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CURRENT POSITIONS

2015–present Professor of Biological Sciences, Vanderbilt University
2015–present Professor of Biomedical Informatics, Vanderbilt University
2013–present Cornelius Vanderbilt Chair in Biological Sciences, Vanderbilt University

PAST POSITIONS

2013–2015 Associate Professor of Biological Sciences and Biomedical Informatics, Vanderbilt University
2007–2012 Assistant Professor of Biological Sciences, Vanderbilt University
2005–2007 Research Scientist, The Broad Institute of MIT & Harvard
2002–2005 Post-doctoral Fellow, University of Wisconsin-Madison, Advisor: S. B. Carroll
1998–2001 Doctoral Student, University of Edinburgh, Advisor: G. N. Stone
1997–1998 Undergraduate Exchange Student, Reading University, Advisor: P. W. H. Holland
1996–1997 Undergraduate Thesis Student, University of Crete, Advisor: E. Zouros

EDUCATION

2001 Ph.D., Evolutionary Biology University of Edinburgh, United Kingdom
1998 B.Sc., Biology University of Crete, Greece

AWARDS AND FELLOWSHIPS

2017 National Finalist, Blavatnik Awards for Young Scientists
2017 Biological Sciences Excellence in Research Award
2017 Littlejohn Faculty Fellow
2015 Biological Sciences Excellence in Research Award
2013–present Cornelius Vanderbilt Chair of Biological Sciences
2013 Biological Sciences Excellence in Research Award
2011 Chancellor's Award for Research
2009 NSF CAREER Award
2008 Searle Scholar
2002–2005 Human Frontier Science Program Long-Term Fellowship
1998–2001 Natural Environment Research Council Studentship
1997–1998 Greek Foundation of State Scholarships for Undergraduate Study Abroad

PROFESSIONAL HONORS

2018 Chair (elected), Cellular and Molecular Fungal Biology Gordon Research Conference
2016 Vice-chair (elected), Cellular and Molecular Fungal Biology Gordon Research Conference
2015 Guest Editor for *Genomes and Evolution* special issue of *Current Opinion in Genetics and Development*

FUNDING

Burroughs Wellcome Trust National Science Foundation	PI (with J. A. Capra, PI), 06/17-05/21, Integrating 'omics and electronic health records to elucidate the genetic architecture of preterm birth, \$300,000 PI (with C. T. Hittinger, PI; C. P. Kurtzman, Co-PI), 02/15-01/20, DIMENSIONS: Collaborative Research: The making of biodiversity across the yeast subphylum, \$851,102
National Institutes of Health	Co-PI (PI R. R. Dinglasan), 07/14-06/16, Midgut transcriptome and proteome analysis of non-model anopheline malaria vectors, \$180,175
National Science Foundation	Advisor, 09/14-08/17, National Plant Genome Initiative Postdoctoral Research Fellowship to Dr. Jennifer H. Wisecaver, The evolution of secondary metabolic gene clusters in plants, \$207,000
March of Dimes	PI / Theme Leader (with P. Abbot, PI; K. Petren, PI), 7/13-6/18, The March of Dimes Prematurity Research Collaborative of Ohio (Director L. J. Muglia), Theme 1: Evolutionary Synthesis of Human Pregnancy, ~\$1,800,000
National Institutes of Health	Co-Advisor (with L. J. Zwiebel), 12/12-11/15, F31 Pre-doctoral Research Fellowship Award to Mr. David C. Rinker, Chemosensory signatures of hematophagy in mosquitoes, \$81,708
National Science Foundation	PI, 09/09-08/14, CAREER: A genomics approach to identifying the factors influencing phylogenetic accuracy, \$688,129
National Institutes of Health	Advisor, 08/10-07/12, F31 Pre-doctoral Research Fellowship Award to Mr. John G. Gibbons, Characterizing the genomic patterns of variation in the fungal pathogen <i>Aspergillus fumigatus</i> , \$50,352
National Science Foundation	Advisor, 09/08-08/10, Postdoctoral Fellowship in Biological Informatics to Dr. Jason C. Slot, Dynamics and ecological significance of the origins, order and inheritance of fungal gene clusters, \$120,000
Searle Scholars Program	PI, 07/08-06/11, Deciphering the origins and assembly of the genetic toolkit for animal development, \$300,000

RESEARCH INTERESTS

- ❖ The evolution of fungal specialized metabolic pathways and chemodiversity
- ❖ The evolution of human pregnancy
- ❖ Phylogenetics, phylogenomics of fungi and animals
- ❖ Evolution of gene families

UNDERGRADUATE TEACHING (LAST 5 YEARS)

BSCI1511	<i>Introduction to Biological Sciences</i> , Vanderbilt Univ., 2015–present
BSCI2205	<i>Evolution</i> , Vanderbilt Univ., 2010–present
BSCI2272	<i>Computational Genomics</i> , Vanderbilt Univ., 2010–2013
BSCI3861-BSCI4999	<i>Research for Academic Credit Courses</i> , Vanderbilt Univ., every semester

INVITED ADVANCED TEACHING (LAST 5 YEARS)

Workshop on Phylogenomics – Europe, 2017
 Workshop on Genomics – Europe, 2011–2016, 2018 (scheduled)
 Workshop on Molecular Evolution – MBL, USA, 2010–2015
 EMBO/Wellcome Trust Computational Molecular Evolution Workshop, 2010–2014
 Workshop on Molecular Evolution – Europe, 2010–2013

ADVISING

Postdocs

Jason C. Slot (2008-2013; now Assistant Professor, The Ohio State Univ.)
Ioannis Stergiopoulos (2011; now Associate Professor, Univ. of California, Davis)
Padmanabhan Mahadevan (2009-2010; now Associate Professor, Tampa Univ.)
Xiaofan Zhou (2011-2016; now Professor, South China Agricultural Univ.)
Kriston L. McGary (2009-2016; now Consultant, Genetic Networks)
Jennifer H. Wisecaver (2013-2017; now Assistant Professor, Purdue Univ.)
Julie B. Phillips (2014-2017; now Assistant Professor, Cumberland Univ.)
Xing-Xing Shen (current)
Matthew E. Mead (current)
Abigail L. LaBella (current)
Mingshuang Wang (current)

