JEFFREY M. GOOD
CURRICULUM VITAE

ADDRESS: University of Montana
Division of Biological Sciences
The University of Montana
Missoula MT 59812
Phone: 406-243-5771
Fax: 406-243-4184
E-mail: jeffrey.good@umontana.edu
Lab website: www.thegoodlab.org

EDUCATION

2002-2007	Ph.D., Ecology & Evol. Biology, Univ. Arizona, (Advisor: Michael Nachman).
1999-2002	M.S., Biology, Univ. Idaho, (Advisor: Jack Sullivan).
1995-1999	B.S., Zoology (*Magna cum Laude*), Univ. Idaho.

ACADEMIC APPOINTMENTS

2018-2019	Visiting Fellow, Centre for Biodiversity Analysis, Australian National University
2018-2019	Distinguished Visiting Researcher, CSIRO, Australia
2016-present	Associate Professor, Division of Biological Sciences, University of Montana.
2015-present	Director, Philip L. Wright Zoological Museum, University of Montana.
2013-present	Director, Genomics Core Facility, University of Montana.
2010-2016	Assistant Professor, Division of Biological Sciences, University of Montana.
2008-2010	NSF International Postdoctoral Fellow (Mentor: Svante Pääbo), Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany.

EMPHASIS OF RESEARCH: Ecological genomics, speciation, population genetics, adaptation, sex chromosome evolution, evolution of mammalian reproduction.

TEACHING EXPERIENCE

2020-2021	Instructor (every fall), Genomics (~35 UG/G students), Univ. of Montana
2012-2019	co-Instructor (every fall), Genomics (~35 UG/G students), Univ. of Montana
2013,15,16	co-Instructor, Population Genomic Data Analysis Short Course, Univ. of Montana
2011,13,15	Instructor, Adv. Topics in Genetics & Evolution (G), Univ. of Montana
2013,16,18,20	Instructor, Foundations in Genetics & Evolution (G), Univ. of Montana
2011-2017	Instructor (alt. spring), Genetics & Evolution (UG, ~225 students), Univ. of Montana
2010	Instructor, Evolutionary & Ecological Genomics (seminar), Univ. of Montana

RESEARCH GRANTS, CONTRACTS, AND OTHER SUPPORT

2021	Surveillance genome sequencing to detect SARS-CoV-2 virus variants in Montana. National Institutes of Health (Project Leader, P20 GM103546-10 CoBRE Supplement), $704,474. June 2021 – July 31, 2022.
2021	COVID-19 Testing and Surveillance, Montana Department of Public Health and Human Services, (contract 21-07-4-41-011-0), up to $2,250,000. October 2020 – December 31, 2021.

2020 CC* Networking Infrastructure: Deploying a Science DMZ to Advance Research at the Univ. Montana. National Science Foundation. (co-PI, CC-2018112), $307,645. June, 2020 – May 31, 2022.

2019 BEE: Mechanisms and scope for adaptive rescue in polymorphic populations. National Science Foundation (co-PI, DEB-1907022), $894,817. August 01, 2018 – July 31, 2021.

2019 CC* Compute: Improved Computing for Advanced Research and Education (ICARE). National Science Foundation (co-PI, OAC-1925267), $394,895. July 31, 2019– June 30, 2020.

2018 The evolution of genomic imprinting. National Institutes of Health (PI, R01-HD094787), $1,481,840. April 01, 2018 – December 31, 2022.

2018 Collaborative Research: Rates of lineage, phenotypic, and genomic diversification in replicated radiations of murine rodents. National Science Foundation (PI, DEB-1754096), $335,008. May 01, 2018 – April 30, 2022. 2021 supplement: $85,699 (total $420,707).

2017 RII Track-2 FEC: Using Natural Variation to Educate, Innovate, and Lead (UNVEIL): A collaborative research network to advance genome-to-phenome connections in the wild. National Science Foundation EPSCoR (co-PI, OIA-1736249), $4,000,000. August 01, 2017 – July 31, 2021.

2017 Doctoral Dissertation Improvement Grant, Matthew Jones (mentor). National Science Foundation, $17,952.

2016 Securing the collection of University of Montana's Zoological Museum. National Science Foundation (PI, DBI-1561748), $499,865. September, 2016 – August, 2020.

