

Michael Lynch

**Center for Mechanisms of Evolution, Biodesign Institute
Arizona State University
Tempe, AZ 85287**

Phone: 480-965-0868
Email: mlynch11@asu.edu

Birth: 6 December 1951, Auburn, New York

Undergraduate education: St. Bonaventure University, Biology - B.S., 1973.

Graduate education: University of Minnesota, Ecology and Behavioral Biology - Ph.D., 1977 (advisor: J. Shapiro).

Areas of Interest and Research: The integration of molecular and cellular biology, genetics, and evolution; population and quantitative genetics; molecular, genomic, and phenotypic evolution.

Select Professional Activities and Service:

Director, Biodesign Center for Mechanisms of Evolution, Arizona State University, 2017 – present.
Professor, School of Life Sciences, Arizona State University, 2017 – present.

Class of 1954 Professor, 2011 – 2017.
Distinguished Professor, Indiana University, 2005 – 2017.
Professor; Biology, Indiana University, 2001 – 2004.
Adjunct Professor, Computer Science, Indiana University, 2014 – 2017.
Adjunct Professor, Physics, Indiana University, 2015 – 2017.

Professor; Biology, University of Oregon, 1989 – 2001.
Director, Ecology and Evolution Program, Univ. of Oregon, 1989 – 1993, 1996 – 2000.

Asst., Assoc., Full Professor; Ecology, Ethology, and Evolution; University of Illinois, 1977 – 1989.

Co-director, NSF IGERT Training Grant in Evolution, Development, and Genomics, 1999 – 2004.
Director, NSF Genetic Mechanisms of Evolution Training Grant, 1990 – 2000.

President, Genetics Society of America, 2013.
President, Society for Molecular Biology and Evolution, 2009.
President, American Genetic Association, 2007.
President, Society for the Study of Evolution, 2000.
Chair-elect, Section on Biological Sciences American Association for the Advancement of Science, 2017-2020.
Vice-president, Genetics Society of America, 2012.
Vice-president, Society for the Study of Evolution, 1994.
Council Member, Society for the Study of Evolution, 1991 – 1993.
Council Member, Society of Molecular Biology and Evolution, 2005 – 2007.
Genetics Society of America committees over multiple years, various including Public Policy, Nominations, Financial.

Board of Scientific Counselors, National Center for Biotechnology Information (NCBI), 2008 – 2012.
NCBI Needs-assessment Panel, 2011.

Associate Editor, Genome Biology and Evolution, 2008 – present.

Associate Editor, Genetics, 1992 – 1996.
 Associate Editor, Conservation Genetics, 1999 – present.
 Associate Editor, Molecular Ecology, 1991 – 1997.
 Associate Editor, Evolution, 1988 – 1990.

Member, NRC/NAS Ecosystems Panel, 1997.
 Member, NRC/NAS Committee on Scientific Issues in the Endangered Species Act, 1993 – 1995.

Organizing Committee, Genetics Society of America Centennial Meeting, 2016.
 Co-chair (with R. Phillips and S. Sazer), Kavli Institute for Theoretical Physics Program on Evolutionary Cell Biology, 2015.
 Co-chair (with H. Goodson and A. Turkewitz), NSF Workshop on Evolutionary Cell Biology, 2012.
 External Reviewer, Barcelona Center for Genomic Regulation, 2012.
 Member, Organizing Committee, Society of Molecular Biology and Evolution Meeting in Kyoto, 2011.
 External Advisory Board, Cornell Center for Comparative and Population Genomics, 2010 -- .
 Advisory Board for Extended Workshop, Evolutionary Perspectives on Mechanisms of Cellular Organization, Kavli Institute for Theoretical Physics, 2010.
 Member, Organizing Committee, FASEB Ciliate Molecular Genetics Meeting, 2009.
 NESCent Working Group on Human Evolution, 2007 – 2009.
 Member, Oversight Committee for Sequencing of the *Daphnia pulex* Genome, 2003 – present.
 Member, Genetics Advisory Team, Oregon Department of Fish and Wildlife, 1990 – 2001.
 Organizer, Symposium on Quantitative Genetics of Natural Populations, Raleigh, NC, 1987.
 Instructor, Itasca Field Station, University of Minnesota, Ecological Genetics course, 1987.
 Co-founder, Midwest Population Biology Conference (with J. Emlen); Chair, 1979, 1983 meetings.

Panel Member, NIH MIRA Study Section, 2015.
 Chair, NIH Genetic Variation and Evolution Study Section, 2009 – 2010.
 Panel Member, NIH Genetic Variation and Evolution Study Section, 2004 – present.
 Panel Member, NIH Genome Study Section, 1999.
 Panel Member, NIH Quantitative Genetics Study Section, 1998.
 Ad hoc Panel Member, NIH Genetics Study Section, 1990, 1997 – 2002.

Panel Member, NSF Molecular and Cellular Evolution Panel, 2016.
 Panel Member, NSF Eukaryotic Genetics / Genes and Genomes Panel, 2001, 2003.
 Panel Member, NSF Advancing Theory in Biology, 2010.
 Panel Member, NSF Frontiers for Integrative Research, 2003.
 Panel Member, NSF IGERT Program, 2000, 2001.
 Advisory Panel Member, NSF Division of Environmental Biology, 1999.
 Panel Member, NSF Population Biology Panel, 1987 – 1988, 1998.
 Panel Member, NSF Research Training Group Program, BBS, 1990.
 Panel Member, NSF Program on Conservation Biology, 1990.

Panel Member, Data Driven Discovery, Gordon and Betty Moore Foundation, 2014.

Professional Societies:

American Association for the Advancement of Science
 Genetics Society of America
 Society for Molecular Biology and Evolution
 Society for the Study of Evolution

Recognition:

Member, US National Academy of Sciences – 2009.

Fellow, American Academy of Arts and Sciences – 2002.
 Fellow, American Association for the Advancement of Science – 1998.
 Fellow, Max Planck Institut für Limnologie, Plön, West Germany – 1982, 1984, 1985.
 Visiting Simon's Scholar, Kavli Institute of Theoretical Physics – 2013.
 Beckman Fellow, Center for Advanced Study, Univ. of Illinois – 1981.
 List of Excellent Instructors, Univ. of Illinois – Limnology, 1978, 1982; Population Biology, 1988.
 Univ. of Illinois Faculty Summer Fellowship, 1978.

Named, keynote, and plenary lectures (since 1995):

1995, Kellogg Biological Station, Eminent Ecologist Lectures.
 1997, Plenary Speaker, Genetics Society of Australia, Perth.
 1998, Keynote Speaker, Zoological Society of London, Origin and Nature of Biodiversity.
 1998, Distinguished Evolutionary Biologist, University of Texas.
 2000, Presidential Address, Society for the Study of Evolution, Bloomington, Indiana.
 2001, Distinguished Speaker Series, Beyond the Human Genome Project, Harvey Mudd College.
 2002, Plenary Speaker, European Population Genetics Symposium, University of Leeds.
 2002, Plenary Speaker, Beckman Symposium on Sequenced Genomes, City of Hope Hospital.
 2003, Plenary Speaker, Stat Day Meeting of Indiana Biostatisticians.
 2003, Plenary Speaker, International Congress of Genetics, Melbourne.
 2005, Lead Speaker, Darwin's Birthday Celebration, University College, London.
 2005, Plenary Speaker, European Society for Evolutionary Biology, Krakow, Poland.
 2006, Keynote Speaker, Bioinformatics 2006, Aarhus, Denmark.
 2007, Keynote Speaker, Symposium on Integration of Genotype and Phenotype, Florida State University.
 2007, Plenary Speaker, Society for Molecular Biology and Evolution, Dalhousie University.
 2007, Keynote Speaker, Gordon Conference on Structural, Functional, and Evolutionary Genomics.
 2008, Keynote Speaker, Keystone Symposium on Complex Traits: Biologic and Therapeutic Insights, Sante Fe.
 2008, Keynote Speaker, Cold Spring Harbor Biology of Genomes Symposium.
 2009, Plenary Speaker, Evolution of Sex and Recombination Symposium, University of Iowa.
 2009, Plenary Speaker, European Cytogenetics Conference.
 2009, Nei Presidential Lecture, Society for Molecular Biology and Evolution.
 2010, Cockerham Lecture, North Carolina State University.
 2010, Casanova Memorial Lecture, University of Valencia.
 2010, Louis Thaler Lecture, University of Montpellier, France.
 2011, Plenary Speaker, International Plant and Animal Genome Conference, San Diego.
 2011, Pfizer Lecture, Iowa State University.
 2011, Plenary Speaker, Penn State Plant Biology Symposium.
 2011, Keynote Speaker, Program in Functional Genomics / Systems Biology, University of Zurich.
 2011, Keynote Speaker, Symposium in Honor of Dr. Masatoshi Nei, Pennsylvania State University.
 2012, Plenary Speaker, Popgen Meeting, University of Nottingham.
 2012, Keynote Speaker, Great Lakes Bioinformatics Conference, University of Michigan.
 2012, Plenary Speaker, Queensland Molecular Biology Meeting, New Zealand.
 2013, Keynote Speaker, Mechanisms of Protein Evolution, University of Colorado Medical School.
 2013, G. E. Hutchinson Distinguished Speaker, Yale University.
 2013, Keynote Speaker, Genome Instability, Mutation, and Human Diseases, St. Petersburg, Russia.
 2013, Keynote Speaker, International Plant Genome Conference, Amsterdam.
 2014, Haldane Lecture, John Innes Centre, UK.
 2014, Plenary Lecture, International Society for the Studies of the Origins of Life, Nara, Japan.
 2014, Keynote Speaker, Symposium in Honor of Tomoko Ohta, National Institute of Genetics, Japan.
 2014, Keynote Speaker, International Cladoceran Symposium, Prague, Czech Republic.
 2014, Keynote Speaker, Computational Biology & Innovation Symposium, Dublin, Ireland.
 2015, Nobel Forum, Karolinska Institute, Stockholm.
 2015, Dynasty Lectures, Moscow State University, St. Petersburg State University, Russia.
 2016, Keynote Lecture, Evolutionary Systems Biology, Hinxton, UK.

2016, Keynote Speaker, Multigenic Bases of Microevolutionary Processes, Guangzhou, China.
 2016, Keynote Speaker, Tribute to James Crow, University of Wisconsin.
 2017, Keynote Speaker, German Society for Protozoology, Dresden.
 2017, Dean's Distinguished Lecture, Temple University.
 2017, Keynote Speaker, Genome Dynamics *Paramecium* and Evolution, Nohfelden, Germany.
 2017, Keynote Speaker, 50th Anniversary, Dept. of Ecology and Evolutionary Biology, University of Minnesota.
 2018, Keynote Speaker, Münster Graduate School of Evolution, Germany.
 2018, Keynote Speaker, 2018 Arthropod Genomics Symposium, Urbana, IL.
 2018, Keynote Speaker, Environmental Mutagenesis and Genomics Society, San Antonio, TX.