Graduate students

John G. Gibbons (2012; postdoc, Harvard Univ.; now Assistant Professor, Clark Univ.)
Leonidas Salichos (2014; postdoc, Yale Univ.)
David C. Rinker (co-advisor with L. J. Zwiebel, 2015; now postdoc, Vanderbilt Univ.)
Yuyu Wang (visiting student; now graduate student, China Agricultural Univ.)
Abigail Lind (2017; now postdoc, Univ. California, San Francisco)
Haley Eidem (current)
Mara Kim (current)
Juan F. Ortiz (current)
Michelle Moon (co-advisor with P. Abbot, current)
Jacob Steenwyk (current)

Masters students

Patricia Soria (2014; now graduate student, University of Florida)
Kenneth Polzin (2014; now independent consultant, biodiversity informatics)

Undergraduates

Matthew E. Campbell (2012; now graduate student, University of Montana)
Mara Kim (2012; now graduate student, Vanderbilt University)
Martha H. Elmore (2013; now graduate student, Harvard University)
George H. Greene (2014; now graduate student, Duke University)
Brian A. Cooper (2015; now software developer, Minibar Delivery)
Sean B. King (2016; now graduate student, Princeton University)
Samuel A. Smith (2017; now graduate student, Brown University)
Rebecca Burke-Aguero (2017; now software developer, Microsoft)
Alexander T. Borowsky (current)
Maddison Johnson (current)
Zackery Ely (current)

SERVICE

Editorial Board Member

Current Biology (2018–)
eLife (2016–)
BMC Genomics (2015–)
Evolution, Medicine, & Public Health (2014–)
Fungal Genetics and Biology (2014–)
PLoS ONE (2014–)
BMC Microbiology (2013–)

G3: Genes/Genomes/Genetics (2011–)
Journal of Biological Research (2010–)
Genomics Insights (2009–)
PLoS Genetics (guest editor)

- Manuscript reviewer** I review many manuscripts per year and have served as a reviewer for more than 50 journals including: *Anim. Biodiv. Conserv.*, *Bioessays*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Biology*, *BMC Evol. Biol.*, *BMC Genomics*, *BMC Microbiol.*, *Cell*, *Chem. & Biol.*, *Curr. Biol.*, *DNA Res.*, *Development*, *Euk. Cell*, *Europ. J. Entomol.*, *Evolution*, *Evol. Med. Public Health*, *Fungal Genet. Biol.*, *Gene*, *Genes Dev. Evol.*, *Genome Biol.*, *Genome Res.*, *Heredity*, *Integr. Comp. Biol.*, *J. Theor. Biol.*, *Mol. Biol. Evol.*, *Mol. Ecol.*, *J. Biol. Rhythms*, *J. Mol. Evol.*, *Mol. Phylog. Evol.*, *Mycologia*, *Nature*, *Nature Ecol. Evol.*, *Nature Comm.*, *New Phytol.*, *Plant Cell*, *Plasmid*, *PLOS Biol.*, *PLOS Comp. Biol.*, *PLOS Genet.*, *PLOS One*, *PLoS Path.*, *Proc. Roy. Soc. Lond. Ser. B.*, *PNAS*, *Science*, *Science Signalling*, *Trends Ecol. Evol.*, *Trends Evol. Biol.*, *Trends Genet.*, *Zoology*.
- Grant reviewer** NIH (USA), NSF (USA), The Wellcome Trust (UK), NASA (USA), BBSRC (UK), Marsden Fund, Royal Society (New Zealand), ANR (France), FCT (Portugal), STW (The Netherlands).
- Book reviewer** W. W. Norton, Princeton University Press, Roberts & Company.

PROFESSIONAL AFFILIATIONS

Society for Molecular Biology and Evolution, Society for the Study of Evolution, Society of Systematic Biologists, Mycological Society of America, Genetics Society of America, American Association for the Advancement of Science.

EDITED VOLUMES

2015 Rokas, A., & P. S. Soltis, Editors. Special issue on Genomes and Evolution. *Curr. Op. Genet. Dev.*, volume **35**: 1-126.

PREPRINT MANUSCRIPTS (Rokas Lab Members in Bold)

Gonçalves, C., **J. H. Wisecaver**, M. Salema-Oom, M. J. Leandro, **X.-X. Shen**, D. Peris, C. T. Hittinger, **A. Rokas** & P. Gonçalves. Evidence for loss and adaptive reacquisition of alcoholic fermentation in an early-derived fructophilic yeast lineage. *bioRxiv*: <http://doi.org/10.1101/213686>

Wang, M., H. Fu, **X.-X. Shen**, R. Ruan, N. Pun, J. Xu, H. Li & **A. Rokas**. Genomic features and evolution of the conditionally dispensable chromosome in the tangerine pathotype of *Alternaria alternata*. *bioRxiv*: <http://doi.org/10.1101/207746>

Lind, A. L., F. Y. Lim, A. Soukup, N. P. Keller & **A. Rokas**. A LaeA- and BrlA-dependent cellular network governs tissue-specific secondary metabolism in the human pathogen *Aspergillus fumigatus*. *bioRxiv*: <http://doi.org/10.1101/196600>

Zhou, X., S. Lutteropp, L. Czech, A. Stamatakis, M. von Looz & **A. Rokas**. Quartet-based computations of internode certainty provide accurate and robust measures of phylogenetic incongruence. *bioRxiv*: <http://doi.org/10.1101/168526>

Moon, J. M., D. M. Aronoff, J. A. Capra, P. Abbot & **A. Rokas**. Genes involved in human sialic acid biology do not harbor signatures of recent positive selection. *bioRxiv*: <http://doi.org/10.1101/137034>

Rinker, D. C., X. Zhou, R. J. Pitts, P. L. Jones, A. Rokas & L. J. Zwiebel. RNAseq in the mosquito maxillary palp: a little antennal RNA goes a long way. *bioRxiv*: <http://doi.org/10.1101/016998>

PEER-REVIEWED PUBLICATIONS (Rokas Lab Members in Bold)

Google Scholar publication statistics
 Number of publications: 118
 Number of citations: ~ 11,000
 H-index: 51

2017 Zhou, X., X.-X. Shen, C. T. Hittinger & A. Rokas. Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. *Mol. Biol. Evol.*: in press.

