

Jianzhi “George” Zhang

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EDUCATION

- 1988–1992 B.S. in Genetics, Fudan University, Shanghai, China
- 1992–1994 M.S. Program in Genetics, Fudan University, Shanghai, China
- 1994–1998 Ph.D. in Genetics, Pennsylvania State University, University Park, PA.
Thesis: Patterns and mechanisms of molecular evolution: statistical methods and data analysis. Advisor: Dr. Masatoshi Nei

EMPLOYMENT

- 1993–1994 Teaching Assistant, Institute of Genetics, Fudan University, Shanghai, China
- 1994–1998 Research Assistant and Teaching Assistant, Department of Biology, Pennsylvania State University
- 1999–2001 Fogarty Postdoctoral Fellow, National Institute of Allergy and Infectious Diseases, National Institutes of Health. Advisor: Dr. Helene F. Rosenberg
- 2001–2005 Assistant Professor, Department of Ecology and Evolutionary Biology, University of Michigan
- 2005–2009 Associate Professor, Department of Ecology and Evolutionary Biology, University of Michigan
- 2009–2013 Professor, Department of Ecology and Evolutionary Biology, University of Michigan
- 2013– Marshall W. Nirenberg Collegiate Professor, Department of Ecology and Evolutionary Biology, University of Michigan

OTHER AFFILIATIONS IN UNIVERSITY OF MICHIGAN

Center for Computational Medicine and Bioinformatics
Center for Statistical Genetics
Michigan Institute for Computational Discovery and Engineering
NIH Training Program in Genetics
NIH Training Program in Genome Sciences

HONORS AND AWARDS

Undergraduate Scholarship, Fudan University, 1989-1992.

Multiple travel awards for traveling to national and international conferences, Institute of Molecular Evolutionary Genetics, Pennsylvania State University, 1996-1998.

Fogarty Fellowship, Fogarty International Center, National Institutes of Health, 1999-2001.

Robert H. Freeman Faculty Award, College of Literature, Science, and the Arts, University of Michigan, 2005

Collegiate Professorship, College of Literature, Science, and the Arts, University of Michigan, 2013

Fellow, American Association for the Advancement of Science, 2017

FUNDING

“Position effects on gene expression level and noise” (R01GM120093), \$1,203,000, National Institute of General Medical Sciences, National Institutes of Health, 9/1/2016-5/31/2020. PI

“A comparative genomics approach to the evolution of marine animals and their genomes”, \$300,000, Korean Institute of Marine Science & Technology, 9/1/2015-4/30/2019. Subcontract PI

"Deep learning for phylogenetic inference", \$80,000, Michigan Institute for Computational Discovery and Engineering (MICDE) Catalyst Grant, 5/1/2018-4/30/2019. PI (Co-PI: Yuanfang Guan)

"Sperm Protamine Proteins: A potential novel carrier of epigenetic memory", \$100,000, Innovation Initiative Award, Endowment for the Basic Sciences, University of Michigan Medical School, 9/1/2017-8/31/2018. Co-PI (PI: Sue Hammound)

“Genomic studies of antagonistic pleiotropy” (R01GM103232), \$1,160,000, National Institute of General Medical Sciences, National Institutes of Health, 9/1/2013-7/31/2018. PI

"DISSERTATION RESEARCH: The fitness landscape of a yeast tRNA gene" (DEB-1501788), \$19,571, National Science Foundation, 4/1/2015-3/31/2017. PI (Co-PI: Chuan Li)

“Yeast as a model for understanding heterosis” (MCB-1329578), \$535,000, National Science Foundation, 12/1/2013-11/30/2016. PI

“MCubed: transcriptome evolution”, \$60,000, Office of the Vice President for Research, University of Michigan, 4/1/2013-3/31/2015. PI (Co-PIs: Stephen Smith and Alexey Kondrashov).

“Yeast as a model organism for understanding heterosis”, \$15,000, Office of the Vice President for Research, University of Michigan, 4/1/2013-3/31/2014. PI.

“Functional genomic approaches to duplicate gene evolution” (R01GM67030), \$1,430,000, National Institute of General Medical Sciences, National Institutes of Health, 3/1/2009-11/28/2013. PI.

“Evolution of vertebrate sensory genes” (R01GM80285), \$808,640, National Institute of General Medical Sciences, National Institutes of Health, 7/1/2007-12/30/2011. PI.

“RNases for understanding the origin of new gene function” (R01GM67030), \$950,000, National Institute of General Medical Sciences, National Institutes of Health, 1/1/2003-12/31/2008. PI.

“Understanding duplicate gene evolution by computational and experimental functional genomics”, \$80,000, Center for Computational Medicine and Biology, University of Michigan, 11/1/2006-10/31/2008. PI (Co-PI: Anuj Kumar).

“Evolution of honeybee sex determination genes”, \$15,000, Office of the Vice President for Research, University of Michigan, 1/1/2004-12/31/2004. PI.

“Molecular evolutionary mechanisms of origins of new gene functions”, \$15,000, Rackham Graduate School, University of Michigan, 1/1/2002-12/31/2003. PI.

RESEARCH INTERESTS

Evolutionary genomics and evolutionary systems biology

TEACHING AT UNIVERSITY OF MICHIGAN

BIO173- Authentic Research Connection: Experimental Evolution of Yeast (2 terms, with Tim James)

BIO305-Genetics (8 terms, with Janine Maddock, Tzvi Tzfira, Andrzej Wierzbicki, or Monica Dus)

EEB490-Population Genetics (2 terms)

EEB512-Molecular Systematics and Evolution (7 terms; 2 with David Mindell)

EEB512-Molecular and Genomic Evolution (3 terms)

EEB800-Molecular Evolution Journal Club (6 terms)

EEB335-Biodiversity Research Seminars (5 terms)

EEB410-EEB Capstone Seminar (6 terms, with Jessica Middlemis-Maher, Knute Nadelhoffer, Mark Hunter, or Lydia Beaudrot)

TEACHING OUTSIDE UNIVERSITY OF MICHIGAN

Molecular evolution (6 hours), Kunming Institute of Zoology, Kunming, China, July 2004

Molecular evolution (6 hours), Chinese Academy of Sciences, Shanghai, China, December 2010

Molecular evolution (5 hours), Tsinghua University, Beijing, China, December 2010

Molecular evolution (3 hours), Zhejiang University, Hangzhou, China, May 2017

PROFESSIONAL MEMBERSHIPS

American Association for the Advancement of Science

Society for Molecular Biology and Evolution

PROFESSIONAL SERVICES

Member, National Center for Biotechnology Information (NCBI) Board of Scientific Counselors, 2014-2019

President-elect (2015), President (2016), and Past President (2017), Society for Molecular Biology and Evolution

Elected Secretary, Society for Molecular Biology and Evolution, 2007-2009

Bylaws Committee, Society for Molecular Biology and Evolution, 2006

Scientific Committee, Annual Meeting of the Society for Molecular Biology and Evolution, 2008

Global Organizing Committee, Annual Meeting of the Society for Molecular Biology and Evolution, 2011

Chair, Awards Committee, Society for Molecular Biology and Evolution, 2018

Selection Committee, *Molecular Biology and Evolution* Best Student Paper of 2018 Award

Senior Editor (2012-), *Molecular Biology and Evolution*

Associate Editor (2009-), *PLOS Genetics*

Highlights Editor (2011-), *Genome Biology and Evolution*

Associate Editor (2009-), *Genome Biology and Evolution*

Advisory Editorial Board member (2012-), *EMBO Reports*

Editorial Board member (2017-), *National Science Review*

Editorial Board member (2013-), *Biology Direct*

Editorial Board member (2009-), *Journal of Genetics and Genomics*

Area Editor of Evolutionary Genetics, Genomes, and Evolution of Development (2018-), *Oxford Bibliographies in Evolutionary Biology*

Editorial Board member (2010-2015), *Mammalian Genome*

Associate Editor (2009-2013), *Journal of Systematics and Evolution*

Editorial Board member (2007-2008), *Journal of Systematics and Evolution*

Editorial Board member (2008-2012), *Current Zoology*

Associate Editor (2004-2010), *Gene*

Associate Editor (2004-2008), *Molecular Biology and Evolution*

Editorial Board member (2007-2009), *Frontiers of Biology in China*

Guest Editor (2015, 2018), *Proceedings of the National Academy of Sciences of USA*