2014 Doctoral Dissertation Improvement Grant, Thomas Brekke (mentor), National Science Foundation. $18,396.

2013 A Multi-User Genomics Core and Training Facility. M. J. Murdock Charitable Trust (PI). $704,000, January, 2014 – December, 2015.

2013 CC-NIE Integration: Advancing research through network improvements (ARNI). National Science Foundation (co-PI, ACI-1341009). $483,979, October, 2013 – September, 2015.

2012 Meiotic sex chromosome inactivation and the developmental basis of hybrid male sterility in house mice. National Institutes of Health (PI, R01HD073439), $1,476,444.

2012 Evolutionary and functional genetics of male reproduction using wild mice as a model system. National Institutes of Health (R01GM098536, co-Investigator), $573,976 (UM subcontract).

2012 The genetic and developmental basis of hybrid male sterility during the early stages of speciation in house mice. National Science Foundation (DEB-1146470), $599,998 – relinquished due to overlap with NIH award (R01-HD073439).

2010 Small Research Grant, University of Montana ($4,500)

2006 Doctoral Dissertation Improvement Grant, National Science Foundation ($11,722)

ACADEMIC HONORS & FELLOWSHIPS

2019 Editor's Choice Award for Outstanding Population Genetics Article published in Genetics Awarded for *"The evolution of polymorphic hybrid incompatibles in house mice"*

2018 Visiting Fellow Award, Australian National University, $10,000 AUD.

2018 Distinguished Visiting Researcher Award, CSIRO, Australia, $15,000 AUD.

2010 AAAS Newcomb Cleveland Prize (annual award to authors of the "Most Outstanding

Paper Published in Science Magazine")
2008 International Research Fellowship Award, National Science Foundation
2007 Max Planck Society Postdoctoral Fellowship
2006 Robert W. Hoshaw Memorial Award for Graduate Excellence, Ecology and Evolutionary Biology, University of Arizona
2006 Galileo Circle Scholarship, College of Science, University of Arizona
2002 NSF IGERT Genomics Fellowship, University of Arizona (3 year award)
2001 Award for Graduate Excellence, University of Idaho Alumni Association

PUBLICATIONS

Overview: >13,800 citations, h-index of 36, i10-index of 62 (Google Scholar, 10/2021).

In preparation:

Ferreira MS, Thurman TJ, Jones MR, Farelo L, Kumar AV, Mortimer SME, Demboski JR, Mills LS, Alves PC, Melo-Ferreira J, Good JM. The evolution of seasonal camouflage in white-tailed jackrabbits in response to past and future climates. *In revision.*

Beckman EJ, Martins F, Suzuki TA, Bi K, Keeble S, Good JM, Chavez A, Nachman MW. The genomic basis of high-elevation adaptation in wild house mice (*Mus musculus domesticus*) from South America. *In review.*

Hunnicutt KE, Good JM, Larson EL. Unraveling patterns of disrupted gene expression in a complex tissue. *In review..*

Herrera, ND, Sarver, BAJ, Callahan CM, Bell KC, Sullivan J, Demboski JR, Good JM. The complex evolutionary history of a cryptic chipmunk species. *In prep.*

Kopania EEK, Larson EL, Callahan CM, Keeble SM, Good JM. Molecular evolution across mouse spermatogenesis. *In review.*

Published:

72. Roycroft EJ, Achmadi A, Callahan CM, Esselstyn JA, Good JM, Moussalli A, Rowe KC. Molecular evolution of ecological specialisation: genomic insights from the adaptive radiation of murine rodents. ***Genome Biology and Evolution***, evab103, https://doi.org/10.1093/gbe/evab103.
71. Brekke* TD, Moore* EC, Campbell-Staton SC, Callahan CM, Cheviron ZA, Good JM. (2021) X chromosome-dependent disruption of placental regulatory networks in hybrid dwarf hamsters. ***Genetics***, iyab043, https://doi.org/10.1093/genetics/iyab043. Preprint: **bioRxiv** doi: 10.1101/2020.09.15.298893 *Equal contribution.
70. Sarver BAJ, Sneddon D, Herrera ND, Hunter SS, Settles ML, Kronenberg Z, Demboski JR, Good JM, Sullivan J. (2021) Diversification, introgression, and rampant cytonuclear discordance in central and southern rocky mountains chipmunks (Sciuridae: *Tamias*). ***Systematic Biology***, syaa085, https://doi.org/10.1093/sysbio/syaa08.
69. Ferreira MS, Jones MR, Callahan CM, Farelo L, Tolesa Z, Suchentrunk F, Mills LS, Alves PC, Good JM, Melo-Ferreira J. (2021) The legacy of recurrent introgression during the radiation of hares. ***Systematic Biology***, syaa088, doi.org/10.1093/sysbio/syaa088. Preprint: **bioRxiv** doi: 10.1101/2020.06.19.160283.