Lind, A. L., J. H. Wisecaver, C. Lameiras, F. Rodrigues, G. H. Goldman & A. Rokas. Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. *PLoS Biol.* **15**: e2003583.

King, N. & **A. Rokas.** Embracing uncertainty in early animal evolution. *Curr. Biol.* **27**: R1081–R1088.

Shi, R., E. A. Mullins, **X.-X. Shen, K. T. Lay, P. K. Yuen, S. S. David, A. Rokas & B. F. Eichman.** Selective base excision repair of DNA damage by the non-base-flipping DNA glycosylase AlkC. *EMBO J.*: in press.

Lojek, L. J., A. J. Farrand, **J. H. Wisecaver, C. E. Blaby-Haas, S. S. Merchant, A. Rokas & E. P. Skaar.** *Chlamydomonas reinhardtii* cMO is an IsdG family heme oxygenase. *mSphere* **2**: e00176-17.

Eidem, H. R.*, K. L. McGary*, J. A. Capra, P. Abbot & A. Rokas. The transformative potential of an integrative approach to pregnancy. *Placenta* **57**: 204–215. (*Equal contributors)

Valsecchi, I., O. Sarikayabayram, J. Wong Sak Hoi, L. Muszkieta, **J. Gibbons, M.-C. Prevost, A. Mallet, J. Krijnse-Locker, O. Granet, I. Mouyna, P. Carr, M. Bromley, V. K. Aimanianda, vishu kumar; J.-H. Yu, A. Rokas, G. Braus, C. Saveanu, O. Bayram & J.-P. Latgé.** MybAp, a transcription factor involved in conidiation and conidial viability of the human pathogen *Aspergillus fumigatus*. *Mol. Microbiol.* **105**: 880-900.

Wu, M.-Y., **M. E. Mead, S.-C. Kim, A. Rokas & J.-H. Yu.** *WetA* bridges cellular and chemical development in *Aspergillus flavus*. *PLoS ONE* **12**: e0179571.

Zhao, L., **X. Zhou, A. Rokas & R. D. Cone (2017).** Functional variants of the melanocortin-4 receptor associated with the Odontoceti and Mysticeti suborders of cetaceans. *Sci. Rep.* **7**: 5684.

Fidler, A. L., C. E. Darris, S. V. Chetyrkin, V. K. Pedchenko, S. P. Boudko, K. L. Brown, W. G. Jerome, J. K. Hudson, **A. Rokas & B. G. Hudson.** Collagen IV and basement membrane at the evolutionary dawn of metazoan tissues. *eLife* **6**: e24176.

Wisecaver, J. H., A. T. Borowsky, V. Tzin, G. Jander, D. J. Kliebenstein & A. Rokas. A global co-expression network approach for connecting genes to specialized metabolic pathways in plants. *The Plant Cell* **29**: 944–959.

Shen, X.-X., C. T. Hittinger & A. Rokas. Contentious relationships in phylogenomic studies can be driven by a handful of genes. *Nature Ecol. Evol.* **1**: 0126.

Steenwyk, J. & A. Rokas. Extensive copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. *G3* **7**: 1475-1485.

- Ortiz, J. F. & A. Rokas.** CTDGFinder: A novel homology-based algorithm for identifying closely spaced clusters of tandemly duplicated genes. *Mol. Biol. Evol.* **34**: 215-229.
- 2016 Lind, A. L., T. Satterlee, T. D. Smith, A. M. Calvo, & A. Rokas.** Regulation of secondary metabolism by the Velvet complex is temperature-responsive in *Aspergillus*. *G3* **6**: 4023-4033.
- Shen, X.-X., X. Zhou, J. Kominek, C. P. Kurtzman, C. T. Hittinger & A. Rokas.** Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data. *G3* **6**: 3927-3939.
- Zhou, X., D. Peris, C. T. Hittinger & A. Rokas.** *in silico* Whole Genome Sequencer & Analyzer (iWGS): a computational pipeline to guide the design and analysis of *de novo* genome sequencing studies. *G3* **6**: 3655-3662.
- Shen, X.-X., L. Salichos & A. Rokas.** A genome-scale investigation of how sequence-, function-, and tree-based gene properties influence phylogenetic inference. *Genome Biol. Evol.* **8**: 2565-2580.
- Riley, R., S. Haridas, K. H. Wolfe, M. R. Lopes, C. T. Hittinger, M. Göker, A. Salamov, **J. H. Wisecaver**, T. M. Long, C. H. Calvey, A. L. Aerts, K. Barry, C. Choi, A. Clum, A. Y. Coughlan, S. Deshpande, A. P. Douglass, S. J. Hanson, H.-P. Klenk, K. LaButti, A. Lapidus, E. Lindquist, A. Lipzen, J. P. Meier-Kolthoff, R. A. Ohm, R. P. Otilar, J. Pangilinan, Y. Peng, **A. Rokas**, C. A. Rosa, C. Scheuner, A. A. Sibirny, J. C. Slot, J. B. Stielow, H. Sun, C. P. Kurtzman, M. Blackwell, I. V. Grigoriev & T. W. Jeffries. Comparative genomics of biotechnologically important yeasts. *Proc. Natl. Acad. Sci. USA* **113**: 9882-9887.
- Ackerman IV, W. E., I. A. Buhimschi, **H. R. Eidem, D. C. Rinker, A. Rokas, K. Rood, G. Zhao, T. L. Summerfield, M. B. Landon & C. S. Buhimschi.** Comprehensive RNA profiling of villous trophoblast and decidua basalis in pregnancies complicated by preterm birth following intra-amniotic infection. *Placenta* **44**: 23-33.
- Wisecaver, J. H., W. G. Alexander, S. B. King, C. T. Hittinger & A. Rokas.** Dynamic evolution of nitric oxide detoxifying flavohemoglobins, a family of single-protein metabolic modules in bacteria and eukaryotes. *Mol. Biol. Evol.* **33**: 1979–1987.
- Eidem, H. R., D. C. Rinker, W. E. Ackerman IV, I. A. Buhimschi, C. S. Buhimschi, C. Dunn-Fletcher, S. G. Kallapur, M. Pavlicev, L. J. Muglia, P. Abbot & A. Rokas.** Comparing human and macaque placental transcriptomes to disentangle preterm birth pathology from gestational age effects. *Placenta* **41**: 74-82.
- Alexander, W. G., **J. H. Wisecaver, A. Rokas & C. T. Hittinger.** Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. *Proc. Natl. Acad. Sci. USA* **113**: 4116–4121.
- Kobert, K., **L. Salichos, A. Rokas, & A. Stamatakis.** Computing the Internode Certainty and related measures from partial gene trees. *Mol. Biol. Evol.* **33**: 1606-1617.
- Stahlin, B. M., **J. G. Gibbons, A. Rokas, T. V. O’Halloran, & J. C. Slot.** Evolution of a heavy metal homeostasis/resistance island reflects increasing copper stress in Enterobacteria. *Genome Biol. Evol.* **8**: 811-826.
- Kim, M., B. A. Cooper, R. Venkat, J. B. Phillips, H. R. Eidem, J. Hirbo, S. Nutakki, S. M. Williams, L. J. Muglia, J. A. Capra, K. Petren, P. Abbot, A. Rokas, & K. L. McGary.** GENE STATION 1.0: a synthetic resource of diverse evolutionary and functional genomic data for studying the evolution of pregnancy-associated tissues and phenotypes. *Nucleic Acids Res.* **44**, Database issue: D908-916.