Guest Academic Editor (2009, 2010), *PLOS Biology*

Guest Associate Editor (2009), *PLOS Genetics*

Guest Associate Editor (2008, 2009, 2017), *PLOS Computational Biology*

Ad hoc reviewer for *Acta Biotheoretica*, *Acta Zoologica Sinica*, *American Journal of Human Biology*, *American Journal of Human Genetics*, *American Naturalist*, *Asian Journal of Andrology*, *Biochemistry*, *Biochimica et Biophysica Acta*, *Bioinformatics*, *Biology Direct*, *Biology Letters*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *BMC Genomics*, *BMC Molecular Biology*, *BMC Systems Biology*, *Briefings in Bioinformatics*, *Cell*, *Cell Reports*, *Cell Research*, *Cell Systems*, *Chaos*, *Chemical Senses*, *Current Biology*, *Current Zoology*, *EMBO Reports*, *Emerging Infectious Diseases*, *eLife*, *Evolution*, *Evolutionary Bioinformatics*, *FEBS Journal*, *FEBS Letters*, *Gene*, *Gene Expression Patterns*, *Genetics*, *Genome*, *Genome Biology*,

Genome Biology and Evolution, Genome Research, Genomics, Heredity, Human Biology, Human Genomics, Human Molecular Genetics, Human Mutation, Journal of Biology, Journal of Evolutionary Biology, Journal of Experimental Zoology, Journal of Genetics and Genomics, Journal of Heredity, Journal of Integrative Plant Biology, Journal of Leukocyte Biology, Journal of Molecular Biology, Journal of Molecular Evolution, Journal of Neuroscience, Journal of Systematics and Evolution, Journal of Theoretical Biology, Mammalian Genome, Mathematical Biosciences, Mechanisms of Development, Molecular Biology and Evolution, Molecular Cancer, Molecular Diversity, Molecular Ecology, Molecular Phylogenetics and Evolution, Molecular Systems Biology, Nature, Nature Communications, Nature Ecology & Evolution, Nature Genetics, Nature Plants, Nature Reviews Genetics, Nature Structural & Molecular Biology, Nucleic Acids Research, PLOS Biology, PLOS Computational Biology, PLOS Genetics, PLOS ONE, Proceedings of the Indian National Science Academy, Proceedings of the National Academy of Sciences of USA, Proceedings of the Royal Society of London (Series B), Science, Scientific Reports, Trends in Ecology and Evolution, Trends in Genetics, and Yeast.

Grant reviewer for US National Science Foundation, UK Research Council (Biotechnology and Biological Sciences), UK Medical Research Council, Poland National Science Center, and China National Natural Science Foundation.

Ad hoc member, NIH Study Section on Genetic Variation and Evolution, 2006, 2007
Regular member, NIH Study Section on Genetic Variation and Evolution, 2007-2012
Ad hoc member, NIGMS ESI-MIRA Study Section, 2018
Member, China National Natural Science Foundation microevolution grant review panel, 2013
Member, NSF Division of Environmental Biology pre-proposal review panel, 2014, 2017
Member, NSF Division of Environmental Biology Doctoral Dissertation Improvement Grants review panel, 2016

Evaluator, State Natural Science Award, Chinese government, 2011, 2012
External evaluator, Beijing Institute of Genomics, Chinese Academy of Sciences, 2012
Overseas Evaluator, Chinese Academy of Sciences, 2012-

Evaluator for promotions and tenure: Arizona State University, Cornell University, Georgia Institute of Technology, Iowa State University, Johns Hopkins University, Kent State University, Michigan State University, National Health Research Institutes of Taiwan, Okinawa Institute of Science and Technology, Peking University, Temple University, Texas A&M University, University of Arizona, University College Dublin, University of California at Los Angeles, University of Chicago, University of Illinois at Urbana-Champaign, University of Iowa, University of Missouri, University of Nebraska, University of Toronto, University of Wisconsin at Madison, US National Institutes of Health, Virginia Polytechnic Institute and State University, Wayne State University, University of Missouri, and University of Washington.

Organizer, Evolutionary Systems Biology Symposium, Annual Meeting of the Society for Molecular Biology and Evolution, Tempe, Arizona, May 2006

Co-organizer, Penn State SMBE Symposium on Molecular and Genomic Evolution, University Park, Pennsylvania, March 2011

Organizer, Evolutionary Systems Biology Symposium, Annual Meeting of the Society for Molecular Biology and Evolution, Kyoto, Japan, July 2011

INVITED SEMINARS

National Institute of Allergy and Infectious Diseases, National Institutes of Health, March 1998
National Center for Biotechnology Information, National Institutes of Health, March 1998
Laboratory of Molecular Systematics, Smithsonian Institution, September 1999
Institute of Genetics, Fudan University, Shanghai, China, December 1999
Center for Advanced Research in Biotechnology, University of Maryland, May 2000
Department of Genetics, University of Washington, October 2000
Department of Biology, Texas A&M University, November 2000
Department of Genetics, Rutgers University, November 2000
Department of Anthropology, Rutgers University, November 2000
Department of Ecology and Evolution, SUNY at Stony Brook, November 2000
Department of Biology, University of Michigan, December 2000
Department of Biology and Biochemistry, University of Houston, January 2001
Department of Biological Sciences, University of Iowa, January 2001
Department of Biological Sciences, University of Maryland Baltimore County, February 2001
Department of Biology and Center for Bioinformatics and Computational Biology, University of Maryland at College Park, February 2001
Kunming Institute of Zoology, Chinese Academy of Sciences, April 2001
School of Life Sciences, Zhejiang University, Hangzhou, China, November 2001
Department of Ecology and Evolution, University of Chicago, October 2002
Institute of Molecular Evolutionary Genetics, Pennsylvania State University, November 2002
School of Life Sciences, Peking University, December 2002
Department of Biology, Arizona State University, February 2003
Department of Ecology and Evolution, Fudan University, Shanghai, China, October 2003
Department of Biology, Western Michigan University, March 2004
Department of Evolution, Ecology, and Organismal Biology, Ohio State University, February 2005
Department of Biology, Emory University, February 2005
School of Life Sciences, Sun Yat-Sen University, Guangzhou, China, June 2005
School of Life Sciences, Xiamen University, Xiamen, China, June 2005
Bioinformatics Program, University of Michigan, September 2005
Institute of Bioinformatics, Zhejiang University, Hangzhou, China, December 2005
Department of Human Genetics, University of Michigan, January 2006
Saturday Morning Physics Series, University of Michigan, February 2006
Perinatology Research Branch, National Institute of Child Health and Human Development, NIH, August 2006
Graduate University for Advanced Studies, Hayama, Japan, March 2007
National Institute of Genetics, Mishima, Japan, March 2007
Department of Ecology and Evolution, University of Chicago, April 2007
Department of Biochemistry, Biophysics & Molecular Biology, Iowa State University, November 2007
Department of Biology, University of Maryland at College Park, February 2008

Department of Biology, Pennsylvania State University, February 2008
Institute of Molecular Evolutionary Genetics, Pennsylvania State University, February 2008
Center for Complex Biological Systems, University of California at Irvine, March 2008
Department of Ecology and Evolutionary Biology, University of California at Irvine, March 2008
Department of Anthropology and Department of Organismic Biology and Evolution, Harvard University, April 2008
Department of Biology, University of Nebraska, April 2008
Fred Hutchinson Cancer Research Center, Seattle, April 2008
California Academy of Sciences, San Francisco, August 2008
National Health Research Institutes, Zhunan Town, Taiwan, March 2009 (two seminars)
Biodiversity Research Center, Academia Sinica, Taipei, Taiwan, March 2009
Interdisciplinary Group Seminar, University of Michigan, July 2009
Primate Research Institute, Kyoto University, July 2009
Department of Bioinformatics and Computational Biology, University of Texas M. D. Anderson Cancer Center, December 2009
Institute for Cellular and Molecular Biology, University of Texas at Austin, March 2010
Center for Integrative Genomics and Department of Ecology and Evolution, University of Lausanne, Switzerland, June 2010
Institute of Biochemistry, University of Zurich, Switzerland, June 2010
School of Life Sciences, East China Normal University, Shanghai, China, August 2010
School of Life Sciences, Zhejiang University, Hangzhou, China, September 2010
College of Life Sciences, Fudan University, Shanghai, China, December 2010
CAS-MPG Partner Institute for Computational Biology, Shanghai, China, December 2010
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China, December 2010
Department of Ecology and Evolutionary Biology, University of Michigan, January 2011
Department of Ecology and Evolutionary Biology and Institute of Systems Biology, Yale University, January 2011
Center for Bioinformatics and Computational Biology, University of Iowa, February 2011
Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, March 2011
Center for Computational Medicine and Bioinformatics, University of Michigan, November 2011
Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China, December 2011
BGI-Shenzhen, Shenzhen, China, December 2011
Department of Genetics, University of Wisconsin at Madison, February 2012
Department of Biology, Wayne State University, April 2012
Buchanan Lecturer, Department of Biological Sciences, Bowling Green State University, April 2012 (a public lecture and a departmental seminar)
Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China, December 2012
Institute of Botany, Chinese Academy of Sciences, Beijing, China, December 2012
School of Life Sciences, Wuhan University, Wuhan, China, July 2013
Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, China, July 2013
School of Life Sciences, Nanjing University, Nanjing, China, July 2013
School of Life Sciences, Peking University, Beijing, China, March 2014 (two seminars)
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China,

