Premal Shah

Department of Genetics
Rutgers University
New Brunswick, NJ 08854

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https://theshahlab.org

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**
Member: Human Genetics Institute of New Jersey
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

BOLD : Members of Shah lab

32. **Favate JS, Liang S**, Yadavalli SS, and **Shah P**.
The landscape of transcriptional and translational changes over 22 years of bacterial adaptation.
bioRxiv : 10.1101/2021.01.12.426406v1 (under revision *eLife*)

31. Vora M, Pyonteck SM, Matlack TL, Prashar A, Kane NS, **Favate JS**, **Shah P**, and Rongo C.
The hypoxia response pathway promotes PEP Carboxykinase expression and gluconeogenesis.
bioRxiv : 10.1101/2021.05.04.442650 (under revision *Nature Communications*)

30. Morishita Y, Fuentes I, **Favate J**, Zushida K, Nishi A, Hevi C, Goldsmith N, Buyske S, Sillivan SE, Miller CA, Kandel ER, Uchida S, **Shah P**, and Shumyastsky GP.
The gastrin-releasing peptide regulates stress-enhanced fear and dopamine signaling.
bioRxiv : 10.1101/2020.12.31.424996v1 (under revision *Biol. Psych.*)

29. **Cope AL** and **Shah P**.
Intragenomic variation in mutation biases causes underestimation of selection on synonymous codon usage. (2022)
PLoS Genetics 18 (6) : e1010256

28. **Cope AL**, Anderson F, **Favate JS**, Jackson M, Mok A, Kurowska A, MacKenzie E, Shivakumar V, **Tilton P**, Winterbourne SM, Xue S, Kavoussanakis K, Lareau LF*, **Shah P***, and Wallace EWJ*. (2022)
riboviz 2: A flexible and robust ribosome profiling data analysis and visualization workflow.
Bioinformatics 38 (8): 2358-2360 *Co-corresponding authors

27. Nikonorova IA, Wang J, **Cope AL**, **Tilton P**, Power KM, Walsh JD, Akella JS, Krauchunas AR, **Shah P**, and Barr MM. (2022)
Isolation, profiling, and tracking of extracellular vesicle cargo in Caenorhabditis elegans.
Current Biology 32 : 1-13

26. **Cope AL***, Vellappan S*, **Favate JS**, Skalenko KS, Yadavalli SS, and **Shah P**. (2022)
Exploring ribosome-positioning on translating transcripts with ribosome-profiling.
In: Dassi E. (eds) Post-Transcriptional Gene Regulation.
Methods in Molecular Biology. vol 2404. Humana, New York, NY.
https://doi.org/10.1007/978-1-0716-1851-6_5. *Equal contribution

25. Skalenko KS, Li L, Zhang Y, Vvedenskaya IO, Winkelman JT, **Cope AL**, Taylor DM, **Shah P**, Ebright RH, Kinney JB, Zhang Y, and Nickels BE. (2021)
Promoter-sequence determinants and structural basis of primer-dependent transcription initiation in Escherichia coli.
Proceedings of the National Academy of Sciences, USA 118 (27) : e2106388118

24. Campos RK, **Wijeratne HRS, Shah P***, Garcia-Blanco MA*, and Bradrick SS.* (2020)
Ribosomal stalk proteins RPLP1 and RPLP2 promote biogenesis of flaviviral and cellular multi-pass transmembrane proteins.
Nucl. Acids Res. 48 (17) : 9872-9885 *Co-corresponding authors

23. Winkelman JT, Pukhrambam C, Vvedenskaya IO, Zhang Y, Taylor DM, **Shah P**, Ebright RH, and Nickels BE. (2020)
XACT-seq comprehensively defines the promoter-position and promoter-sequence determinants for initial-transcription pausing.
Mol. Cell. 79: 1-15

22. Gupta R, Walvekar A, **Liang S**, Rashida Z, **Shah P***, and Laxman S*. (2019)
A tRNA modification balances carbon and nitrogen metabolism by regulating phosphate homeostasis.
eLife 8:e44795 *Co-corresponding authors

21. Holmes MJ, **Shah P**, Wek RC, and Sullivan WJ. (2019)
Simultaneous ribosome profiling of human host cells infected with Toxoplasma gondii.
mSphere 4 (3) : e00292-19

20. Dierschke SK, Miller WP, **Favate JS, Shah P**, Imamura Y, Salzberg AC, Kimball SR, Jefferson LS, and Dennis MD. (2019)
O-GlcNAcylation alters the selection of mRNAs for translation and promotes 4E-BP1-dependent mitochondrial dysfunction in retina.
Jour. Biol. Chem. 294 (14) : 5508-5520