68. Jones MR, Mills LS, Jensen JD, Good JM (2020) Convergent evolution of seasonal camouflage to reduced snow cover across the snowshoe hare range. ***Evolution***, 74:2033-2045. doi.org/10.1111/evo.13976. PMID: 32282064
67. Jones MR, Mills LS, Jensen JD, Good JM. (2020) The origin and spread of locally adaptive seasonal camouflage in snowshoe hares. ***The American Naturalist***, 196:316-332. doi:10.1086/710022. ****Recipient of 2020 American Naturalist Student Paper Award.***
66. Ferreira M, Alves P, Callahan C, Giska I, Farelo L, Hannes J, Mills LS, Hackländer K, Good JM, Melo-Ferreira J. (2020) Transcriptomic regulation of seasonal coat color change in hares. ***Ecology and Evolution***, 10:1180-1192. doi:10.1002/ece3.5956
65. Marques JP, Seixas FA, Farelo L, Callahan CM, Good JM, Montgomery WI, Reid N, Alves PC, Boursot P, Melo-Ferreira J. (2020) An annotated draft genome of the mountain hare (*Lepus timidus*). ***Genome Biology and Evolution***, 12:3656-3662. doi:10.1093/gbe/evz273
64. Harris RB, Irwin K, Jones MR, Laurent S, Barrett RDH, Nachman MW, Good JM, Linnen CR, Jensen JD, Pfeifer SP. (2019) The population genetics of crypsis in vertebrates: recent insights from mice, hares, and lizards. ***Heredity***, doi:10.1038/s41437-019-0257-4.
63. Bi K, Linderoth T, Singhal S, Vanderpool D, Patton JL, Nielsen R, Moritz C, Good JM. (2019) Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. ***PLoS Genetics***, 15(5): e1008119; doi: 10.1371/journal.pgen.1008119.
62. Skinner BM, Bacon J, Rathje CC, Larson EL, Kopania EEK, Good JM, Affara NA, Ellis PJI. (2019) Automated nuclear cartography reveals conserved sperm chromosome territory localisation across 2 million years of mouse evolution. ***Genes***, 10; doi: 10.3390/genes10020109.
61. Skinner BM, Rathje CC, Bacon J, Johnson EEP, Larson EL, Kopania EEK, Good JM, Yousafzai G, Affara NA, Ellis PJI. (2019) A high-throughput method for unbiased quantitation and categorisation of nuclear morphology. ***Biology of Reproduction***, 100:1250-1260; doi: 10.1093/biolre/ioz013.
60. Phifer-Rixey M, Bi K, Ferris KG, Sheehan MJ, Lin D, Mack KL, Keeble SM, Suzuki TA, Good JM, Nachman MW (2018) The genomic basis of environmental adaptation in house mice. ***PLoS Genetics***, 14:e1007672.
59. Jones MR, Mills LS, Alves PC, Callahan CM, Alves JM, Lafferty DJR, Jiggins FM, Jensen JD, Melo-Ferreira J, Good JM (2018) Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. ***Science***, 360:1355-1358.
58. Larson EL, Kopania E, Good JM (2018) Spermatogenesis and the evolution of mammalian sex chromosomes. ***Trends in Genetics***, 34(9):722-732. doi: 10.1016/j.tig.2018.06.003.
57. Bracewell RR, Vanderpool D, Good* JM, Six* DL (2018) Cascading speciation among mutualists and antagonists in a tree-beetle-fungi interaction. ***Proceedings of the Royal Society B***, 285:20180694; doi: 10.1098/rspb.2018.0694. *Shared senior authorship.
56. Larson EL, Vanderpool D, Sarver BAJ, Callahan C, Keeble S, Provencio LP, Kessler MD, Stewart V, Nordquist E, Dean MD, Good JM (2018) The evolution of polymorphic hybrid incompatibilities in house mice. ***Genetics***, 209:845-859; doi: 10.1534/genetics.118.300840 ****Editor's Choice Award for outstanding population genetics article in 2018***
55. Mills LS, Bragina E, Kumar A, Zimova M, Lafferty D, Feltner J, Davis BW, Hacklander K, Alves P, Good JM, Melo-Ferreira J, Dietz A, Abramov AV, Lopatina N, Fay K (2018) Winter color

polymorphisms identify global hot spots for evolutionary rescue from climate change. ***Science***, 359:1033-1036.