March 2014

Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan, March 2014
Department of Life Science, National Taiwan University, Taipei, Taiwan, March 2014
National Health Research Institutes, Zhunan Town, Taiwan, March 2014 (two seminars)
Department of Biological Sciences, University of Southern California, November 2014
Department of Biology and Institute for Genetic Medicine, Johns Hopkins University, March 2015

National Center for Biotechnology Information (NCBI), NLM, NIH, April 2015
Division of EcoScience, Ewha Womans University, Seoul, Korea, June 2015
Institute of Biotechnology, National Autonomous University of Mexico, Cuernavaca, Mexico, October 2015 (two seminars)

Bioinformatics Seminar, University of California, Los Angeles, February 2016
Institute for Genomics and Evolutionary Medicine, Temple University, May 2016
Life Sciences Institute, Zhejiang University, July 2016

Department of Molecular and Cellular Biology, University of Arizona, September 2016

Department of Biochemistry and Biophysics, University of Rochester, March 2017

School of Life Sciences, Zhejiang University, May 2017

Sun Yat-sen University School of Medicine, April 2018

Department of Integrated Biosciences, University of Tokyo, July 2018

Department of Biological Sciences, University of Southern Mississippi, October 2018

Quantitative Biology Program, University of California, San Diego, November 2018

Genetics Institute, University of Florida, November 2018

THEOCHEM (The Greater Boston Area Theoretical Chemistry Lecture Series), Massachusetts Institute of Technology, November 2018 (student invited speaker; two seminars)

CONFERENCE PRESENTATIONS

“Color vision of ancestral organisms of higher primates”, The Fourth Annual Meeting of the Society for Molecular Biology and Evolution, Tucson, Arizona, June 1996

“Detection of convergent and parallel evolution at the amino acid sequence level”, Annual Meeting of American Society of Naturalists, Society of Systematic Biology, and Society for the Study of Evolution, Boulder, Colorado, June 1997

“Positive Darwinian selection after gene duplication in primate ribonuclease genes”, The Sixth Annual Meeting of the Society for Molecular Biology and Evolution, Vancouver, Canada, June 1998

“Independent adaptive expansions of the ribonuclease gene family in rodents”, The Fifth International Meeting on Ribonucleases, Warrenton, Virginia, May 1999

“Protein-length distributions for the three domains of life”, Symposium on Genome Diversity and Evolution, and the Annual Meeting of the American Genetic Association, State College, Pennsylvania, June 1999

“Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection”, Joint Annual Meeting of the Society for Molecular Biology and Evolution and American Genetic Association, New Haven, Connecticut, June 2000

“Diversifying selection of the tumor-growth promoter angiogenin in primate evolution”, Symposium on Primate Evolutionary Genetics and Annual Meeting of the American Genetic Association, San Diego, California, May 2001

“Diversifying selection on the tumor-growth promoter angiogenin in primate evolution”, Annual Meeting of American Society of Naturalists, Society of Systematic Biology, and Society for the Study of Evolution, Knoxville, Tennessee, June 2001

“Adaptive evolution of a duplicated pancreatic ribonuclease gene in a leaf-eating monkey”, Symposium on Evolutionary Genomics, Atami, Japan, November 2001 INVITED SPEAKER

“Complementary advantageous substitutions in the evolution of an antiviral RNase of higher primates”, Annual Meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy, June 2002

“Adaptive evolution of a duplicated pancreatic ribonuclease gene in a leaf-eating monkey”, The Sixth International Meeting on Ribonucleases, Bath, UK, June 2002 INVITED SPEAKER

“Accelerated protein evolution and origins of human-specific features”, Symposium on Human Origins and Disease, Cold Spring Harbor, New York, October 2002

“Accelerated protein evolution and origins of human-specific features: FOXP2 as an example”, Symposium on the Molecular Basis of Evolution, Tokyo, Japan, December 2002 INVITED SPEAKER

“Gene duplication and adaptive evolution”, Symposium on Advances in Modern Zoology, Beijing, China, December 2002 INVITED SPEAKER

“Evolutionary deterioration of the vomeronasal pheromone transduction pathway in catarrhine primates”, Annual Meeting of the Society for Molecular Biology and Evolution, Newport Beach, California, June 2003

“Positive selection on protein-length in the evolution of a primate sperm ion channel”, Xiangshan Symposium on Evolutionary Biology, Beijing, China, October 2003 INVITED SPEAKER

“Testing the chromosomal speciation hypothesis for humans and chimpanzees”, Gordon Conference on "Structural, Functional and Evolutionary Genomics", Ventura, California, February 2004 INVITED SPEAKER

“Parallel gene duplication and adaptive evolution of a digestive enzyme in leaf-eating monkeys”, Joint Annual Meetings of the Society for Molecular Biology and Evolution and American Genetic Association, University Park, Pennsylvania, June 2004 INVITED SPEAKER

“Evolution of duplicate genes”, 10th SCBA International Symposium, Beijing, China, July 2004 INVITED SPEAKER

“Evolutionary genetics of human speech/language emergence”, National Academy of Sciences Frontiers of Science Symposia, Beckman Center, California, November 2004 INVITED SPEAKER

“Evolution of the vertebrate RNase A superfamily: glimpses from genome sequences”, The Seventh International Meeting on Ribonucleases, Stara Lesna, Slovak Republic, June 2005 INVITED SPEAKER (presentation read by Dr. Jaap Beintema)

“Why do hubs tend to be essential in protein networks?”, Annual Meeting of the Society for Molecular Biology and Evolution, Tempe, Arizona, May 2006 INVITED SPEAKER

“Evolution of the complementary sex determination gene of honey bees”, International Symposium on Genomics and Evolution, Guangzhou, China, January 2007 INVITED SPEAKER

“Evolution of vertebrate taste receptor genes”, Annual Meeting of the Association for Chemoreception Sciences, Sarasota, Florida, April 2007 INVITED SPEAKER

“Accelerated protein evolution and positive selection in human and chimp lineages”, Wellcome Trust Conference on Evolution of Brain, Behaviour and Intelligence, Hinxton, Cambridge, UK, September 2007 INVITED SPEAKER

“Molecular dissection of primate evolution and human origins”, Wenner-Gren Foundations International Symposium on "Human Evolution", Stockholm, Sweden, November 2008 INVITED SPEAKER

“Contrasting genetic paths to morphological and physiological evolution”, Annual Meeting of the Society for Molecular Biology and Evolution, Iowa City, Iowa, June 2009

“Evolution of vertebrate chemosensory genes”, The 3rd International Symposium of the Biodiversity and Evolution Global COE Project, Kyoto, July 2009 INVITED SPEAKER

“Gene expression noise and evolution”, Darwin-China 200 Conference, Beijing, October 2009 INVITED SPEAKER

“The genetics basis of evolution”, Darwin 2009 Symposium, Stony Brook University, Stony Brook, November 2009 INVITED SPEAKER

“Gene expression noise and evolution”, Symposium on “Biological complexity and

hierarchy: From molecules to cellular networks", Rice University, Houston, December 2009
INVITED SPEAKER

"Measuring the evolutionary rate of protein-protein interaction", Penn State SMBE Symposium on Molecular and Genomic Evolution, Pennsylvania State University, University Park, March 2011 INVITED SPEAKER

"Gene expression noise and evolution", Summer Symposium on Transcriptional Dynamics, Evolution, and Systems Biology, Michigan State University, East Lansing, July 2011 INVITED SPEAKER

"Gene expression noise and evolution", Annual Meeting of the Society for Molecular Biology and Evolution, Kyoto, Japan, July 2011 INVITED SPEAKER

"Evolution of vertebrate *Tlr* taste receptor genes", Annual Meeting of the Japanese Society for Evolutionary Studies, Kyoto, Japan, July 2011 INVITED SPEAKER