Current Lab Research Emphases:

- **The 5000 *Daphnia pulex* genome project.** The goal is to sequence the genomes of 96 genotypes from each of 50 populations in this model organism for evolutionary and ecological genomics. In addition to developing a resource for the research community, the results are being used to test ideas on the origin of introns, the genetic consequences of loss of recombination, and the genetic consequences of long-term population bottlenecks. This project is also now extending to similar analyses with other species.
- **The genome biology of the *Paramecium aurelia* complex.** The goal is to determine the causes and consequences of the differential retention of duplicate genes following whole-genome duplication in this cryptic species complex. In addition, we are attempting to resolve the regulatory vocabulary in this genus, as well studying the evolution of vesicle transport pathways.
- **Development of methods for the analysis of population-genomic data.** We are developing a series of maximum-likelihood methods for ascertaining the population-genetic features using high-throughput genome sequence data. These methods, which take into account uncertainties due to low coverage and error-prone sequences, are being made available to the general public in the form of user-friendly software.
- **Experimental molecular evolution in microbial populations.** We are pursuing highly replicated experiments (~500 lines) with multiple bacterial species grown at different population sizes, mutation rates, and nutritional status in an effort to reveal general principles regarding the mechanisms of evolution. The work involves periodic population-level, whole-genome sequencing, transcriptomics, and proteomics
- **Mutation rates.** We are utilizing a mutation-accumulation strategy, followed by whole-genome sequencing, to measure the rate and complete molecular spectrum of mutations across the Tree of Life. This work is focused on testing the drift-barrier hypothesis. Parallel work is being done on the transcription-error rate and on the rate of somatic mutation, and will soon be extended to the issue of translation error rates.
- In various ways, we are attempting to establish a formal field of **evolutionary cell biology**, with a goal of integrating ideas from cell biology, evolutionary biology, biophysics, and biochemistry. Specific projects underway include the estimation of the bioenergetic costs of genes and various cellular parts, and the evolution of multimeric protein structure.

Current Support:

US Department of Army, MURI award W911NF-14-1-0411, 2014-2019, Innovation in Prokaryotic Evolution (co-PI, with Pat Foster, Jay Lennon, Jake McKinlay, and Allan Drummond).

US Department of Army, MURI award W911NF-09-1-0444, 2010-2018, Bacterial Genome Instability (PI, with Pat Foster, Haixu Tang, and Steven Finkel).

National Institutes of Health, R01-GM101672, 2013-2017, Population Genomics of *Daphnia pulex*.

National Institutes of Health, R35-GM122566-01, 2017-2022, Causes and Population-genetic Consequences of Molecular Variation.

National Institutes of Aging, R01 AG054641-01, 2017-2022, Understanding the Role of Transcription Errors in Aging and Disease. (coPI with Marc Vermulst).

National Science Foundation, DEB-1257806, 2013-2016, Methods for the Analysis of Population-genomic Data.

National Science Foundation, MCB-1518060, 2015-2018, Evolution of the Transcriptional Vocabulary: the *Paramecium aurelia* complex.

Publications:

Lynch, M. 1974. The phytoplankton of the Allegheny Reservoir from May 1972 to September 1973. *Science Studies* (St. Bonaventure University) 30: 5-29.

Shapiro, J., V. Lamarra, and Lynch, M. 1975. Biomanipulation: An ecosystem approach to lake restoration, pp. 85-96. In P. L. Brezonik and J. L. Fox (eds.) *Water Quality Management Through Biological Control*. Proc. Symp. Univ. Florida.

Lynch, M. 1977. Zooplankton competition and plankton community structure. *Limnology and Oceanography* 22: 775-777.

Lynch, M. 1977. Fitness and optimal body size in zooplankton populations. *Ecology* 58: 763-774.

Lynch, M. 1978. Complex interactions between natural coexploiters - *Daphnia* and *Ceriodaphnia*. *Ecology* 59: 552-564.

Lynch, M. 1979. Predation, competition, and zooplankton community structure: An experimental study. *Limnology and Oceanography* 24: 253-272.

Lynch, M. 1980. The evolution of cladoceran life histories. *Quarterly Review of Biology* 55: 23-42.

Lynch, M. 1980. Predation, enrichment, and the evolution of cladoceran life histories: A theoretical approach. In W. C. Kerfoot (ed.) *The Evolution and Ecology of Zooplankton Communities*. American Society of Limnology and Oceanography Special Symposium No. 3: 367-376.

Lynch, M. 1980. *Aphanizomenon* blooms: Alternate control and cultivation by *Daphnia pulex*. In W.C. Kerfoot (ed.) *The Evolution and Ecology of Zooplankton Communities*. American Society of Limnology and Oceanography Special Symposium No. 3: 299-304.

Lynch, M., and J. Shapiro. 1981. Predation, enrichment, and phytoplankton community structure. *Limnology and Oceanography* 26: 86-102.

Lynch, M., B. Monson, M. Sandheinrich, and L. Weider. 1981. Patterns of size-specific mortality in zooplankton populations. *Verh. Internat. Verein. Limnol.* 21: 363-368.

Lynch, M. 1982. How well does the Edmondson-Paloheimo model approximate instantaneous birth rates? *Ecology* 63: 12-18.

Lynch, M. 1983. Ecological genetics of *Daphnia pulex*. *Evolution* 37: 358-374.

- Weis, A., P. Price, and M. Lynch. 1983. Selection for clutch size in the gall-maker *Asteromyia carbonifera*. *Ecology* 64: 688-695.
- Lynch, M. 1983. Estimation of size-specific mortality rates in zooplankton populations by periodic sampling. *Limnology and Oceanography* 28: 533-545.
- Lynch, M., and R. Ennis. 1983. Resource availability, maternal effects, and longevity. *Exper. Gerontology* 18: 147-165.
- Lynch, M., and W. Gabriel. 1983. Phenotypic evolution and parthenogenesis. *American Naturalist* 122: 745-764.
- Lynch, M. 1984. The genetic structure of a cyclical parthenogen. *Evolution* 38: 186-203.
- Lynch, M. 1984. The limits to life history evolution in *Daphnia*. *Evolution* 38: 465-482.
- Lynch, M. 1984. Destabilizing hybridization, general-purpose genotypes, and geographic parthenogenesis. *Quarterly Review of Biology* 59: 257-290.
- Lynch, M. 1984. The selective value of alleles underlying polygenic traits. *Genetics* 108: 1021-1033.
- Lynch, M. 1985. Elements of a mechanistic theory for the life history consequences of food limitation. *Ergeb. Limnol.* 21: 351-362.
- Lynch, M. 1985. Speciation in the Cladocera. *Verh. Internat. Verein. Limnol.* 22: 3116-3123.
- Lynch, M. 1985. Spontaneous mutations for life history characters in an obligate parthenogen. *Evolution* 39: 804-818.
- Lynch, M., L. Weider, and W. Lampert. 1986. Measurement of the carbon balance in *Daphnia*. *Limnology and Oceanography* 31: 17-33.
- Lynch, M. 1986. Random drift, uniform selection, and the degree of population differentiation. *Evolution* 40: 640-643.
- Lynch, M., and W. G. Hill. 1986. Phenotypic evolution by neutral mutation. *Evolution* 40: 915-935.
- Lynch, M. 1987. The consequences of fluctuating selection for isozyme polymorphisms in *Daphnia*. *Genetics* 115: 657-669.
- Lynch, M., and W. Gabriel. 1987. Environmental tolerance. *American Naturalist* 129: 283-303.
- Lynch, M., and W. Gabriel. 1987. Evolution of breadth of biochemical adaptation, pp. 67-83. In P. Calow (ed.) *Evolutionary Physiological Ecology*. Cambridge Univ. Press, Cambridge, UK.
- Kerfoot, W. C., and M. Lynch. 1987. Branchiopod communities: associations with planktivorous fish in space and time, pp. 367-378. In W.C. Kerfoot and A. Sih (eds.) *Predation*. Univ. Press New England, Hanover, NH.
- Lynch, M. 1987. The evolution of intrafamilial interactions. *Proc. Natl. Acad. Sci. USA* 84: 8507-8511.
- Lynch, M. 1988. The rate of polygenic mutation. *Genetical Research* 51: 137-148.
- Lynch, M. 1988. The divergence of neutral quantitative characters among partially isolated populations. *Evolution* 42: 455-466.

- Lynch, M. 1988. Path analysis of ontogenetic data, pp. 29-46. In L. Persson and B. Ebenman (eds.) *The Dynamics of Size-structured Populations*. Springer-Verlag.
- Lynch, M., and S. J. Arnold. 1988. Measurement of selection on size and growth, pp. 47-59 In L. Persson and B. Ebenman (eds.) *The Dynamics of Size-structured Populations*. Springer-Verlag.
- Lynch, M. 1988. Estimation of relatedness by DNA fingerprinting. *Mol. Biol. Evol.* 5: 584-599.
- Lynch, M. 1988. Design and analysis of experiments on random drift and inbreeding. *Genetics* 120: 791-807.
- Lynch, M. 1989. Phylogenetic hypotheses under the assumption of neutral quantitative genetic variation. *Evolution* 43: 1-17.
- Lynch, M., K. Spitze, and T. Crease. 1989. The distribution of life history variation in *Daphnia pulex*. *Evolution* 43: 1724-1736.
- Lynch, M. 1989. The life history consequences of resource depression in *Daphnia pulex*. *Ecology* 70: 246-256.
- Lynch, M. 1990. The rate of morphological evolution in mammals from the standpoint of the neutral expectation. *American Naturalist* 136: 727-741.
- Lynch, M., and T. Crease. 1990. The analysis of population survey data on DNA sequence variation. *Mol. Biol. Evol.* 7: 377-394.
- Crease, T., M. Lynch, and K. Spitze. 1990. A hierarchical analysis of population genetic variation in nuclear and mitochondrial genes in *Daphnia*. *Mol. Biol. Evol.* 7: 444-458.
- Lynch, M. 1990. The similarity index and DNA fingerprinting. *Mol. Biol. Evol.* 7: 478-484.
- Lynch, M., and W. Gabriel. 1990. Mutation load and the survival of small populations. *Evolution* 44: 1725-1737.
- Gabriel, W., R. Bürger, and M. Lynch. 1991. Population extinction by mutational load and demographic stochasticity, pp. 49-59. In A. Seitz, and V. Loeschcke (eds.) *Species Conservation: a Population Biological Approach*. Birkhäuser Verlag, Basel.
- Lynch, M. 1991. Methods for the analysis of comparative data in evolutionary biology. *Evolution* 45: 1065-1080.
- Lynch, M. 1991. The genetic interpretation of inbreeding depression and outbreeding depression. *Evolution* 45: 622-629.
- Lynch, M. 1991. Analysis of population genetic structure by DNA fingerprinting, pp. 113-126. In T. Burke, G. Dolf, A. J. Jeffreys, and R. Wolff (eds.) *DNA Fingerprinting: Approaches and Applications*. Birkhäuser Verlag, Basel.
- Crease, T. J., and M. Lynch. 1991. Ribosomal DNA variation in *Daphnia pulex*. *Mol. Biol. Evol.* 8: 620-640.
- Spitze, K., J. Burnson, and M. Lynch. 1991. The covariance structure of life history characters in *Daphnia pulex*. *Evolution* 45: 1081-1090.
- Lynch, M., W. Gabriel, and A. M. Wood. 1991. The adaptive and demographic response of plankton populations to environmental change. *Limnol. Oceanogr.* 36: 1301-1312.
- Cohen, J. E., M. Lynch, and C. E. Taylor. 1991. Forensic DNA tests and Hardy-Weinberg equilibrium. *Science* 253: 1037.

