

**Dmitri A. Petrov**

Department of Biology  
Stanford University  
Stanford CA 94305

Telephone: (650) 736-1169  
Fax: (650) 723-6132  
email: [dpetrov@stanford.edu](mailto:dpetrov@stanford.edu)  
<http://petrov.stanford.edu>

**Academic Position.**

Michelle and Kevin Douglas Professor and Associate Chair, Department of Biology, Stanford University

**Date and Place of Birth.**

February 8, 1969 in Moscow, Russia

**Citizenship.**

USA

**Education.**

Harvard University Society of Fellows  
Harvard University, Department of Organismic and Evolutionary Biology  
Moscow Institute of Physics and Technology

Junior Fellow (1997-2000)  
Ph.D. in Biology (1997)  
M.Sc. in Physics and  
Molecular Biology (1989)

**Research Experience.**

|           |  |
|-----------|--|
| 2011-now  | Michelle and Kevin Douglas Professor of Biology,<br>Department of Biology, Stanford University, Stanford, USA                |
| 2009-2011 | Professor, Department of Biology,<br>Stanford University, Stanford, USA  |
| 2005-2009 | Associate Professor, Department of Biology,<br>Stanford University, Stanford, USA  |
| 2000-2005 | Assistant Professor, Department of Biology,<br>Stanford University, Stanford, USA  |
| 1998-2000 | Research Fellow, Department of Genetics,<br>Harvard Medical School, Cambridge, Massachusetts, USA                            |
| 1992-1997 | Graduate Student, Harvard University,<br>Department of Organismic and Evolutionary Biology,<br>Cambridge, Massachusetts, USA |
| 1990-1992 | Research Assistant, Washington University School of Medicine,<br>Department of Genetics, St. Louis, Missouri, USA            |
| 1989-1990 | Research Assistant,<br>Institute of Molecular Genetics, Moscow, Russia   |
| 1987-1989 | M.S. Student,<br>Institute of Molecular Genetics, Moscow, Russia   |

**Awards.**

|           |   |
|-----------|---|
| 2013      | Walter P. Kistler Prize and Research Award in Population Genetics and Society |
| 2008      | Chambers Fellow   |
| 2005      | Hellman Faculty Award   |
| 2003-2006 | Terman Award, Stanford University   |
| 2003-2004 | Alfred P. Sloan Foundation Research Fellow                                    |
| 1998      | Harvard University William F. Milton Fund Award                               |

|           |  |
|-----------|--|
| 1995-1997 | Teaching excellence awards<br>Genetics (1995 and 1997) and Introductory Molecular Biology (1995), Harvard University, Cambridge, Massachusetts |
| 1996      | Walter Fitch Prize for Best Student Paper<br>The Society for Molecular Biology and Evolution, Tucson, Arizona                                  |

**Editorial responsibilities.**

|              |  |
|--------------|--|
| 2007-present | Associate Editor, PLoS Genetics                  |
| 2009-2014    | Associate Editor, Mobile DNA                     |
| 2009-2012    | Associate Editor, GBE                            |
| 2003-2012    | Associate Editor, Journal of Molecular Evolution |

**Other professional responsibilities.**

|              |  |
|--------------|--|
| 2013-now     | Director, Genetics Society of America  |
| 2013-now     | Founding Executive Board member of the Center of Computational, Evolutionary, and Human Genomics, Stanford University  |
| 2012-now     | Scientific Advisory Board, Institute of Advanced Studies, Hebrew University  |
| 2012         | Member, NIH Genetic Variation and Evolution Study Section  |
| 2009         | External program reviewer for Austrian Science Foundation (FWF)  |
| 2006-2009    | Member, NIH Kirschstein-NRSA Individual Fellowship Panel   |
| 2006         | Member, NSF Evolutionary Genetics Panel  |
| 2003-present | Outside reviewer, Population Biology panel at the NSF  |
| 2003-present | Outside reviewer, Science Foundation Ireland   |
| 2003-present | Outside reviewer, Israel Science Foundation  |
| 2000-2002    | Edited a special issue of the journal <i>Genetica</i> on "Evolution of Genome size" (volume 115)   |
| 2001         | Organized a workshop (together with Paul Sniegowski, University of Pennsylvania) "Role of mutation in evolution" at the 2001 Conference of the Society for Molecular Biology and Evolution |

**Grants**

|           |  |
|-----------|--|
| 2015-2019 | National Institutes of Health RO1, " High-resolution study of adaptation in haploid and diploid populations of yeast", Principal Investigator  |
| 2012-2016 | National Institutes of Health RO1, "Adaptation in Six Dimensions", Principal Investigator (together with Paul Schmidt (U. Penn) (co-PI))   |
| 2012      | NESCENT, "Tracking the biotic response to global climate change through genomic analysis", co-Principal Investigator (together with co-PIs Alan Bergland (Stanford) and Paul Schmidt (U. Penn))                        |
| 2011-2016 | National Institutes of Health RO1, "Sequencing Yeast Lines to Measure Rates of Neutral and Deleterious Mutations", co-Principal Investigator (together with Mark Siegal (NYU) (PI), David Hall (UGA) (co-PI))          |
| 2010-2015 | National Institutes of Health RO1, "Population Genomics of Adaptive Transposition in <i>Drosophila</i> ", Principal Investigator   |
| 2007-2012 | National Institutes of Health, Center For Excellence in Genomic Science Grant, co-Principal Investigator (together with David Kingsley (PI), Richard Myers (co-PI), William Talbot (co-PI), Katherine Peichel (co-PI)) |
| 2006-2011 | National Institutes of Health RO1, "Patterns of Background Nucleotide Substitution in the Human Lineage", Principal Investigator   |

