OMB No. 0925-0001 and 0925-0002 (Rev. 03/2020 Approved Through 02/28/2023)

BIOGRAPHICAL SKETCH

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NAME: Turner, Paul Eugene

eRA COMMONS USER NAME: PETURNER

POSITION TITLE: Rachel Carson Professor of Ecology and Evolutionary Biology, Yale University; Microbiology Faculty, Yale School of Medicine

EDUCATION/TRAINING

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| University of Rochester; Rochester, NY | BA | 05/1988 | Biological Sciences |
| Michigan State University; East Lansing, MI | PhD | 11/1995 | Microbial Evolution |
| University of Maryland; College Park, MD | Postdoc | 12/1998 | Phage Evolution |
| University of Valencia; Valencia, Spain | Postdoc | 12/1999 | Virus Evolution |
| National Institutes of Health | Postdoc | 08/2001 | Molecular Virology |

A. Personal Statement

I have a broad background in microbial genetics, genomics and evolution, including specific training and expertise in the evolutionary genetics of bacteria, bacteriophages (bacteria-specific viruses), and RNA virus pathogens. As a grad student and postdoc, I successfully conducted basic research on a wide variety of microbes, to elucidate the evolutionary biology of infectious disease agents and non-pathogenic microbes. After moving to Yale, as PI and Co-PI on externally funded grants I continued to expand my toolkit and to perform studies laying the groundwork for my current research program, which includes basic research in molecular and evolutionary microbiology of human pathogens, and applied studies of using viruses in medical therapy (virotherapy). I successfully administered these projects by hiring staff, obtaining permits to work with disease agents, and managing budgets. I have an excellent track record of collaborating with researchers at Yale, and at other domestic and international institutions. In addition, I have achieved great success in training researchers at all levels (undergraduate, Master’s, PhD and postdoctoral), and in using external funds to produce many peer-reviewed publications from each externally funded project. My departmental leadership experience at Yale includes service as Department Chair (7 years), Director of Graduate Studies (3 years), and Chair of the Diversity, Equity and Inclusion Committee (current). My institutional leadership at Yale includes Interim Dean of Science (1.5 years), where I helped develop cluster-hire initiatives to recruit diverse faculty, as well as Chair of the Biological Sciences Area Committee and Tenure Appointments Committee (3 years), which evaluated tenure cases in biology for both Yale U and Yale School of Medicine.

B. Positions, Scientific Appointments and Honors

Positions and Employment

2019-21 Chair of the Biological Sciences Advisory Committee, Yale U

2017-18 Interim Dean of Science, Yale U

2011- Full Professor and Departmental Chair, Department of Ecology & Evolutionary Biology, Yale U

2011- Visiting Faculty Fellow, The Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, The Marine Biological Laboratory, Woods Hole, MA

2006-11 Associate Professor with tenure, Department of Ecology & Evolutionary Biology, Yale U

2004-05 Visiting Scholar, Division of Biological Sciences, University of California, San Diego

2002- Faculty Member, Graduate Program in Microbiology, Yale School of Medicine

2001-06 Assistant Professor, Department of Ecology & Evolutionary Biology, Yale U

Selected Other Experience and Professional Memberships

2020 Committee on Data Needs to Monitor Evolution of SARS-CoV-2, National Academies of Science, Engineering and Medicine

2019-21 Council Delegate, Biosciences Section, American Association for Advancement of Science

2019-22 Biological Sciences Advisory Committee of the National Science Foundation

2015-16 Committee on Gene Drive Research in Non-Human Organisms, National Research Council

2015- Associate Editor, *Virus Evolution*

2014-17 Biological Sciences Advisory Committee of the National Science Foundation

2012-15 Associate Editor, *Evolution, Medicine and Public Health*

2010 -13 Councilor, American Genetic Association

2010- Member, American Genetic Association

2009-11 Associate Editor, *Evolution: International Journal of Organic Evolution*

2009-10 Chair, American Society for Microbiology Division R: Evolutionary and Genomic Microbiology

2007-16 Committee on Minority Education, American Society for Microbiology

2007-10 Director of Graduate Studies, Department of Ecology and Evolutionary Biology, Yale U

2005-09 Scientific Advisory Board, NSF NESCent: National Evolutionary Synthesis Center

2005- Diversity Coordinator, Department of Ecology and Evolutionary Biology, Yale U

2004- Member, American Society for Virology

2003-04 Advisor, Science Network of the New England Board of Higher Education

2002-04 Committee: Biological Confinement of Genetically Engineered Organisms, National Research