- Lynch, M. 1992. The life history consequences of resource depression in *Ceriodaphnia quadrangula* and *Daphnia ambigua*. *Ecology* 73: 1620-1629.
- Gabriel, W., and M. Lynch. 1992. The selective advantage of reaction norms for environmental tolerance. *J. Evol. Biol.* 5: 41-59.
- Lynch, M., and R. Lande. 1993. Evolution and extinction in response to environmental change, pp. 234-250. In P. Kareiva, J. Kingsolver, and R. Huey (eds.) *Biotic Interactions and Global Change*. Sinauer Assocs., Inc. Sunderland, MA.
- Lynch, R. Bürger, D. Butcher, and W. Gabriel. 1993. Mutational meltdowns in asexual populations. *J. Heredity* 84: 339-344.
- Lynch, M., and P. Jerol. 1993. A method for calibrating molecular clocks and its application to animal mitochondrial DNA. *Genetics* 135: 1197-1208.
- Lynch, M., and K. Spitze. 1994. Evolutionary genetics of *Daphnia*, pp. 109-128. In L. Real (ed.) *Ecological Genetics*. Princeton Univ. Press.
- Lynch, M. 1994. The neutral theory of phenotypic evolution, pp. 86-108. In L. Real (ed.) *Ecological Genetics*. Princeton Univ. Press.
- Gabriel, W., M. Lynch, and R. Bürger. 1994. Muller's ratchet and mutational meltdowns. *Evolution* 47: 1744-1757.
- Lynch, M., and B. Milligan. 1994. Analysis of population-genetic structure using RAPD markers. *Molecular Ecology* 3: 91-99.
- Bürger, R., and M. Lynch. 1994. Evolution and extinction in a changing environment: a quantitative-genetic analysis. *Evolution* 49: 151-163.
- Lynch, M., and H. W. Deng. 1994. Genetic slippage in response to sex. *American Naturalist* 144: 242-261.
- Toline, C. A., and M. Lynch. 1994. Mutational divergence of life-history traits in an obligate parthenogen. *Genome* 37: 33-35.
- Avise, J. C., S. M. Haig, O. A. Ryder, M. Lynch, and C. J. Geyer. 1995. Descriptive genetic studies: applications in population management and conservation biology, pp. 183-244. In J. D. Ballou, M. Gilpin, and T. J. Foose (eds.) *Population Management for Survival and Recovery*. Columbia Univ. Press, New York.
- Conery, J. S., M. Lynch, and T. Hovland. 1995. Irregular computations on SIMD machines: a case study. *Proc. 5th Symp. Frontiers of Massively Parallel Computation*: 222-230.
- Lehman, N., M. E. Pfrender, P. A. Morin, T. J. Crease, and M. Lynch. 1995. A hierarchical molecular phylogeny of the genus *Daphnia*. *Mol. Phylog. Evol.* 4: 395-407.
- Lynch, M., J. Conery, and R. Bürger. 1995. Mutational meltdowns in sexual populations. *Evolution* 49: 1067-1080.
- Lynch, M., J. Conery, and R. Bürger. 1995. Mutation accumulation and the extinction of small populations. *American Naturalist* 146: 489-518.
- Lynch, M. 1996. A quantitative-genetic perspective on conservation issues, pp. 471-501. In J. Avise and J. Hamrick (eds.) *Conservation Genetics: Case Histories from Nature*. Chapman and Hall, New York.
- Lynch, M. 1996. Mutation accumulation in transfer RNAs: molecular evidence for Muller's ratchet in mitochondrial genomes. *Mol. Biol. Evol.* 13: 209-220.

- Deng, H.-W., and M. Lynch. 1996. Change of genetic architecture in response to sex. *Genetics* 143: 203-212.
- Deng, H.-W., and M. Lynch. 1996. Estimation of deleterious-mutation parameters in natural populations. *Genetics* 144: 349-360.
- Houle, D., R. Morikawa, and M. Lynch. 1996. Comparing mutational variabilities. *Genetics* 143: 1467-1483.
- Kibota, T., and M. Lynch. 1996. Estimate of the genomic mutation rate deleterious to overall fitness in *Escherichia coli*. *Nature* 381: 694-696.
- Crease, T., S. K. Sung, S. L. Sung, N. Lehman, K. Spitze, and M. Lynch. 1997. Allozyme and mitochondrial DNA variation in populations of the *Daphnia pulex* complex from both sides of the Rocky Mountains. *Heredity* 79: 242-251.
- Deng, H.-W., and M. Lynch. 1997. Inbreeding depression and inferred deleterious mutation parameters in *Daphnia*. *Genetics* 147: 147-155.
- Lynch, M. 1997. Mutation accumulation in nuclear, organelle, and prokaryotic genomes: transfer RNA genes. *Mol. Biol. Evol.* 14: 914-925.
- Schultz, S. T., and M. Lynch. 1997. Deleterious mutation and extinction: effects of variable mutational effects, synergistic epistasis, beneficial mutations, and degree of outcrossing. *Evolution* 51: 1363-1371.
- Bürger, R., and M. Lynch. 1997. Adaptation and extinction in changing environments, pp. 209-240. In R. Bijlsma and V. Loeschcke (eds.) *Environmental Stress, Adaptation and Evolution*. Birkhäuser Verlag, Basel.
- Lynch, M., and J. Blanchard. 1998. Deleterious mutation accumulation in organelle genomes. *Genetica* 102/103: 29-39.
- Deng, H.-W., Y.-X. Fu, and Lynch, M. 1998. Inferring the major genomic mode of dominance and overdominance. *Genetica* 102/103: 559-567.
- Lynch, M., and R. Lande. 1998. The critical effective size for a genetically secure population. *Anim. Cons.* 1: 70-72.
- Lynch, M., L. Latta, J. Hicks, and M. Giorgianni. 1998. Mutation, selection, and the maintenance of life-history variation in a natural population. *Evolution* 52: 727-733.
- Vassilieva, L., and M. Lynch. 1999. Accumulation of spontaneous mutations in *Caenorhabditis elegans*. *Genetics* 151: 119-129.
- Lynch, M., M. Pfrender, K. Spitze, N. Lehman, D. Allen, J. Hicks, L. Latta, M. Ottene, F. Bogue, and J. Colbourne. 1999. The quantitative and molecular genetic architecture of subdivided species. *Evolution* 53: 100-110.
- Lynch, M., and K. Ritland. 1999. Estimation of relatedness with molecular markers. *Genetics* 152: 1753-1766.
- Lynch, M. 1999. The age and relationships of the major animal phyla. *Evolution* 53: 319-325.
- Force, A., M. Lynch, B. Pickett, A. Amores, Y.-L. Yan, and J. Postlethwait. 1999. Preservation of duplicate genes by complementary, degenerative mutations. *Genetics* 151: 1531-1545.
- Lynch, M., J. Blanchard, D. Houle, T. Kibota, S. Schultz, L. Vassilieva, and J. Willis. 1999. Spontaneous deleterious mutation. *Evolution* 53: 645-663.
- Conery, J. S., and M. Lynch. 1999. Genetic simulation library. *Bioinformatics* 15: 85-86.

- Lynch, M. 1999. Estimation of genetic correlations in natural populations. *Genetical Research* 74: 255-264.
- Schultz, S. T., M. Lynch, and J. H. Willis. 1999. Spontaneous deleterious mutation in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* 96: 11393-11398.
- Lynch, M., and A. Force. 2000. The probability of duplicate-gene preservation by subfunctionalization. *Genetics* 154: 459-473.
- Vassilieva, L., A. M. Hook, and M. Lynch. 2000. The fitness effects of spontaneous mutations in *Caenorhabditis elegans*. *Evolution* 54: 1234-1246.
- Blanchard, J., and M. Lynch. 2000. Why do mitochondrial genes end up in the nuclear genome? *Trends in Genetics* 16: 315-320.
- Denver, D., K. Morris, M. Lynch, L. L. Vassilieva, and W. K. Thomas. 2000. High direct estimate of the mutation rate in the mitochondrial genome of *C. elegans*. *Science* 289: 2342-2344.
- Pfrender, M. E., and M. Lynch. 2000. Quantitative genetic variation in *Daphnia*: temporal changes in genetic architecture. *Evolution* 54: 1502-1509.
- Lynch, M., and A. Force. 2000. Gene duplication and the origin of interspecific genomic incompatibility. *American Naturalist* 156: 590-605.
- Pfrender, M. E., K. Spitze, J. Hicks, K. Morgan, L. Latta, and M. Lynch. 2000. Lack of concordance between genetic diversity estimates at the molecular and quantitative-trait levels. *Conservation Genetics* 1: 263-269.
- Lynch, M., and J. S. Conery. 2000. The evolutionary fate and consequences of duplicate genes. *Science* 290: 1151-1154.
- Lynch, M. 2000. The limits to knowledge in quantitative genetics. *Evol. Biol.* 32: 225-237.
- Lynch, M., and J. S. Conery. 2001. Gene duplication and evolution: response to Long and Thornton and Zhang et al. *Science* 293: 1551a.
- Higgins, K., and M. Lynch. 2001. Metapopulation extinction due to mutation accumulation. *Proc. Natl. Acad. Sci. USA* 98: 2928-2933.
- Morgan, K. K., J. Hicks, K. Spitze, L. Latta, M. Pfrender, C. Ottone, and M. Lynch. 2001. Patterns of genetic architecture for life-history traits and molecular markers in a subdivided species. *Evolution* 55: 1753-1761.
- Lynch, M. 2001. The molecular natural history of the human genome. *Trends in Ecology and Evolution* 16: 420-422.
- Lynch, M., and M. O'Hely. 2001. Supplementation and the genetic fitness of natural populations. *Conservation Genetics* 2: 363-378.
- Lynch, M., M. O'Hely, B. Walsh, and A. Force. 2001. The probability of preservation of a newly arisen gene duplicate. *Genetics* 159: 1789-1804.
- Lynch, M. 2002. Intron evolution as a population-genetic process. *Proc. Natl. Acad. Sci. USA* 99: 6118-6123.
- Lynch, M., and A. Richardson. 2002. The evolution of spliceosomal introns. *Curr. Opin. Gen. Devel.* 12: 701-710.
- Lynch, M. 2002. Chromosomal repatterning by gene duplication. *Science* 297: 945-947.