- 2003-2006 National Science Foundation, "Population Analysis of All Transposable Elements in the Sequenced Drosophila Genome", Principal Investigator
- 2003-2004 National Science Foundation, "Genomic Analysis of the Sporophyte to Gametophyte Transition in Maize", co-Principal Investigator (PI Prof. Virginia Walbot, Stanford University)
- 2001 Stanford University OTL award

### Invited Presentations.

2015

- SMBE, Plenary Presentation, Vienna, Austria
- MMEE Conference, Paris
- Ecole Superier Normal, Paris, Departmental Seminar
- NC State, Department of Genetics, Student invited speaker
- Harvard University, OEB and Systems Biology Program Departmental Seminar

2014

- Division of Biology, UCSD
- Department of Genetics, University of Pennsylvania, Postdoc invited speaker
- 1st ASM Conference on Experimental Microbial Evolution
- SMBE Annual Conference in Puerto Rico
- Department of Ecology and Evolution, University of Chicago
- "The Causes of Genome Evolution" Conference, Mishima, Japan

2013

- Museum of Vertebrate Zoology, Berkeley, CA
- Max-Planck Institute for Biology of Aging, Cologne, Germany
- Department of Genetics, University of Wisconsin
- SMBE Annual Conference in Chicago
- USC, Molecular & Computational Biology Department
- Department of Ecology and Evolution, Stony Brook University

2012

- Max-Planck Institute for Molecular Genetics, Berlin, Germany
- Jacques Monod conference "Theoretical and empirical advances in evolutionary genomics", Roscoff, France
- Vienna Graduate School of Population Genetics
- Radcliffe workshop "Population Genetics of Natural Selection", Harvard University
- Department of Cell Research and Immunology, Tel Aviv University
- Department of Integrative Biology, UC Berkeley
- 3<sup>rd</sup> International Conference, "Genomic Impact of Eukaryotic Transposable Elements", Asilomar, CA

2011

- Otto Warburg International Summer School and Research Symposium "Evolutionary Genomics", Berlin, Germany
- Frontiers in Genomics 2011, National University of México, Campus Cuernavaca, Mexico
- Department of Ecology and Evolution, University of Arizona
- International Symposium "Genomics Days", University of Lausanne, Lausanne, Switzerland
- Department of Biology, Indiana University, Departmental Seminar

2010

- University of Pennsylvania, Department of Biology, Departmental Seminar
  - UCSD, The Center for Theoretical Biological Physics, "The Physics of Evolution"
  - International symposium "Molecular Basis of Evolutionary Innovations", Marche-en-Famenne (Belgium)
  - Cold Spring Harbor "Genomes" Meeting, invited speaker and chair of "Evolutionary Genomics" session
  - International symposium "Populations, Evolution, and Physics", Aspen Center for Physics
- 2009
- International symposium "From sparse entities to crowded environments: numbers in living systems" (European interdisciplinary graduate school "Frontiers in Life Sciences", graduate student invitation)
  - Harvard University, School of Medicine, Department of Genetics
  - Institute of Science and Technology, Austria
  - 2nd Stanford Workshop in Biodemography, Stanford, CA
  - University of Washington, Dept. of Genome Sciences, Departmental Seminar
  - University of Toronto, Dept. of Ecology and Evolution, Departmental Seminar
  - Institute of Molecular Genetics of the Russian Academy of Sciences, Moscow, Russia
  - Moscow Conference on Computational Molecular Biology (MCCMB'09), Moscow, Russia
  - International Congress of SMBE, Iowa City, Iowa
  - USC, Dept. of Molecular and Cellular Biology
  - UCLA, Dept. of Ecology and Evolution, Departmental Seminar
  - Cold Spring Harbor, Biology of Genomes Meeting, (contributed presentation)
  - Buck Institute Seminar
- 2008
- Cornell University, Dept. of Molecular Biology and Genetics Seminar Series
  - Wright State, Dept. of Biology "Darwin Bicentennial" Seminar Series
  - University of Santa Barbara, KITP, Workshop "Population Genetics and Genomics"
  - International Congress of SMBE, Barcelona, Spain
  - International Congress on Transposable Elements, Saint Malo, France
  - University of Georgia, Athens, Georgia
  - University of Auckland, New Zealand
- 2007
- Statistical Approaches to Inference of Selection Workshop, Vienna, Austria
  - National Center for Biological Sciences, Bangalore, India
  - UC Irvine, Ecology and Evolution Seminar Series
  - BioX "Talks in English"
  - Max Plank Institute for Molecular Genetics, Berlin, Germany
- 2006
- Beckman Symposium on Evolution, Stanford University
  - Hebrew University, Departmental Seminar
  - University of Chicago, Dept. of Ecol. and Evol., Departmental Seminar
  - 1<sup>st</sup> International Conference, "Genomic Impact of Eukaryotic Transposable Elements", Asilomar, CA
  - "Mobile DNA" ASM Meeting, Banff, Canada
- 2005
- UC Davis, Ecology and Evolution Seminar Series
  - ESEB Annual Meeting, Krakow, Poland
  - Universitat Autònoma de Barcelona, Barcelona, Spain, Departmental Seminar
  - Institut Jacques Monod, Departmental Seminar, Paris, France
  - 7<sup>th</sup> International SocBIN conference "Bioinformatics 2005", Tartu, Estonia
  - UC Riverside, Dept. of Biology, Departmental Seminar

