

Dmitri A. Petrov

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Academic Position.

Michelle and Kevin Douglas Professor, 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.

2014-2020	Associate Chair, Department of Biology, Stanford University, Stanford, USA
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.

2007-2017	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.

2019-now	Chair, NIH Genetic Variation and Evolution Study Section
2016-now	Director, Program for Conservation Genomics, Center for Computational, Evolutionary, and Human Genomics
2016-2019	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

2019-2021	American Lung Association, Lung Cancer Discovery Award, Principal Investigator
2019-2021	Tobacco Related Disease Research Program (TRDRP), High Impact Pilot Research Award, Principal Investigator
2019-2024	National Institutes of Health R01CA234349 (Winslow/Petrov) Unraveling mechanisms of tumor suppression in lung cancer, Co-Principal

	Investigator
2018-2022	National Institutes of Health R01CA231253 (PQ4) (Winslow/Petrov) “Quantitative and multiplexed analysis of gene function in cancer in vivo”, Co-Principal Investigator
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 (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-Principle 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 Drosophila", 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

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

On Biorxiv/In review:

166. Garud, N., Messer, P.W., **Petrov, D.A.** (2020). Detection of hard and soft sweeps from *Drosophila melanogaster* genomic data. *PLoS Genetics* (in revision); <https://www.biorxiv.org/content/10.1101/2020.06.20.163261v1>; doi: <https://doi.org/10.1101/2020.06.20.163261>
165. **Kinsler, G., Geiler-Samerotte, K., Petrov, D.A.** (2020). A genotype-phenotype-fitness map reveals local modularity and global pleiotropy of adaptation. *Elife* in review. <https://www.biorxiv.org/content/10.1101/2020.06.25.172197v1>; doi: <https://doi.org/10.1101/2020.06.25.172197>
164. Harpak, A., **Garud, N.**, Rosenberg, N.A., **Petrov, D.A.**, Combs, N., **Pennings, P.S.**, Munshi-South, J. (2020). Genetic adaptation in New York City rats. *Nature Communications* (in review).

<https://www.biorxiv.org/content/10.1101/2020.02.07.938969v1>;
doi: <https://doi.org/10.1101/2020.02.07.938969>