- Jackson, R. B., C. R. Linder, M. Lynch, M. Purugannan, and S. Somerville. 2002. Linking molecular insights and ecological research. *Trends in Ecology and Evolution* 17: 409-414.
- Azevedo, R. B. R., P. D. Keightley, C. Lauren-Maatta, L. L. Vassilieva, M. Lynch, and A. M. Leroi. 2002. Spontaneous mutational variation for body size in *Caenorhabditis elegans*. *Genetics* 162: 755-765.
- Lynch, M., and J. S. Conery. 2003. The evolutionary demography of duplicate genes, pp. 35-44. In A. Meyer and Y. Van de Peer (eds.), *Genome Evolution*. Kluwer Academic Publishers, Dordrecht.
- Keightley, P. D., and M. Lynch. 2003. Towards a realistic model of mutations affecting fitness. *Evolution* 57: 683-685.
- Lynch, M., and A. Kewalramani. 2003. Messenger RNA processing and the evolutionary proliferation of introns. *Mol. Biol. Evol.* 20: 563-571.
- Baer, C. F., and M. Lynch. 2003. Correlated evolution of life-history with size at maturity in *Daphnia pulicaria*: patterns within and between populations. *Genetical Research* 81: 123-132.
- Estes, S., and M. Lynch. 2003. Rapid recovery of mutation-accumulation lines by compensatory mutation. *Evolution* 57: 1022-1030.
- Housworth, E., E. Martins, and M. Lynch. 2003. The phylogenetic mixed model. *American Naturalist* 163: 84-96.
- Lynch, M., and J. S. Conery. 2003. The origins of genome complexity. *Science* 302: 1401-1404.
- Katju, V., and M. Lynch. 2003. The structure and early evolution of recently arisen gene duplicates in the *Caenorhabditis elegans* genome. *Genetics* 165: 1793-1803.
- Denver, D. R., S. L. Swenson, and M. Lynch. 2003. An evolutionary analysis of the helix-hairpin-helix superfamily of DNA repair glycosylases. *Molecular Biology and Evolution* 20: 1603-1611.
- Lynch, M. 2004. Gene duplication and evolution, pp. 33-47. In A. Moya and E. Font (eds.), *Evolution: From Molecules to Ecosystems*. Oxford University Press, New York, NY.
- Estes, S., P. C. Phillips, D. R. Denver, W. K. Thomas, and M. Lynch. 2004. Mutation accumulation in populations of varying size: The distribution of mutational effects for fitness correlates in *Caenorhabditis elegans*. *Genetics* 166: 1269-1279.
- Denver, D. R., K. Morris, M. Lynch, and W. K. Thomas. 2004. High mutation rate and predominance of insertions in the *Caenorhabditis elegans* nuclear genome. *Nature* 430: 679-682.
- Lynch, M., and V. Katju. 2004. The altered evolutionary trajectories of gene duplicates. *Trends in Genetics* 20: 544-549.
- Denver, D. R., K. Morris, A. Kewalramani, K. Harris, A. Chow, S. Randell-Estes, M. Lynch, and W. K. Thomas. 2004. Abundance, distribution and mutation rates of homopolymeric nucleotide runs in the genome of *Caenorhabditis elegans*. *J. Mol. Evol.* 58: 584-595.
- Pfrender, M. E., J. Hicks, and M. Lynch. 2004. Biogeographic patterns and current distribution of molecular-genetic variation among populations of speckled dace, *Rhinichthys osculus* (Girard). *Mol. Phylogenet. Evol.* 30: 490-502.
- Dudycha, J. L., and M. Lynch. 2005. Ontogeny and allometry of resource allocation in animals with indeterminate growth. *Evolution* 59: 565-576.

- Lynch, M., D. G. Scofield, and X. Hong. 2005. The evolution of transcription-initiation sites. *Mol. Biol. Evol.* 22: 1137-1146.
- Denver, D. R., K. Morris, J. T. Strelman, S. K. Kim, M. Lynch, and W. K. Thomas. 2005. The transcriptional consequences of mutation and natural selection in *Caenorhabditis elegans*. *Nature Genetics* 37: 544-548.
- Denver, D. R., S. Feinberg, S. Estes, W. K. Thomas, and M. Lynch. 2005. Mutation rates, spectra and hotspots in mismatch repair-deficient *Caenorhabditis elegans*. *Genetics* 170: 107-113.
- Baer, C. F., F. Shaw, C. Steding, M. Baumgartner, A. Hawkins, A. Houppert, N. Mason, M. Reed, F. Shaw, K. Simonelic, W. Woodward, and M. Lynch. 2005. Comparative evolutionary genetics of spontaneous mutations affecting fitness in rhabditid nematodes. *Proc. Natl. Acad. Sci. USA* 102: 5785-5790.
- Colbourne, J. K., B. Robison, K. Bogart, and M. Lynch. 2005. Five hundred and twenty eight microsatellite markers for ecological genomic investigations using *Daphnia*. *Mol. Ecol. Notes* 4: 485-490.
- Force, A., W. Cresko, F. B. Pickett, S. Proulx, C. Amemiya, and M. Lynch. 2005. The origin of gene subfunctions and modular gene regulation. *Genetics* 170: 433-446.
- Paland, S., J. K. Colbourne, and M. Lynch. 2005. Evolutionary history of contagious asexuality in *Daphnia pulex*. *Evolution* 59: 800-813.
- Ajie, B. C., S. Estes, M. Lynch, and P. C. Phillips. 2005. Behavioral degradation under mutation accumulation. *Genetics* 170: 655-660.
- Estes, S., Ajie, B. C., M. Lynch, and P. C. Phillips. 2005. Spontaneous mutational correlations for life-history, morphological, and behavioral characters in *Caenorhabditis elegans*. *Genetics* 170: 645-653.
- Lynch, M. 2005. Intelligent design vs. intelligent evolution. *Nature* 435: 276.
- Lynch, M. 2005. Simple evolutionary pathways to complex proteins. *Protein Science* 14: 2217-2225.
- Lynch, M., X. Hong, and D. G. Scofield. 2006. Nonsense-mediated decay and the evolution of eukaryotic gene structure, pp. 197-211. In L. E. Maquat (ed.) *Nonsense-mediated mRNA Decay*. Landes Bioscience, Georgetown, TX.
- Robinson, C. D., S. Lourido, S. P. Whelan, J. L. Dudycha, M. Lynch, and S. Isern. 2006. Viral transgenesis of embryonic cell cultures from the freshwater microcrustacean *Daphnia*. *J. Exp. Zool.* 305: 62-67.
- Lynch, M. 2006. The origins of eukaryotic gene structure. *Mol. Biol. Evol.* 23: 450-468.
- Paland, S., and M. Lynch. 2006. Transitions to asexuality result in excess amino-acid substitutions. *Science* 311: 990-902.
- Lynch, M., B. Koskella, and S. Schaack. 2006. Mutation pressure and the evolution of organelle genome architecture. *Science* 311: 1727-1730.
- Katju, V., and M. Lynch. 2006. On the formation of novel genes by duplication in the *Caenorhabditis elegans* genome. *Mol. Biol. Evol.* 23: 1056-1067.
- Cristescu, M. E., J. K. Colbourne, J. Radivojac, and M. Lynch. 2006. A microsatellite-based genetic linkage map of the waterflea, *Daphnia pulex*: on the prospect of crustacean genomics. *Genomics* 88: 415-430.
- Denver, D. R., S. Feinberg, C. Steding, M. Durbin, and M. Lynch. 2006. The relative roles of three DNA repair pathways in preventing *Caenorhabditis elegans* mutation accumulation. *Genetics* 174: 57-65.

- Hong, X., D. G. Scofield, and M. Lynch. 2006. Intron size, abundance, and distribution within untranslated regions of genes. *Mol. Biol. Evol.* 23: 2392-2404.
- Snoke, M. S., T. U. Berendonk, D. Barth, and M. Lynch. 2006. Large global effective population sizes in *Paramecium*. *Mol. Biol. Evol.* 23: 2474-2479.
- Lynch, M. 2006. Streamlining and simplification of microbial genome architecture. *Ann. Rev. Microbiol.* 60:327-349.
- Omilian, A. R., M. E. A. Cristescu, J. L. Dudyca, and M. Lynch. 2006. Aneiotic recombination in asexual lineages. *Proc. Natl. Acad. Sci. USA* 103: 18638-18643.
- Scofield, D. G., X. Hong, and M. Lynch. 2007. Position of the final intron in full-length transcripts: determined by NMD? *Mol. Biol. Evol.* 24: 896-899.
- Lynch, M. 2007. The frailty of adaptive hypotheses for the origins of organismal complexity. *Proc. Natl. Acad. Sci. USA* 104 (Suppl.): 8597-8604.
- Rho, M., J. H. Choi, S. Kim, M. Lynch, and H. Tang. 2007. *De novo* identification of LTR retrotransposons in eukaryotic genomes. *BMC Genomics* 8: 90.
- Lynch, M. 2007. The evolution of genetic networks by nonadaptive processes. *Nature Reviews Genetics* 8: 803-813.
- Lynch, M., W. Sung, K. Morris, N. Crown, C. R. Landry, E. B. Dopman, W. J. Dickinson, K. Okamoto, S. Kulkarni, D. L. Hartl, and W. K. Thomas. 2008. A genome-wide view of the spectrum of spontaneous mutations in yeast. *Proc. Natl. Acad. Sci. USA* 105: 9272-9277.
- Seyfert, A. L., M. E.A. Cristescu, L. Frisse, S. Schaack, W. K. Thomas, and M. Lynch. 2008. The rate and spectrum of microsatellite mutation in *Caenorhabditis elegans* and *Daphnia pulex*. *Genetics* 178: 2113-2121.
- Allen, D. E., and M. Lynch. 2008. Both costs and benefits of sex correlate with relative frequency of asexual reproduction in cyclically parthenogenic *Daphnia pulicaria* populations. *Genetics* 179: 1497-1502.
- Haag-Liautard, C., N. Coffey, D. Houle, M. Lynch, B. Charlesworth, and P. D. Keightley. 2008. Direct estimation of the mitochondrial DNA mutation rate in *D. melanogaster*. *PLoS Biology* 6: 1706-1714.
- Omilian, A. R., D. G. Scofield, and M. Lynch. 2008. Intron presence-absence polymorphisms in *Daphnia*. *Mol. Biol. Evol.* 25: 2129-2139.
- Lynch, M., A. Seyfert, B. Eads, and E. Williams. 2008. Localization of the genetic determinants of meiosis suppression in *Daphnia pulex*. *Genetics* 180: 317-327.
- Lynch, M. 2008. Estimation of nucleotide diversity, disequilibrium coefficients, and mutation rates from high-coverage genome-sequencing projects. *Mol. Biol. Evol.* 25: 2421-2431.
- Lynch, M. 2008. The cellular, developmental, and population-genetic determinants of mutation-rate evolution. *Genetics* 180: 933-943.
- Scofield, D. G., and M. Lynch. 2008. Evolutionary diversification of the Sm family of RNA-associated proteins. *Mol. Biol. Evol.* 25: 2255-2267.
- Catania, F., and M. Lynch. 2008. Where do introns come from? *PLoS Biology* 6: e283.