- 2015 Wang, Y., X. Zhou, D. Yang, & A. Rokas.** A genome-scale investigation of incongruence in Culicidae mosquitoes. *Genome Biol. Evol.* **7**: 3463-3471.
- Hirbo, J., **H. R. Eidem, A. Rokas, & P. Abbot.** Integrating diverse types of genomic data to identify genes that underlie adverse pregnancy phenotypes. *PLoS ONE* **10**: e0144155.
- Hittinger, C. T., **A. Rokas, F.-Y. Bai, T. Boekhout, P. Gonçalves, T. W. Jeffries, J. Kominek, M.-A. Lachance, D. Libkind, C. A. Rosa, J. P. Sampaio, & C. P. Kurtzman.** Genomics and the making of yeast biodiversity. *Curr. Opin. Genet. Dev.* **35**: 100–109.
- Zhou, X., A. Rokas, S. L. Berger, J. Liebig, A. Ray & L. J. Zwiebel.** Chemoreceptor evolution in Hymenoptera and its implications for the evolution of eusociality. *Genome Biol. Evol.* **7**: 2407-2416.
- Phillips, J. B., P. Abbot & A. Rokas.** Is preterm birth a human-specific syndrome? *Evol. Med. Public Health* **2015**: 136-148.
- Eidem, H. R., W. E. Ackerman IV, K. L. McGary, P. Abbot & A. Rokas.** Gestational tissue transcriptomics in term and preterm human pregnancies: A systematic review and meta-analysis. *BMC Med. Genomics* **8**: 27.
- Lind, A. L., J. H. Wisecaver, T. D. Smith, X. Feng, A. M. Calvo & A. Rokas.** Examining the evolution of the regulatory circuit controlling secondary metabolism and development in the fungal genus *Aspergillus*. *PLoS Genet.* **11**: e1005096.
- Eidem, H. R.*, K. L. McGary* & A. Rokas.** Shared selective pressures on fungal and human metabolic pathways lead to divergent yet analogous genetic responses. *Mol. Biol. Evol.* **32**: 1449–1455. (*Equal contributors)
- Wisecaver, J. H. & A. Rokas.** Fungal metabolic gene clusters – caravans traveling across genomes and environments. *Front. Microbiol.* **6**: 161.
- Elmore, M. H.*, K. L. McGary*, J. H. Wisecaver, J. C. Slot, D. M. Geiser, S. Sink, K. O'Donnell & A. Rokas.** Clustering of two genes putatively involved in cyanate detoxification evolved recently and independently in multiple fungal lineages. *Genome Biol. Evol.* **7**: 789-800. (*Equal contributors)
- Neafsey, D. E., R. M. Waterhouse, 117 other authors including **X. Zhou, D. C. Rinker, A. Rokas** and L. J. Zwiebel, & N. J. Besansky. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science* **347**: 43.
- 2014 Wisecaver, J. H.*, J. C. Slot* & A. Rokas.** The evolution of fungal metabolic pathways. *PLoS Genet.* **10**: e1004816. (*equal contributors)
- Zhou, X.*, D. C. Rinker*, R. J. Pitts, A. Rokas & L. J. Zwiebel.** Divergent and conserved elements comprise the chemoreceptive repertoire of the non-blood feeding mosquito *Toxorhynchites amboinensis*. *Genome Biol. Evol.* **6**: 2883-2896. (*equal contributors)
- Polzin, K. & A. Rokas.** Evaluating rare amino acid substitutions (RGC_CAMs) in a yeast model clade. *PLoS ONE* **9**: e92213.
- Salichos, L., A. Stamatakis & A. Rokas.** Novel information theory-based measures for quantifying incongruence among phylogenetic trees. *Mol. Biol. Evol.* **31**: 1261-1271.
- Zhou, X. & A. Rokas.** Prevention, diagnosis, and treatment of high throughput sequencing data pathologies. *Mol. Ecol.* **23**: 1679-1700.
- Soria, P. S.*, K. L. McGary* & A. Rokas.** Functional divergence for every paralog. *Mol. Biol. Evol.* **31**: 984-992. (*equal contributors)