"Measuring the evolutionary rate of protein-protein interaction", Young Researchers Conference on Evolutionary Genomics, Tokyo, Japan, August 2011 INVITED SPEAKER

"Evolution of orthologs and paralogs: function, expression, and fitness effect", Annual Meeting of the Society for Molecular Biology and Evolution, Dublin, Ireland, June 2012 INVITED SPEAKER

"Robust developmental cell lineages underlie canalization", International Symposium on "Genetics, Development, and Evolution", Kunming, China, August 2012 INVITED SPEAKER

"The genomic landscape of antagonistic pleiotropy in yeast", EMBO Conference on "Experimental Approaches to Evolution and Ecology", Heidelberg, Germany, October 2012 INVITED SPEAKER

"The genetic architecture of complex traits: A reverse genetic perspective", Symposium on "Multigenic Interactions in Microevolution", Tengchong, China, January 2013 KEYNOTE SPEAKER

"Development cell lineages are robust to cell deaths", Symposium on "Mathematical Tools for Evolutionary Systems Biology", Banff International Research Station, Canada, May 2013 INVITED SPEAKER

"Differential mRNA folding optimizes the tradeoff between translational speed and accuracy", Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, July 2013

"Differential mRNA folding optimizes the tradeoff between translational speed and accuracy", International Symposium of Evolutionary Genetics for Young Investigators, Guangzhou, China, August 2013 INVITED SPEAKER

“Human coding RNA editing is generally nonadaptive”, Symposium on “Molecular Evolution in All Fields of Biology”, Mishima, Japan, November 2013 INVITED SPEAKER

“Yeast intra- and inter-specific variations of gene expression levels are largely neutral”, Annual Meeting of the Society for Molecular Biology and Evolution, Puerto Rico, June 2014 INVITED SPEAKER

“Yeast intra- and inter-specific variations of gene expression levels are largely neutral”, Cold Spring Harbor Asia Meeting on Evolutionary Genetics and Genomics, Suzhou, China, October 2014 INVITED SPEAKER

"Nascent RNA folding mitigates transcription-associated mutagenesis", SMBE Satellite Meeting on Mutation, Repair, and Evolution, Bloomington, May 2015 INVITED SPEAKER

“Evolution of vertebrate taste senses inferred from comparative genomics”, International Symposium on Marine Genomics, Seoul, Korea, June 2015 KEYNOTE SPEAKER

“Human coding RNA editing is generally nonadaptive”, Annual Meeting of the Society for Molecular Biology and Evolution, Vienna, Austria, July 2015

"Diversity in post-transcriptional modifications: adaptive or not?" SMBE Satellite Meeting on RNA Modification and Its Implication on Adaptation and Evolution, Valencia, Spain, May 2016 KEYNOTE SPEAKER

"Testing the neutral hypothesis of phenotypic evolution", Annual Meeting of the Society for Molecular Biology and Evolution, Gold Coast, Australia, July 2016 PLENARY SPEAKER (NEI LECTURER)

"Testing the neutral hypothesis of phenotypic evolution" Forum for Early-Career Evolutionary Geneticists, Kunming, China, July 2016 KEYNOTE SPEAKER

"Diversity in post-transcriptional modifications: adaptive or not?" Genomics Frontiers Symposium, Shenyang, China, July 2016 KEYNOTE SPEAKER

"Diversity in post-transcriptional modifications: adaptive or not?" Symposium on Microevolutionary Processes, Guangzhou, China, December 2016 KEYNOTE SPEAKER

"Evolutionary adaptations to new environments generally reverse plastic phenotypic changes" Forum for Early-Career Evolutionary Geneticists, Chengdu, China, May 2017 KEYNOTE SPEAKER

"The fitness landscapes of a tRNA gene in multiple environments: G×E is pervasive yet simple", Annual Meeting of the Society for Molecular Biology and Evolution, Austin, July 2017

"Evolutionary adaptations to new environments generally reverse plastic phenotypic changes", Molecular Evolution & Medicine Symposium, Philadelphia, September 2017 INVITED SPEAKER

"Multi-environment fitness landscapes of a yeast tRNA gene", The 1st AsiaEvo Conference, Shenzhen, China, April 2018 INVITED SPEAKER

"Diversity in posttranscriptional modification: Adaptations or cellular errors?", Annual Meeting of the Society for Molecular Biology and Evolution, Yokohama, Japan, July 2018 INVITED SPEAKER

"Evolution of RNA editing", Gordon Research Conference on RNA editing, Ciocco, Italy, March 2019 INVITED SPEAKER

PUBLICATIONS

1. **Zhang, J.**, and M. Nei (1996) Evolution of Antennapedia-class homeobox genes. *Genetics* 142:295-303.
2. **Zhang, J.**, and M. Nei (1997) Accuracies of ancestral amino acid sequences inferred by parsimony, likelihood, and distance methods. *J. Mol. Evol.* 44:S139-S146.
3. **Zhang, J.**, and S. Kumar (1997) Detection of convergent and parallel evolution at the amino acid sequence level. *Mol. Biol. Evol.* 14:527-536.
4. **Zhang, J.**, S. Kumar, and M. Nei (1997) Small-sample tests of episodic adaptive evolution: a case study of primate lysozyme genes. *Mol. Biol. Evol.* 14:1335-1338.
5. Gu, X., and **J. Zhang** (1997) A simple method for estimating the parameter for substitution rate variation among sites. *Mol. Biol. Evol.* 14:1106-1113.
6. Nei, M., **J. Zhang**, and S. Yokoyama (1997) Color vision of ancestral organisms of higher primates. *Mol. Biol. Evol.* 14:611-618.
7. **Zhang, J.**, and X. Gu (1998) Correlation between the substitution rate and rate variation among sites in protein evolution. *Genetics* 149:1615-1625.
8. **Zhang, J.**, H. F. Rosenberg, and M. Nei (1998) Positive Darwinian selection after gene duplication in primate ribonuclease genes. *Proc. Natl. Acad. Sci. USA* 95:3708-3713.
9. Nei, M., and **J. Zhang** (1998) Molecular origin of species. *Science* 282:1428-1429. (Perspective)
10. Brown, J. R., **J. Zhang**, and J. E. Hodgson (1998) A bacterial antibiotic resistance gene with eukaryotic origins. *Curr. Biol.* 8:R365-R367.
11. **Zhang, J.** (1999) Performance of likelihood ratio tests of evolutionary hypotheses under inadequate substitution models. *Mol. Biol. Evol.* 16:868-875.
12. Rooney, A. P., and **J. Zhang** (1999) Rapid evolution of a primate sperm protein: relaxation of functional constraint or positive Darwinian selection? *Mol. Biol. Evol.* 16:706-710.
13. Singhanian, N. A., K. D. Dyer, **J. Zhang**, M. S. Deming, C. A. Bonville, J. B. Domachowske, and H. F. Rosenberg (1999) Rapid evolution of the Ribonuclease A superfamily: adaptive expansion of independent gene clusters in rats and mice. *J. Mol. Evol.* 49:721-728.
14. **Zhang, J.** (2000) Rates of conservative and radical nonsynonymous nucleotide substitutions in mammalian nuclear genes. *J. Mol. Evol.* 50:56-68.