163. Genetic determinants of EGFR-driven lung cancer growth and therapeutic response in vivo. Foggetti, G., **Li, C.**, Cai, H., Hellyer, J., Ayeni, D., Hastings, K., Choi, J., Wurtz, A., Andrejka, L., Maghini, D., Rashleigh, N., Levy, S., Homer, R., Gettinger, S., Diehn, M., Wakelee, H., **Petrov, D.A.**, Winslow, M.M., Politi, K.; *Nature Cancer*, in review;
<https://www.biorxiv.org/content/10.1101/2020.04.13.036921v1.abstract>
162. A functional taxonomy of tumour suppression in lung cancer. Cai, H.* , Chew, S.-K.* , **Li, C.***, Tsai, M., Andrejka, L., Murray, C., Hughes, N., **Shuldiner, E.**, Tang, E., Hung, K., Chen, L., Lee, C., Yousefi, M., **McFarland, C.M.**, Lin, W.-Y., Kunder, C., Cong, L., **Petrov, D.A.#**, Swanton, C.#, and Winslow, M.M.# (* - contributed equally; # corresponding authors);
161. Quantitative *in vivo* analyses reveal a complex pharmacogenomic landscape in lung adenocarcinoma. **Li, C.***, Lin, W.-Y.* , Rizvi, H., Cai, H., **McFarland, C.M.**, **Rogers, Z.**, Yousefi, M., Winters, I.P., Rudin, C.M., **Petrov, D.A.#**, and M.M., Winslow#. (* - contributed equally; # corresponding authors); *Nature Cancer*, in review;
<https://www.biorxiv.org/content/10.1101/2020.01.28.923912v1>
160. **Tilk, S.**, Curtis, C., **Petrov, D.A.**, **McFarland, C.D.** Most cancers carry a substantial deleterious load due to Hill-Robertson interference. *Nature*, in review.
<https://www.biorxiv.org/content/10.1101/764340v2>
159. **Armstrong, E.E.**, Khan, A., **Taylor, R.W.**, Gouy, A., Greenbaum, G., Thiery, A., Kang, J.T.L., Redondo, S.A., Prost, S., Barsh, G., Kaelin, C., Phalke, S., Chugani, A., Gilbert, M., Miquelle, D., Zachariah, A., Borthakur, U., Reddy, A., Louis, E., Ryder, O., Jhala, Y., **Petrov, D.A.**, Excoffier, L., Hadly, E.A., and Ramakrishnan, U. Recent evolutionary history of tigers highlights contrasting roles of genetic drift and selection. *MBE* (in review);
<https://www.biorxiv.org/content/10.1101/696146v1.abstract>
158. Kolodny, O., McLaren, M.R., Greenbaum, G., Ramakrishnan, U., Feldman, M.W., **Petrov, D.A.**, **Taylor, R.W.** Reconsidering the management paradigm of fragmented populations. <https://www.biorxiv.org/content/10.1101/649129v1>
157. **Machado***, **H.E.**, **Bergland***, **A.O.**, **Taylor, R.**, **Tilk, S.**, Behrman, E., Dyer, K., Fabian, D.K, Flatt, T., Gonzalez, J., Karasov, T.L., Kozeretska, I., Lazzaro B.P., Merritt, T.J.S., O'Brien, K., Rajpurohit, S., Roy, P.R., Schaeffer, S.W., Schmidt, P.# and **D. A. Petrov#**. Broad geographic sampling reveals predictable and pervasive seasonal adaptation in *Drosophila*. *Elife*, (in review); (* and # - contributed equally);
<https://www.biorxiv.org/content/early/2018/06/03/337543>
156. **Venkataram, S.**, **Sellis, D.**, and **Petrov, D.A.** Backward predictability of evolution in the diploid Fisher's geometric model. *Theor. Pop. Biol.*, (in revision); <http://biorxiv.org/content/early/2013/12/02/001016>

Published/in press after peer review:

155. **Feder, A.F.**, Pennings, P.S, and **Petrov, D.A.** (2018). The clarifying role of time series data in the population genetics of HIV. *PLoS Genetics* (in press); <https://www.biorxiv.org/content/early/2018/12/29/495275>; doi: <https://doi.org/10.1101/495275>
154. **Enard, D.** and **Petrov, D.A.** (2020). Ancient epidemics through the lens of recent adaptation in human genomes. *Phil. Trans. B*, (in press); <https://www.biorxiv.org/content/10.1101/2020.03.18.997346v1>
153. **Armstrong, E.E.**, Taylor, R.W., Miller, D.E., Kaelin, C., Barsh, G., Hadly E.A., **Petrov, D.A.** (2020). Long live the king: chromosome-level assembly of the lion (*Panthera leo*) using linked-read, HiC, and long read data. *BMC Biology*, **18**: 3; <http://biorxiv.org/cgi/content/short/705483v1>
152. **Tilk, S.**, **Bergland, A.O.**, **Goodman, A.**, Schmidt, P., **Petrov, D.A.**, **Greenblum, S.** (2019). High accuracy haplotype-derived allele frequencies from ultra-low coverage pool-seq samples. *G3*, **9**, 4159-4168; <https://www.biorxiv.org/content/early/2018/01/11/244004>
151. **Machado, H.E.**, Lawrie, D.S., and **D. A. Petrov.** (2019). Strong selection at the level of codon usage bias: evidence against the Li-Bulmer model. *Genetics*, **214**, 511–528; <http://biorxiv.org/content/biorxiv/early/2017/02/09/106476.full.pdf>
150. Rudman, S.M., **Greenblum, S.**, Hughes, R.C., Rajpurohit, S., Kiratli, O., Lowder, D.B., Lemmon, S.G, **Petrov, D.A.**, Chaston, J.M., Schmidt, P. (2019). Microbiome composition shapes rapid genomic adaptation of *Drosophila melanogaster*. *Proc. Natl. Acad. of Sci.*, **116**: 20035-20032; <https://www.biorxiv.org/content/10.1101/632257v1>
149. **Li, Y.**, **Petrov, D.A*** and Sherlock, G.*. (2019). Single nucleotide mapping of the locally accessible trait space in yeast reveals pareto fronts that constrain initial adaptation, *Nature Ecology and Evolution*, **3**: 1539–1551; <https://www.biorxiv.org/content/10.1101/593947v1> (* - contributed equally).
148. **Feder, A.F.**, Pennings, P.S, Hermisson, J. and **Petrov, D.A.** (2019). Evolutionary dynamics in structured populations under strong population genetic forces. *G3*, **9**, 3395-3407 in press; <https://www.biorxiv.org/content/10.1101/579854v1>
147. Uricchio, L.H., **Petrov, D.A.**, and **Enard, D.** (2019). Exploiting selection at linked sites to infer the rate and strength of adaptation. *Nature Ecology and Evolution*, **3**, 977; originally posted on <https://www.biorxiv.org/content/early/2018/09/26/427633>
146. Natesh, M.#, **Taylor, R.W#**, Truelove, N., Hadly, E.A., Palumbi, S., **Petrov, D.A*** and Ramakrishnan, U.* (2019). Empowering conservation science and practice with efficient and economical genotyping from poor quality samples. *Methods in Ecology and Evolution*, (in press); (* and #- contributed equally); <https://www.biorxiv.org/content/early/2018/06/20/349472>
145. Rech, G.E., Bogaerts-Marquez, M., Barron, M.G, Merenciano, M., Villanueva-Canas, J.L., Horvath, V., Fiston-Lavier, A.-F., Luyten, I., **Venkataram, S.**, Quesneville, H., **Petrov, D.A.***, and Gonzalez, J.* (2019). Stress response, behavior, and development are shaped by transposable element-induced mutations in *Drosophila*. *PLoS Genetics*, **15**, e1007900; <https://www.biorxiv.org/content/early/2018/07/30/380618> (* - contributed equally).

144. **Feder, A.F.**, Pennings, P.S., and **Petrov, D.A.** (2018). The clarifying role of time series data in the population genetics of HIV. <https://www.biorxiv.org/content/early/2018/12/29/495275>
143. Combs, P.A., Krupp, J.J., Khosla, N.M., Bua, D., **Petrov, D.A.**, Levine, J.D, Fraser, H.B. (2018). Tissue-specific cis-regulatory divergence implicates *eloF* in inhibiting interspecies mating in *Drosophila*. *Current Biology*, **28**, 1-7.
142. **Armstrong, E.E., Taylor, R.W., Prost, S.**, Blinston, P., van der Meer, E., Madzikanda, H., Mufute, O., Mandisodza, R., Stuelpnagel, J., Sillero-Zubiri, C., and **Petrov, D.A.** (2018) Cost-effective assembly of the African wild dog genome using linked long reads. *GIGAScience*, giy124; originally posted at <https://www.biorxiv.org/content/biorxiv/early/2017/09/27/195180.full.pdf>
141. **Enard, D.** and **Petrov, D.A.** (2018) RNA viruses drove adaptive introgressions between Neanderthals and modern humans. *Cell*, **175**, 360-371; <http://biorxiv.org/content/early/2017/03/24/120477>
140. Theys, K., **Feder, A.F.**, Gelbart, M., Hart, I.M., Stern, A., Pennings, P.S. (2018) Within-patient mutation frequencies reveal fitness costs of CpG dinucleotides and drastic amino acid changes in HIV. *PLoS Genetics* **14**: e1007420
139. Rajpurohit, S., Gefen, E., **Bergland, A.O., Petrov, D.A.**, Gibbs, A.G., and Schmidt, P.S. Spatiotemporal patterns of desiccation tolerance in natural populations of *Drosophila melanogaster*. (2018). *Mol. Ecol.* **27**: 3525-3540; <http://biorxiv.org/content/early/2016/10/07/079616>
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>
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