- Greene, G. H., K. L. McGary, A. Rokas & J. C. Slot.** Ecology drives the distribution of specialized tyrosine metabolism modules in fungi. *Genome Biol. Evol.* **6**: 121-132.
- 2013** Samuels, D. C., C. Li, B. Li, Z. Song, E. Torstenson, H. B. Clay, **A. Rokas**, T. Thornton-Wells, J. H. Moore, T. Hughes, R. Hoffman, J. L. Haines, D. G. Murdock, D. P. Mortlock & S. M. Williams. Recurrent tissue-specific mtDNA mutations are common in humans. *PLoS Genetics* **9**: e1003929.
- Rinker, D. C.*, X. Zhou***, R. J. Pitts, The AGC Consortium, **A. Rokas** & L. J. Zwiebel. Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in *Anopheles gambiae*. *BMC Genomics* **14**: 749. (*equal contributors)
- Dhingra, S., **A. L. Lind**, H-C. Lin, Y. Tang, **A. Rokas** & A. M. Calvo. The fumagillin gene cluster, an example of hundreds of genes under veA control in *Aspergillus fumigatus*. *PLoS ONE* **8**: e77147.
- Campbell, M. A.**, M. Staats, J. L. A. van Kan, **A. Rokas** & **J. C. Slot**. Repeated loss of an anciently horizontally transferred gene cluster in *Botrytis*. *Mycologia* **105**: 1126–1134.
- McGary, K. L., J. C. Slot & A. Rokas.** The physical linkage of metabolic genes in fungi is an adaptation against the accumulation of toxic intermediate compounds. *Proc. Natl. Acad. Sci. USA* **110**: 11481-11486.
- Salichos, L. & A. Rokas.** Accurately inferring ancient divergences requires genes with strong phylogenetic signal. *Nature* **497**: 327-331.
- Predazzi, I. M., **A. Rokas**, A. Deinard, N. Schnetz-Boutaud, N. D. Williams, W. S. Bush, A. Tacconelli, K. Friedrich, S. Fazio, G. Novelli, J. L. Haines, G. Sirugo & S. M. Williams. Putting pleiotropy and selection into context defines a new paradigm for interpreting genetic data. *Circ. Cardiovasc. Genet.* **6**: 299-307.
- Rinker, D. C.**, R. J. Pitts, **X. Zhou**, E. Suh, **A. Rokas** & L. J. Zwiebel. Blood meal-induced changes to antennal transcriptome profiles reveal shifts in odor sensitivities in the malaria vector mosquito *Anopheles gambiae*. *Proc. Natl. Acad. Sci. USA* **110**: 8260-8265.
- Bradshaw, R. E., **J. C. Slot**, G. G. Moore, P. Chettri, P. J. G. M. de Wit, K. C. Ehrlich, A. R. D. Ganley, M. A. Olson, **A. Rokas**, I. Carbone & M. P. Cox. Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. *New Phytol.* **198**: 525–535.
- Xu, Y., P. Ma, P. Shah, **A. Rokas**, Y. Liu & C. H. Johnson. Non-optimal codon usage is a post-transcriptional mechanism to achieve conditionality of circadian clock function. *Nature* **495**: 116-120.
- Adhikary, S., M. C. Cato, **K. L. McGary**, **A. Rokas** & B. F. Eichman. Non-productive DNA damage binding by DNA glycosylase-like protein Mag2 from *Schizosaccharomyces pombe*. *DNA Repair* **12**: 196-204.
- Muszkietka, L., A. Beauvais, V. Pätz, **J. G. Gibbons**, V. A. Leberre, R. Beau, K. Shibuya, **A. Rokas**, J. M. Francois, O. Kniemeyer, A. A. Brakhage & J. P. Latge. Investigation of *Aspergillus fumigatus* biofilm formation by various “omics” approaches. *Front. Microbiol.* **4**: 13.
- Ubaida Mohien, C., D. R. Colquhoun, D. K. Mathias, **J. G. Gibbons**, J. S. Armistead, M. del Carmen-Rodriguez, M. H. Rodriguez, N. J. Edwards, J. Hartler, G. G. Thallinger, D. R. Graham, J. Martinez-Barnette, **A. Rokas**, & R. R. Dinglasan. A bioinformatics approach for integrated transcriptomic and proteomic comparative analyses of model and non-sequenced anopheline vectors of human malaria parasites. *Mol. Cell. Proteomics* **12**: 120-131.