Council

1995- Member, American Society for Microbiology

1990- Member, International Society for the Study of Evolution

Selected Honors

2021 Named President Elect of the International Society for Evolution, Medicine and Public Health

2021 Rolla E. Dyer Memorial Lecture, National Institutes of Health

2020 John H. Blaffer Distinguished Lecture, MD Anderson Cancer Center

2020 Named as one of Cell Press’s 1000 Inspiring Black Scientists in America

2019 Elected to Fellowship in National Academy of Sciences

2019 Elected to Fellowship in American Academy of Arts & Sciences

2019 Elected to Fellowship in American Academy of Microbiology

2019 MLK Week Memorial Lecture. Virginia Polytechnic Institute & State U, Blacksburg, VA

2019 American Academy of Microbiology Honorary Diversity Lecturer, ASM Microbe, San Francisco

2018 Edwin H. Lennette Memorial Lecturer. American Society for Virology conference. U Maryland

2017 Named endowed professor of ecology & evolutionary biology, Yale University

2014 Elected Chair of 2018 CNRS Jacques Monod Conference on Viral Emergence

2013 Elected Faculty Affiliate, BEACON Center for the Study of Evolution in Action, NSF Science and Technology Center

2011 E.E. Just Endowed Research Fellowship, and William Townsend Porter Award. The Marine Biological Laboratory, Woods Hole, MA

2010 Elected Contributing Faculty Member for Faculty of 1000; Microbial Evolution and Genomics Section in the Microbiology Faculty

2009 Elected Chair of 2013 Gordon Research Conference on Microbial Population Biology

2009 Participant, American Academy of Microbiology Colloquium, Galapagos Islands, Ecuador

2009 Dean’s Lecture, Houston 2009 Darwin Bicentennial Celebration. U Houston

2007 8th Annual James P. Holland Memorial Lecture, Indiana University

2007 ASM Division R (Evolutionary and Genomic Microbiology) Lecturer, 107th General Meeting of the American Society for Microbiology, Toronto, Canada

2004-05 Career Enhancement Fellowship for Junior Faculty, Woodrow Wilson Foundation

2004-05 Yale University Junior Faculty Fellowship in the Natural Sciences

2003 Top Ten Emerging Scholars Award, *Diverse Issues in Higher Education* (formerly

*Black Issues in Higher Education*).

2002 USA Delegate, USA-Russia Workshop on Infectious Disease, Novosibirsk, Russia

**C. Contribution to Science**

**1. My early work concerned the evolutionary consequences of RNA virus co-infection, especially disentangling the fitness advantages and disadvantages to virus genotypes when replicating within the same host cell. These studies were highly interdisciplinary, harnessing mathematical game theory and experimental evolution studies of viruses in the laboratory, as well as subjecting wild samples of viruses to phylogenetic and genomic analyses to infer effects of co-infection on virus population structure in nature. These studies provided a comprehensive roadmap for examining positive effects of co-infection such as the role of genetic exchange (recombination, reassortment) in generating variation that fuels natural selection, and for elucidating negative effects of co-infection such as virus-virus competition within host cells.**

**a.** Turner, P.E., and L. Chao. 1999. Prisoner's dilemma in an RNA virus. *Nature* 398:441-443.

**b.** Turner, P.E., C. Burch, K. Hanley, and L. Chao. 1999. Hybrid frequencies confirm limit to coinfection in the RNA bacteriophage phi-6. *Journal of Virology* 73:2420-2424. PMCID: PMC104488.

**c.** Silander, O., D. Weinreich, K. Wright, K. O’Keefe, C. Rang, P.E. Turner, and L. Chao. 2005. Widespread genetic exchange among terrestrial bacteriophages. *Proceedings of the National Academy of Sciences USA* 102:19009-19014. PMCID: PMC1323146.

**d.** McDonald, S.M., M.I. Nelson, P.E. Turner, and J.T. Patton. 2016. Reassortment in segmented RNA viruses: mechanisms and outcomes. *Nature Reviews Microbiology* 14:448-460. PMCID: PMC5119462.

**2. Some viruses specialize on relatively few host species, whereas other viruses are capable of generalizing on a wider variety of host species for infection. My RNA virus studies examined the evolutionary genetics of specialism versus generalism, to determine how and why viruses evolutionarily change to become broader versus narrower in their host breadth. These projects identified molecular substitutions associated with changes in viral host range, demonstrated that viruses can evolve genetic robustness to better withstand effects of deleterious mutations, and that point mutations in RNA viruses can minimally govern virus speciation events.**

**a.** Turner, P.E., and S.F. Elena. 2000. Cost of host radiation in an RNA virus. *Genetics* 156:1465-1470. PMCID: PMC1461356.

**b.** Montville, R., R. Froissart, S.K. Remold, O. Tenaillon, and P.E. Turner. 2005. Evolution of mutational robustness in RNA viruses. *PLoS Biology* 3:1939-1945. PMCID: PMC1456243.

**c.** Remold, S.K., A. Rambaut, and P.E. Turner. 2008. Evolutionary genomics of host adaptation in VSV. *Molecular Biology and Evolution* 25(6):1138-1147.

**d.** Duffy, S., C. L. Burch, and P.E. Turner. 2007. Evolution of host specificity drives reproductive isolation among RNA viruses. *Evolution* 61:2614-2622.