54. Zimova M, Hacklaender K, Good JM, Melo-Ferreira J, Alves P, Mills LS (2018) Function and underlying mechanisms of seasonal colour moulting in mammals and birds: What keeps them changing in a warming world? ***Biological Reviews***, doi:10.1111/brv.12405.
53. Marques JP, Ferreira M, Farelo L, Callahan C, Hackländer K, Jenny H, Montgomery W, Reid N, Good JM, Alves P, Melo-Ferreira J (2017) Mountain hare transcriptome and diagnostic markers as resources to monitor hybridization with European hares. ***Scientific Data***, 4:170178. doi: 10.1038/sdata.2017.178.
52. Bracewell RR, Bentz BJ, Sullivan BT, Good JM (2017) Rapid neo-sex chromosome evolution and incipient speciation in a major forest pest. ***Nature Communications***, 8:1593, doi:10.1038/s41467-017-01761-4.
51. Chang P, Kopania E, Keeble S, Sarver BAJ, Larson EL, Orth A, Belkhir K, Boursot P, Bonhomme F, Good JM, Dean MD (2017) Whole exome sequencing of wild-derived inbred strains of mice improves power to link phenotype and genotype. ***Mammalian Genome***, 28:416-425. [Featured cover image]
50. Ferreira MS, Alves PC, Callahan CM, Marques JP, Mills LS, Good* JM, Melo-Ferreira* J (2017) The transcriptional landscape of seasonal coat color molt in the snowshoe hare. ***Molecular Ecology,*** 26:4173-4185. *Shared senior authorship.
49. Sarver BAJ, Keeble S, Cosart T, Tucker PK, Dean MD, Good JM (2017) Phylogenomic insights into mouse evolution using a pseudoreference approach. ***Genome Biology and Evolution,*** 9: 726-739, doi: 10.1093/gbe/evx034.
48. Marques JP, Farelo L, Vilela J, Alves PC, Good JM, Boursot P, Melo-Ferreira J (2017) Range expansion underlies historical introgressive hybridization in the Iberian hare. ***Scientific Reports***, 7:40788.
47. Larson EL, Vanderpool D, Keeble S, Dean MD, Good JM (2017) The composite regulatory basis of the large X-effect in mouse speciation. ***Molecular Biology and Evolution***, 34:282-295.
46. Sarver BAJ, Demboski JR, Good JM, Forshee N, Hunter SS, Sullivan J (2017) Comparative phylogenomic assessment of mitochondrial introgression among several species of chipmunks (*Tamias*). ***Genome Biology and Evolution***, 9:7-19, doi: 10.1093/gbe/evw254.
45. Brekke TD, Henry LA, Good JM (2016) Genomic imprinting, disrupted placental expression, and speciation. ***Evolution***, 70:2690-2703.
44. Larson EL, Vanderpool D, Keeble S, Zhou M, Sarver BAJ, Smith AD, Dean MD, Good JM (2016) Contrasting levels of molecular evolution on the mouse X chromosome. ***Genetics***, 203:1841-1857. – August, 2016, Issue Highlight.
43. Abbott RJ, Barton NH, Good JM (2016) Genomics of hybridization and its evolutionary consequences. ***Molecular Ecology***, 25:2325-2332.
42. Andrews KR, Good JM, Miller MR, Luikart G, Hohenlowe PA (2016) Harnessing the power of RADseq for ecological and evolutionary genomics. ***Nature Reviews Genetics***, 17:81-92.
41. Jones MR, Good JM (2015) Targeted capture in evolutionary and ecological genomics. ***Molecular Ecology,*** *doi:* 10.1111/mec.13304.
40. Good JM, Vanderpool D, Keeble S, Bi K (2015) Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. ***Evolution,*** 69:1961-1972.

– Featured cover article.