- Gibbons, J. G. & A. Rokas.** The function and evolution of the *Aspergillus* genome. *Trends Microbiol.* **21**: 14-22.
- 2012 Elmore, M. H.* , J. G. Gibbons* & A. Rokas.** Assessing the genome-wide effect of promoter region tandem repeat natural variation on gene expression. *G3* **2**: 1643-1649. (*equal contributors)
- Rokas, A., J. G. Gibbons, X. Zhou, A. Beauvais & J. P. Latge.** The diverse applications of RNA-Seq for functional genomics studies in *Aspergillus fumigatus*. *Ann. N.Y. Acad. Sci.* **1273**: 25-34.
- Zhou, X.* , J. D. Slone* , A. Rokas, S. L. Berger, J. Liebig, A. Ray, D. Reinberg & L. J. Zwiebel.** Phylogenetic and transcriptomic analysis of chemosensory receptors in a pair of divergent ant species reveals sex-specific signatures of odor coding. *PLoS Genet.* **8**: e1002930. (*equal contributors)
- League, G. P., J. C. Slot & A. Rokas.** The *ASP3* locus in *Saccharomyces cerevisiae* originated by horizontal gene transfer from *Wickerhamomyces*. *FEMS Yeast Res.* **12**: 859-863.
- Zhang, H., A. Rokas & J. C. Slot.** Two different secondary metabolism gene clusters occupied the same ancestral locus in fungal dermatophytes of the Arthrodermataceae. *PLoS ONE* **7**: e41903.
- Gibbons, J. G., L. Salichos, J. C. Slot, D. C. Rinker, K. L. McGary, J. G. King, M. A. Klich, D. L. Tabb, W. H. McDonald & A. Rokas.** The evolutionary imprint of domestication on microbe genome variation and function. *Curr. Biol.* **22**: 1403-1409.
- Stergiopoulos, I., Y. A. I. Kourmpetis, J. C. Slot, F. T. Bakker, P. J. G. M. De Wit & A. Rokas.** *In silico* characterization and molecular evolutionary analysis of a novel superfamily of fungal effector proteins. *Mol. Biol. Evol.* **29**: 3371-3384.
- Floudas, D., M. Binder, 68 other authors including **A. Rokas** and **J. C. Slot** & D. S. Hibbett. The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* **336**: 1715-1719.
- Martinez-Barnetche, J., R. E. Gómez-Barreto, M. Ovilla-Muñoz, J. Téllez-Sosa, D. E. García-López, R. R. Dinglasan, C. Ubaida Mohien, R. M. MacCallum, S. N. Redmond, **J. G. Gibbons, A. Rokas, C. M. Machado, F. Cazares-Raga, L. González-Cerón, S. Hernández-Martínez & M. H. Rodríguez-Lopez.** Transcriptome of the adult female malaria mosquito vector *Anopheles albimanus*. *BMC Genomics* **13**: 207.
- Wei, C., **L. Salichos, C. M. Wittgrove, A. Rokas & J. G. Patton.** Transcriptome-wide analysis of small RNA expression in early zebrafish development. *RNA* **18**: 915-929.
- Campbell, M. A., A. Rokas & J. C. Slot.** Horizontal transfer and death of a fungal secondary metabolic gene cluster. *Genome Biol. Evol.* **4**: 289-293.
- Gibbons, J. G., A. Beauvais, R. Beau, K. L. McGary, J.-P. Latge & A. Rokas.** Global transcriptome changes underlying colony growth in the opportunistic human pathogen *Aspergillus fumigatus*. *Euk. Cell* **11**: 68-78.
- Klaassen, C. H. W.* , **J. G. Gibbons***, N. D. Fedorova, J. F. Meis & **A. Rokas.** Evidence for genetic differentiation and variable recombination rates among Dutch populations of the opportunistic human pathogen *Aspergillus fumigatus*. *Mol. Ecol.* **21**: 57-70. (*equal contributors)
- 2011 Rokas, A.** Phylogenetic analysis of protein sequence data using the Randomized Accelerated Maximum Likelihood (RAxML) program. *Curr. Prot. Mol. Biol.*: **96**: 19.11.1-19.11.14.

- Pitts, R. J.*, **D. C Rinker***, P. L. Jones*, **A. Rokas** & L. J. Zwiebel. Transcriptome profiling of chemosensory appendages in the malaria vector *Anopheles gambiae* reveals tissue- and sex-specific signatures of odor coding. *BMC Genomics*: **12**: 271. (*equal contributors)
- Zill, O. A., D. R. Scannell, **A. Rokas**, C. Payen, M. J. Dunham, M. B. Eisen, J. Rine, M. Johnston & C. T. Hittinger. The awesome power of yeast evolutionary genetics: New genome sequences and strain resources for the *Saccharomyces sensu stricto* genus. *G3* **1**: 11-25.
- Salichos, L. & A. Rokas.** Evaluating ortholog prediction algorithms in a yeast model clade. *PLoS One* **6**: e18755.
- Kent, B. N., **L. Salichos, J. G. Gibbons, A. Rokas**, I. L.G. Newton, M. E. Clark & S. R. Bordenstein. Complete Bacteriophage Transfer in a Bacterial Endosymbiont (*Wolbachia*) Determined by Targeted Genome Capture. *Genome Biol. Evol.* **3**: 209-218.
- Slot, J. C. & A. Rokas.** Horizontal transfer of a large and highly toxic secondary metabolic gene cluster between fungi. *Curr. Biol.* **21**: 134-139.
- 2010** Carnahan, R. H.*, **A. Rokas***, E. A. Gaucher & A. B. Reynolds. The molecular evolution of the p120-catenin subfamily and its functional associations. *PLoS One* **5**: e15747. (*equal contributors)
- Slot, J. C. & A. Rokas.** Multiple *GAL* pathway gene clusters evolved independently and by different mechanisms in fungi. *Proc. Natl. Acad. Sci. USA* **107**: 10136-10141.
- Hittinger, C. T., P. Gonçalves, J. P. Sampaio, J. Dover, M. Johnston & **A. Rokas.** Remarkably ancient balanced polymorphisms in a multi-locus gene network. *Nature*: **464**: 54-58.
- Salichos, L. & A. Rokas.** The diversity and evolution of circadian clock proteins in fungi. *Mycologia* **102**: 269-278.
- Gibbons, J. G., M. A. Klich & A. Rokas.** Developing highly conserved microsatellite markers: a case study in the filamentous fungal genus *Aspergillus*. *Mol. Ecol. Resources* **10**: 404-408.
- Hittinger, C. T., M. Johnston, **J. T. Tossberg & A. Rokas.** Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. *Proc. Natl. Acad. Sci. USA* **107**: 1476-1481.
- 2009** **Gibbons, J. G., E. Janson, C. T. Hittinger, M. Johnston, P. Abbot & A. Rokas.** Benchmarking next-generation transcriptome sequencing for functional and evolutionary genomics. *Mol. Biol. Evol.* **26**: 2731-2744.
- Rokas, A. & P. Abbot.** Harnessing genomics for evolutionary insights. *Trends Ecol. Evol.*: **24**: 192-200.
- Gibbons, J. G. & A. Rokas.** Comparative and functional characterization of intragenic tandem repeats in ten *Aspergillus* genomes. *Mol. Biol. Evol.* **26**: 591-602.
- Rokas, A.** The effect of domestication on the fungal proteome. *Trends Genet.* **25**: 60-63.
- 2008** **Rokas, A.** The origins of multicellularity and the early history of the genetic toolkit for animal development. *Ann. Rev. Genet.* **42**: 235-251.
- Rokas, A.** The molecular origins of multicellular transitions. *Curr. Opin. Genet. Dev.* **18**: 472-478.
- Rokas, A., & S. B. Carroll.** Frequent and widespread parallel evolution of protein sequences. *Mol. Biol. Evol.*: **25**: 1943-1953.