15. **Zhang, J.** (2000) Protein-length distributions for the three domains of life. *Trends Genet.* 16:107-109.
16. **Zhang, J.**, and M. Nei (2000) Positive selection in the evolution of mammalian interleukin-2 genes. *Mol. Biol. Evol.* 17:1413-1416.
17. **Zhang, J.**, and H. F. Rosenberg (2000) Sequence variation at two eosinophil-associated ribonuclease loci in humans. *Genetics* 156:1949-1958.
18. **Zhang, J.**, K. D. Dyer, and H. F. Rosenberg (2000) Evolution of the rodent eosinophil-associated RNase gene family by rapid gene sorting and positive selection. *Proc. Natl. Acad. Sci. USA* 97:4701-4706.
19. Rooney, A. P., **J. Zhang**, and M. Nei (2000) An unusual form of purifying selection in a sperm protein. *Mol. Biol. Evol.* 17:278-283.
20. Rosenberg, H. F., **J. Zhang**, Y.-D. Liao, and K. D. Dyer (2001) Rapid diversification of RNase A superfamily ribonucleases from the bullfrog, *Rana catesbeiana*. *J. Mol. Evol.* 53:31-38.
21. **Zhang, J.**, and H. F. Rosenberg (2002) Complementary advantageous substitutions in the evolution of an antiviral RNase of higher primates. *Proc. Natl. Acad. Sci. USA* 99:5486-5491.
22. **Zhang, J.**, and H. F. Rosenberg (2002) Diversifying selection of the tumor-growth promoter angiogenin in primate evolution. *Mol. Biol. Evol.* 19:438-445.
23. **Zhang, J.**, K. D. Dyer, and H. F. Rosenberg (2002) RNase 8, a novel RNase A superfamily ribonuclease expressed uniquely in placenta. *Nucleic Acids Res.* 30:1169-1175.
24. **Zhang, J.**, D. M. Webb, and O. Podlaha (2002) Accelerated protein evolution and origins of human-specific features: FOXP2 as an example. *Genetics* 162:1825-1835.
25. **Zhang, J.**, Y.-P. Zhang, and H. F. Rosenberg (2002) Adaptive evolution of a duplicated pancreatic ribonuclease gene in a leaf-eating monkey. *Nat. Genet.* 30:411-415.
26. Wang, X., **J. Zhang**, and Y.-P. Zhang (2002) Erratic evolution of SRY in higher primates. *Mol. Biol. Evol.* 19:582-584.
27. **Zhang, J.** (2003) Parallel functional changes in the digestive RNases of ruminants and colobines by divergent amino acid substitutions. *Mol. Biol. Evol.* 20:1310-1317.
28. **Zhang, J.** (2003) Evolution by gene duplication-an update. *Trends Ecol. Evol.* 18:292-298. (Review)
29. **Zhang, J.** (2003) Evolution of the human *ASPM* gene, a major determinant of brain size. *Genetics* 165:2063-2070.
30. **Zhang, J.** (2003) Paleomolecular biology unravels the evolutionary mystery of vertebrate ultraviolet vision. *Proc. Natl. Acad. Sci. USA* 100:8045-8047. (Commentary)
31. **Zhang, J.**, and D. M. Webb (2003) Evolutionary deterioration of the vomeronasal pheromone transduction pathway in catarrhine primates. *Proc. Natl. Acad. Sci. USA* 100:8337-8341.
32. **Zhang, J.**, and Y.-P. Zhang (2003) Pseudogenization of the tumor-growth promoter angiogenin in a leaf-eating monkey. *Gene* 308:95-101.
33. **Zhang, J.**, K. D. Dyer, and H. F. Rosenberg (2003) Human RNase 7: a new cationic ribonuclease of the RNase A superfamily. *Nucleic Acids Res.* 31:602-607.
34. Gao, L., and **J. Zhang** (2003) Why are some human disease-associated mutations fixed in mice? *Trends Genet.* 19:678-681.

35. Nei, M., and **J. Zhang** (2003) Evolutionary distance: estimation. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp1-4. (Review)
36. Podlaha, O., and **J. Zhang** (2003) Positive selection on protein-length in the evolution of a primate sperm ion channel. *Proc. Natl. Acad. Sci. USA* 100:12241-12246.
37. Shi, P., **J. Zhang**, H. Yang, and Y. P. Zhang (2003) Adaptive diversification of bitter taste receptor genes in mammalian evolution. *Mol. Biol. Evol.* 20:805-814.
38. **Zhang, J.** (2004) Evolution of *DMY*, a recently emergent sex determination gene in medaka fish. *Genetics* 166:1887-1895.
39. **Zhang, J.** (2004) Frequent false detection of positive selection by the likelihood method with branch-site models. *Mol. Biol. Evol.* 21:1332-1339.
40. **Zhang, J.** (2004) The infancy of duplicate genes. *Heredity* 92:479-480. (News and Commentary)
41. **Zhang, J.**, and D. M. Webb (2004) Rapid evolution of primate antiviral enzyme APOBEC3G. *Hum. Mol. Genet.* 13:1785-1791.
42. **Zhang, J.**, X. Wang, and O. Podlaha (2004) Testing the chromosomal speciation hypothesis for humans and chimpanzees. *Genome Res.* 14:845-851.
43. Grus, W. E., and **J. Zhang** (2004) Rapid turnover and species-specificity of vomeronasal pheromone receptor genes in mice and rats. *Gene* 340:303-312.
44. Podlaha, O., and **J. Zhang** (2004) Non-neutral evolution of the transcribed pseudogene *Makorin1-pl* in mice. *Mol. Biol. Evol.* 21:2202-2209.
45. Wang, X., and **J. Zhang** (2004) Rapid evolution of mammalian X-linked testis-expressed homeobox genes. *Genetics* 167:879-888.
46. Dyer, K., H. F. Rosenberg, and **J. Zhang** (2004) Isolation, characterization and evolutionary divergence of mouse RNase 6: evidence for unusual evolution in rodents. *J. Mol. Evol.* 59:657-665.
47. Wang, X., S. D. Thomas, and **J. Zhang** (2004) Relaxation of selective constraint and loss of function in the evolution of human bitter taste receptor genes. *Hum. Mol. Genet.* 13:2671-2678.
48. Webb, D. M., L. Cortés-Ortiz, and **J. Zhang** (2004) Genetic evidence for the coexistence of pheromone perception and full trichromatic vision in howler monkeys. *Mol. Biol. Evol.* 21:697-704.
49. **Zhang, J.** (2005) On the evolution of codon volatility. *Genetics* 169:495-501.
50. **Zhang, J.** (2005) Brain size (genetics). In: *McGraw-Hill 2005 Yearbook of Science & Technology*. McGraw-Hill, New York, Pp34-36. (Review)
51. **Zhang, J.** (2005) Evolution for bioinformaticians and bioinformatics for evolutionists. *Evolution* 59:2281-2283. (Book review)
52. **Zhang, J.**, and X. He (2005) Significant impact of protein dispensability on the instantaneous rate of protein evolution. *Mol. Biol. Evol.* 22:1147-1155.
53. **Zhang, J.**, R. Nielsen, and Z. Yang (2005) Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level. *Mol. Biol. Evol.* 22:2472-2479.
54. He, X., and **J. Zhang** (2005) Rapid subfunctionalization accompanied by prolonged and substantial neofunctionalization in duplicate gene evolution. *Genetics* 169:1157-1164.
55. He, X., and **J. Zhang** (2005) Gene complexity and gene duplicability. *Curr. Biol.* 15:1016-1021.

56. Webb, D. M., and **J. Zhang** (2005) FoxP2 in song-learning birds and vocal learning mammals. *J. Heredity* 96:212-216.
57. Cho, S., J. J. Beintema, and **J. Zhang** (2005) The Ribonuclease A superfamily of mammals and birds: identifying new members and tracing evolutionary histories. *Genomics* 85:202-220.
58. Grus, W. E., P. Shi, Y. P. Zhang, and **J. Zhang** (2005) Dramatic variation of the vomeronasal pheromone receptor gene repertoire among five orders of placental and marsupial mammals. *Proc. Natl. Acad. Sci. USA* 102:5767-5772.
59. Podlaha, O., D. M. Webb, P. K. Tucker, and **J. Zhang** (2005) Positive selection for indel substitutions in the rodent sperm protein Catsper1. *Mol. Biol. Evol.* 22:1845-1852.
60. Yang, H., P. Shi, Y.-P. Zhang, and **J. Zhang** (2005) Composition and evolution of the V2R vomeronasal receptor gene repertoire in mice and rats. *Genomics* 86:306-315.
61. **Zhang, J.** (2006) Parallel adaptive origins of digestive RNases in Asian and African leaf monkeys. *Nat. Genet.* 38:819-823.
62. Cho, S., and **J. Zhang** (2006) Ancient expansion of the ribonuclease A superfamily revealed by genomic analysis of placental and marsupial mammals. *Gene* 373:116-125.
63. Cho, S., Z. Y. Huang, D. R. Green, D. R. Smith, and **J. Zhang** (2006) Evolution of the complementary sex-determination gene of honey bees: balancing selection and trans-species polymorphisms. *Genome Res.* 16:1366-1375.
64. Grus, W. E., and **J. Zhang** (2006) Origin and evolution of the vertebrate vomeronasal system viewed through system-specific genes. *BioEssays* 28:709-718. (Review)
65. He, X., and **J. Zhang** (2006) Higher duplicability of less important genes in yeast genomes. *Mol. Biol. Evol.* 23:144-151.
66. He, X., and **J. Zhang** (2006) Transcriptional reprogramming and backup between duplicate genes: is it a genome-wide phenomenon? *Genetics* 172:1363-1367.
67. He, X., and **J. Zhang** (2006) Toward a molecular understanding of pleiotropy. *Genetics* 173:1885-1891.
68. He, X., and **J. Zhang** (2006) Why do hubs tend to be essential in protein networks? *PLoS Genet.* 2:e88 (9 pages).
69. Liao, B.-Y., and **J. Zhang** (2006) Evolutionary conservation of expression profiles between human and mouse orthologous genes. *Mol. Biol. Evol.* 23:530-540.
70. Liao, B.-Y., and **J. Zhang** (2006) Low rates of expression-profile divergence in highly-expressed genes and tissue-specific genes during mammalian evolution. *Mol. Biol. Evol.* 23:1119-1128.
71. Liao, B.-Y., and **J. Zhang** (2006) Impacts of gene essentiality, expression pattern, and gene compactness on the evolution rate of mammalian proteins. *Mol. Biol. Evol.* 23:2072-2080.
72. Shi, P., and **J. Zhang** (2006) Contrasting modes of evolution between vertebrate sweet/umami receptor genes and bitter receptor genes. *Mol. Biol. Evol.* 23:292-300.
73. Shi, P., M. A. Bakewell, and **J. Zhang** (2006) Did brain-specific genes evolve faster in humans than in chimpanzees? *Trends Genet.* 22:608-613.
74. Wang, X., and **J. Zhang** (2006) Remarkable expansions of an X-linked reproductive homeobox gene cluster in rodent evolution. *Genomics* 88:34-43.
75. Wang, X., W. E. Grus, and **J. Zhang** (2006) Gene losses during human origins. *PLoS Biol.* 4:366-377.