- University of Idaho, Dept. of Biol. Sciences, Departmental Seminar
  - NYU, Dept. of Biology, Departmental Seminar
- 2004
- UC San Diego, Ecology, Behavior, and Evolution Section Seminar
  - UC Berkeley, Computational and Genomic Biology Seminars Series
  - University of Arizona, Dept. of Ecology and Evolution, Departmental Seminar
- 2003
- The Iowa State University, Dept. of Ecol, Evol. & Org. Biology, Departmental Seminar
  - The Angiosperm Genome Size Workshop and Discussion meeting, RBG, Kew, London, UK
  - Human Genome Conference sponsored by DOE and JGI, Santa Fe, New Mexico
- 2002
- The University of Chicago, Dept. of Human Genetics, Departmental Seminar
  - University of Montpellier, France, Departmental Seminar
  - CNRS, Gif-sur-Yvette, France, Departmental Seminar.
  - Harvard University, Dept. of Org. and Evol. Biol., Departmental Seminar.
  - Intraclonal Genetic Variation Meeting, The Linnean Society of London, London, UK
- 2001
- Stanford University, Hopkins Marine Station, Departmental Seminar
  - University of Santa Barbara, Institute of Theoretical Physics, Workshop "Statistical Physics and Biological Information" (2 lectures)
- 1999
- University of Chicago, EEB Departmental Seminar
  - University of Massachusetts, Departmental Seminar
- 1998
- Evolutionary Genetics Meeting in honor of Richard Lewontin, Harvard University, Cambridge, MA
- 1994
- New England Molecular Evolutionary Biology Conference, Harvard University, Cambridge, MA

### Teaching.

- |           |   |
|-----------|---|
| 2013      | Summer school on quantitative population genetics and evolution, Cargese, Corsica   |
| 2011      | Frontiers in Genomics, National University of México, Campus Cuernavaca, Mexico   |
| 2006      | Second International Postgraduate Course in Genomics, Barcelona, Spain  |
| Annually  | Fundamentals of Molecular Evolution (Winter Quarter) (Bio113/244)   |
| Annually  | Evolution (in the Biological Core sequence) (Spring Quarter) (Bio43)  |
| 2002-2007 | Ecology, Evolution, and Natural History of Baja California (2 week-long Summer class with 12 students in Baja California taught jointly with 3 other instructors) (Bio 100) |

### Publications by D. Petrov and from the Petrov lab (lab members are in bold):

123. **Venkataram, S.\***, Dunn, B.\*, **Li, Y.**, Argawala, A., Chang, J., **Ebel, E.**, **Geiler-Samerotte**, Herrisant, L., Blundell, J., Levy, S.F., Fisher, D., Sherlock, G.\*, and **Petrov, D.A\***. A comprehensive genotype-fitness map for adaptive mutations in yeast. *Cell*, (in preparation); (\* contributed equally).
121. **Enard, D.**, **Cai, L.**, Gwennap, C., and **Petrov, D.A.** Viruses are a dominant driver of protein adaptation in mammals. *ELife*, submitted; biorXiv <http://dx.doi.org/10.1101/029397>

120. **Venkataram, S., Sellis, D., and Petrov, D.A.** Forward and backward predictability of evolution in Fisher's geometric model. *Theor. Pop. Biology*, in preparation; <http://biorxiv.org/content/early/2013/12/02/001016>
119. **Zhu, Y., Sherlock, G. and Petrov, D.A.** Extremely rare polymorphisms recapitulate AT-biased mutational spectrum from the mutation-accumulation experiments in yeast. *Proc. Natl. Acad. Sci. USA*, (in preparation).
118. **Zhu, Y., Sherlock, G. and Petrov, D. A.** Population structure and origins of clinical *Saccharomyces cerevisiae* strains. *G3*, (in preparation).
117. **Garud, N. and Petrov, D.A.** Elevation of linkage disequilibrium above neutral expectations in ancestral and derived populations of *Drosophila melanogaster*. *Genetics*, (in preparation).
116. **Sellis, D., Kvitek, D.J., Dunn, B., Swartz, K., Sherlock, G., and Petrov, D.A.** Empirical evidence for heterozygote advantage in adapting diploid populations of *Saccharomyces cerevisiae*. *Genetics*, (in review).
115. **Feder, A.F., Rhee, S.Y., Shafer, R.W., Petrov, D.A.\***, and **Pennings, P.S.\*** (2016). More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. *ELife*, (in press); (\* contributed equally).
114. **Wilson, B., Garud, N.R., Feder, A.F., Assaf, Z.J., and Pennings, P.S.** (2015). The population genetics of drug resistance evolution in natural 2 populations of viral, bacterial, and eukaryotic pathogens. *Mol. Ecol.*, **25**, 42-66.
113. **Machado, H.E., Bergland, A.O., O'Brien, K.R., Behrman, E.L., Schmidt, P.S. and D. A. Petrov.** (2016). Comparative population genomics of latitudinal variation in *D. simulans* and *D. melanogaster*. *Mol. Ecology*, (in press). 10.1111/mec.13446
112. **Bergland, A.O., Tobler, R., González, J., Schmidt, P., and Petrov, D.A.** (2016). Secondary contact has contributed to genome-wide patterns of clinal variation in North American and Australian populations of *Drosophila melanogaster*. *Mol. Ecology*, doi:10.1111/mec.13455; posted on bioRxiv at <http://www.biorxiv.org/content/early/2014/09/13/009084>
111. **McCoy, R. C., Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Petrov, D. A.** (2015). Evidence of selection against complex mitotic-origin aneuploidy during preimplantation development. *PLoS Genetics*, **11**: e1005601. doi:10.1371/journal.pgen.1005601
110. Glemin, S., Arndt, P.F., **Messer, P.W., Petrov, D.A.**, Galtier, N., and L. Duret. (2015). Quantification of GC-biased gene conversion in the human genome. *Genome Research*, **25**:1215-1228.
109. **Garud, N.** and Rosenberg, N.A. (2015). Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. *Theor. Pop. Biology*, **102**: 94-101.
108. Moreno-Gamez, S., Hill, A.L, Rosenbloom, D. I. S., **Petrov, D.A.**, Nowak, M.A., and **P. Pennings.** (2015). Imperfect drug penetration leads to spatial monotherapy and rapid evolution of multi-drug resistance. *Proc. Natl. Acad. Sci.*, doi: 10.1073/pnas.1424184112.