- Mathee, K. *et al.* (19 co-authors, including **A. Rokas**). Dynamics of *Pseudomonas aeruginosa* genome evolution. *Proc. Natl. Acad. Sci. USA* **105**: 3100-3105.
- King, N. *et al.* (34 co-authors, including **A. Rokas** and JGI Sequencing). The genome of the choanoflagellate *Monosiga brevicollis* and the origins of metazoan multicellularity. *Nature* **451**: 783-788.
- Stone, G. N., R. J. Atkinson, **A. Rokas**, J.-L. Nieves-Aldrey, G. Melika, Z. Acs, G. Csóka, A. Hayward, R. Bailey, C. Buckee & G. A. T. McVean. Evidence for widespread cryptic sexual generations in apparently purely asexual *Andricus* gallwasps. *Mol. Ecol.* **17**: 652-665.
- 2007 Rokas, A. et al.** (15 co-authors). What can comparative genomics tell us about species concepts in the genus *Aspergillus*? *Studies in Mycology* **59**: 11-17.
- Stone, G. N., R. J. Challis, R. J. Atkinson, G. Csóka, A. Hayward, G. Melika, S. Mutun, S. Preuss, **A. Rokas**, E. Sadeghi, & K. Schönrogge. The phylogeographic clade trade: Tracing the impact of human-mediated dispersal on the colonisation of northern Europe by the oak gallwasp *Andricus kollari*. *Mol. Ecol.* **16**: 2768-2781.
- Stone, G. N., R. J. Challis, S. Mutun, J.-L. Nieves-Aldrey, S. Preuss, **A. Rokas**, A. Aebi, E. Sadeghi, & M. Tavakoli. Longitudinal range expansion and cryptic eastern species in the western Palaearctic oak gallwasp *Andricus coriarius*. *Mol. Ecol.* **16**: 2103-2114.
- Ane, C., B. Larget, D. A. Baum, S. D. Smith, & **A. Rokas**. Bayesian estimation of concordance among trees. *Mol. Biol. Evol.* **24**: 412-426.
- 2006 Rokas, A. & Carroll, S. B.** Bushes in the Tree of Life. *PLOS Biol.* **11**: e352.
- Jeong, S., **A. Rokas** & S. B. Carroll. Regulation of body pigmentation by the Abdominal-B Hox protein and its gain and loss in *Drosophila* evolution. *Cell* **125**: 1387-1399.
- Prud'homme, B., N. Gompel, **A. Rokas**, V. A. Kassner, T. M. Williams, S.-D. Yeh, J. R. True & S. B. Carroll. Repeated morphological evolution through cis-regulatory changes in a pleiotropic gene. *Nature* **440**: 1050-1053.
- 2005 Rokas, A., D. Krueger & S. B. Carroll.** Animal evolution and the molecular signature of radiations compressed in time. *Science* **310**: 1933-1938.
- Rokas, A. & S. B. Carroll.** More genes or more taxa? The relative contribution of gene number and taxon number to phylogenetic accuracy. *Mol. Biol. Evol.* **22**: 1337-1344.
- 2004 Hittinger, C. T., A. Rokas & S. B. Carroll.** Parallel inactivation of multiple *GAL* pathway genes and ecological diversification in yeasts. *Proc. Natl. Acad. Sci. USA* **101**: 14144-14149.
- 2003 Rokas, A.***, B. L. Williams*, N. King & S. B. Carroll. Genome-scale approaches to resolving incongruence in molecular phylogenies. *Nature* **425**: 798-804. (*equal contributors)
- Rokas, A., E. Ladoukakis, & E. Zouros.** Animal mitochondrial DNA recombination revisited. *Trends Ecol. Evol.* **18**: 411-417.
- Rokas, A., R. J. Atkinson, L. W. I. Webster & G. N. Stone.** Out of Anatolia: Longitudinal gradients in genetic diversity support a Turkish origin for a circum-mediterranean oak gallwasp *Andricus quercustozae*. *Mol. Ecol.* **12**: 2153-2174.
- Cummings, M. P., S. A. Handley, D. S. Myers, D. L. Reed, **A. Rokas** & K. Winka. Comparing bootstrap and posterior probability values in the four taxon case. *Syst. Biol.* **52**: 477-487.
- Rokas, A.***, N. King*, J. R. Finnerty & S. B. Carroll. Conflicting phylogenetic signals at the base of the metazoan tree. *Evol. Devel.* **5**: 346-359. (*equal contributors)