39. Mangels R, Young B, Keeble S, Ardekani R, Meslin C, Ferreira Z, Clark NL, Good JM, Dean MD (2015) Genetic and phenotypic influences on copulatory plug survival in mice. ***Heredity*,** doi: 10.1038/hdy.2015.50.
38. Crino OL, Prather CT, Driscoll SC, Good JM, Bruener CW (2014) Developmental stress increases reproductive success in male zebra finches. ***Proceedings of the Royal Society B***, 281:20141266.
37. Carneiro M, Rubin CJ, Di Palma,F, Albert FW, Alföldi J, Barrio AM, Pielberg G, Rafati N, Sayyab S, Turner-Maier J, Younis S, Afonso S, Aken B, Alves JM, Barrell D, Bolet G, Boucher S, Burbano HA Campos R, Chang JL, Duranthon V, Fontanesi L, Garreau H, Heiman D, Johnson J, Mage RG, Peng Z, Queney G, Rogel-Gaillard C, Ruffier M, Searle S, Villafuerte R, Xiong A, Young S, Forsberg-Nilsson K, Good JM, Lander ES, Ferrand N, Lindblad-Toh K, Andersson L (2014) Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. ***Science***, 345:1074-1079.
36. Brekke TD, Good JM (2014) Parent-of-origin growth effects and the evolution of hybrid inviability in dwarf hamsters. ***Evolution***, 68:3134-3148.
35. Sullivan J, Demboski JR, Bell KC, Hird S, Sarver B, Reid N, Good JM (2014) Divergence-with-gene-flow within the recent chipmunk radiation (*Tamias*). ***Heredity***, doi:10.1038/hdy.2014.27.
34. Carneiro M, Albert FW, Afonso S, Pereira RJ, Burbano H, Campos R, Melo-Ferreira J, Blanco-Aguiar JA, Villafuerte R, Nachman MW, Good JM, Ferrand N (2014) The genomic architecture of population divergence between subspecies of the European rabbit. ***PLoS Genetics***, 10(8):e1003519.
33. Bi K, Linderoth T, Vanderpool D, Good JM, Nielsen R, Moritz C (2013) Unlocking the vault: next-generation museum population genomics. ***Molecular Ecology***, 24:6018-6032.
32. Good JM, Wiebe V, Albert FW, Burbano HA, Kircher M, Green RE, Halbwax M, André C, Atencia R, Fischer A, Pääbo S (2013) Comparative population genomics of the ejaculate in humans and the great apes. ***Molecular Biology and Evolution***, 30:964–976.
31. Campbell P, Good JM, Nachman MD (2013) Meiotic sex chromosome inactivation is disrupted in sterile hybrid male house mice. ***Genetics***, 193:819-828.
30. Good JM (2012) The conflict within and the escalating war between the sex chromosomes. ***PLoS Genetics***, 8:e1002955.
29. Bi K, Vanderpool D, Singhal S, Linderoth T, Moritz C, Good JM (2012) Transcriptome-based exon capture enables highly cost-effective comparative genomic data collection at moderate evolutionary scales. ***BMC Genomics***, 13:403.
28. Campbell P, Good JM, Dean MD, Tucker PK, Nachman MD (2012) The contribution of the Y chromosome to hybrid male sterility in house mice. ***Genetics***, 191:1271-1281.
27. Prüfer K, Munch K, Hellmann I, Akagi K, Miller JR, Walenz B, Koren S, Sutton G, Kodira C, Winer R, Knight JR, Mullikin JC, Meader SJ, Ponting CP, Lunter G, Higashino S, Hobolth A, Dutheil J, Karakoç E, Alkan C, Sajjadian S, Catacchio CR, Ventura M, Marques-Bonet T, Eichler EE, André C, Atencia R, Mugisha L, Junhold J, Patterson N, Siebauer M, Good JM, Fischer A, Ptak SE, Lachmann M, Symer DE, Mailund T, Schierup MK, Andrés AM, Kelso J, Pääbo S (2012) The bonobo genome compared with the chimpanzee and human genomes. ***Nature***, 486:527-531.