19. Chatterji P, Williams PA, Whelan KA, Samper FC, Andres SF, Simon LA, Parham LR, Mizuno R, Lundsmith ET, Lee DSM, **Liang S**, **Wijeratne HRS**, Marti S, Chau L, Giroux V, Wilkins BJ, Wu GD, **Shah P**, Tartaglia GG, and Hamilton KE. (2019)
Posttranscriptional regulation of colonic epithelial repair by RNA binding protein IMP1/IGF2BP1.
EMBO reports 20 : e47074

18. Chatterji P*, Hamilton KE*, **Liang S**, Andres SF, **Wijeratne HRS**, Mizuno R, Simon LA, Hicks PD, Foley SW, Pitarresi JR, Klein-Szanto AJ, Mah AT, Landeghem LV, Gregory BD, Lengner CJ, Madison BB, **Shah P**, and Rustgi AK. (2018)
The LIN28B–IMP1 post-transcriptional regulon has opposing effects on oncogenic signaling in the intestine.
Genes Dev. 32: 1020-1034.

17. Carja, O, **Xing T**, Wallace EWJ, Plotkin JB, and **Shah P**. (2017)
riboviz: analysis and visualization of ribosome profiling datasets.
BMC Bioinformatics 18 : 461

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

2017-2022 NIDDK R01 DK056645
The LIN28B-LET7 axis in intestinal epithelial biology.
PI: Anil Rustgi (Columbia University)
Role: Co-I

2020-2024 NIDDK R01 DK124369
Defining post-transcriptional regulons in intestinal epithelial regeneration.

PI: Kathryn Hamilton (University of Pennsylvania)
Role: Co-I

2021-2025 NIGMS R01 GM139695
Functional analysis of mammalian midbody RNA in post-mitotic signaling functions.
PI: Ahna Skop (University of Wisconsin)
Role: Co-I

2022-2027 NICHD R01
Novel mechanisms regulating translation elongation during male germ cell differentiation.
PI: Elizabeth Snyder (Rutgers University)
Role: Co-I

2022-2024 NIAID R21 AI170977
The temporal dynamics of translation efficiency during an innate immune response.
PI: Ann Tate (Vanderbilt University)
Role: Co-I

Pending

2022-2027 R01
Molecular and Cellular Mechanisms of Maternal Behavior.
PI: Gleb Shumyatsky (Rutgers University)
Role: Co-I

Completed

2019-2022 NSF/BBSRC 1936046
RiboViz for reliable, reproducible and rigorous quantification of protein synthesis.
Role: PI

2021-2022 NSF 2133405
MoCelS-DCL: Planning Workshops for Synthesis of Massively Parallel Assays and Molecular Physiology.
Role: Co-PI with Drs. Edward P O'Brien, Devarajan Thirumalai, Susan Marqusee, and Liana Lareau

2021 SAS Student Computing Fee (SCF) Award
Role: Co-PI with Drs. Christopher Ellison and Tara Matise

2016-2021 NIDDK R01 DK109714
Homeostatic responses to amino acid insufficiency.
PI: Tracy Anthony (Rutgers University)
Role: Co-I

2021 Provosts COVID Impact on Scholarly Productivity Faculty Grant
Role: PI

2021 Doctoral Student Academic Advancement Support Program
Role: Mentor

2009-2011 National Institute for Mathematical and Biological Synthesis (NIMBioS)
Graduate Research Assistantship.

2009 University of Tennessee Graduate Summer Research Assistantship.

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.

HONORS AND AWARDS

2021 School of Arts and Sciences Distinguished Contributions to Undergraduate Education

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.

Trainee awards

2021-2024 Alexander Cope (postdoc) - INSPIRE/IRACDA Postdoctoral fellowship.

2020-2022 Alexandra Logerfo (grad student) - Rutgers/NIH-NIGMS Biotechnology Training Program fellowship.

2019 Sadhana Chidambaran (undergrad) - Jackson Labs: Summer Student Program fellowship.

2018 Sadhana Chidambaran (undergrad) - National Institute of Mathematical and Biological Synthesis Summer Research Experience fellowship.

INVITED TALKS

2022 *The landscape of molecular changes underlying 22 years of bacterial adaptation.*

23. ASBMB Evolution and core processes in gene expression, Kansas City, MO.

2021 *Ribosome profiling across the tree of life.*

22. Biochemical Society Ribosome profiling workshop, UK.

A generalized framework for quantifying isoform-specific translation.