- Catania, F., F. Wurmser, A. A. Potekhin, E. Przyboś, and M. Lynch. 2009. Genetic diversity in the *Paramecium aurelia* complex. *Mol. Biol. Evol.* 26: 421-431.
- Penalva-Arana, D. C., M. Lynch, and H. M. Robertson. 2009. The chemoreceptor genes of the waterflea *Daphnia pulex*: many Grs but no Ors. *BMC Evol. Biol.* 9:79
- Omilian, A. R., and M. Lynch. 2009. Patterns of intraspecific DNA variation in the *Daphnia* nuclear genome. *Genetics* 182: 325-336.
- Lynch, M. 2009. Estimation of allele frequencies from high-coverage genome-sequencing projects. *Genetics* 182: 295-301.
- Lucas-Lledó, J. I., and M. Lynch. 2009. Evolution of mutation rates: phylogenomic analysis of the photolyase/cryptochrome family. *Mol. Biol. Evol.* 26: 1143-1153.
- Rho, M., M. Zhou, X. Gao, S. Kim, H. Tang, and M. Lynch. 2009. Parallel mammalian genome contractions following the KT boundary. *Genome Biol. Evol.* 1: 2-12.
- Denver, D. D., P. C. Dolan, L. J. Wilhelm, W. Sung, J. I. Lucas-Lledó, D. K. Howe, S. C. Lewis, K. Okamoto, M. Lynch, W. K. Thomas, and C. F. Baer. 2009. A genome-wide view of *Caenorhabditis elegans* base-substitution mutation processes. *Proc. Natl. Acad. Sci. USA* 106: 16310-16314.
- Li, W. A. E. Tucker, W. Sung, W. K. Thomas, and M. Lynch. 2009. Extensive, recent intron gains in *Daphnia* populations. *Science* 326: 1260-1262.
- Gao, X., and M. Lynch. 2009. Ubiquitous internal gene duplication and intron creation in eukaryotes. *Proc. Natl. Acad. Sci. USA* 106: 20818-20823.
- Lynch, M. 2009. Rate, molecular spectrum, and consequences of spontaneous mutations in man. *Proc. Natl. Acad. Sci. USA* 107: 961-968.
- Ossowski, S., K. Schneeberger, J. Lucas-Lledó, N. Warthmann, R. M. Clark, R. G. Shaw, D. Weigel, and M. Lynch. 2010. The rate and molecular spectrum of spontaneous mutations in *Arabidopsis thaliana*. *Science* 327: 92-94.
- Schaack, S., E. Choi, M. Lynch, and E. J. Pritham. 2010. DNA transposons and the role of recombination in mutation accumulation in *Daphnia pulex*. *Genome Biology* 11: R46.
- Haubold, B., P. Pfaffelhuber, and M. Lynch. 2010. mlRho – A program for estimating the population mutation and recombination rates from shotgun-sequenced genomes. *Molecular Ecology* 19, Suppl. 1: 277-284.
- Gleick, P. H., et al. 2010. Climate change and the integrity of science. *Science* 328: 689-690.
- Lynch, M., and A. Abegg. 2010. The rate of origin of complex adaptations. *Mol. Biol. Evol.* 27: 1404-1414.
- Lynch, M. 2010. Evolution of the mutation rate. *Trends in Genetics* 26: 345-352.
- Catania, F., and M. Lynch. 2010. Evolutionary dynamics of a conserved sequence motif in the ribosomal genes of the ciliate *Paramecium*. *BMC Evol. Biol.* 10: 129.
- Schaack, S., E. J. Pritham, A. Wolf, and M. Lynch. 2010. DNA transposon dynamics in populations of *Daphnia pulex* with and without sex. *Proc. R. Soc. Lond. B* 277: 2381-2387.
- Rho, M., S. Schaack, X. Gao, S. Kim, M. Lynch, and H. Tang. 2010. LTR retroelements in the genome of *Daphnia pulex*. *BMC Genomics* 11: 425.

- Lynch, M. 2010. Scaling expectations for the time to establishment of complex adaptations. *Proc. Natl. Acad. Sci. USA* 107: 16577-16582.
- Sung, W., A. Tucker, R. D. Bergeron, M. Lynch, and W. K. Thomas. 2010. Simple sequence repeat variation in the *Daphnia pulex* genome. *BMC Genomics* 11: 691.
- Lipinski, K. J., K. A. Fitzpatrick, M. Lynch, V. Katju, and U. Bergthorsson. 2011. High spontaneous rate of gene duplication in *Caenorhabditis elegans*. *Curr. Biol.* 21: 306-310.
- Colbourne, J., et al. 2011. The ecoresponsive genome of *Daphnia pulex*. *Science* 331: 555-561.
- Lucas-Lledó, J. I., R. Maddamsetti, and M. Lynch. 2011. Phylogenomic analysis of the uracil-DNA glycosylase superfamily. *Mol. Biol. Evol.* 28: 1307-1317.
- Lynch, M. 2011. Statistical inference on the mechanisms of genome evolution. *PLoS Genetics* 7(6): e1001389.
- Lynch, M., L.-M. Bobay, F. Catania, J.-F. Gout, and M. Rho. 2011. The repatterning of eukaryotic genomes by random genetic drift. *Ann. Rev. Genomics Hum. Genet.* 12: 347-366.
- Lynch, M. 2011. The lower bound to the evolution of mutation rates. *Genome Biol. Evol.* 3: 1107-1118.
- Eads, B., D. Tsuchiya, M. Lynch, J. Andrews, and M. E. Zolan. 2012. Evolution of *REC8* in *Daphnia*: the spread of a transposon insertion associated with obligate asexuality. *Proc. Natl. Acad. Sci. USA* 109: 858-863.
- Xu, S., S. Schaack, A. Seyfert, E. Choi, M. Lynch, and M. E. Cristescu. 2012. High mutation rates in the mitochondrial genomes of *Daphnia pulex*. *Mol. Biol. Evol.* 29: 763-769.
- Lynch, M. 2012. The evolution of multimeric protein assemblages. *Mol. Biol. Evol.* 29: 1353-1366.
- Allen, D. E., and M. Lynch. 2012. The effect of variable frequency of sexual reproduction on the genetic structure of natural populations of a cyclical parthenogen. *Evolution* 66: 919-926.
- Sung, W., A. Tucker, T. G. Doak, J. Choi, W. K. Thomas, and M. Lynch. 2012. Extraordinary genome stability in the ciliate *Paramecium tetraurelia*. *Proc. Natl. Acad. Sci. USA* 109: 19339-19344.
- Sung, W., M. S. Ackerman, S. F. Miller, T. G. Doak, and M. Lynch. 2012. The drift-barrier hypothesis and mutation-rate evolution. *Proc. Natl. Acad. Sci. USA* 109: 18488-18492.
- Lynch, M. 2012. Evolutionary layering and the limits to cellular perfection. *Proc. Natl. Acad. Sci. USA* 109: 18851-18856.
- McGrath, C. L., and M. Lynch. 2012. Evolutionary significance of whole-genome duplication, p. 1-20. In P. S. Soltis and D. E. Soltis (eds.) *Polyploidy and Genome Evolution*. Springer-Verlag, New York, NY.
- Latta, L. C. 4th, K. K. Morgan, C. S. Weaver, D. Allen, S. Schaack, and M. Lynch. 2013. Genomic background and generation time influence deleterious mutation rates in *Daphnia*. *Genetics* 193: 539-544.
- Schaack, S., D. E. Allen, L. C. Latta 4th, K. K. Morgan, and M. Lynch. 2013. The effect of spontaneous mutations on competitive ability. *J. Evol. Biol.* 26: 451-456.
- Catania, F., C. L. McGrath, T. G. Doak, and M. Lynch. 2013. Spliced DNA sequences in the *Paramecium* germline: their properties and evolutionary potential. *Genome Biol. Evol.* 5: 1200-1211.
- Ibarra-Laclette, E., E. Lyons, G. Hernández-Guzmán, C. A. Pérez-Torres, L. Carretero-Paulet, T. H. Chang, T. Lan, A. J. Welch, M. J. Juárez, J. Simpson, A. Fernández-Cortés, M. Arteaga-Vázquez, E. Góngora-Castillo, G. Acevedo-

