

# Premal Shah

Department of Genetics  
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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

- 2016 McCandlish DM, **Shah P**, and Plotkin JB.  
*Epistasis and the dynamics of reversion in molecular evolution.*  
Genetics 10.1101/042895
- 2016 Weinberg DE\*, **Shah P\***, Eichhorn SW, Hussmann JA, Plotkin JB, and Bartel DP.  
*Improved ribosome-footprint and mRNA measurements provide insights into dynamics and regulation of yeast translation.*  
Cell Reports 14 (7): 1787-1799 \*Equal contribution
- 2016 Kubatko L, **Shah P**, Herbei R, and Gilchrist MA.  
*A codon model of nucleotide substitution with selection on synonymous codon usage.*  
Molecular Phylogenetics and Evolution 94: 290-297
- 2015 **Shah P**, McCandlish DM, and Plotkin JB.  
*Contingency and entrenchment in protein evolution under purifying selection.*  
Proceedings of the National Academy of Sciences, USA E3226–E3235

- 2015 Gilchrist MA, Chen WC, **Shah P**, Landerer C, and Zaretzki R.  
*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
- 2014 Fordyce JA, **Shah P**, and Fitzpatrick BM.  
*iteRates: An R package for implementing a parametric rate comparison on phylogenetic tree.*  
Evolutionary Bioinformatics (10): 127-130
- 2013 **Shah P**, Ding Y, Niemczyk M, Kudla G, and Plotkin JB.  
*Rate-limiting steps in yeast protein translation.*  
Cell 153 (7): 1589-1601
- 2013 Xu Y, Ma P, **Shah P**, Rokas A, Liu Y and Johnson CH.  
*Non-optimal codon usage is a mechanism to achieve circadian clock conditionality.*  
Nature 495: 116-120
- 2013 McCandlish DM, Rajon E, **Shah P**, Ding Y and Plotkin JB.  
*The role of epistasis in protein evolution.*  
Nature 497: E1-E2
- 2013 **Shah P**, Fitzpatrick BM, and Fordyce JA.  
*A parametric method for assessing diversification rate variation in phylogenetic trees.*  
Evolution 67 (2): 368-377
- 2013 Niemiller ML, Fitzpatrick BM, **Shah P**, Schmitz L, and Near TJ.  
*Evidence for repeated loss of selective constraint in rhodopsin of amblyopsid cavefishes (Teleostei: Amblyopsidae).*  
Evolution 67 (3): 732-748
- 2012 Ding Y, **Shah P** and Plotkin JB.  
*Weak 5' mRNA structure in short eukaryotic genes.*  
Genome Biology and Evolution 4 (10): 1046-1053
- 2011 **Shah P**, and Gilchrist MA.  
*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
- 2010 **Shah P**, and Gilchrist MA.  
*Effect of correlated tRNA abundances on translation errors and evolution of codon usage bias.*  
PLOS Genetics 6 (9): e1001128
- 2010 **Shah P**, and Gilchrist MA.  
*Is thermosensing property of RNA thermometers unique?*  
PLOS ONE 5 (7): e11308
- 2009 Gilchrist MA, **Shah P**, and Zaretzki R.  
*Measuring and detecting molecular adaptation in codon usage against nonsense errors during protein translation.*  
Genetics 183 (4): 1493-505

## HONORS AND AWARDS

- 2011 Jim Tanner Award for Outstanding Dissertation.
- 2009-2011 National Institute for Mathematical and Biological Synthesis (NIMBioS) Graduate Research Assistantship (\$20,000 p.a.).
- 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 University of Tennessee Graduate Summer Research Assistantship (\$3,600).
- 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

- 2015 *Opportunities and pitfalls in modeling protein translation using ribosome-profiling.*  
Tel Aviv University, Tel Aviv, Israel
- 2015 *Insights from mechanistic models of protein translation.*  
University of Maryland, Baltimore County, MD
- 2015 *Insights from mechanistic models of protein translation.*  
Rutgers University, New Brunswick NJ
- 2014 *Dynamics of protein translation in yeast.*  
National Center for Biological Sciences, Bangalore, INDIA
- 2013 *Rate-limiting steps in protein translation.*  
University of Utah, Salt Lake City UT
- 2011 *Population genetics of codon usage bias.*  
University of Pennsylvania, Philadelphia PA
- 2011 *Insights from mechanistic models of protein translation on the evolution of codon usage bias.*  
Vanderbilt University, Nashville TN
- 2009 *Measuring the adaptedness of a gene: Nonsense-error Adaptation Index.*  
University of Tennessee, Knoxville TN
- 2006 *Agent-based models in economics.*  
Computable and Experimental Economics Laboratory (CEEL), Trento, Italy

## CONFERENCE PRESENTATIONS

- 2015 **Shah P** and Plotkin JB.  
*Opportunities and pitfalls in modeling protein translation using ribosome-profiling.*  
Society for Molecular Biology and Evolution (SMBE) - Vienna, Austria.
- 2015 **Shah P**, McCandlish DM and Plotkin JB.  
*Contingency and entrenchment in protein evolution.*  
Forecasting evolution - Lisbon, Portugal.
- 2015 **Shah P** and Plotkin JB.  
*Dynamics and regulation of protein translation.*  
Biomedical Postdoc Research Symposium - Philadelphia, PA.
- 2015 **Shah P** and Plotkin JB.  
*Local DNA topography predicts genomic mutation rates.*  
Society for Molecular Biology and Evolution (SMBE) - Bloomington, IN.
- 2014 **Shah P**, Krishnan A, Gilchrist MA and Plotkin JB.  
*Redefining the context in context-dependent mutation.*  
Society for Molecular Biology and Evolution (SMBE) - San Juan, PR.

- 2014 **Shah P**, Krishnan A, Gilchrist MA and Plotkin JB.  
*Redefining the context in context-dependent mutation.*  
Society for Study of Evolution (SSE) - Raleigh, NC.
- 2013 **Shah P** and Plotkin JB.  
*Characterizing epistasis in proteins under purifying selection.*  
Society for Molecular Biology and Evolution (SMBE) - Chicago, IL.
- 2013 **Shah P** and Plotkin JB.  
*Characterizing epistasis in proteins under purifying selection.*  
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.*  
Society for Molecular Biology and Evolution (SMBE) - Lyon, France.
- 2010 **Shah P** and Gilchrist MA.  
*Correlated tRNAs, translation errors and evolution of codon usage bias.*  
Society for Study of Evolution (SSE) - Portland, OR.
- 2010 **Shah P** and Gilchrist MA.  
*Genome-wide determinants of codon composition.*  
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.*  
Society for Study of Evolution (SSE) - Moscow, ID.
- 2009 Gilchrist MA, **Shah P**, and Zaretzki R.  
*Making Wright's metaphor a reality: Quantifying and detecting molecular adaptation.*  
SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) - Dahlenega, GA.
- 2009 Gilchrist MA, **Shah P**, and Zaretzki, R.  
*Measuring and detecting molecular adaptation against nonsense errors.*  
The 7th Georgia Tech - Oak Ridge National Lab International Conference – "Genome Biology and Bioinformatics" - Atlanta, GA.
- 2009 **Shah P**, Strielkowski W, and Sinha, S.  
*Mechanisms of immigrants' clusters formation using networks dynamic modeling.*  
Santa Fe Institute - Summer Complex Systems School, Chennai, India.

## PROFESSIONAL SERVICE

### Reviewer

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

## PROFESSIONAL AFFILIATIONS

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

**TEACHING EXPERIENCE****Graduate Teaching Assistant:**

2007 Genetics

2006 Biology for non-majors

**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.

**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.