26. Good JM (2011) Reduced representation methods for sub-genomic enrichment and next-generation sequencing. *In*: **Molecular Methods in Evolutionary Genetics** (V Orgogozo and MV Rockman, eds.). Humana Press.
25. Crisci JL, Wong A, Good JM, Jensen JD (2011) On characterizing adaptive events unique to modern humans. ***Genome Biology and Evolution***, 3:791-798.
24. Fischer A, Prüfer K, Good JM, Halbwax M, Wiebe V, André C, Atencia R, Mugisha L, Ptak SE, Pääbo S (2011) Bonobos fall within the genomic variation of chimpanzees. ***PLoS ONE*** 6:e21605.
23. Good JM, Vanderpool D, Smith KL, Nachman MW (2011) Extraordinary sequence divergence at *Tsga8*, an X-linked gene involved in mouse spermiogenesis. ***Molecular Biology and Evolution***, 28:1675-1686.
22. Albert FW, Hodges E, Jensen JD, Besnier F, Xuan Z, Rooks M, Bhattacharjee A, Brizuela L, Good JM, Green RE, Burbano HA, Plyusnina IZ, Trut L, Andersson L, Schöneberg T, Carlborg Ö, Hannon GJ, Pääbo S, (2011) Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. ***Heredity***, 107:205-214.
21. Reich D, Green RE, Kircher M, Krause J, Patterson N, Durand EY, Viola B, Briggs AW, Stenzel U, Johnson PLF, Maricic M, Good JM, Marques-Bonet T, Alkan C, Fu Q, Mallick S, Li H, Meyer M, Eichler EE, Stoneking M, Richards M, Talamo S, Shunkov MV, Derevianko AP, Hublin JJ, Kelso J, Slatkin M, Pääbo S (2010) Genetic history of an archaic hominin group from Denisova Cave in Siberia. ***Nature***, 468:1053-1060.
20. Good JM, Giger T, Dean MD, Nachman MW (2010) Widespread over-expression of the X chromosome in sterile F1 mice. ***PLoS Genetics***, 6(9):e1001148.
19. Green RE, Krause J, Briggs AW, Maricic M, Stenzel U, Kircher M, Patterson N, Li L, Zhai W, Fritz MH-Y, Hansen N, Durand EY, Malaspinas A-S, Jensen JJ, Marques-Bonet T, Alkan C, Prüfer K, Meyer M, Burbano HA, Good JM, Schultz R, Aximu-Petri A, Butthof A, Höber B, Höffner B, Siegemund M, Weihmann A, Nusbaum C, Lander ES, Russ C, Novod N, Affourtit J, Egholm M, Verna C, Rudan P, Brajkovic D, Kucan Z, Guic I, Doronichev VB, Golovanova LV, Lalueza-Fox C, Rasilla M, Fortea J, Rosas A, Schimtz RW, Johnson PLF, Eichler EE, Falush D, Birney E, Mullikan JC, Slatkin M, Nielsen R, Kelso J, Lachmann M, Reich D, Pääbo S (2010) A draft sequence of the Neandertal genome. ***Science***, 328:710-722.
18. Burbano HA, Hodges E, Green RE, Briggs AW, Krause J, Meyer M, Good JM, Maricic M, Johnson PLF, Xuan Z, Rooks M, Bhattacharjee A, Brizuela L, Albert FW, de la Rasilla M, Fortea J, Rosas A, Lachmann M, Hannon GJ, Pääbo S (2010) Targeted investigation of the Neandertal genome by array-based sequence capture. ***Science***, 328:723-725.
17. Krause J, Fu Q, Good JM, Viola B, Shunkov MV, Derevianko AP, Pääbo S (2010) The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. ***Nature***, 464:894-897.
16. Briggs AW, Good JM, Green RE, Krause J, Maricic T, Stenzel U, Pääbo S (2009) Primer Extension Capture: targeted sequence retrieval from heavily degraded DNA sources. ***Journal of Visualized Experiments***, 31, doi:10.3791/1573.
15. Briggs AW, Good JM, Green RE, Krause J, Maricic T, Stenzel U, Lalueza-Fox C, Rudan P, Brajkovic D, Kucan Z, Gusic I, Schmitz R, Doronichev VB, Golovanova LV, Rasilla M, Fortea

J, Rosas A, Pääbo S (2009) Targeted retrieval and analysis of five Neandertal mtDNA genomes. ***Science***, 325:318-321.