- Hernández, S. C. Schuster, H. Himmelbauer, A. E. Minoche, S. Xu, M. Lynch, A. Oropeza-Aburto, S. A. Cervantes-Pérez, M. de Jesús Ortega-Estrada, J. I. Cervantes-Luevano, T. P. Michael, T. Mockler, D. Bryant, A. Herrera-Estrella, V. A. Albert, and L. Herrera-Estrella. 2013. Architecture and evolution of a minute plant genome. *Nature* 498: 94-98.
- Sung, W., M. S. Ackerman, S. F. Miller, T. G. Doak, and M. Lynch. 2013. Reply to Massey: Drift does influence mutation-rate evolution. *Proc. Natl. Acad. Sci. USA* 110: E860.
- Lynch, M. 2013. Evolutionary diversification of the multimeric states of proteins. *Proc. Natl. Acad. Sci. USA* 110: E2821-E2828.
- Catania, F., and M. Lynch. 2013. A simple model to explain evolutionary trends of eukaryotic gene architecture and expression: how competition between splicing and cleavage/polyadenylation factors may affect gene expression and splice-site recognition in eukaryotes. *Bioessays* 35: 561-570.
- Raymann, K., L. M. Bobay, T. G. Doak, M. Lynch, and S. Gribaldo. 2013. A genomic survey of Reb homologs suggests widespread occurrence of R-bodies in proteobacteria. *G3 (Bethesda)* 3: 505-516.
- Schrider, D., D. Houle, M. Lynch, and M. Hahn. 2013. Genetic variation in the mutation rate in *Drosophila melanogaster*. *Genetics* 194: 937-954.
- Xu, S., D. J. Innes, M. Lynch, and M. E. Cristescu. 2013. The role of hybridization in the origin and spread of asexuality in *Daphnia*. *Mol. Ecol.* 22: 4549-4561.
- Tucker, A., M. Ackerman, B. Eads, S. Xu, and M. Lynch. 2013. Population-genomic insights into the evolutionary origin and fate of obligately asexual *Daphnia pulex*. *Proc. Natl. Acad. Sci. USA* 110: 15740-15745.
- Gout, J. F., W. K. Thomas, Z. Smith, K. Okamoto, and M. Lynch. 2013. Large-scale detection of *in vivo* transcription errors. *Proc. Natl. Acad. Sci. USA* 110: 18584-18589.
- Boscaro, V., M. Felletti, C. Vannini, M. S. Ackerman, P. S. G. Chain, S. Malfatti, L. M. Vergez, M. Shin, T. G. Doak, M. Lynch, and G. Petroni. 2013. *Polynucleobacter necessarius*, a new model for genome reduction in both free-living and symbiotic bacteria. *Proc. Natl. Acad. Sci. USA* 110: 18590-18595.
- Lynch, M., D. Bost, S. Wilson, and T. Maruki. 2014. Population-genetic inference from pooled-sequencing data. *Genome Biol. Evol.* 6: 1210-1218.
- Maruki, T., and M. Lynch. 2014. Genome-wide estimation of linkage disequilibrium from population-level high-throughput sequencing data. *Genetics* 197: 1303-1313.
- McGrath, C. L., J. F. Gout, T. G. Doak, A. Yanagi, and M. Lynch. 2014. Insights into three whole-genome duplications gleaned from the *Paramecium caudatum* genome sequence. *Genetics* 197: 1417-1428.
- McGrath, C. L., J. F. Gout, P. Johri, T. G. Doak, and M. Lynch. 2014. Differential retention and divergent resolution of duplicate genes following whole-genome duplication. *Genome Research* 24: 1665-1675.
- Lynch, M., S. Xu, T. Maruki, P. Pfaffelhuber, and B. Haubold. 2014. Genome-wide linkage-disequilibrium profiles from single individuals. *Genetics* 198: 269-281.
- Li, W., R. Kuzoff, K. W. Chen, A. Tucker, and M. Lynch. 2014. Characterization of newly gained introns in *Daphnia* populations. *Genome Biol. Evol.* 6: 2218-2234.
- Lynch, M., M. C. Field, H. Goodson, H. S. Malik, J. B. Pereira-Leal, D. S. Roos, A. Turkewitz, and S. Sazer. 2014. Evolutionary cell biology: two origins, one objective. *Proc. Natl. Acad. Sci. USA* 111: 16990-16994.

- Sazer, S., M. Lynch, and D. Needleman. 2014. Deciphering the evolutionary history of open and closed mitosis. *Curr. Biol.* 24: R1099-R1103.
- Lynch, M., and K. Hagner. 2014. Evolutionary meandering of intermolecular interactions along the drift barrier. *Proc. Natl. Acad. Sci. USA* 112: E30-E38.
- Long, H., W. Sung, S. F. Miller, M. S. Ackerman, T. G. Doak, and M. Lynch. 2014. Mutation rate, spectrum, topology and context-dependency in the DNA mismatch repair (MMR) deficient isolate *Pseudomonas fluorescens* Migula ATCC948. *Genome Biol. Evol.* 7: 262-271.
- Dillon, M. M., W. Sung, M. Lynch, and V. S. Cooper. 2015. The rate and molecular spectrum of spontaneous mutations in the GC-rich multi-chromosome genome of *Burkholderia cenocepacia*. *Genetics* 200: 935-946.
- Gout, J. F., and M. Lynch. 2015. Maintenance and loss of duplicated genes by dosage subfunctionalization. *Mol. Biol. Evol.* 32: 2141-2148.
- Lynch, M. 2015. Feedforward loop for diversity. *Nature* 523: 414-416.
- Sung, W., M. S. Ackerman, J. F. Gout, S. F. Miller, P. Foster, and M. Lynch. 2015. Asymmetric context-dependent mutation patterns revealed through mutation-accumulation experiments. *Mol. Biol. Evol.* 32: 1672-1683.
- Long, H., S. Kucukyildirim, W. Sung, E. Williams, M. Ackerman, T. G. Doak, and M. Lynch. 2015. Background mutational features of the radiation-resistant bacterium *Deinococcus radiodurans*. *Mol. Biol. Evol.* 32: 2383-2392.
- Maruki, T., and M. Lynch. 2015. Genotype-frequency estimation from high-throughput sequencing data. *Genetics* 201: 473-486.
- Xu, S., M. S. Ackerman, H. Long, L. Bright, K. Spitze, J. S. Ramsdell, W. K. Thomas, and M. Lynch. 2015. A male-specific genetic map of the microcrustacean *Daphnia pulex* based on single sperm whole-genome sequencing. *Genetics* 201: 31-38.
- Farlow, A., H. Long, S. Arnoux, W. Sung, T. G. Doak, C. Schlötterer, M. Nordborg, and M. Lynch. 2015. The spontaneous mutation rate in the fission yeast *Schizosaccharomyces pombe*. *Genetics* 201: 737-744.
- Xu, S., K. Spitze, M. Ackerman, Z. Ye, L. Bright, R. Keith, C. Jackson, J. Shaw, and M. Lynch. 2015. Hybridization and the origin of contagious asexuality in *Daphnia pulex*. *Mol. Biol. Evol.* 32: 3215-3225.
- Suzuki, H., A. Dapper, C. Jackson, H. Lee, V. Pejaver, T. Doak, M. Lynch, and J. Preer, Jr. 2015. Draft genome sequence of *Caedibacter varicaedens*, a Kappa killer endosymbiont bacterium of the ciliate *Paramecium biaurelia*. *Genome Announcements* 3: 1-2.
- Lynch, M., and G. K. Marinov. 2015. The bioenergetic costs of a gene. *Proc. Natl. Acad. Sci. USA* 112: 15690-15695.
- Marinov, G. K., and M. Lynch. 2015. Diversity and divergence of dinoflagellate histone proteins. *G3: Genes|Genomes|Genetics* 6: 397-422.
- Keith, N., A. E. Tucker, C. E. Jackson, W. Sung, J. I. Lucas-Lledó, D. Schrider, S. Schaack, J. L. Dudycha, and M. Lynch. 2016. High mutational rates of large-scale duplication and deletion in *Daphnia pulex*. *Genome Res.* 26: 60-69.
- Lynch, M., and G. K. Marinov. 2016. Reply to Lane and Martin: Mitochondria do not boost the bioenergetic capacity of eukaryotic cells. *Proc. Natl. Acad. Sci. USA* 113: E667-E668.
- Lynch, M. 2016. Mutation and human exceptionalism: our future genetic load. *Genetics* 202: 869-875.

- Marinov, G. K., and M. Lynch. 2016. Conservation and divergence of the histone code in nucleomorphs. *Biol. Direct* 11: 18.
- Oughton, D., C. Mays, L. W. Barnthouse, J. C. Beasley, A. Bonisoli-Alquati, C. Bradshaw, J. Brown, S. Dray, S. Geras'kin, T. Glenn, K. Higley, K. Ishida, L. A. Kapustka, W. Kuhne, M. Lynch, T. Mappes, S. Mihok, A. P. Møller, C. Mothersill, T. A. Mousseau, J. Otaki, E. Pryakhin, O. E. Rhodes, Jr., B. Salbu, and P. Strand. 2016. Addressing ecological effects of radiation on populations and ecosystems to improve protection of the environment against radiation: Agreed statements from a consensus symposium. *J. Environ. Radioactivity* 158/159: 21-29.
- Long, H., S. F. Miller, C. Strauss, C. Zhao, L. Cheng, Z. Ye, K. Griffin, R. Te, H. Lee, C. C. Chen, and M. Lynch. 2016. Antibiotic treatment enhances the genome-wide mutation rate of target cells. *Proc. Natl. Acad. Sci. USA* 113: E2498-E2505.
- Kucukyildirim, S., H. Long, W. Sung, S. F. Miller, T. G. Doak, and M. Lynch. 2016. The rate and spectrum of spontaneous mutations in *Mycobacterium smegmatis*, a bacterium naturally devoid of the post-replicative mismatch repair pathway. *G3: Genes|Genomes|Genetics* 6: 2157-2163.
- Sung, W., M. S. Ackerman, M. Dillon, T. Platt, C. Fuqua, V. Cooper, and M. Lynch. 2016. Evolution of the insertion-deletion mutation rate across the tree of life. *G3: Genes|Genomes|Genetics* 6: 2583-2591.
- Lynch, M., M. Ackerman, J.-F. Gout, H. Long, W. Sung, W. K. Thomas, and P. L. Foster. 2016. Genetic drift, selection, and evolution of the mutation rate. *Nature Rev. Genetics* 17: 704-714.
- Lynch, M. 2016. Mutation, eugenics, and the boundaries of science. *Genetics* 204: 825-827.
- Raborn, R. T., K. Spitze, V. P. Brendel, and M. Lynch. 2016. An atlas of promoters in the *Daphnia* genome revealed by comprehensive mapping of 5'-mRNA ends. *Genetics* 204: 593-612.
- Long, H., M. G. Behringer, E. Williams, R. Te, and M. Lynch. 2016. Similar mutation rates but highly diverse mutation spectra in ascomycete and basidiomycete yeasts. *Genome Biol. Evol.* 8: 3815-3821.
- Long, H., D. J. Winter, A. Y.-C. Chang, W. Sung, S. H. Wu, M. Balboa, R. B. R. Azevedo, R. A. Cartwright, M. Lynch, and R. A. Zufall. 2016. Low base-substitution mutation rate in the germline genome of the ciliate *Tetrahymena thermophila*. *Genome Biol. Evol.* 8: 3629-3639.
- Dillon, M. M., W. Sung, M. Lynch, R. Sebra, and V. S. Cooper. 2017. Genome-wide biases in the rate and molecular spectrum of spontaneous mutations in *Vibrio cholera* and *Vibrio fischeri*. *Mol. Biol. Evol.* 34: 93-109.
- Lynch, M., and G. K. Marinov. 2017. Membranes, energetics, and evolution across the prokaryote-eukaryote divide. *ELife* 6: e20437.
- Jiang, X., H. Tang, Z. Ye, and M. Lynch. 2017. Insertion polymorphisms of mobile elements in sexual and asexual populations of *Daphnia pulex*. *Genome Biol. Evol.* 9: 362-374.
- Johri, P., S. Krenek, G. K. Marinov, T. G. Doak, T. Berendonk, and M. Lynch. 2017. Population genomics of *Paramecium* species. *Mol. Biol. Evol.* 34: 1194-1216.
- Bright, L. J., J.-F. Gout, and M. Lynch. 2017. Early stages of functional diversification in the Rab GTPase gene family revealed by genomic and functional studies in *Paramecium* species. *Mol. Biol. Cell* 28: 1101-1110.
- Lynch, M., M. Ackerman, K. Spitze, Z. Ye, and T. Maruki. 2017. Population genomics of *Daphnia pulex*. *Genetics* 206: 315-332.

