Tauras P. Vilgalys

Department of Medical Genetics
University of Chicago, Chicago, IL

taur.vil@gmail.com
425.466.0784

Education & Training

Postdoc	2020-present	Genetic Medicine, Department of Medicine, University of Chicago
Ph.D.	2019	Evolutionary Anthropology, Duke University
B.S.	2014	Biology, Loyola Marymount University

Publications

** indicates co-first author. ^ indicates co-corresponding author.*

2025 **Vilgalys TP**, Klunk J, Demeure CE, Cheng X, Shiratori M, Madej J, Beau R, Elli D, Patino MI, Redfern R, DeWitte SN, Gamble JA, Boldsen JL, Carmichael A, Varlik N, Eaton K, Grenier J-C, Golding GB, Devault A, Rouillard J-M, Yotova V, Sindeaux R, Ye CJ, Bikaran M, Dumaine A, Brinkworth JF, Missiakas D, Rouleau GA, Steinrücken M, Pizarro-Cerdá J, Poinar H^, Barreiro LB^. Reply to: Insufficient evidence for natural selection associated with the Black Death. *Nature* 638, E23-E29.

2024 Woitowich NC*, Hengel SR*, **Vilgalys TP**, Babdor J, Tyrrell DJ. Analysis of NIH K99/R00 Awards and the Career Progression of Awardees. *eLife* 12:RP88984. doi:10.7554/eLife.88984.1

2022 Klunk J*, **Vilgalys TP***, Demeure CE, Cheng X, Shiratori M, Madej J, Beau R, Elli D, Patino MI, Redfern R, DeWitte SN, Gamble JA, Boldsen JL, Carmichael A, Varlik N, Eaton K, Grenier J-C, Golding GB, Devault A, Rouillard J-M, Yotova V, Sindeaux R, Ye CJ, Bikaran M, Dumaine A, Brinkworth JF, Missiakas D, Rouleau GA, Steinrücken M, Pizarro-Cerdá J, Poinar H^, Barreiro LB^. Evolution of immune genes is associated with the Black Death. *Nature* 611, 312–319.

2022 **Vilgalys TP***, Fogel AS*, Anderson JA, Mututua RF, Warutere JK, Kim SY, Voyles TN, Robinson JA, Wall JD, Archie EA, Alberts SC, Tung J. Selection against admixture and gene regulatory divergence in a long-term primate field study. *Science* 377(6606): 635-641.

2020 Batra SS, Levy-Sakin L, Robinson J, Guillory J, Durinck S, **Vilgalys TP**, Kwok PY, Cox LA, Seshagiri S, Song YS, Wall JD. Accurate assembly of the olive baboon (*Papio anubis*) genome using long-read and Hi-C data. *GigaScience* 9(12):giaa134.

2020 Anderson JAA, **Vilgalys TP**, Tung J. Diversifying primate genomics: new insights into the ecology and evolution of primate gene regulation. *Current Opinions in Genetics and Development* 62:16-22.

2019 Fan Y, **Vilgalys TP**, Sun S, Peng Q, Tung J, Zhou X. IMAGE: high-powered detection of genetic effects on DNA methylation using integrated methylation QTL mapping and allele-specific analysis. *Genome Biology* 20:1-18.

2019 **Vilgalys TP**, Rogers J, Jolly C, Mukherjee S, Baboon Genome Analysis Consortium, Tung J. Evolution of DNA methylation in *Papio* baboons. *Molecular Biology & Evolution* 36(3): 527-540.

2019 Rogers J, et al., Baboon Genome Analysis Consortium (including **Vilgalys TP**). The comparative genomics and complex population history of *Papio* baboons. *Science Advances* 5(1): eaau6947.

2019 Watts HE, Jiminez D, Pacheco V, **Vilgalys TP**. Effects of temperature on the timing of breeding and molt transitions in house finches. *Journal of Experimental Biology* 221: 185058.

2018 Watts HE, Jiminez D, Pacheco V, **Vilgalys TP**. Temperature-correlated shifts in the timing of egg laying in house finches *Haemorhous mexicanus*. *International Journal of Avian Science*: doi.org/10.1111/ibi.12676.

2017 Lea AJ, **Vilgalys TP**, Durst PAP, Tung J. Maximizing ecological and evolutionary insight from bisulfite sequencing data sets. *Nature Ecology & Evolution* 1(8): 1074.

2014 **Vilgalys TP**, Sears R, Hand E, Morlege-Hampton S, Carmona-Galindo V. Exploration of climate influences on the abundance of galls on red willows (*Salix laevitigata*) across two riparian communities in Southern California. *Journal of Ecology and the Natural Environment* 5(5): 164-169.

Grants

2024 NIH K99/R00 Pathway to Independence Award, NHGRI: *Genomic basis of variation in the transcriptional response to pathogens among primates.* March 2024-February 2029, $982,435. Role: PI.

2022 Emory Primate Research Center Pilot Research Program: *Genetic variation in the response to yellow fever in non-human primates*. May 2022-April 2023, $69,980. Role: PI.

2020 NIH F32 Ruth B Kirschstein NRSA Fellowship, NIGMS: *Characterizing variation and adaptation in the immune response to plague (Y. pestis) through single-cell sequencing and ancient genomics.* February 2021 – January 2024, $210,000. Role: PI.

2018 Leakey Foundation Research Grant: *Natural selection on gene regulation following admixture in wild baboons*. June 2018 – Dec 2019, $14,136. Role: PI.

2018 National Science Foundation: Doctoral Dissertation Research Improvement Grant, *Leveraging natural hybridization to understand the evolution of primate gene regulation*. March 2018 – February 2020, $19,995. Role: co-PI.

