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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, Department of Biology, Stanford University, Stanford, USA
2009-2011	Professor, Department of Biology, Stanford University, Stanford, USA
2005-2009	Associate Professor, Department of Biology, Stanford University, Stanford, USA
2000-2005	Assistant Professor, Department of Biology, Stanford University, Stanford, USA
1998-2000	Research Fellow, Department of Genetics, Harvard Medical School, Cambridge, Massachusetts, USA (advisor Chao-Ting Wu)
1992-1997	Graduate Student, Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, Massachusetts, USA (advisors Richard Lewontin and Daniel Hartl)
1990-1992	Research Assistant, Washington University School of Medicine, Department of Genetics, St. Louis, Missouri, USA
1989-1990	Research Assistant, Institute of Molecular Genetics, Moscow, Russia
1987-1989	M.S. Student, 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 Genetics (1995 and 1997) and Introductory Molecular Biology (1995), Harvard University, Cambridge, Massachusetts
1996	Walter Fitch Prize for Best Student Paper 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.

2016-now	Member, NIH Genetic Variation and Evolution Study Section
2015-now	Director, Program for Conservation Genomics, Stanford University
2013-2016	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

2016-2021	National Institutes of Health R35 (MIRA), "Genomics of rapid adaptation in the lab and in the wild", Principal Investigator
2016-2019	National Institutes of Health R01CA207133-01 (Winslow/Petrov) "A Quantitative multiplexed platform for the pharmacogenomic analysis of lung cancer", Co-Principal Investigator
2015-2018	NSF, Collaborative Research: ABI Innovation: Computational population-genetic analysis for detection of soft selective, Co-Principal Investigator
2015-2016	National Institutes of Health RO1, " High-resolution study of adaptation in haploid and diploid populations of yeast", Principal Investigator (terminated due to acceptance of the R35 MIRA grant; see above)
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 <i>Drosophila</i> 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

Publications from the Petrov lab (lab members are in bold):

138. McCoy, R.C., Newnham, L.J., Ottolini, C., Hoffmann, E., Chatzimeletiou, K. Cornejo, O.E., Zhan, Q., Zaninovic, N., Rosenwaks, Z., **Petrov, D.A.**, Demko, Z.P., Sigurjonsson S., Handyside, A.H. (2018) Tripolar mitosis drives the association between maternal genotypes of *PLK4* and aneuploidy in human preimplantation embryos. *Human Molecular Genetics*, ddy147; <http://www.biorxiv.org/content/early/2017/08/29/182303>
137. **Rogers***, **Z.N.**, **McFarland***, **C.D.**, Winters, I.P., Seoane, J.A., Brady, J.J., Yoon, S., Curtis, C., **Petrov, D.A.** and Winslow, M.M. (2018). The fitness landscape of tumor suppression in lung adenocarcinoma *in vivo*. *Nature Genetics*, **50**, 483–486. (* - contributed equally).
136. **Li, Y.**, **Venkataram, S.**, Agarwala, A., Dunn, B., **Petrov, D.A.***, Sherlock, G.*, Fisher, D.S.* (2018). Hidden complexity of yeast adaptation under "simple" evolutionary conditions. *Current Biology*, **28**: 515-525.
135. Behrman, E.L., Howick, V.M., Kapun, M., **Staubach, F.**, **Bergland, A.O.**, **Petrov, D.A.**, Lazzaro, B.P., Schmidt, P.S. (2018). Rapid seasonal evolution in innate immunity of wild *Drosophila melanogaster*. *Proc. Royal Soc. B.*, **285**: 20172599; <http://www.biorxiv.org/content/early/2017/09/10/186882>.
134. Winters, I.P., Chiou, S.-H., Paulk, N.K., **McFarland, C.D.**, Lalgudi, P.V., Ma, R.K., Lisowski, L., Connolly, A.J., **Petrov, D.A.**, Kay, M.K., and Winslow, M.M. (2017). Multiplexed *in vivo* homology-directed repair and tumor barcoding enables parallel quantification of Kras variant oncogenicity. *Nature Communications*, **8**: 2053.
133. **Ebel, E.R.**, Tellis, N., **Venkataram, S.**, **Petrov, D.A.***, and **Enard, D.*** (2017). Accelerated evolution of mammalian proteins that interact with *Plasmodium* and related parasites. *PLoS Genetics*, **13**: e1007023; originally posted at <http://biorxiv.org/content/early/2016/10/17/081216>.
132. Sherlock, G. and **Petrov, D. A.** (2017). Seeking Goldilocks during evolution of drug resistance. *PLoS Biology*, **15**: e2001872.