- Ackerman, M. S., P. Johri, K. Spitze, S. Xu, T. Doak, K. Young, and M. Lynch. 2017. Estimating coefficients of pairwise relatedness using population-genomic data. *Genetics* 206: 105-118.
- Maruki, T., and M. Lynch. 2017. Genotype calling from population-genomic sequencing data. G3: Genes|Genomes|Genetics 7: 1393-1404.
- Ye, Z., S. Xu, K. Spitze, J. Asselman, X. Jiang, M. S. Ackerman, J. Lopez, B. Harker, R. T. Raborn, M. E. Pfrender, and M. Lynch. 2017. Comparative genomics of the *Daphnia pulex* species complex. G3: Genes|Genomes|Genetics 7: 1405-1416.
- Sun, Y., K. E. Powell, W. Sung, M. Lynch, M. A. Moran, and H. Luo. 2017. Spontaneous mutations of a model heterotrophic marine bacterium. *ISME J.* 11: 1713-1718.
- Strauss, C., H. Long, C. E. Patterson, R. Te, and M. Lynch. 2017. Genome-wide mutation rate response to pH change in the coral reef pathogen *Vibrio shilonii* AK1. *MBio* 8: e01021-17.
- Gout, J.-F., W. Li, C. Fritsch, A. Li, S. Haroon, L. Singh, D. Hua, H. Fazelinia, S. Seeholzer, M. Lynch, and M. Vermulst. 2017. The landscape of transcription errors in eukaryotic cells. *Science Advances* 3: e1701484.
- Tincher, C., H. Long, M. G. Behringer, N. Walker, and M. Lynch. 2017. The glyphosate-based herbicide Roundup® does not elevate genome-wide mutagenesis of *Escherichia coli*. G3: Genes|Genomes|Genetics 7: 3331-3335.
- Marasco, M., W. Li, M. Lynch, and C. S. Pikaard. 2017. Catalytic properties of RNA polymerases IV and V: accuracy, nucleotide incorporation, and rNTP/dNTP discrimination. *Nucleic Acids Res.* 45: 11315-11326.
- Long, H., W. Sung, S. Kucukyildirim, E. Williams, S., W. Guo, C. Patterson, C. Gregory, C. Strauss, C. Stone, C. Berne, D. Kysela, W. R. Shoemaker, M. Muscarella, H. Luo, J. T. Lennon, Y. V. Brun, and M. Lynch. 2017. Evolutionary determinants of genome-wide nucleotide composition. *Nature Ecol. Evol.* 2: 237-240.
- Warren, W. C., R. García-Pérez, S. Xu, K. P. Lampert, D. Chalopin, M. Stöck, L. Kuderna, P. Minx, M. J. Montague, C. Tomlinson, L. W. Hillier, D. N. Murphy, J. Wang, Z. Wang, T. Marques-Bonet, C. Macias Garcia, G. W. C. Thomas, M. W. Hahn, J.-N. Volff, F. Farias, B. Aken, K. D. Pruitt, S. Kneitz, M. Lynch, and M. Schartl. 2018. The celibate genome of the Amazon molly, *Poecilia formosa*. *Nature Ecol. Evol.* 2: 669-679.
- Senra, M. V. X., W. Sung, M. Ackerman, S. F. Miller, V. F. Vizzoni, M. Lynch, and C. A. G. Soares. 2018. An unbiased genome-wide view of the mutation rate and spectrum of the endosymbiotic bacterium *Teredinibacter turnerae*. *Genome Biol. Evol.* 10: 723-730.
- Lynch, M. 2018. Phylogenetic diversification of cell biological features. *Elife* 7: e34820.
- McCully, A. L., M. G. Behringer, J. R. Gliessman, E. V. Pilipenko, J. L. Mazny, M. Lynch, D. A. Drummond, J. B. McKinlay. 2018. An *Escherichia coli* nitrogen starvation response is important for mutualistic coexistence with *Rhodospseudomonas palustris*. *Appl. Environ. Microbiol.* (in press).
- Long, H., T. G. Doak, and M. Lynch. 2018. Limited mutation rate variation within the *Paramecium aurelia* species complex. G3: Genes|Genomes|Genetics (in press).
- Long, H., and M. Lynch. 2018. Specificity of the DNA mismatch repair system (MMR) and mutagenesis bias in bacteria. *Mol. Biol. Evol.* (in press).
- Jiang, X., H. Tang, and M. Lynch. 2018. A maximum-likelihood approach to estimating the insertion frequencies of transposable elements from population sequencing data. *Mol. Biol. Evol.* (in revision).

Hagner, K., S. Setayeshgar, and M. Lynch. 2018. The effect of stochastic gene expression on protein multimerization. *Biophys. J.* (submitted).

Hagner, K., S. Setayeshgar, P. Higgs, and M. Lynch. 2018. The evolution of protein multimerization. *Phys. Rev.* (submitted).

Books:

Lynch, M., and J. B. Walsh. 1998. *Genetics and Analysis of Quantitative Traits*. Sinauer Assocs., Inc., Sunderland, MA.

With 14 other committee members, for the National Research Council. 1995. *Science and the Endangered Species Act*. National Academy Press, Washington, DC.

Lynch, M. 2007. *The Origins of Genome Architecture*. Sinauer Assocs., Inc., Sunderland, MA.

Walsh, J. B., and M. Lynch. 2018. *Evolution and Selection of Quantitative Traits*. Sinauer Assocs., Inc., Sunderland, MA.

Lynch, M. *The Origins of Cellular Features*. (expected publication, 2020).

Post-doctoral associates (current and former): Charles Baer, Robert Belsey, Megan Behringer, Jeffrey Blanchard, Lydia Bright, Francesco Catania, John Colbourne, Teresa Crease, Melania Cristescu, Dee Denver, Thomas Doak, Jeffrey Dudycha, Brian Eads, Suzanne Edmands, Allan Force, Michael Fugate, Xiang Gao, Jean Francois Gout, Kevin Higgins, Laura Higgins, Wei-Chin Ho, David Houle, Jason Jia, Xiao-qian Jiang, Sibel Kucukyildirim, Niles Lehman, Hong-An Long, Ignasi Lucas, Georgi Marinov, Emilia Martins, Takahiro Maruki, Paul McElheny, Phil Morin, Martin O’Hely, Carolina Penalva-Arana, Susan Ratner, Barrie Robison, Stewart Schultz, Douglas Scofield, Ken Spitze, Way Sung, Yoshi Tanaka, Abraham Tucker, Larissa Vassilieva, John Willis, Sen Xu, Zhiqiang Ye.

Visiting associates (current and former): Erika Aguirre, Ricardo Alia, Scott Baird, Louis Marie Bobay, Vittorio Boscaro, Reinhard Bürger, John Conery, Teresa Crease, Yana Eglit, Wilfried Gabriel, Thomas Hansen, Elizabeth Housworth, Lawrence Kirkendall, Alex Kondrashov, Peter Larsen, Thomas Little, Marcus Senra, Thomas Titus, Sara Via, Ting Wang, Francois Wurmser, Fumin Zhang, Jianye Zhang.

Ph. D. students (current and former): Matthew Ackerman, Desiree Allen, Stephan Baehr, Elizabeth Bohuski, Jennifer Britt, David Butcher, Chi Chun Chen, Hong-Wen Deng, Suzanne Estes, Allan Force, Kyle Hagner, Parul Johri, Vaishali Katju, Travis Kibota, Britt Koskella, Wenli Li, Weiyi Li, Timothy Licknack, Casey McGrath, Samuel Miller, Kendall Morgan, Angela Omilian, Susanne Paland, Michael Pfrender, Aaron Richardson, Sarah Schaack, Margaret Snoke, Ryan Stikeleather, Barry Sullender, Ken Spitze, Michael Vanni, Lawrence Weider.

Masters students (current and former): Deborah Allen, Gary Henderson, Justin Hicks, Xin Hong, Micah Jordan, Scott Kolpak, Leigh Latta, Lisa Nass, Kevin Simonelic, Hui-Hua Sun, Anna Toline.

Additional Invited Speaking Engagements (since 1995):

1995, National Marine Fisheries Service, Symposium on Genetic Issues in Salmonid Hatcheries.

1995, Pennsylvania State University.

1995, Arizona State University.

1995, Duke University.

1995, University of Chicago.
1996, University of Alaska.
1996, North American Forestry Genetics Association.
1996, University of British Columbia.
1996, National Marine Fisheries Service, Symposium on Risk Analysis in Salmonids.
1997, Special Symposium on Inbreeding and Outbreeding in Salmonids, Juneau.
1997, University of Michigan.
1997, University of Arizona.
1997, Environmental Mutagen Society, Symposium Speaker, Minneapolis.
1997, University of Minnesota.
1997, University of Maryland, Symposium on Small Populations.
1997, Society for the Study of Evolution, Symposium on Deleterious Mutation, Boulder.
1997, University of Queensland, Australia.
1997, LaTrobe University, Australia.
1997, Florida State University.
1998, Sloan Symposium on Limits to Knowledge in Evolution, University of California at Riverside.
1998, Oregon State University.
1998, University of Madrid, El Escorial, Conservation of Genetic Resources.
1998, University of Texas Health Science Center, Houston.
1998, Symposium on Evolution of Asexual vs. Sexual Reproduction, La Sage, Switzerland.
1998, University of Nevada at Reno.
1998, University of California at Davis.
1999, Indiana University.
1999, Washington State University.
1999, New Mexico State University.
1999, North Carolina State University.
1999, European Society of Evolutionary Biology, Barcelona.
1999, University of Helsinki, Finland.
1999, Uppsala University, Norway.
1999, AIBS Presidents' Summit, Washington, D. C.
1999, University of Oklahoma.
1999, NSF/EC Workshop on the Use of Molecular Tools in the Study of Ecology.
2000, Salmon Research in the Next Millenium, Santa Barbara, CA.
2000, University of Florida.
2000, State University of New York at Stony Brook.
2000, University of Missouri at Kansas City.
2000, Evolution: From Molecules to Ecosystems, University of Valencia, Spain.
2000, Sloan Symposium on Limits to Knowledge in Science, Columbia University.
2001, Distinguished Speaker Series, Beyond the Human Genome Project, Harvey Mudd College.
2001, Jacques Monod Symposium on Gene Duplication, Aussois, France.
2001, Fred Hutchinson Cancer Research Center, Seattle.
2001, University of Southern California.
2001, Whole Genome Workshop, DIMACS Conference, Rutgers University.
2001, Biophysics and Biochemistry, Oregon State University.
2001, Ecological and Evolutionary Genomics Symposium, University of Lausanne.
2001, Wright State University.
2001, Hatchery Symposium, National Marine Fisheries Service, Seattle.
2001, University of Utah.
2001, Linking Molecular Insights and Ecological Research, Stanford University.
2001, University of Kentucky.
2002, Workshop on the Development of an Evolutionary Synthesis Center, NSF.
2002, University of Illinois.
2002, Stanford University.
2002, Symposium on Ecological Genomics, Ecological Society of America.
2002, American Genetics Association, Symposium on Molecular Evolutionary Genetics.