107. **Assaf, Z.J., Petrov, D.A.\* and Blundell, J.R.\*** (2015). Staggered sweeps: The obstruction of adaptation in diploids by recessive deleterious alleles. *Proc. Natl. Acad. Sci. USA*, [www.pnas.org/cgi/doi/10.1073/pnas.1424949112](http://www.pnas.org/cgi/doi/10.1073/pnas.1424949112); (\* contributed equally).
106. **McCoy, R. C.**, Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Fraser, H. B., **Petrov, D. A.** Common variants spanning *PLK4* are associated with increased rate of mitotic-origin aneuploidy in human embryos. (2015). *Science*, **348**: 235-238.
105. Levy\*, S., **Blundell\*, J.R., Venkataram, S., Petrov, D.A.**, Fisher, D.S., and Sherlock, G. (2015). Quantitative evolutionary dynamics using high-resolution lineage tracking. *Nature*, doi:10.1038/nature14279; (\* contributed equally).
104. Barrón, M.G., **Fiston-Lavier, A.-S., Petrov, D.A.**, and González-Perez, J. (2015). Population genomics of transposable elements in *Drosophila*. *Annual Review of Genetics*, **48**: 561–81.
103. **Fiston-Lavier, A.-S**, Barrón, M.G., **Petrov, D.A.**, González, J. (2015). T-lex2: genotyping, frequency estimation and re-annotation of transposable elements using single or pooled next-generation sequencing data. *Nucleic Acids Research*, **43**, e22 doi: 10.1093/nar/gku1250; originally posted on <http://www.biorxiv.org/content/early/2014/02/24/002964>
102. **Garud, N. Messer, P.W.**, Buzbas, E., and **Petrov, D.A.** (2015). Evidence that selective sweeps in *Drosophila melanogaster* are primarily soft. *PLoS Genetics*, **11**: e1005004; originally posted at [arXiv:1303.0906](http://arxiv.org/abs/1303.0906)
101. **Zhu, Y.**, Siegal, M.L., Hall, D.W., and **Petrov, D.A.** (2014). Reply to Chen and Zhang: On interpreting genome-wide trends from yeast mutation accumulation data. *Proc. Natl. Acad. Sci.*, **111**: E4063-E4063.
100. **Bergland, A.O**, Behrman, E.L., O'Brien, K.R., Schmidt, P.S., and **Petrov, D.A.** (2014). Genomic evidence of rapid and stable adaptive oscillations over seasonal time scales in *Drosophila*. *PLoS Genetics*, **10**: e1004775. doi:10.1371/journal.pgen.1004775; originally posted on [arXiv:1303.5044](http://arxiv.org/abs/1303.5044)
99. **McCoy, R.C., Taylor, R.W.**, Blauwkamp, T.A., Kelley, J.L., Kertesz, M., Pushkarev, D., **Petrov, D.A., Fiston-Lavier, A.-S.** (2014) Illumina TruSeq synthetic long-reads empower *de novo* assembly and resolve complex, highly-repetitive transposable elements. *PLoS ONE* **9**: e106689; originally posted at <http://www.biorxiv.org/content/early/2014/01/21/001834>
98. **Wilson, B., Petrov, D.A., and Messer, P.W.** (2014). Soft selective sweeps in complex demographic scenarios. *Genetics*, **198**: 669-684; originally posted on <http://www.biorxiv.org/content/early/2014/04/23/004424>
97. **Zhu, Y.**, Siegal, M.L., Hall, D.W., and **Petrov, D.A.** (2014). Precise estimates of mutation rate and spectrum in yeast. *Proc. Natl. Acad. Sci.*, **111**: E2310-E2318
96. **Enard, D., Messer, P.W., and Petrov, D.A.** (2014). Evidence of abundant positive selection in the human genome. *Genome Research*, **24**, 885–895; posted on [arxiv.org:1308.4951](http://arxiv.org/abs/1308.4951)
95. **Lawrie, D.S. and Petrov, D.A.** (2014). Comparative population genomics: power and principles for the inference of functionality. *Trends in Genetics*, **30**, 133-139.