131. **Assaf, Z.J., Tilk, S., Park, J., Siegal, M.L., and Petrov, D.A.** (2017) . Deep sequencing of natural and experimental populations of *Drosophila melanogaster* reveals biases in the spectrum of new mutations. *Genome Res.*, 27:1988-2000.
130. **Wittman, M. J., Bergland, A.O., Feldman, M.W., Schmidt, P.S., and D. A. Petrov.** (2017) Segregation lift: A general mechanism for the maintenance of polygenic variation under seasonally fluctuating selection. *Proc. Natl. Acad. Sci.*, **114**: E9932-E9941; <http://biorxiv.org/content/biorxiv/early/2017/03/09/115444.full.pdf>
129. **Rogers, Z.N., McFarland, C.D., Winters, I.P., Naranjo, S., Chuang, C.-H., Petrov, D.A., and Winslow, M.** (2017). Tuba-seq: a quantitative and multiplexed approach to uncover the fitness landscape of tumor suppression in vivo. *Nature Methods*, doi:10.1038/nmeth.4297.
128. **Machado, H.E., Lawrie, D.S., and D. A. Petrov.** Strong selection at the level of codon usage bias: evidence against the Li-Bulmer model. *Genetics*, (submitted); <http://biorxiv.org/content/biorxiv/early/2017/02/09/106476.full.pdf>
127. **Feder, A.F., Kline, C., Polacino, P., Cottrell, M., Kashuba A.D.M., Keele, B.F., Hu, S.-L., Petrov, D.A., Pennings, P.S., and Ambrose, Z.** (2017). High resolution spatio-temporal assessment of simian/human immunodeficiency virus (SHIV) evolution reveals a highly dynamic process within the host. *PLOS Pathogens*, **13**: e1006358; <http://biorxiv.org/content/early/2017/01/04/097980>
124. **Wilson, B.A, Pennings, P.S. and Petrov, D.A.** (2017). Soft selective sweeps in evolutionary rescue. *Genetics*, **205**: 1573-1586; <http://biorxiv.org/content/early/2016/05/12/052993>
123. Rajpurohit, S., Hanus, R., Vrkoslav, V., Behrman, E.L., **Bergland, A.O., Petrov, D.A.**, Cvačka, J., Schmidt, P.S. Adaptive dynamics of cuticular hydrocarbons in *Drosophila*. (2017). *J. Evol. Biol.*, **30**: 66-80
122. **Zhu, Y., Sherlock, G. and Petrov, D.A.** Extremely rare polymorphisms recapitulate AT-biased mutational spectrum from the mutation-accumulation experiments in yeast. (2017). *PLoS Genetics*, **13**: e10064.
121. **Venkataram, S.***, Dunn, B.***, Li, Y., Argawala, A., Chang, J., Ebel, E., Geiler-Samerotte, K., Herrisant, L., Blundell, J., Levy, S.F., Fisher, D., Sherlock, G.***, and **Petrov, D.A.***. (2016). A comprehensive genotype-fitness map for adaptive mutations in yeast. *Cell*, **167**, 1–12; (* contributed equally).
120. Lou, D., Kim, E., Meyerson, N., Pancholi, N., Mohni, K., **Enard, D., Petrov, D.**, Weller, S., Weitzman, M., and S. Sawyer. (2016). An intrinsically disordered region of Nbs1 constitutes a species-specific barrier to Herpes Simplex Virus 1 in primates. *Cell Host Microbe*, **20**, 178–188.
119. **Zhu, Y., Sherlock, G.* and Petrov, D. A.*** (2016). Population structure and origins of clinical *Saccharomyces cerevisiae* strains. *G3*, **6**, 2421-2434. <http://biorxiv.org/content/early/2016/03/21/044958>; (* contributed equally).
118. **Sellis, D.**, Kvitek, D.J., Dunn, B., Schwartz, K., Sherlock, G., and **Petrov, D.A.** (2016). Empirical evidence for heterozygote advantage in adapting diploid populations of *Saccharomyces cerevisiae*. *Genetics*, **203**, 1401-1413; <http://biorxiv.org/content/early/2015/12/02/033563>

117. **Enard, D., Cai, L.,** Gwennap, C., and **Petrov, D.A.** (2016). Viruses are a dominant driver of protein adaptation in mammals. *ELife*, **5**, e12469.
116. **Garud, N. and Petrov, D.A.** (2016). Elevation of linkage disequilibrium above neutral expectations in ancestral and derived populations of *Drosophila melanogaster*. *Genetics*, **203**, 863–880.
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*, **5**, e10670; (* contributed equally).
114. **Wilson, B., Garud, N.R., Feder, A.F., Assaf, Z.J., and Pennings, P.S.** (2016). 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. Ecol.*, **25**: 723–740. doi:10.1111/mec.13446
112. **Bergland, A.O., Tobler, R.,** González, J., Schmidt, P., and **Petrov, D.A.** (2016). Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in *Drosophila melanogaster*. *Mol. Ecol.*, **25**: 1157–117 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; (* 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](https://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](https://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). Genome wide signals of pervasive positive selection in human evolution. *Genome Research*, **24**, 885–895; posted on [arxiv.org:1308.4951](https://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 21st 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
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