76. Podlaha, O., D. M. Webb, and **J. Zhang** (2006) Accelerated evolution and loss of a domain of the sperm-egg binding protein SED1 in ancestral primates. *Mol. Biol. Evol.* 23:1828-1831.
77. **Zhang, J.** (2007) Disulfide-bond reshuffling in the evolution of an ape placental ribonuclease. *Mol. Biol. Evol.* 24:505-512.
78. **Zhang, J.** (2007) The drifting human genome. *Proc. Natl. Acad. Sci. USA* 104:20147-20148. (Commentary)
79. Shi, P., and **J. Zhang** (2007) Comparative genomic analysis identifies an evolutionary shift of vomeronasal receptor gene repertoires in the vertebrate transition from water to land. *Genome Res.* 17:166-174.
80. Bakewell, M. A., P. Shi, and **J. Zhang** (2007) More genes underwent positive selection in chimpanzee evolution than in human evolution. *Proc. Natl. Acad. Sci. USA* 104:7489-7494.
81. Cho, S., and **J. Zhang** (2007) Zebrafish ribonucleases are bactericidal: Implications for the origin of the vertebrate RNase A superfamily. *Mol. Biol. Evol.* 24:1259-1268.
82. Wang, Z., and **J. Zhang** (2007) In search of the biological significance of modular structures in protein networks. *PLoS Comput. Biol.* 3:e107 (11 pages).
83. Liao, B.-Y., and **J. Zhang** (2007) Mouse duplicate genes are as essential as singleton genes. *Trends Genet.* 23:378-381.
84. Wang, X., and **J. Zhang** (2007) Rapid evolution of primate *ESX1*, an X-linked placenta- and testis-expressed homeobox gene. *Hum. Mol. Genet.* 16:2053-2060.
85. Grus, W. E., P. Shi, and **J. Zhang** (2007) Largest vertebrate vomeronasal type 1 receptor (V1R) gene repertoire in the semi-aquatic platypus. *Mol. Biol. Evol.* 24:2153-2157.
86. Cho, S., Huang, Z. Y., and **J. Zhang** (2007) Sex-specific splicing of the honey bee *doublesex* gene reveals 300 million years of evolution at the bottom of the insect sex-determination pathway. *Genetics* 173:1733-1741.
87. Qian, W., and **J. Zhang** (2008) Evolutionary dynamics of nematode operons: easy come, slow go. *Genome Res.* 18:412-421.
88. Liao, B.-Y., and **J. Zhang** (2008) Null mutations in human and mouse orthologs frequently result in different phenotypes. *Proc. Natl. Acad. Sci. USA* 105:6987-6992.
89. Zhang, Z., and **J. Zhang** (2008) Accuracy and application of the motif expression decomposition method in dissecting transcriptional regulation. *Nucleic Acids Res.* 36:3185-3193.
90. Liao, B.-Y., and **J. Zhang** (2008) Co-expression of linked genes in mammalian genomes is generally disadvantageous. *Mol. Biol. Evol.* 25:1555-1565.
91. Grus, W. E., and **J. Zhang** (2008) Distinct evolutionary patterns between chemoreceptors of two vertebrate olfactory systems and the differential tuning hypothesis. *Mol. Biol. Evol.* 25:1593-1601.
92. Qian, W., and **J. Zhang** (2008) Gene dosage and gene duplicability. *Genetics* 179:2319-2324.
93. **Zhang, J.** (2008) Positive selection, not negative selection, in the pseudogenization of *rcsA* in *Yersinia pestis*. *Proc. Natl. Acad. Sci. USA* 105:E69. (Letter to Editor)
94. Grus, W. E., and **J. Zhang** (2008) Human lineage-specific gene inactivation. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp1-6. (Review)

95. Bakewell, M. A., and **J. Zhang** (2008) Positive selection on genes in humans as compared to chimpanzees. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp1-7. (Review)
96. Shi, P., and **J. Zhang** (2009) Extraordinary diversity of chemosensory receptor gene repertoires among vertebrates. In: *Chemosensory Systems in Mammals, Fishes, and Insects*. (W. Meyerhof & S. Korsching, eds., Springer, Berlin). Pp.1-23. (Review)
97. Grus, W. E., and **J. Zhang** (2009) Origin of the genetic components of the vomeronasal system in the common ancestor of all extant vertebrates. *Mol. Biol. Evol.* 26:407-419.
98. Wang, Z., and **J. Zhang** (2009) Why is the correlation between gene importance and gene evolutionary rate so weak? *PLoS Genet.* 5:e1000329 (11 pages).
99. He, X., and **J. Zhang** (2009) On the growth of scientific knowledge: Yeast biology as a case study. *PLoS Comput. Biol.* 5:e1000320 (12 pages).
100. Wang, Z., and **J. Zhang** (2009) Abundant indispensable redundancies in cellular metabolic networks. *Genome Biol. Evol.* 1:23-33.
101. Zhang, Z., and **J. Zhang** (2009) A big world inside small-world networks. *PLoS ONE* 4:e5686 (6 pages).
102. Zhang, Z., W. Qian, and **J. Zhang** (2009) Positive selection for elevated gene expression noise in yeast. *Mol. Syst. Biol.* 5:299 (12 pages).
103. **Zhang, J.** (2009) Phylogenetic evidence for parallel adaptive origins of digestive RNases in Asian and African leaf monkeys: A response to Xu et al. (2009). *Mol. Phylogenet. Evol.* 53:608-609.
104. Qian, W., and **J. Zhang** (2009) Protein subcellular relocalization in the evolution of yeast singleton and duplicate genes. *Genome Biol. Evol.* 1:198-204.
105. Podlaha, O., and **J. Zhang** (2009) Processed pseudogenes: the 'fossilized footprints' of past gene expression. *Trends Genet.* 25:429-434.
106. Barkman, T., and **J. Zhang** (2009) Evidence for escape from adaptive conflict? *Nature* 462:E1-E2. (Brief Communication Arising)
107. Liao, B.-Y., M.-P. Weng, and **J. Zhang** (2010) Impact of extracellularly on the evolutionary rate of mammalian proteins. *Genome Biol. Evol.* 2:39-43.
108. He, X., W. Qian, Z. Wang, Y. Li, and **J. Zhang** (2010) Prevalent positive epistasis in *Escherichia coli* and *Saccharomyces cerevisiae* metabolic networks. *Nat. Genet.* 42:272-276.
109. Li, Y., Z. Liu, P. Shi, and **J. Zhang** (2010) The hearing gene *Prestin* unites echolocating bats and whales. *Curr. Biol.* 20:R55-R56.
110. Liao, B.-Y., M.-P. Weng, and **J. Zhang** (2010) Contrasting genetic paths to morphological and physiological evolution. *Proc. Natl. Acad. Sci. USA* 107:7353-7358.
111. **Zhang, J.** (2010) Evolutionary genetics: Progress and challenges. In: *Evolution Since Darwin: The First 150 Years*. (M. A. Bell, et al., eds., Sinauer, Sunderland, Mass.). Pp. 87-118. (Review)
112. **Zhang, J.** (2010) Positive Darwinian selection in gene evolution. In: *Darwin's Heritage Today: Proceedings of the Darwin 200 Beijing International Conference* (M. Long, et al., eds, High Education Press, Beijing), Pp. 288-309. (Review)
113. Podlaha, O., and **J. Zhang** (2010) Pseudogenes and their evolution. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp1-8. (Review)