94. **McCoy, R.C., Garud, N.R.,** Kelley, J.K., Boggs, C.L., and **Petrov, D.A.** (2014). Demographic inference accurately times recent bottleneck in an introduced butterfly population. *Mol. Ecol.*, **23**, 136–150.
93. **Petrov, D.A.** (2013). Searching for adaptation in the genome. *Princeton Guide to Evolution*, Princeton University Press, edited by Losos, J.B., ISBN: 9780691149776.
92. **Messer, P.W.,** and **Petrov, D.A.** (2013). Population genomics of rapid adaptation by soft selective sweeps. *Trends in Ecology and Evolution*, **28**, 659-669.
91. **Staubach, F.,** J. F. Baines, S. Kuenzel, E. M. Bik, and **Petrov, D.A.** (2013). Bacterial diversity associated with *Drosophila* in the laboratory and in the natural environment. *PLoS ONE*, **8**, e70749. doi:10.1371/journal.pone.0070749; originally posted at [arXiv:1211.3367](https://arxiv.org/abs/1211.3367).
90. **Lawrie, D. S., Messer, P.W., Hershberg, R.,** and **Petrov, D.A.** (2013). Strong purifying selection at synonymous sites in *D. melanogaster*. *PLoS Genetics*, **9**, e1003527. doi:10.1371/journal.pgen.10003527; originally posted at [arXiv:1301.3325](https://arxiv.org/abs/1301.3325)
89. **Messer, P.W.** (2013). *SLiM*: simulating evolution with selection and linkage. *Genetics*, **194**, 1037-1039; originally posted at [arXiv:1301.3109](https://arxiv.org/abs/1301.3109)
88. **Messer, P.W.** and **Petrov, D.A.** (2013). McDonald-Kreitman test under frequent adaptation: problems and solutions. *Proc. Natl. Acad. Sci. USA*, **110**: 8615-8620; originally posted at [arXiv:1211.0060](https://arxiv.org/abs/1211.0060)
87. Losos, J.B, Arnold, S.J., Bejerano, G., Brodie, E.D., Hibbett, D., Hoekstra, H.E., Mindell, D.P., Monteiro, A., Moritz, C., Orr, H.A., **Petrov, D.A.**, Renner, S.S., Ricklefs, R.E., Soltis, P.S., and Turner, T.L. (2013). Evolutionary biology for the 21<sup>st</sup> century. *PLoS Biology*, **11**: e1001466. doi:10.1371/journal.pbio.1001466.
86. **Feder, A.F., Petrov, D.A,** and **A.O. Bergland.** (2012). LDx: maximum likelihood estimation of linkage disequilibrium from high-throughput pooled resequencing data. *PLoS ONE* **7**: e48588. doi:10.1371/journal.pone.0048588; originally posted at [arXiv:1210.2363](https://arxiv.org/abs/1210.2363)
85. **Hershberg, R.** and **D.A. Petrov.** (2012). On the limitations of using ribosomal genes as a reference for the study of codon usage: a rebuttal. *PLoS ONE*, **7**: e49060. doi:10.1371/journal.pone.0049060.
84. **Staubach, F.,** Lorenc, A., **Messer, P.,** Tang, K., **Petrov, D.A.** and Tautz, D. (2012). Adaptive genome dynamics and introgression of haplotypes in natural populations of the house mouse (*Mus musculus*). *PLoS Genetics*, **8**: e1002891. doi:10.1371/journal.pgen.1002891.
83. **Zhu, Y., Bergland, A.O.,** González, J., and **Petrov, D.A.** (2012). One lane, one population: empirical validation of pooled whole genome population re-sequencing. *PLoS ONE*, **7**, e41901; doi:10.1371/journal.pone.0041901
82. **Messer, P.W.** and Neher, R.A. (2012). Estimating the strength of selective sweeps from deep population diversity data. *Genetics*, **191**, 593-605.
81. González, J. and **D. A. Petrov.** (2012). Evolution of genome content: population dynamics of transposable elements in flies and humans. *Evolutionary Genomics: statistical and computational methods*. Springer-Humana, ed. Maria Anisimova (in press).



80. Rabinowitz, M., Ryan, R., Gemelos, G., Hill, M., Baner, J., Cinnioglu, C., Banjevic, M., Potter, D., **Petrov, D.A.**, and Demko, Z. (2012). Origins and rates of aneuploidy in human blastomeres. *Fertility and Sterility*, **97**, 395-401.
79. **Sellis, D.**, Callahan, B.J., **Petrov, D.A.** and **P.W., Messer**. (2011). Heterozygote advantage as a natural consequence of adaptation in diploids. *Proc. Natl. Acad. Sci., USA*, **108**: 20666-20671.
78. **Lawrie, D.**, **Petrov, D.A.** and **P.W., Messer**. (2011). Faster than neutral evolution of constrained sequences: the complex interplay of mutational biases and weak selection. *Gen. Biol. Evol.*, **3**: 383–395. doi:10.1093/gbe/evr032.
77. **Markova, P.** and **Petrov, D.A.** (2011). The choice of aligner significantly impacts estimates of positive selection in *Drosophila*. *Genome Research*, **21**: 863-874. doi:10.1101/gr.115949.110.
76. **Fiston-Lavier, A.-S.**, **Carrigan, M.**, **Petrov, D.A.**, and **González, J.** (2011). *T-lex*: a tool for fast and accurate assessment of transposable element presence in next-generation sequencing data. *Nucl. Acids Res.*, doi:10.1093/nar/gkq1291
75. **Petrov, D.A.**, **Fiston-Lavier, A.-S.**, **Lipatov, M.**, **Lenkov, K.**, and **González, J.** (2011). Population genomics of transposable elements in *Drosophila melanogaster*. *Mol. Biol. Evol.*, doi: 10.1093/molbev/msq337
74. **Cai, J.**, Borenstein, E. and **D.A. Petrov**. (2010). Broker genes in human disease. *Gen. Biol. and Evol.*, **2**, 815-825; doi: 10.1093/gbe/evq064
73. **Hershberg, R.** and **D.A. Petrov**. (2010). Evidence that mutation is universally biased towards AT in bacteria. *PLoS Genetics*, **6**(9): e1001115; doi:10.1371/journal.pgen.1001115
72. **Cai, J.J.** and **D. A. Petrov**. (2010). Relaxed purifying selection and possibly high rate of adaptation in primate lineage-specific genes. *Gen. Biol. and Evol.*, doi:10.1093/gbe/evq019
71. **Fiston-Lavier\*, A.-S.**, **Singh\*, N.D.**, **Lipatov, M.**, and **D. A. Petrov**. (2010). *Drosophila melanogaster* recombination rate calculator. *Gene*, doi:10.1016/j.gene.2010.04.015. (\*these authors contributed equally).
70. **Karasov, T.\***, **Messer, P.\***, and **D.A. Petrov**. (2010). Evidence that adaptation in *Drosophila* is not limited by mutation at single sites. *PLoS Genetics* **6**: e1000924. doi:10.1371/journal.pgen.1000924). (\*these authors contributed equally).
69. **González, J.**, **Karasov, T.**, **Messer, P.W.**, and **D. A. Petrov**. (2010). Genome-wide patterns of adaptation to temperate environments associated with transposable elements in *Drosophila*. *PLoS Genetics*, **6**: e1000905. doi:10.1371/journal.pgen.1000905
68. Chan, Y.F., Marks, M.E., Jones, F.C., Villarreal, G., Shapiro, M.D., Fisher, S., Southwick, A.M., Absher, D.M., Grimwood, J., Schmutz, J., Myers, R., **Petrov, D.**, Jónsson, B., Schluter, D., Bell, M.B., and D. M. Kingsley. (2010). Adaptive evolution of pelvic reduction in sticklebacks by recurrent deletion of a Pitx1 enhancer. *Science*, **327**, 302-305. doi:10.1126/science.11182213.
67. D. E. Krane, V. Bahn, D. Balding, B. Barlow, H. Cash, B. L. Desportes, P. D'Eustachio, K. Devlin, T. E. Doom, I. Dror, S. Ford, C. Funk, J. Gilder, G. Hampikian, K. Inman, A. Jamieson, P. E. Kent, R. Koppl, I. Kornfield, S. Krinsky, J. Mnookin, L. Mueller, E. Murphy, D. R. Paoletti, **D. A. Petrov**, M. Raymer, D. M. Risinger, A. Roth, N. Rudin, W. Shields, J. A. Siegel, M.

