

Michael Lynch

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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 Committee on Assessing the Taxonomic Status of the Red Wolf and the Mexican Gray Wolf, 2018.

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.
 Induction, Auburn Alumni Hall of Distinction – 2019.
 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.
 2018, Distinguished Lecture Series, University of North Carolina, Charlotte.
 2019, Distinguished Speaker, National Science Foundation.
 2020, Opening Speaker, International Conference of Quantitative Genetics, Brisbane, Australia.

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. Loeschke (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. Loescheke (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.
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- Mahmoudabadi, G., R. Phillips, M. Lynch, and R. Milo. 2019. Defining the energetic costs of cellular structures. (Submitted to *J. Cell Biol.*).
- Zheng, W., C. Wang, M. Lynch, and S. Gao. 2019. The compact macronuclear genome of the ciliate *Halteria grandinella*: a transcriptome-like genome with 29,000 nanochromosomes. (Submitted to *Proc. Natl. Acad. Sci. USA*).
- Maruki, T., Z. Ye, and M. Lynch. 2019. Genomic analyses of population structure reveal food as a primary driver of local adaptation in *Daphnia pulex*. (Submitted to *Genetics*).
- Lynch, M., B. Haubold, P. Pfaffelhuber, and T. Maruki. 2019. Inference of historical population-size changes with allele-frequency data. (Submitted to *Genetics*).
- Lynch, M., Z. Ye, and T. Maruki. 2019. The recombinational landscape in *Daphnia pulex*. (Submitted to *Genetics*).
- Li, W., and M. Lynch. 2019. Universally high transcript error rates in bacteria. (Submitted to *Elife*).
- Lynch, M., W.-C. Ho, and C. P. Kempes. 2019. Evolutionary scaling of maximum growth rates with the drift barrier. (Submitted to *Science Advances*).
- Frisch, C., J.-F. Gout, S. Haroon, A. Towheed, X. Zhang, Y. Song, S. Simpson, D. Wallace, K. Thomas, M. Lynch, and M. Vermulst. 2019. Genome-wide surveillance of transcription errors in response to genotoxic stress. (In revision, *Nature Comm.*)
- Keith, N., C. E. Jackson, K. Young, S. P. Glaholt, M. Lynch, and J. R. Shaw. 2019. Genome-wide analysis of cadmium-induced germline mutations over 1,123 generations. (Submitted to *Genome Research*).
- Gout, J.-F., P. Johri, O. Arnaiz, T. G. Doak, A. Couloux, K. Labadie, F. Guérin, S. Duharcourt, S. Malinsky, S. Bhullar, E. Meyer, L. Sperling, and M. Lynch. 2019. Universal trends of post-duplication evolution revealed by the genomes of 14 *Paramecium* species sharing an ancestral whole-genome duplication. (in prep.)

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*. Oxford Univ. Press, Oxford, UK.

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, Boguljub Trickovic, 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, Shannon Snyder, 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, Biodesign Institute, 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, 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, SMBE Satellite Meeting, Uniting Molecular Population Genetics and Quantitative Genetics, Vienna.
2019, Center for Advanced Studies, Oslo, Norway.
2019, University of Otago, New Zealand.
2019, University of Auckland, New Zealand.
2019, University of Canterbury, New Zealand.
2019, Evolution and Ecology of Cancer, Hinxton, UK.
2019, Environmental Mutagenesis and Genomics Society, Washington, DC.
2019, Institute for Quantitative and Computational Biosciences, UCLA.
2019, Origin of Eukaryotes, Agouron Institute, Pasadena.
2020, Biology, Portland State University.