114. Zhao, H., Y. Zhou, C. M. Pinto, P. Charles-Dominique, J. Galindo-González, S. Zhang, and **J. Zhang** (2010) Evolution of the sweet taste receptor gene *Tas1r2* in bats. *Mol. Biol. Evol.* 27:2642-2650.
115. Zhao, H., J.-R. Yang, H. Xu, and **J. Zhang** (2010) Pseudogenization of the umami taste receptor gene *Tas1r1* in the giant panda coincided with its dietary switch to bamboo. *Mol. Biol. Evol.* 27:2669-2673.
116. Qian, W., B.-Y. Liao, A. Y.-F. Chang, and **J. Zhang** (2010) Maintenance of duplicate genes and their functional redundancy by reduced expression. *Trends Genet.* 26:425-430.
117. Yang, J.-R., S.-M. Zhuang, and **J. Zhang** (2010) Impact of translational error-induced and error-free misfolding on the rate of protein evolution. *Mol. Syst. Biol.* 6:421 (13 pages).
118. Wang, Z., B.-Y. Liao, and **J. Zhang** (2010) Genomic patterns of pleiotropy and the evolution of complexity. *Proc. Natl. Acad. Sci. USA* 107:18034-18039.
119. Xiong, Y., X. Chen, Z. Chen, X. Wang, S. Shi, X. Wang, **J. Zhang**, and X. He (2010) RNA sequencing shows no dosage compensation of the active X-chromosome. *Nat. Genet.* 42:1043-1047.
120. Zhao, H., D. Xu, S. Zhang, and **J. Zhang** (2011) Widespread losses of vomeronasal signal transduction in bats. *Mol. Biol. Evol.* 28:7-12.
121. Wagner, G. P., and **J. Zhang** (2011) The pleiotropic structure of the genotype-phenotype map: the evolvability of complex adaptations. *Nat. Rev. Genet.* 12:204-213. (Review)
122. Park, C., and **J. Zhang** (2011) Genome-wide evolutionary conservation of N-glycosylation sites. *Mol. Biol. Evol.* 28:2351-2357.
123. Wang, Z., and **J. Zhang** (2011) Impact of gene expression noise on organismal fitness and the efficacy of natural selection. *Proc. Natl. Acad. Sci. USA* 108:E67-E76.
124. Qian, W., X. He, E. Chan, H. Xu, and **J. Zhang** (2011) Measuring the evolutionary rate of protein-protein interaction. *Proc. Natl. Acad. Sci. USA* 108:8725-8730.
125. Park, S. H., O. Podlaha, W. E. Grus, and **J. Zhang** (2011) The microevolution of *V1r* vomeronasal receptor genes in mice. *Genome Biol. Evol.* 3:401-412.
126. **Zhang, J.** (2011) A panorama of mammalian gene expression evolution. *Mol. Syst. Biol.* 7:552 (2 pages). (News & Views)
127. He, X. X. Chen, Y. Xiong, Z. Chen, X. Wang, S. Shi, X. Wang, and **J. Zhang** (2011) Response to the comments on “RNA sequencing shows no dosage compensation of the active X-chromosome”. *Nat. Genet.* 43:1171-1172.
128. Zhao, H., D. Xu, S. Zhang, and **J. Zhang** (2012) Genomic and genetic evidence for the loss of umami taste in bats. *Genome Biol. Evol.* 4:73-79.
129. Qian, W., J.-R. Yang, N. M. Pearson, C. Maclean, and **J. Zhang** (2012) Balanced codon usage optimizes eukaryotic translational efficiency. *PLoS Genet.* 8: e1002603 (18 pages).
130. Wagner, G. P., and **J. Zhang** (2012) Universal Pleiotropy is not a valid null hypothesis: Reply to Hill and Zhang. *Nat. Rev. Genet.* 13:296.
131. **Zhang, J.** (2012) Genetic redundancies and their evolutionary maintenance. In *Evolutionary Systems Biology* (O. Soyer, eds, Springer), Pp. 279-300. (Review)
132. Yang, J.-R., B.-Y. Liao, S.-M. Zhuang, and **J. Zhang** (2012) Protein misinteraction avoidance causes highly expressed proteins to evolve slowly. *Proc. Natl. Acad. Sci. USA* 109:E831-E840.
133. Park, C., and **J. Zhang** (2012) High expression hampers horizontal gene transfer. *Genome Biol. Evol.* 4:523-532.

134. Zhao, H., and **J. Zhang** (2012) Mismatches between feeding ecology and taste receptor evolution: An inconvenient truth. *Proc. Natl. Acad. Sci. USA* 109:E1464. (Letter to Editor)
135. Lin, F., K. Xing, **J. Zhang**, and X. He (2012) Expression reduction in mammalian X chromosome evolution refutes Ohno's hypothesis of dosage compensation. *Proc. Natl. Acad. Sci. USA* 109:11752-11757.
136. Park, C., W. Qian, and **J. Zhang** (2012) Genomic evidence for elevated mutation rates in highly expressed genes. *EMBO Rep.* 13:1123-1129.
137. Qian, W., D. Ma, C. Xiao, Z. Wang, and **J. Zhang** (2012) The genomic landscape and evolutionary resolution of antagonistic pleiotropy in yeast. *Cell Rep.* 2:1399-1410.
138. Chen, X., and **J. Zhang** (2012) The ortholog conjecture is untestable by the current gene ontology but is supported by RNA sequencing data. *PLoS Comput. Biol.* 8:e1002784 (13 pages).
139. Park, C., X. Chen, J.-R. Yang, and **J. Zhang** (2013) Differential requirements for mRNA folding partially explain why highly expressed proteins evolve slowly. *Proc. Natl. Acad. Sci. USA* 110:E678-E686.
140. Chen, X., and **J. Zhang** (2013) No gene-specific optimization of mutation rate in *Escherichia coli*. *Mol. Biol. Evol.* 30:1559-1562.
141. **Zhang, J.**, and G. P. Wagner (2013) On the definition and measurement of pleiotropy. *Trends Genet.* 29:383-384. (Letter to Editor)
142. Li, C., Z. Wang, and **J. Zhang** (2013) Toward genome-wide identification of Bateson-Dobzhansky-Muller incompatibilities in yeast: A simulation study. *Genome Biol. Evol.* 5:1261-1272.
143. **Zhang, J.** (2013) Gene duplication. In *Princeton Guide to Evolution* (J. Losos, eds, Princeton University Press, Princeton, NJ), Pp 397-405. (Review)
144. Grus, W. E., and **J. Zhang** (2013) Human lineage-specific gene inactivation. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp 1-8. (Updated review)
145. Chen, X., and **J. Zhang** (2013) Why are genes encoded on the lagging strand of the bacterial genome? *Genome Biol. Evol.* 5:2436-2439.
146. **Zhang, J.** (2014) Gene duplication. In *Oxford Bibliographies in Evolutionary Biology* (J. Losos, eds, Oxford University Press, Oxford). DOI: 10.1093/OBO/9780199941728-0002. (Review)
147. Li, D., and **J. Zhang** (2014) Diet shapes the evolution of the vertebrate bitter taste receptor gene repertoire. *Mol. Biol. Evol.* 31:303-309.
148. Xu, G., and **J. Zhang** (2014) Human coding RNA editing is generally nonadaptive. *Proc. Natl. Acad. Sci. USA* 111:3769-3774.
149. Ho, W.-C., and **J. Zhang** (2014) The genotype-phenotype map of yeast complex traits: basic parameters and the role of natural selection. *Mol. Biol. Evol.* 31:1568-1580.
150. Xu, J., and **J. Zhang** (2014) Why human disease-associated residues appear as the wild-type in other species: genome-scale structural evidence for the compensation hypothesis. *Mol. Biol. Evol.* 31:1787-1792.
151. Yang, J.-R., S. Ruan, and **J. Zhang** (2014) Determinative developmental cell lineages are robust to cell deaths. *PLOS Genet.* 10:e1004501 (17 pages).
152. Yang, J.-R., X. Chen, and **J. Zhang** (2014) Codon-by-codon modulation of translational speed and accuracy via mRNA folding. *PLOS Biol.* 12:e1001910 (14 pages).