**3. The rise of antibiotic resistance in bacterial pathogens presents an increasing challenge in public health and in agricultural systems. We examined the evolution of conjugative plasmids that contribute to the spread of resistance genes in bacterial populations, especially previously unknown evolutionary correlations between rates of plasmid transfer and expression of resistance genes. In addition, we used mathematical modeling and *in vitro* studies to examine novel therapies to target bacterial pathogens, especially the use of phages as alternatives to traditional antibiotics.**

**a.** Turner, P.E., E.S.C.P. Williams, C. Okeke, V. Cooper, S. Duffy, and J. Wertz. 2014. Antibiotic resistance correlates with transmission in plasmid evolution. *Evolution* 68:3368-3380.

b. Chan, B.K., M. Sistrom, J.E. Wertz, K.E. Kortright, D. Narayan, and P.E. Turner. 2016. Phage selection restores antibiotic sensitivity in MDR *Pseudomonas aeruginosa*. *Scientific Reports* 6:26717. DOI: 10.1038/srep26717. PMCID: PMC4880932.

**c.** Kortright, K., B.K. Chan, J.L. Koff and P.E. Turner. 2019. Phage therapy: a renewed approach to combat antibiotic resistant bacteria. Special Focus issue on Bacteriophages for *Cell Host & Microbe* 25(2):219-232. DOI:https://doi.org/10.1016/j.chom.2019.01.014

d. Kortright, K., B.K. Chan, and P.E. Turner. 2020. High-throughput discovery of phage receptors using transposon insertion sequencing of bacteria. *Proceedings of the National Academy of Sciences USA*. https://doi.org/10.1073/pnas.2001888117

**4. Genetic trade-offs occur when organisms evolve adaptive traits for one purpose while suffering reduced performance in an unselected trait. Our work showed that RNA viruses often experienced evolution of trade-offs, under various selection pressures. We demonstrated that evolution of increased virus stability generally traded-off with viral reproduction, obeying a classic survival-reproduction trade-off seen in higher organisms. Also, we showed that viruses suffered evolutionary trade-offs across selective temperatures and across differing innate immune profiles of hosts. These studies uncovered evolutionary constraints of RNA viruses, which should be useful in designing therapies that target these weaknesses in virus performance across environments.**

**a.** Dessau, M., D. Goldhill, R.C. McBride, P.E. Turner, and Y. Modis. 2012. Selective pressure causes an RNA virus to trade reproductive fitness for increased structural and thermal stability of a viral enzyme. *PLoS Genetics* 8(11):e1003102. doi:10.1371/journal.pgen.1003102. PMCID: PMC3510033.

**b.** Alto, B., B. Wasik, N. Morales, and P.E. Turner. 2013. Stochastic temperatures impede RNA virus adaptation. *Evolution* 67:969-979.

**c.** Foxman, E., J.A. Storer, M.E. Fitzgerald, B.R. Wasik, L. Hou, H. Zhao, P.E. Turner, A.M. Pyle, and A. Iwasaki. 2015. Temperature-dependent innate defense against the common cold virus limits viral replication at warm temperature in mouse airway cells. *Proceedings of the National Academy of Sciences USA* 112(3):827-832. PMCID: PMC4311828.

d. Wasik, B.R., A.R. Munoz-Rojas, K.W. Okamoto, K. Miller-Jensen, and P.E. Turner. 2016. Generalized selection to overcome innate immunity selects for host breadth in an RNA virus. *Evolution* 70(2):270-281. DOI: 10.1111/evo.12845.

**5. RNA viruses are especially capable of jumping to new host species and causing emerging virus diseases in humans and other organisms. My work used both phages and viruses of eukaryotes as laboratory models for elucidating evolutionary rules of RNA virus emergence. These studies demonstrated that mutations underlying host shifts could be beneficial on both the novel and current hosts, and that an evolutionary history of multiple host infection fostered future emergence success. Also, we showed that the rate of novel host invasion in the environment affected fixation of beneficial virus mutations and performance on the novel host. Although RNA virus emergence remains difficult to predict, our work establishes fundamental rules of viral pathogen emergence.**

**a.** Duffy, S., P.E. Turner, and C. L. Burch. 2006. Pleiotropic costs of niche expansion in the RNA bacteriophage Φ6. *Genetics* 172:751-757. PMCID: PMC1456241.

**b.** Dennehy, J.J., N.A. Friedenberg, R.D. Holt, and P.E. Turner. 2006. Virus ecology and the maintenance of novel host use. *American Naturalist* 167:429-439.

**c.** Turner, P.E., N.M. Morales, B.W. Alto, and S.K. Remold. 2010. Role of evolved host breadth in the initial emergence of an RNA virus. *Evolution* 64(11):3273-3286.

**d.** Morley, V., S. Mendiola, and P.E. Turner. 2015. Rate of novel host invasion affects adaptive outcomes for an evolving RNA virus. *Proceedings of the Royal Society of London: Biological Sciences* 282:20150801. DOI: 10.1098/rspb.2015.0801. PMCID: **PMC4632612.**

**Complete List of Published Work in MyBibliography:**

http://www.ncbi.nlm.nih.gov/sites/myncbi/1HE8bZ0bB9hAN/bibliograpahy/49923152/public/?sort=date&direction=ascending