB. (2013)

Rate-limiting steps in yeast protein translation.

Cell 153 (7): 1589-1601

9. Xu Y, Ma P, Shah P, Rokas A, Liu Y and Johnson CH. (2013)

Non-optimal codon usage is a mechanism to achieve circadian clock conditionality.

Nature 495: 116-120

8. McCandlish DM, Rajon E, Shah P, Ding Y and Plotkin JB. (2013)

The role of epistasis in protein evolution.

Nature 497: E1-E2

7. Shah P, Fitzpatrick BM, and Fordyce JA. (2013)

A parametric method for assessing diversification rate variation in phylogenetic trees.

Evolution 67 (2): 368-377

6. Niemiller ML, Fitzpatrick BM, Shah P, Schmitz L, and Near TJ. (2013)

Evidence for repeated loss of selective constraint in rhodopsin of amblyopsid cavefishes (Teleostei: Amblyopsidae).

Evolution 67 (3): 732-748

5. Ding Y, Shah P and Plotkin JB. (2012)

Weak 5' mRNA structure in short eukaryotic genes.

Genome Biology and Evolution 4 (10): 1046-1053

4. Shah P, and Gilchrist MA. (2011)

Explaining complex codon usage patterns with selection for translational efficiency, mutation bias, and genetic drift.

Proceedings of the National Academy of Sciences, USA 108 (25): 10231-6

3. Shah P, and Gilchrist MA. (2010)

Effect of correlated tRNA abundances on translation errors and evolution of codon usage bias.

PLOS Genetics 6 (9): e1001128

2. Shah P, and Gilchrist MA. (2010)

Is thermosensing property of RNA thermometers unique?

PLOS ONE 5 (7): e11308

1. Gilchrist MA, Shah P, and Zaretzki R. (2009)

Measuring and detecting molecular adaptation in codon usage against nonsense errors during protein translation.

Genetics 183 (4): 1493-505

SOFTWARE

- 1. riboviz: Analysis and visualization of ribosome profiling datasets.
- 2. SMoPT: Stochastic Model of Protein Translation

Simulates the dynamics of protein synthesis within an entire cell.

3. iteRates: Parametric rate comparison

Iterates through a phylogenetic tree to identify regions of rate variation using the parametric rate comparison test.

FUNDING

Current

2017-2022 NIGMS R35 (ESI - MIRA) GM124976

Dynamics and evolution of translational regulation.

Role: PI, Total direct costs: \$1,250,000

2016-2021 NIDDK R01 DK109714

Homeostatic responses to amino acid insufficiency. PI: Dr. Tracy Anthony (IFNH, Rutgers University) Role: Subcontract, Total direct costs: \$23,000

Pending

2017-2022 NIDDK R01 DK056645

The LIN28B-LET7 axis in intestinal epithelial biology.

PI: Dr. Anil Rustgi (Perelman School of Medicine, University of Pennsylvania)

Role: Subcontract Score: 20, Percentile: 5

2018-2023 NIAID R01

Impact of translation initiation on the temporal dynamics of an innate immune response.

PI: Dr. Ann Tate (Vanderbilt University)

Role: Co-I

2018-2021 CMND CSR R21

The proteome of CMT mutations.

PI: Dr. Ya-Ming Hou (Thomas Jefferson University)

Role: Co-I

Completed

2009-2011 National Institute for Mathematical and Biological Synthesis (NIMBioS) Graduate Research Assistantship. (\$40,000 + Fringe).

2009 University of Tennessee Graduate Summer Research Assistantship (\$3,600).

HONORS AND AWARDS

2011 Jim Tanner Award for Outstanding Dissertation.

2009-2010 EEB Summer Research Grant.

2009-2010 EEB Travel Award.

2010 College of Arts and Sciences, UTK Travel Award.

2009-2010 Graduate Researchers in Ecology, Behavior and Evolution Travel Grant.