14. Good JM, Dean MD, Nachman MW (2008) A complex genetic basis to X-linked hybrid male sterility between two species of house mice. ***Genetics***, 179:2213-2228.
13. Green RE, Malaspinas A-S, Krause J, Briggs AW, Johnson PLF, Uhler C, Meyer M, Good JM, Maricic T, Stenzel U, Prufer K, Siebauer M, Burbano HA, Ronan M, Rothberg JM, Egholm M, Rudan P, Brajkovic D, Kucan Z, Gusic I, Wikstrom M, Laakkonen L, Kelso J, Slatkin M, Pääbo S (2008) A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. ***Cell***, 134:416-426.
12. Good JM, Handel MA, Nachman MW (2008) Asymmetry and polymorphism of hybrid male sterility during the early stages of speciation in house mice. ***Evolution***, 62: 50-65.
11. Good JM, Hird S, Reid N, Demboski JR, Steppan SJ, Martin-Nims TR, Sullivan J (2008) Ancient hybridization and mitochondrial capture between two species of chipmunks. ***Molecular Ecology***, 17:1313-1327.
10. Dean MD, Good JM, Nachman MW (2008) Adaptive evolution of proteins secreted during sperm maturation: an analysis of the mouse epididymal transcriptome. ***Molecular Biology and Evolution***, 25:383-392.
9. Good JM, Hayden CA, Wheeler TJ (2006) Adaptive protein evolution and regulatory divergence in *Drosophila*. ***Molecular Biology and Evolution***, 23:1101-1103.
8. Saunders MA, Good JM, Lawrence EC, Ferrel RE, Li W-H, Nachman MW (2006) Human adaptive evolution at *Myostatin*, a regulator of muscle growth. ***American Journal of Human Genetics***, 79:1089-1097.
7. Good JM, Ross CL, Markow TA (2006) Multiple paternity in wild-caught *Drosophila mojavensis*. ***Molecular Ecology***, 15:2253-2260.
6. Carstens BC, Brunsfeld SJ, Demboski JR, Good JM, Sullivan J (2005) Investigating the evolutionary history of the Pacific Northwest mesic forest ecosystem: hypothesis testing within a comparative phylogeography framework. ***Evolution***, 59:1639-1652.
5. Good JM, Nachman MW (2005) Rates of protein evolution are positively correlated with timing of expression during mouse spermatogenesis. ***Molecular Biology and Evolution*** 22:1044-1052.
4. Cutter AD, Good JM, Pappas CT, Saunders MA, Starrett DM, Wheeler T (2005) Transposable element orientation bias in the *Drosophila melanogaster* genome. ***Journal of Molecular Evolution***, 61:1-19.
3. Good JM, Demboski JR, Nagorsen D, Sullivan J (2003) Phylogeography and introgressive hybridization: chipmunks (genus *Tamias*) in the northern Rocky Mountains. ***Evolution***, 57:1900-1916.
2. Cutter AD, Payseur BA, Salcedo T, Estes AM, Good JM, Wood E, Hartl T, Maughan H, Strempel J, Wang B, Bryan AC, Dellos M (2003) Molecular correlates of genes exhibiting RNAi phenotypes in *Caenorhabditis elegans*. ***Genome Research***, 13:2651-2657.
1. Good JM, Sullivan J (2001) Phylogeography of the red-tailed chipmunk (*Tamias ruficaudus*), a northern Rocky Mountain endemic. ***Molecular Ecology***, 10:2683-2696.

SYMPOSIA, CONTRIBUTED PAPERS, & INVITED SEMINARS (SELECT, 2010-PRESENT)

2021: University of Memphis; University of Virginia; University of California, Berkeley; University of Utah (student invited speaker). **2020:** Texas A&M; Princeton; University of California, Davis. **2019:** Arizona State University; University of Pennsylvania; Gordon Research Conference on Ecol & Evol Genomics; Monash University; University of Tasmania; Australian National University; National Research Collections Australia, CSIRO; CSIRO Hobart; The Australian Museum, Sydney; Museums Victoria. **2018:** University of Nebraska, Lincoln **2017:** Genomics and Collections Symposium, Australian National University & National Research Collections Australia, CSIRO [Invited Symposium], Biogenomics 2017, Smithsonian National Museum of Natural History [Invited Symposium]. **2016**: The Allied Genetics Conference; University of California, Santa Cruz; University of Porto, Porto, Portugal; Uppsala University, Uppsala, Sweden; Texas Tech University. **2015**: Cornell University; Louisiana State University; University of Southern California; University of California, Los Angeles; Genomes 10K, Santa Cruz, California [Invited Symposium]; American Genetics Association, President's Symposium, Bainbridge Island, Washington [Invited Symposium]. **2014:** Inland Northwest Genomics Symposium, University of Idaho [Invited Symposium]; University of Wyoming; University of New Mexico [3 presentations]; École polytechnique fédérale de Lausanne, Lausanne, Switzerland. **2013:** University of Utah. **2012:** 1ST Joint Congress on Evolutionary Biology, Ottawa, Canada; Trends in Biodiversity and Evolution Meeting, Porto, Portugal [Plenary Lecture]; Ohio State University [2 presentations]. **2011**: 13th Congress of the European Society for Evolutionary Biology, Tuebingen, Germany; Evolution Annual Meetings, University of Oklahoma, Norman, OK [Invited Symposium]; University of Idaho; University of Nebraska, Lincoln; Indiana University; University of California, Berkeley. **2010**: Evolution Annual Meetings, Portland, OR; Complex Trait Community, 9th Annual Meeting, Chicago, IL; University of Montana (Wildlife Biology).