153. Qian, W., and **J. Zhang** (2014) Genomic evidence for adaptation by gene duplication. *Genome Res.* 24:1356-1362.
154. Chen, X., and **J. Zhang** (2014) Mutation accumulation experiment supports elevated mutation rates at highly transcribed sites. *Proc. Natl. Acad. Sci. USA* 111:E4062 (Letter to Editor)
155. Moyers, B. A., and **J. Zhang** (2015) Phylostratigraphic bias creates spurious patterns of genome evolution. *Mol. Biol. Evol.* 32:258-267.
156. Xu, G., and **J. Zhang** (2015) In search of beneficial coding RNA editing. *Mol. Biol. Evol.* 32:536-541.
157. Wei, X., and **J. Zhang** (2015) A simple method for estimating the strength of natural selection on overlapping genes. *Genome Biol. Evol.* 7:381-390.
158. Zhao, H., J. Li, and **J. Zhang** (2015) Molecular evidence for the loss of three basic tastes in penguins. *Curr. Biol.* 25:R141-R142.
159. Yang, J.-R., and **J. Zhang** (2015) Human long noncoding RNAs are substantially less folded than messenger RNAs. *Mol. Biol. Evol.* 32:970-977.
160. Zou, Z., and **J. Zhang** (2015) No genome-wide convergence for echolocation. *Mol. Biol. Evol.* 32: 1237-1241.
161. Chen, X., and **J. Zhang** (2015) No X-chromosome dosage compensation in human proteomes. *Mol. Biol. Evol.* 32:1456-1460.
162. **Zhang, J.**, and J.-R. Yang (2015) Determinants of the rate of protein sequence evolution. *Nat. Rev. Genet.* 16:409-420.
163. Zou, Z., and **J. Zhang** (2015) Are convergent and parallel amino acid substitutions in protein evolution more prevalent than neutral expectations? *Mol. Biol. Evol.* 32:2085-2096.
164. Chen, X., J.-R. Yang, and **J. Zhang** (2016) Nascent RNA folding mitigates transcription associated mutagenesis. *Genome Res.* 26:50-59.
165. Xu, J., and **J. Zhang** (2016) Are human translated pseudogenes functional? *Mol. Biol. Evol.* 33:755-760.
166. Xu, J., and **J. Zhang** (2016) Impact of structure space continuity on protein fold classification. *Sci. Rep.* 6:23263 (12 pages).
167. Ho, W.-C., and **J. Zhang** (2016) Adaptive genetic robustness of *Escherichia coli* metabolic fluxes. *Mol. Biol. Evol.* 33:1164-1176.
168. Moyers, B. A., and **J. Zhang** (2016) Evaluating phylostratigraphic evidence for widespread *de novo* gene birth in evolution. *Mol. Biol. Evol.* 33:1245-1256.
169. Li, C., Qian, W., Maclean, C. J., and **J. Zhang** (2016) The fitness landscape of a tRNA gene. *Science* 352:837-840.
170. Chen, X., and **J. Zhang** (2016) The genomic landscape of position effects on protein expression level and noise in yeast. *Cell Syst.* 2:347-354.
171. He, X., and **J. Zhang** (2016) X-chromosome dosage compensation. *Encyclopedia of Life Sciences*. John Wiley & Sons, Chichester, UK, Pp1-7. (Review).
172. **Zhang, J.** (2016) Neutral theory. In *Oxford Bibliographies in Evolutionary Biology* (K. Pfennig, eds, Oxford University Press, New York), DOI: 10.1093/OBO/9780199941728-0081. (Review)
173. **Zhang, J.** (2016) Toward predicting evolution. *Cell Syst.* 2:290. (Commentary)
174. Zou, Z., and **J. Zhang** (2016) Morphological and molecular convergences in mammalian phylogenetics. *Nat. Commun.* 7:12758 (9 pages).

175. Chen, X., and **J. Zhang** (2016) The X to autosome expression ratio in haploid and diploid human embryonic stem cells. *Mol. Biol. Evol.* 33:3104-3107.
176. Wei, X., and **J. Zhang** (2017) The genomic architecture of interactions between natural genetic polymorphisms and environments in yeast growth. *Genetics* 205:925-937.
177. **Zhang, J.** (2017) Epistasis analysis goes genome-wide. *PLOS Genet.* 13:e1006558. (Perspective)
178. Zou, Z., and **J. Zhang** (2017) Gene tree discordance does not explain away the temporal decline of convergence in mammalian protein sequence evolution. *Mol. Biol. Evol.* 34:1682-1688.
179. Moyers, B. A., and **J. Zhang** (2017) Further simulations and analyses demonstrate open problems of phylostratigraphy. *Genome Biol. Evol.* 9:1519-1527.
180. Yang, J.-R., C. J. Maclean, C. Park, H. Zhao, and **J. Zhang** (2017) Intra and interspecific variations of gene expression levels in yeast are largely neutral. *Mol. Biol. Evol.* 34:2125-2139.
181. Maclean, C. J., B. P. H. Metzger, J.-R. Yang, W.-C. Ho, B. A. Moyers, and **J. Zhang** (2017) Deciphering the genic basis of yeast fitness variation by simultaneous forward and reverse genetics. *Mol. Biol. Evol.* 34:2486-2502.
182. Ho, W.-C., Y. Ohya, and **J. Zhang** (2017) Testing the neutral hypothesis of phenotypic evolution. *Proc. Natl. Acad. Sci. USA* 114:12219-12224.
183. **Zhang, J.** (2017) Toward understanding the evolutionary histories and mechanisms of mangroves. *Natl. Sci. Rev.* 4:737. (Commentary)
184. Wei, X., and **J. Zhang** (2017) Why phenotype robustness promotes phenotype evolvability. *Genome Biol. Evol.* 9:3509-3515.
185. Ho, W.-C., and **J. Zhang** (2018) Evolutionary adaptations to new environments generally reverse plastic phenotypic changes. *Nat. Commun.* 9:350 (11 pages).
186. Liu, Z., and **J. Zhang** (2018) Most m⁶A RNA modifications in protein-coding regions are evolutionarily unconserved and likely nonfunctional. *Mol. Biol. Evol.* 35:666-675.
187. Liu, Z., and **J. Zhang** (2018) Human C-to-U coding RNA editing is largely nonadaptive. *Mol. Biol. Evol.* 35:963-969.
188. Li, C., and **J. Zhang** (2018) Multi-environment fitness landscapes of a tRNA gene. *Nat. Ecol. Evol.* 2:1025-1032.
189. **Zhang, J.** (2018) Neutral theory and phenotypic evolution. *Mol. Biol. Evol.* 35:1327-1331.
190. Xu, C., and **J. Zhang** (2018) Alternative polyadenylation of mammalian transcripts is generally deleterious, not adaptive. *Cell Syst.* 6:734-742.
191. Vijay, N., C. Park, J. Oh, S. Jin, E. Kern, H. W. Kim, **J. Zhang**, and J.-K. Park (2018) Population genomic analysis reveals contrasting demographic changes of two closely related dolphin species in the last glacial. *Mol. Biol. Evol.* 35:2026-2033.
192. Wei, X., and **J. Zhang** (2018) On the origin of compositional features of ribosomes. *Genome Biol. Evol.* 10:2010-2016.
193. Moyers, B. A., and **J. Zhang** (2018) Toward reducing phylostratigraphic errors and biases. *Genome Biol. Evol.* 10:2037-2048.
194. Wei, X. and **J. Zhang** (2018) The optimal mating distance resulting from heterosis and genetic incompatibility. *Sci. Adv.* 4:eaau5518. (7 pages)

195. Wei, X., and **J. Zhang** (2019) Environment-dependent pleiotropic effects of mutations on the maximum growth rate r and carrying capacity K of population growth. *PLOS Biol.* 17:e3000121. (18 pages)
196. Liu, H., C. J. Maclean, and **J. Zhang** (2019) Evolution of the yeast recombination landscape. *Mol. Biol. Evol.* 36:412-422.
197. Ho, W.-C., and **J. Zhang** (2019) Genetic gene expression changes during environmental adaptations tend to reverse plastic changes even after the correction for statistical nonindependence. *Mol. Biol. Evol.* 36:604-612.
198. Xu, C. J.-K. Park, and **J. Zhang** (2019) Evidence that alternative transcriptional initiation is largely nonadaptive. *PLOS Biol.* 17:e3000197. (22 pages)
199. Wei, X., and **J. Zhang** (2019) Patterns and mechanisms of diminishing returns from beneficial mutations. *Mol. Biol. Evol.*, in press.
200. Liu, H., and **J. Zhang** (2019) Yeast spontaneous mutation rate and spectrum vary with environment. *Curr. Biol.*, in press.