Scientific Presentations

Invited presentations

2025 Max Planck Research Group Selection Symposium, Max Planck Society, Berlin, Germany.
2025 University of New Mexico, Department of Anthropology, New Mexico.
2025 University of Wisconsin - Madison, Department of Pathobiological Sciences, Wisconsin.
2025 University of Georgia Athens, Department of Genetics, Georgia.
2024 Pennsylvania State University, Department of Biology, Pennsylvania.
2024 Clemson University, Center for Human Genetics, South Carolina.
2023 University of Zurich, One Health Symposium, Zurich, Switzerland.
2023 'Rising Stars in Genetics and Genomics' Symposium, University of Utah, Utah.
2023 University of Texas at Austin, Department of Anthropology, Texas.
2023 University of Utah, Department of Anthropology, Salt Lake City, Utah.

Select conference presentations (presenting author)

Oral Presentations

2024 Biology of Genomes, Cold Spring Harbor Laboratory, NY, USA. *Immunogenetic pleiotropy in the response to Yersinia pestis.*

2023 American Association of Biological Anthropologists, Reno, NV. *Genetic variation affecting the immune response to Y. pestis during the Black Death.*

2022 Biology of Genomes, Cold Spring Harbor Laboratory, NY, USA. *Natural selection on immune genes during the Black Death.*

2020 Biology of Genomes (virtual). *Selection against gene regulatory divergence shapes genome-wide introgression in wild baboons.*

Poster presentations

2025 Biology of Genomes, Cold Spring Harbor Laboratory, NY, USA. *Immune pleiotropy and evolution in the response to Yersinia pestis.*
2024 American Society of Human Genetics, Denver, CO, USA. *Immunogenetic pleiotropy and context-specific gene regulation in the response to Yersinia pestis.*
2023 Society for Molecular Biology and Evolution, Ferrara, Italy. *Common genetic variation affecting the transcriptomic response to Yersinia pestis.*
2023 Biology of Genomes, Cold Spring Harbor Laboratory, NY, USA. *Genetic variation shaping the transcriptomic immune response to Yersinia pestis.*
2021 Society for Molecular Biology and Evolution (virtual). *Ancient genomics reveal positive selection on immune genes during the Black Plague.*
2019 Society for Molecular Biology and Evolution, Manchester, UK. *Local ancestry influences gene regulation in naturally hybridizing wild baboons.*
2017 Society for Molecular Biology and Evolution, Austin, TX, USA. *The evolution of DNA methylation among baboon species.*

Select Honors and Awards

2025 Young Investigator Attendance Award, Society for Molecular Biology and Evolution
2023, 25 Career Advancement for Postdocs (CAP) Travel Award, Biological Society Division, University of Chicago
2017 Young Investigator Travel Award, Society for Molecular Biology and Evolution
2017 Duke University Summer Research Fellowship
2016 Graduate Research Fellowship Program (NSF GRFP) Honorable Mention, National Science Foundation
2014 James B. Duke Fellowship, Duke University
2014 Carl G. Kadner Award, Loyola Marymount University
2013 Towner Scholarship, Loyola Marymount University
2012 Research Experience for Undergraduates Program (NSF REU), Mote Marine Laboratory
2012 William McLaughlin Memorial Scholarship, Loyola Marymount University
2010 Eagle Scout, Boy Scouts of America

Teaching & Mentorship

Graduate students mentored

Mohamed Hawash, PhD student (Barreiro Lab), University of Montreal
Ravneet Sidhu, PhD student (Poinar Lab), McMaster University
Tania Guerrero, PhD rotation student (Tung Lab), Duke University
Alexandra Soto, 2021 Ecology & Evolutionary Biology Mentor Match Program

Teaching Assistant, Duke University

Evolutionary Medicine and Global Health (Fall 2014, Fall 2016, Fall 2017)
Primate Field Biology (Spring 2017, Spring 2018, Fall 2018)
Intro to Evolutionary Anthropology (Spring 2014, Fall 2015, Spring 2019)

Teaching Assistant, Loyola Marymount University

General Biology 1 Lab (Fall 2012, Fall 2013)
General Biology 2 Lab (Spring 2013)
Hormones and Behavior (Spring 2014)

Teaching and mentorship training

Diversity and Inclusion Course for Postdocs (2021-2022)
Postdoc Mentor Training, University of Chicago (2021)
Certificate in College Teaching, Duke University (2017-2019)

Academic Service

Public outreach

Skype a scientist program reaching 5 classrooms and ~150 students (2021-2023)

Free-to-the-public events at the North Carolina Museum of Natural Sciences (2016-2019) and the Art of Science series of public talks at art galleries (2023)

Developing lesson plans for high school biology courses through the North Carolina Scientific Research and Education Network (SciREN) (2016-2018)

Peer review

Grants: Leakey Foundation research awards

Manuscripts: 7 journals including *Molecular Biology and Evolution*, *Molecular Ecology, the American Journal of Human Genetics*, *Science*, *Nature Communications*, and *Proceedings of the National Academy of Sciences*.

University of Chicago

Postdoc Representative on the Division-level Faculty Search (2024-2025)

Ecology & Evolution of Infectious Disease Journal Club (co-founder, 2022-2023)

DEI Committee, Department of Human Genetics (founding member, 2020-2023)

Duke University

Evolutionary Anthropology representative on the Graduate and Professional Student Council (2015-2016)

Loyola Marymount University

Academic Chair, Tri-Beta Biological Honors Society (2012-2013)

Student Honors Advisory Council (2010-2014)

Executive Board, Alpha Sigma Nu (Jesuit Honors Society) (2013-2014)