21. Translation UK 2021 - Sheffield, UK

2020 *Dynamics and evolution of translational regulation.*

20. University of Edinburgh, Scotland
19. Department of Biochemistry and Microbiology, Rutgers University, New Brunswick NJ (postponed due to COVID)

2019 *Dynamics and evolution of translational regulation.*

18. University of California, Berkeley CA

2018 *Dynamics and evolution of translational regulation.*

17. Cancer Institute of New Jersey, Rutgers University, New Brunswick NJ
16. Johns Hopkins University, Baltimore MD
15. University of Rochester Medical Center, Rochester NY

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

2020 **Shah P**
Quantifying changes in transcription and translation over 22 years of bacterial adaptation.

22. The Allied Genetics Conference of The Genetics Society of America - Zoom meeting.
21. Translation UK 20 - Sheffield, UK (postponed due to COVID-19).

2017 **Shah P**
Evolution 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. South Eastern 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:

2019 - Current Computational genetics of big data

2019 - Current Computational genomics (Graduate)

2018 - Current Fundamentals of molecular biosciences (Graduate)

Spring 2018 Computational genetics of big data

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

Guest Lecturer:

2017 Genomics Jam

2017 Freshman Honors Computational Genetics – Modeling protein synthesis: simulations and data mining

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

Postdocs

1. Alexander Cope (07/20 -)
2. Theresa Rogers (02/21 - 06/22)
3. Kirti Gupta (08/18 - 07/19)

Graduate students

1. Sangeevan Vellappan (Ph.D., 2020 -) co-mentored with Dr. Srujana Yadavalli
2. John Favate (Ph.D., 2018 -)
3. Sukanya Das (Ph.D., 2018 -)
4. Tongji Xing (Ph.D., 2016 - 2022)
5. Alexander Salibi (Masters, 2017 - 2020)
6. Alexandra Logerfo (Ph.D., 2020 - 2021) mentored by Dr. Michael Verzi

Graduate students - Other

1. Matthew Lawlor (Ph.D. committee, 2021 -)
2. Zishuo Zheng (Ph.D. committee, 2020 -)
3. Iva Salamon (Ph.D. committee, 2020 -)
4. William Kion-Crosby (Ph.D. committee, 2019)
5. Vaidhyanathan Mahaganapathy (Masters committee, 2017 - 2020)
6. Candice Craig (rotation, 2016)
7. Srividya Venkatramanan (rotation, 2016)

Undergraduate students

1. Peter Tilton (06/20 - 05/22)
2. Anna Mackinnon (09/19 - 07/21)
3. Anjali Patel (08/19 - 12/20)
4. Kush Patel (06/18 - 05/20)
5. Kevin Shen (11/18 - 05/20)
6. Yasasvi Talagadadeevi (02/17 - 05/20)
7. Sadhana Chidambaran (03/17 - 05/20)
8. Madhuri Bhupathiraju (08/16 - 05/18)
9. Dana Goldrich (08/17 - 12/17)
10. Albert Sultan (04/16 - 05/17)
11. Darya Pavlenko (04/16 - 12/16)

Undergraduate students - Other

1. Sadhana Chidambaran (Mentor, Honors thesis, Department of Genetics, 2020)
2. Aparna Anand (Committee member, Honors thesis, Department of Genetics, 2020)
3. Chinmay Rele (Committee member, Honors thesis, Department of Genetics, 2019)
4. Shirley Luo (Committee member, Honors thesis, Department of Genetics, 2018)
5. Mones Aba Elatto (Committee member, Honors thesis, Department of Genetics, 2018)
6. Vasvi Patel (Reader, senior thesis for G.H. Cook Scholars Program, 2017 - 2018)

PROFESSIONAL SERVICE

Reviewer: Science, 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, Nucleic Acids Research, RNA, Molecular Biology & Evolution, Genome Biology & Evolution, Evolution, Virus Evolution, Journal of Theoretical Biology, Journal of Molecular Evolution, Current Bioinformatics, BMC Bioinformatics, Biochemical Society Transactions, and Biotechnology Journal

Invited:

2019 Mentor: Bay Area RNA Club, University of California, San Fransisco CA.

2017 Discussion leader: Gordon Research Seminar in Molecular Mechanisms in Evolution, Easton MA.

2017 Presentation judge - EPiC: Evolution in Philadelphia Conference, Philadelphia PA.

2015 Panelist: Center for Teaching and Learning - Teaching portfolios, University of Pennsylvania, Philadelphia PA.

Rutgers:

2018 - Current Presentation judge - MBGSO Annual Symposium.

2017 - Current Panelist: Redefining the Postdoctoral Experience: New Training for New Careers.

2017 - Current Molecular Biosciences Graduate Student Recruiting committee

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

2018 Faculty Workshop in Mentoring Biomedical PhD Students at Rutgers University, Piscataway NJ.

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.