2009 EEB Summer Research Grant.

- 2004 Indian Academy of Sciences, Summer Research Fellowship.
- 2000 National Scholarship from the Central Board of Secondary Education, New Delhi awarded to top 0.01% in Mathematics at the National level.

INVITED TALKS

- 2017 Dynamics and evolution of translational regulation.
 - 14. Queens College, CUNY NY
 - 13. University of Pennsylvania, Perelman School of Medicine, Philadelphia PA
 - 12. University of Delaware, Newark DE
 - 11. New York University, NYC NY
 - 10. Fred Hutchinson Cancer Research Center, Seattle WA
 - 9. Pennsylvania State College of Medicine, Hershey PA
- 2015 Opportunities and pitfalls in modeling protein translation using ribosome-profiling.
 - 8. Tel Aviv University, Tel Aviv, Israel

Insights from mechanistic models of protein translation.

- 7. University of Maryland, Baltimore County, MD
- 2014 Dynamics of protein translation in yeast.
 - 6. National Center for Biological Sciences, Bangalore, INDIA
- 2013 Rate-limiting steps in protein translation.
 - 5. University of Utah, Salt Lake City UT
- 2011 Population genetics of codon usage bias.
 - 4. University of Pennsylvania, Philadelphia PA

Insights from mechanistic models of protein translation on the evolution of codon usage bias.

- 3. Vanderbilt University, Nashville TN
- 2009 Measuring the adaptedness of a gene: Nonsense-error Adaptation Index.
 - 2. University of Tennessee, Knoxville TN
- 2006 Agent-based models in economics.
 - 1. Computable and Experimental Economics Laboratory (CEEL), Trento, Italy

CONFERENCE PRESENTATIONS

2017 Shah P

Evolutional of transcriptional and translational regulation during adaptation.

- 20. European Society for Evolutionary Biology Groningen, Netherlands.
- 19. Society for Molecular Biology and Evolution (SMBE) Austin, TX.
- 18. Gordon Research Conference in Molecular Mechanisms in Evolution Easton MA.
- 2016 Shah P and Plotkin JB.

Opportunities and pitfalls in modeling protein translation using ribosome-profiling.

- 17. Translational Control, CSHL, NY
- 2015 Shah P and Plotkin JB.

Opportunities and pitfalls in modeling protein translation using ribosome-profiling.

- 16. Society for Molecular Biology and Evolution (SMBE) Vienna, Austria.
- 15. Computational Modeling of Gene Expression and its Evolution Tel Aviv, Israel.

Shah P. McCandlish DM and Plotkin JB.

Contingency and entrenchment in protein evolution.

14. Forecasting evolution - Lisbon, Portugal.

Shah P and Plotkin JB.

Local DNA topography predicts genomic mutation rates.

13. Society for Molecular Biology and Evolution (SMBE) - Bloomington, IN.

Shah P and Plotkin JB.

Dynamics and regulation of protein translation.

12. Biomedical Postdoc Research Symposium - Philadelphia, PA.

2014 Shah P, Krishnan A, Gilchrist MA and Plotkin JB.

Redefining the context in context-dependent mutation.

- 11. Society for Molecular Biology and Evolution (SMBE) San Juan, PR.
- 10. Society for Study of Evolution (SSE) Raleigh, NC.

2013 Shah P and Plotkin JB.

Characterizing epistasis in proteins under purifying selection.

- 9. Society for Molecular Biology and Evolution (SMBE) Chicago, IL.
- 8. Society for Study of Evolution (SSE) Salt Lake City, UT.

2010 Shah P and Gilchrist MA.

Correlated tRNAs, translation errors and evolution of codon usage bias.

- 7. Society for Molecular Biology and Evolution (SMBE) Lyon, France.
- 6. Society for Study of Evolution (SSE) Portland, OR.

Shah P and Gilchrist MA.

Genome-wide determinants of codon composition.

5. SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) - Madison, FL.

2009 Gilchrist MA. Shah P. and Zaretzki R.

Making Wright's metaphor a reality: Quantifying and detecting molecular adaptation.

- 4. Society for Study of Evolution (SSE) Moscow, ID.
- 3. SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) Dahlonega, GA.
- 2. The 7th Georgia Tech Oak Ridge National Lab International Conference "Genome Biology and Bioinformatics" Atlanta, GA.

2006 Shah P, Strielkowski W, and Sinha, S.

Mechanisms of immigrants' clusters formation using networks dynamic modeling.

1. Santa Fe Institute - Summer Complex Systems School, Chennai, India.

TEACHING

Faculty:

Spring 2017 Special topics in genetics - Computational genetics of big data.

Guest Lecturer:

- 2010 Biometry Introduction to bayesian inference.
- 2010 Evolution in society Explaining genomic patterns in the light of evolution.
- 2008 Genetics Codon usage bias: evolution and consequences.

Graduate Teaching Assistant:

2007 Genetics

2006 Biology for non-majors

MENTORING

Graduate students

1. Tongji Xing (Ph.D. 2016 -)

Graduate students - Other

- 1. Sukanya Das (rotation, 2017)
- 2. Alexander Salibi (rotation, 2017)
- 3. Vaidhyanathan Mahaganapathy (Ph.D. committee, 2017)
- 4. Candice Craig (rotation, 2016)
- 5. Srividya Venkatramanan (rotation, 2016)

Undergraduate students

- 1. Madhuri Bhupathiraju (08/2016)
- 2. Yasasvi Talagadadeevi (02/2017)
- 3. Sadhana Chidambaran (03/2017)
- 4. Dana Goldrich (08/2017)
- 5. Albert Sultan (04/2016 05/2017)
- 6. Darya Pavlenko (04/2016 12/2016)

Undergraduate students - Other

1. Vasvi Patel (Reader, senior thesis for G.H. Cook Scholars Program, 2017 -)

PROFESSIONAL SERVICE

Reviewer: Nature, Nature Structural & Molecular Biology, Nature Molecular Systems Biology, Nature Communications, Elife, Cell Reports, EMBO Reports, PLOS Biology, PLOS Computational Biology, PLOS ONE, Genome Research, Molecular Biology & Evolution, Genome Biology & Evolution, Evolution, RNA, Journal of Theoretical Biology, Journal of Molecular Evolution, Current Bioinformatics, and Biotechnology Journal

Invited panelist:

- 2017 Discussion leader: Gordon Research Seminar in Molecular Mechanisms in Evolution, Easton MA.
- 2017 Panelist: Redefining the Postdoctoral Experience ? New Training for New Careers, Rutgers University, Piscataway NJ.
- 2017 Presentation judge EPiC ? Evolution in Philadelphia Conference, Philadelphia PA.
- 2015 Panelist: Center for Teaching and Learning Teaching portfolios, University of Pennsylvania, Philadelphia PA.

PROFESSIONAL AFFILIATIONS

Society for Study of Evolution (SSE) Society for Molecular Biology and Evolution (SMBE) RNA Society

OUTREACH EXPERIENCE

- 2010-2011 NIMBioS Teacher Collaboration Program.
 - 2010 Undergraduate Mentor in Society for Molecular Biology and Evolution (SMBE) Mentorship Program.
- 2007-2009 Member of Organizing committee for Darwin Day.
 - 2009 Mentor: NIMBioS Undergraduate Research Conference.

WORKSHOPS AND SUMMER SCHOOLS

- 2016 Helmsley/NAS Summer Institutes On Undergraduate Education, University of Connecticut, Storrs CT.
- 2006 CEEL program in Adaptive Economic Dynamics. Organized by: Computable and Experimental Economics Laboratory (CEEL), Trento, Italy. (Invited)
- 2006 Complex Systems School. Organized by: Santa Fe Institute and Institute for Mathematical Sciences, India.