- Slatkin, Y. S. Song, T. Speed, C. Spiegelman, P. Sullivan, A. R. Swienton, T. Tarpey, W. C. Thompson, E. Ungvarsky, and S. Zabell. (2009). Time for DNA disclosure. *Science*, **326**, 1631-1632. DOI: 10.1126/science.326.5960.1631
66. **González, J. and D.A. Petrov.** (2009). MITEs - the ultimate parasites. *Science*, **325**, 1352-53. doi:10.1126/science.1179556.
  65. **Hershberg, R. and D.A. Petrov.** (2009). General rules for the choice of optimal codons. *PLoS Genetics*, **5**: e1000556. doi:10.1371/journal.pgen.1000556
  64. **González, J. and D.A. Petrov.** (2009). Transposable elements and adaptation. *Gene*, doi:10.1016/j.gene.2009.06.008.
  63. **Messer, P.M.** (2009). Measuring rates and patterns of spontaneous mutation from deep and large-scale polymorphism data. *Genetics*, **182**, 1219-1232; doi:10.1534/genetics.109.105692
  62. Sella, G., **Petrov, D.A.**, Przeworski, M., and P. Andolfatto. (2009). Pervasive natural selection in the *Drosophila* genome? *PLoS Genetics*, **5**, e1000495; doi:10.1371/journal.pgen.1000495
  61. Cai, J.J., Borenstein, E., Chen, R., and **D. A. Petrov.** (2009). Similarly strong purifying selection acts on disease genes of all ages. *Gen. Biol. Evol.*, **2009**, 131; doi: 10.1093/gbe/evp013.
  60. **González, J., Macpherson, J.M., and D.A. Petrov.** (2009). A recent adaptive transposable element insertion near highly conserved developmental loci in *Drosophila melanogaster*. *Mol. Biol. Evol.*, **26**, 513-526; doi: 10.1093/molbev/msp107.
  59. Li, V.C, **Davis, J.C., Lenkov, K., Bolival, B., Fuller, M.T., and D. A. Petrov.** (2009). Rapid and correlated evolution of the testis TAFs in *Drosophila* due to low constraint and high rates of positive selection. *Mol. Biol. Evol.*, **26**, 1103-1116.
  58. **González, J.\*, Macpherson, J.M.\*, Messer, P.\*, and D. A. Petrov.** (2009). Inferring the strength of natural selection in *Drosophila* under complex demographic scenarios. *Mol. Biol. Evol.*, **26**, 513-526. (\*these authors contributed equally and are listed alphabetically).
  57. **Cai, J., Macpherson, J.M., Sella, G.\* and D.A. Petrov\*.** (2009). Pervasive hitchhiking at coding and regulatory sites in humans. *PLoS Genetics*, **5**, e1000336. (\*co-senior authors).
  56. **Hershberg, R.\***, Lipatov, M.\*, Small, P.M., Sheffer, H., Niemann, S., Homolka, S., Roach, J.C., Kremer, K., **Petrov, D.A.**, Feldman, M.W., and Gagneux, S. (2008). High functional diversity in *M. tuberculosis* driven by genetic drift and human demography. *PLoS Biology*, **6**(12), e311. (\*these authors contributed equally).
  55. **Hershberg, R. and D.A., Petrov.** Selection on codon bias. (2008). *Annu. Rev. Genet.*, **42**, 14.1-14.13.
  54. **González, J., Lenkov, K., Lipatov, M., Macpherson, J.M., and D.A. Petrov.** (2008). High rate of recent transposable element-induced adaptations in *Drosophila melanogaster*. *PLoS Biology*, **6**, e251.
  53. Dean, J., **Davis, J.C.**, Davis, R.W., and **D.A. Petrov.** (2008). Pervasive redundancy and little new functionality among duplicated genes in yeast. *PLoS Genetics*, **4**, e1000113.