2002, Bioinformatics 2002, Bergen, Norway.
2002, Symposium on Long-term Selection, University of Illinois.
2002, Michigan State University.
2002, Duke University.
2003, Yale University.
2003, University of Wisconsin, Madison.
2003, Bioinformatics in the Post-genomic Era, Stockholm.
2003, Symposium on Ecological Genetics, Leuven, Belgium.
2003, Symposium Celebrating William Hill's Honorary Doctorate, North Carolina State University.
2003, Mol. Biol. Evol. Symposium, Functional Evolutionary Genomics of Gene Duplication.
2003, Symposium on the Developmental Basis of Evolutionary Change, University of Chicago.
2003, Mathematical and Statistical Problems in Genome Science, University of Minnesota.
2003, University of Wisconsin, Milwaukee.
2004, Committee on Genetics, University of Chicago.
2004, Center for Gene Research and Biotechnology, Oregon State University.
2004, Gordon Conference on Molecular Evolution.
2004, Evolutionary Genomics Symposium, University of Arizona.
2004, Comparative Genomics of Vertebrates, La Londe Les Maures, France.
2004, Department of Biology, Notre Dame University.
2004, Ecological Genomics Symposium, Kansas State University, Kansas City.
2004, Brown University.
2004, University of Michigan.
2004, Harvard University.
2004, University of Valencia.
2005, Department of Genome Sciences, University of Washington.
2005, Department of Biology, McMaster University.
2005, University of New Mexico.
2005, University of Buffalo.
2005, Princeton University.
2005, Department of Biology, University of Pennsylvania.
2005, Max Planck Institute for Developmental Biology, Tübingen.
2005, Symposium on Phenotypic Diversity and Evolution, Wenner-Gren Foundation, Sweden.
2005, NESCent Viral Tree of Life Working Group, Durham, NC.
2005, Symposium on Computational Genomics and Evolutionary Biology, Georgia Tech.
2006, University of Maryland.
2006, University of Massachusetts.
2006, University of Idaho.
2006, University of Iowa.
2006, NAS Sackler Colloquium on Adaptation and Complex Design, Irvine.
2006, University of Lausanne.
2006, Pennsylvania State University.
2006, Autonomous University of Barcelona.
2007, University of Rochester.
2007, Evolutionary Genomics Workshop, Instituto Gulbenkian de Ciencia, Lisbon, Portugal.
2007, University of Michigan.
2007, University of Iceland.
2007, FASEB Ciliate Molecular Genetics Meeting, Tucson.
2008, University of Lyon, France.
2008, Portugaliae Genetica Symposium, University of Porto, Portugal.
2008, Advance Talk, Kansas State University.
2008, Genetics Society Symposium on Evolution of Recombination, University of Bath.
2008, Public Lecture on the Genomic Revolution, Sao Paulo, Brazil.
2008, Evolution Symposium, University of Pennsylvania.
2008, Department of Biology, New York University.
2008, Memorial Symposium of the International Prize for Biology 2008, Sendai, Japan.

2008, Marine Biology Laboratory, Woods Hole.
2009, University of Calgary.
2009, University of Lyon.
2009, Dean's Darwin Symposium, University of California, San Diego.
2009, Conservation Genetics Symposium, University of Chicago.
2009, Evolution Symposium, Max Planck Society.
2009, National Academy of Sciences Sackler Colloquium on Evolution in Health and Medicine.
2009, Monterey Bay Aquarium.
2009, FASEB Ciliate Molecular Biology Meetings.
2009, Evolution Symposium, State University of New York at Stony Brook.
2009, Conference on Next-Generation Sequencing, Barcelona.
2009, Jackson Lab, Bar Harbor, Maine.
2009, Mathematics Institute, University of Tennessee.
2009, Center for Genome Research and Biocomputing, Oregon State University.
2009, Center for Advanced Studies, Princeton University.
2009, University of Arizona.
2010, University of Missouri.
2010, Kavli Institute, Workshop on Cellular Evolution, Santa Barbara.
2010, University of California at Santa Barbara.
2010, Department of Biology, Georgia Tech.
2010, Mutagenesis: What it means and how it has changed, Banbury Center, Cold Spring Harbor.
2010, SMBE Symposium on Population-size and Genome Evolution, University of Lyon.
2010, Workshop on Ciliate Endosymbionts, Pisa, Italy.
2010, Center for Comparative and Population Genomics, Cornell University.
2010, Biodiversity Research Center, University of British Columbia.
2010, Gulbenkian Institute, Lisbon, Portugal.
2010, Graduate-student Invited Speaker, North Carolina State University.
2011, Ecology and Evolutionary Biology, University of Arizona.
2011, Ecology and Evolutionary Biology, University of California, Irvine.
2011, Kavli Institute, Workshop on Origins of Complex Adaptations, Aspen.
2011, University of Massachusetts Medical School.
2011, Gordon Conference, Ecological and Evolutionary Genomics.
2011, Otto Warburg Summer School on Evolutionary Genomics, Max Planck Institute for Molecular Genetics.
2011, Summer School on Quantitative Evolutionary and Comparative Genomics, Okinawa, Japan.
2011, Evolutionary Genomics Summer Course, Kunming Institute of Zoology, Chinese Academy of Science.
2011, Biological Sciences, University of Nebraska.
2011, Genetics Colloquium, University of Wisconsin.
2011, National Center for Biotechnology Information, NIH, Bethesda.
2012, Department of Biology, Duke University.
2012, Evolution of Eukaryotes, National Centre for Biological Sciences, Bangalore, India.
2012, Dept. of Genome Sciences, University of Washington.
2012, Symposium on the Neutral Theory, Society for Molecular Biology and Evolution, Dublin, Ireland.
2012, Symposium on the Analysis of High-throughput Sequence Data, Society for Molecular Biology and Evolution.
2012, Summer School on Quantitative Evolutionary and Comparative Genomics, Okinawa, Japan.
2012, Harvard University.
2012, University of Nebraska.
2012, Colorado State University.
2012, University of Chicago.
2013, University of Miami.
2013, Kavli Institute of Theoretical Physics, Cooperation and Major Evolutionary Transitions, Santa Barbara.
2013, Max Planck Institute for Developmental Biology, Tübingen, Germany.
2013, Evolutionary Systems Biology, Konrad Lorenz Institute, Vienna.
2013, University of Wyoming.
2013, Max Planck Institute of Immunology and Epigenetics, Freiburg, Germany.
2013, OIST Summer School on Integrative Biology, Okinawa, Japan.

2013, Genetics Symposium, University of Florida.
2014, Baylor College of Medicine.
2014, California Institute of Technology.
2014, University of Southern California.
2014, Uppsala University, Sweden.
2014, Ohio State University.
2014, University of Laval.
2014, EMBO Junior Investigator Program, Barcelona.
2014, Frontiers in Ciliate Genome Evolution, Adaptation, and Symbiosis, Pisa, Italy.
2015, Genetics, University of Georgia.
2015, Gordon Conference on Evolutionary Mechanisms.
2015, Nanjing University, China.
2015, Fudan University, China.
2015, National Institute for Mathematical and Biological Synthesis, Knoxville, Tennessee.
2015, Evolutionary Cell Biology Symposium, Janelia Farms.
2015, University of South Carolina.
2015, Ciliate Molecular Biology Conference, Camerino, Italy.
2015, Human Mutation Rate Symposium, Max Planck Institute for Evolutionary Anthropology.
2015, University of Texas Southwest Medical School.
2015, Modern Problems of Genetics, Radiobiology, Radioecology, and Evolution, St. Petersburg, Russia.
2015, Ecological Genomics Symposium, Manhattan, Kansas.
2015, University of Umea, Sweden.
2015, Molecular, Cell, and Developmental Biology, U. Colorado.
2015, International Consensus Symposium, International Union of Radioecology, Miami.
2016, Applied Bioinformatics in the Life Sciences, Leuven, Netherlands.
2016, Frontiers in Biology, Wake Forest University.
2016, Canadian Institute for Advanced Research, Integrated Microbial Biodiversity Program, Toronto.
2016, Georgia Institute of Technology.
2016, University of Rochester.
2016, Weizmann Institute of Science, Israel.
2017, Vienna Biocenter, Austria.
2017, Arizona State University.
2017, University of Toronto.
2017, McGill University.
2017, EMBO Meeting, Comparative Genomics of Eukaryotic Microorganisms, Costa Brava, Spain.
2017, Frontiers in Evolutionary Ecology and Genomics, Beijing Normal University.
2017, Evolution in the Time of Genomics, Stazione Zoologica, Naples, Italy.
2017, Evolutionary Systems Biology of Cells, SMBE Symposium, Austin, Texas.
2017, International Centre for Theoretical Science, Bangalore, India.
2017, University of Minnesota.
2017, Hopkins Marine Station, Monterey, CA.
2017, Pennsylvania State University.
2018, Department of Ecology and Evolutionary Biology, University of Michigan.
2018, Department of Systems Biology, Columbia University.
2018, University of California, San Diego.
2018, Ocean University of China, Qingdao.
2018, Evolution of Biomolecular Networks, Lorentz Workshop, Netherlands.
2018, Origin of the Eukaryotic Cell, Janelia Farms.
2018, Max Planck Institute, Plön, Germany.
2018, Asian Science Camp, Manado, Indonesia.
2018, Cell Biology and Physiology Center, National Heart, Lung and Blood Institute, NIH.
2018, University of Colorado School of Medicine.
2018, Chan Zuckerberg Biohub, San Francisco.
2019, Center for Advanced Studies, Oslo, Norway.