SOCIETY MEMBERSHIPS

Society for Molecular Biology and Evolution
Society for the Study of Evolution
Genetics Society of America
American Society of Mammalogists
American Society of Naturalists
American Genetics Association

PROFESSIONAL SERVICE

Editorial:	*PLoS Genetics* (Guest Associate Editor), *Evolution* (Associate Editor, January, 2013-2015), *Molecular Ecology* (Guest co-Editor for special issue on "Genomics and Hybridization", 2016).
Panel Service:	*American Genetics Association Council* (2020-2023), *National Science Foundation* (Fall 2012; Fall 2020), *National Institutes of Health* (GGG, 2019; GVE, Fall 2014, 2016)
Peer Review (select):	*Nature, Science, Proceedings of the National Academy of Sciences, eLife, Genetics, Evolution, Molecular Ecology, Evolution, Systematic Biology, Molecular Biology and Evolution, PLoS Genetics, Primates, Animal Conservation, Proceedings of the Royal Society*

	(B), Genome Research, Current Biology, BioTechniques, Systematic Biology, Axious, Genetics, Murdock Charitable Trust (ad hoc), National Science Foundation (ad hoc), Oxford Bibliographies, Journal of Evolutionary Biology, Czech Science Foundation (ad hoc), G3: Genes, Genomes, Genetics.
2018	Symposium organizer, UNVEIL - Genomics of Adaptation 2018 Meeting. University of Montana
2017	Symposium organizer, Society for Molecular Biology and Evolution 2017 Meeting
2011	Symposium organizer, 13th Congress of the European Society for Evolutionary Biology. Tuebingen, Germany.
2010	Symposium organizer, Society for Molecular Biology and Evolution 2010 Meeting

OTHER SYNERGISTIC ACTIVITIES

Development of Genomics Research Infrastructure — I have put considerable effort into developing research infrastructure at UM, which in turn has played a critical role in my teaching and outreach activities. I established and direct the UM Genomics Core facility through an instrumentation grant from the Murdock Charitable trust ($704,000, PI). I have also worked with others to greatly expanded research computing resources at UM (three NSF infrastructure grants, $1,186,519 total, co-PI). Over the last year I helped lead the UMGC's efforts to provide high throughput COVID-19 testing and variant of concern surveillance for the University and state of Montana, supported by a standing MT state contract (MT DPHHS, up to $2,250,000) and an NIH grant ($704,474, project leader).

Development of Biological Collections Infrastructure — I am the faculty director of the UM Philip L. Wright Zoological Museum director (UMZM), an outstanding regional collection (~22,000 bird and mammal specimens spanning >100yrs) that was in a state of near complete decay when I started in 2010. I have worked to revitalize this critical resource for science and outreach, including inventorying and transitioning all records to the publicly accessible databases, designing and moving to new archive space and remodeling existing teaching lab space with the support of an NSF infrastructure grant ($499,865, PI) and private philanthropy. These new facilities will enable several decades of future growth of the research and teaching collection.

Genomics Training Infrastructure — My lab is a leader in using genomic approaches and museum collections to answer diverse questions in ecology and evolution. At UM, these efforts have helped establish a large research and training network focused on the science and application of genomic studies in natural populations. The UNVEIL (Using Natural Variation to Educate, Innovate, and Lead) network is supported by a four year National Science foundation grant ($4,000,000; co-PI) to promote genome-to-phenome science in collaboration with the University of Nebraska (https://www.unveilnetwork.org). In addition of student and postdoctoral training, the UNVEIL network has allowed us to develop dedicated workshops and mini-symposia on genomics, which have advanced training in ecological genomics.