52. **Macpherson, J.M., González, J.,** Witten, D., **Davis, J.C.,** Rosenberg, N., Hirsh, A.E., and **D. A. Petrov.** (2008). Nonadaptive explanations for signatures of partial selective sweeps in *Drosophila*. *Mol. Biol. Evol.*, **25**, 1025-1042.
51. **Macpherson, J.M. \*, Sella, G. \*, Davis, J.C., and D. A. Petrov.** (2007). Genomewide spatial correspondence between nonsynonymous divergence and neutral polymorphism reveals extensive adaptation in *Drosophila*. *Genetics*, **177**, 2083-2099. (\*these authors contributed equally).
50. **Singh, N.D., Macpherson, M.J.,** Jensen, J., and **D.A. Petrov.** (2007). Similar levels of X-linked and autosomal nucleotide variation in African and non-African populations of *Drosophila melanogaster*. *BMC Evol. Biol.*, 2007, **7**, 202.
49. **Hershberg, R.,** Tang, H., and **D.A. Petrov.** (2007). Reduced selection leads to accelerated gene loss in *Shigella*. *Genome Biology*, **8**, R164.
48. Oliver, M.J., **Petrov, D.A.,** Ackerly, D., Falkowski, P.G., and O.M. Schofield. (2007). The mode and tempo of genome size evolution in eukaryotes. *Genome Research*, **17**, 594-601.
47. **Singh, N.D.** and **D. A. Petrov.** (2007). Evolution of sex chromosomes. Genome Dynamics issue "Gene and Protein Evolution", ed. J.N., Volff. (in press).
46. **Singh, N.D.,** Arndt, P.F., and **D. A. Petrov.** (2006). Minor shift in background substitutional patterns in the *Drosophila saltans* and *willistoni* lineages is insufficient to explain GC content of coding sequences. *BMC Biology*, **4**, 37.
45. Boissinot, S. \*, **Davis, J.C.\***, Entezam, A. \*, **Petrov, D.A** and Furano, A.V. (2006). Fitness cost of LINE-1 (L1) activity in humans. *Proc. Natl. Acad. Sci.*, **103**, 9590-9594. (\*these authors contributed equally).
44. **Petrov, D.A.** and J. F. Wendel. (2006). Evolution of eukaryotic genome structure. In "Evolutionary Genetics: Concepts and Case Studies", Oxford University Press, edited by C.W. Fox and J. B. Wolf.
43. **Lipatov, M.,** Arndt, P.F., Hwa, T., and **D.A. Petrov.** (2006). A novel method distinguishes between mutation rates and fixation biases in patterns of single-nucleotide substitution. *J. Mol. Evol.*, **62**, 168-175.
42. **Lipatov, M., Lenkov, K., D.A. Petrov,** and C.Bergman. (2005) Gene-transposable element chimeras in *Drosophila*: bioinformatic and population genetic analyses. *BMC Biology*, **3**: 24.
41. **Davis, J.C.** and **D.A. Petrov.** (2005). Do disparate mechanisms of duplication contribute similar types of genes to the *Saccharomyces cerevisiae* genome? *Trends in Genetics*, **21**, 548-555.
40. **Singh, N.D., Davis, J.C.,** and **D.A. Petrov.** (2005). Increase in codon bias on the X chromosome in eukaryotes. *Genetics*, **171**, 145-155.
39. **Singh, N.D. Davis, J.C.,** and **D.A. Petrov.** (2005). Codon bias and GC content on the X chromosome in *Drosophila* correlate negatively with recombination rate. *J. Mol. Evol.*, **61**, 315-324.

38. **Aminetzach, Y.T., M. J., Macpherson, and D.A. Petrov.** (2005). Pesticide resistance via transposition-mediated adaptive gene truncation in *Drosophila*. *Science*, **309**, 764-767.
37. Arndt, P.F., Hwa, T., and **D. A. Petrov.** (2005). Substantial regional variation in substitution rates in the human genome: importance of GC content, gene density and telomere-specific effects. *J. Mol. Evol.*, **60**, 748-763.
36. **Davis, J.C\***, Brandman, O.\*, and **D. A. Petrov.** (2005). Protein evolution in the context of *Drosophila* development. *J. Mol. Evol.*, **60**, 774-785. (\*these authors contributed equally).
35. Gu, Z., David, L., **Petrov D.A.**, Jones, T., Davis, R.W., Steinmetz, L.W. (2005). Elevated evolutionary rates in the laboratory strain of *Saccharomyces cerevisiae*. *Proc. Natl. Acad. Sci.*, **102**, 1092-1097.
34. **Singh, N.D.**, Arndt, P.F., and **D.A. Petrov.** (2005). Effect of recombination on patterns of substitution in *Drosophila*. *Genetics*, **169**, 709-722.
33. Knight, C. A., Molinari, N., and **D.A. Petrov.** (2005). The large genome constraint hypothesis: evolution, ecology, and phenotype. *Annals of Botany*, **95**, 177-190.
32. Morris, J.R., **Petrov, D.A.**, Lee, A. M., and C.-T. Wu. (2004). Enhancer choice *in cis* and *in trans* in *Drosophila melanogaster*: role of the promoters. *Genetics*, **167**, 1739-1747.
31. **Singh, N.D.** and **D. A. Petrov.** (2004). Dramatic sequence turnover at an intergenic locus in *Drosophila*. *Mol. Biol. Evol.*, **21**, 670-680.
30. **Davis, J. C.** and **D.A. Petrov.** (2004). Preferential duplication of slowly evolving proteins in eukaryotic genomes. *PLOS Biology*, **2**, E55.
29. Arndt, P.F., **Petrov, D.A.**, and Hwa, T. (2003). A distinct shift in the genomic pattern of substitution at the time of mammalian radiation. *Mol. Biol. Evol.*, **20**, 1887-1896.
28. **Bensasson, D.**, Feldman, M. W., and **D. A. Petrov.** (2003). High rates of DNA duplication and mitochondrial DNA insertion in the human genome. *J. Mol. Evol.*, **57**, 343-354.
27. **Petrov, D.A, Aminetzach, Y.T., Davis, J.C., Bensasson, D., & Hirsh, A.E.** (2003). Size matters: non-LTR retrotransposable elements and ectopic recombination in *Drosophila*. *Mol. Biol. Evol.*, **20**, 880-892.
26. Nuzhdin, S.V. and **D. A. Petrov.** (2003) Transposable elements in clonal lineages: lethal hangover from sex. *Biol. J. Linn. Soc.*, **79**, 33-41.
25. Ptak, S. and **D. A. Petrov.** (2002). How intron splicing affects the deletion and insertion profile in *D. melanogaster*. *Genetics*, **162**, 1233-1244.
24. **D. A. Petrov.** (2002). Mutational equilibrium model of genome size evolution. *Theor. Pop. Biol.*, **61**, 531-543.
23. Sakharkar, M.K., Kanguene P., **Petrov, D.A.**, Kolaskar, A.S., & Subbiah, S. A. (2002) Database on "Intron-less/single exonic" genes from eukaryotes (SEGE). *Bioinformatics*, **18**, 1266-1267.

22. **D. A. Petrov.** (2002). Evolution of genome size. *Encyclopedia of Evolution*. Ed. Mark Pagel, Oxford University Press.
21. **D.A. Petrov.** (2002). DNA loss and evolution of genome size in *Drosophila*. *Genetica*, **115**, 81-91.
20. Walbot, V. and **D.A. Petrov.** (2001). Gene galaxies in the maize genome. *Proc. Natl. Acad. Sci. USA*, **98**, 8163-8164.
19. **D. A. Petrov.** (2001). Evolution of genome size: new approaches to an old problem. *Trends in Genetics*, **17**, 23-28.
18. Bensasson, D., **Petrov, D.A.**, Zhang, D.-X., Hartl, D.L., Hewitt, G. (2001). Genomic Gigantism: DNA loss is slow in mountain grasshoppers. *Mol. Biol. Evol.*, **18**, 246-253.
17. **Petrov, D.A.**, Sangster, T.A., Johnston, J. S., Hartl, D.L., & Shaw, K.L. (2000). Evidence for DNA loss as a determinant of genome size. *Science*, **287**, 1060-1062 (see comments *Science* **287**, 985-986).
16. **Petrov, D.A.** & Hartl, D. L. (2000). Pseudogene evolution and natural selection for a compact genome. *J. of Heredity*, **91**, 221-227.
15. Lozovskaya, E.R., Nurminsky, D.I., **Petrov, D.A.**, & Hartl, D.L. (1999). Genome size as a mutation-selection-drift process. *Genes and Genet. Syst.*, **74**, 201-207.
14. **Petrov, D.A.** & Hartl, D. L. (1999). Patterns of nucleotide substitution in *Drosophila* and mammalian genomes. *Proc. Natl. Acad. Sci. USA*, **96**, 1475-1479.
13. **Petrov, D.A.**, Chao, Y.-C., Stephenson, E.C., & Hartl, D. L. (1998). Pseudogene evolution in *Drosophila* suggests a high rate of DNA loss. *Mol. Biol. Evol.*, **15**, 1562-1567.
12. Moriyama, E.N., **Petrov, D.A.**, & Hartl, D.L. (1998). Genome size and intron size in *Drosophila*. *Mol. Biol. Evol.*, **15**, 770-773.
11. **Petrov, D.A.** & Hartl, D. L. (1998). High rate of DNA loss in the *D. melanogaster* and *D. virilis* species groups. *Mol. Biol. Evol.*, **15**, 293-302.
10. **Petrov, D.A.** & Hartl, D. L. (1997). Trash DNA is what gets thrown away: High rate of DNA loss in *Drosophila*. *Gene*, **205**, 279-289.
9. **Petrov, D.A.** (1997). Slow but steady: genome reduction through spontaneous mutation. *The Plant Cell*, **9**, 1900-1901.
8. **Petrov, D.A.**, Lozovskaya, E. R., & Hartl, D. L. (1996). High intrinsic rate of DNA loss in *Drosophila*. *Nature*, **384**, 346-349.
7. Siegal, M. L., **Petrov, D. A.**, & Deaguier, D. (1996). Triple-ligation strategy with advantages over directional cloning. *Biotechniques*, **21**, 614-619.
6. Lozovskaya, E. R., Hartl, D. L., & **Petrov, D. A.** (1995). Genomic regulation of transposable elements in *Drosophila*. *Cur. Opin. in Gen. and Dev.*, **5**, 768-773.

5. **Petrov, D. A.**, Schutzman, J. L., Hartl, D. L., & Lozovskaya, E. R. (1995). Diverse transposable elements are mobilized in hybrid dysgenesis in *Drosophila virilis*. *Proc. Natl. Acad. Sci. USA*, **92**, 8050-8054.
4. Lozovskaya, E. R., **Petrov, D. A.**, & Hartl, D. L. (1993). A combined molecular and cytogenetic approach to genome evolution in *Drosophila* using large-fragment DNA cloning. *Chromosoma*, **102**, 253-266.
3. Krane, D. E., Allen, R. W., Sawyer, S. A., **Petrov, D. A.**, & Hartl, D. L. (1992). Genetic differences at four DNA typing loci in Finnish, Italian, and mixed Caucasian populations. *Proc. Natl. Acad. Sci. USA*, **89**, 10583-10587.
2. Danilevskaya, O. N., **Petrov, D. A.**, Pavlova, M. N., Koga, A., Kurenova, E. V., & Hartl, D. L. (1992). A repetitive DNA element, associated with telomeric sequences in *Drosophila melanogaster*, contains open reading frames. *Chromosoma*, **102**, 32-40.
1. Smoller, D. A., **Petrov, D.A.**, & Hartl, D. L. (1991). Characterization of bacteriophage P1 library containing inserts of *Drosophila* DNA of 75-100 kilobase pairs. *Chromosoma*, **100**, 487-494.