- Rokas, A.**, G. Melika, Y. Abe, J.-L. Nieves-Aldrey, J. M. Cook & G. N. Stone. Lifecycle closure, lineage sorting, and hybridization revealed in a phylogenetic analysis of European oak gallwasps (Hymenoptera: Cynipidae: Cynipini) using mitochondrial sequence data. *Mol. Phylog. Evol.* **26**: 36-45.
- 2002** Cook, J. M., **A. Rokas**, M. Pagel & G. N. Stone. Evolutionary shifts between host oak species and host plant organs in *Andricus* gallwasps. *Evolution* **56**: 1821-1830.
- Stone, G. N., R. J. Atkinson, G. Brown, & **A. Rokas**. The population genetic consequences of range expansion: a review of pattern and process, and the value of oak gallwasps as a model system. *Biodiversity Science*, **10**: 80-97.
- Rokas, A.**, R. J. Atkinson, J.- L. Nieves-Aldrey, S. A. West & G. N. Stone. The incidence and diversity of *Wolbachia* in gallwasps (Hymenoptera; Cynipidae) on oak. *Mol. Ecol.* **11**: 1815-1829.
- Rokas, A.**, J. A. A. Nylander, F. Ronquist & G. N. Stone. A maximum likelihood analysis of eight phylogenetic markers in gallwasps (Hymenoptera: Cynipidae); implications for insect phylogenetic studies. *Mol. Phylog. Evol.* **22**: 206-219.
- 2001** **Rokas, A.**, R. J. Atkinson, G. S. Brown, S. A. West & G. N. Stone. Understanding patterns of genetic variation in the oak gallwasp *Biorhiza pallida*: demographic history or a *Wolbachia* selective sweep? *Heredity* **87**: 294-304.
- Stone, G. N., R. J. Atkinson, **A. Rokas**, G. Csóka & J.- L. Nieves-Aldrey. Differential success in northwards range expansion between ecotypes of the marble gallwasp *Andricus kollari*: a tale of two refugia. *Mol. Ecol.* **10**: 761-778.
- 2000** **Rokas, A.** & P. W. H. Holland. Rare genomic changes as a tool for phylogenetics. *Trends Ecol. Evol.* **15**: 454-459.
- Averof, M., **A. Rokas**, K. H. Wolfe & P. M. Sharp. Evidence for a high frequency of simultaneous double-nucleotide substitutions. *Science* **287**: 1283-1286.
- 1999** **Rokas, A.**, J. Kathirithamby & P. W. H. Holland. Intron insertion as a phylogenetic character: the *engrailed* homeobox of Strepsiptera does not indicate affinity with Diptera. *Insect Mol. Biol.* **8**: 527-530.

BOOK CHAPTERS

- 2016** **Rokas, A.** Systematics in the age of genomics. In “Next Generation Systematics”, P. D. Olson, J. Hughes, & J. A. Cotton (Eds.), Cambridge University Press, pp. 219-228.
- 2008** **Rokas, A.** & S. Chatzimanolis. From gene-scale to genome-scale phylogenetics; the data flood in but the challenges remain. In “Phylogenomics” W. J. Murphy (Ed.), Methods in Molecular Biology series, Humana Press, Totowa, NJ, pp. 1-12.
- Geiser, D. M., R. A. Samson, J. Varga, **A. Rokas** and S. M. Witiak. A review of molecular phylogenetics in *Aspergillus*, and prospects for a robust genus-wide phylogeny. In “*Aspergillus* in the Genomics Era”, Varga, J., and R. A. Sampson (Eds.), Wageningen Academic Publishers, pp. 17-32.
- Rokas, A.** & J. E. Galagan. The *Aspergillus nidulans* genome and comparative analysis with other Aspergilli. In “The Aspergilli: Genomics, Medical Applications, Biotechnology, and Research Methods”, Osmani, S. A. and G. H. Goldman, CRC Press, pp. 43-55.
- 2006** Atkinson, R. J., **A. Rokas** & G. N. Stone. Longitudinal patterns in species richness and genetic diversity in European oaks and oak gallwasps. In: “Phylogeography in southern

European refugia: Evolutionary Perspectives on the origins and conservation of European Biodiversity”, S. Weiss, N. Ferrand (Eds). Kluwer, The Netherlands.

- 2003** Stone, G. N., R. J. Atkinson, G. Brown, **A. Rokas** & G. Csóka. The population genetic consequences of range expansion: oak gallwasps as a model system. In: “Genes in the Environment”, R. S. Hails, J. E. Beringer and H. C. J. Godfray (Eds), Blackwell and the British Ecological Society, pp. 46-62.

SELECT COMMENTARIES (LAST5 YEARS)

- 2017** Shropshire, J. D. & **A. Rokas**. The gene family that cheats Mendel. *eLife* **6**: e28567.
 Abbot, P. & **A. Rokas**. Mammalian pregnancy. *Curr. Biol.* **27**: R127-R128.
- 2013** **Rokas, A.** My oldest sister is a sea walnut? *Science* **342**: 1327-1329.
Rokas, A. *Aspergillus*. *Curr. Biol.* **23**: R187-R188.

INVITED TALKS

- 2017** Keynote Speaker, iGenolevures Meeting on “The Future of Yeast Genomics”, Paris, France
 Invited Speaker, XIII International Meeting on Paracoccidioidomycosis 2017, Iguassu Falls, Brazil
 Invited Speaker, no 29º Congresso Brasileiro de Microbiologia 2017, Iguassu Falls, Brazil
 Department of Pathology, Microbiology, and Immunology, Vanderbilt University, Nashville, TN
 Bridging Speaker, International Congress of Mycology and Eukaryotic Microbiology, Singapore
 Heidelberg Institute for Theoretical Studies, Heidelberg, Germany
 Plenary Speaker, 7th Advanced Lecture Course on Human Fungal Pathogens, Nice, France
 Invited Speaker, Society for Reproductive Investigation Annual Meeting, Orlando, FL
 March of Dimes Prematurity Research Centers Annual Symposium, Orlando, FL
- 2016** Plenary Speaker, Burroughs Wellcome-Fund/March of Dimes Biennial Preterm Birth Symposium, Research Triangle Park, NC
 Graduate Student-Invited Speaker, Department of Organismal Biology, Uppsala University, Uppsala, Sweden
 Distinguished Lectures in Microbiology, Department of Bacteriology, University of Wisconsin-Madison, WI
 Division of Biological Sciences, University of Missouri, MO
 Dimensions of Fungal Biodiversity Symposium, Mycological Society of America Meeting, Berkeley, CA
 Department of Biology, Middle Tennessee State University, Murfreesboro, TN
 March of Dimes Prematurity Research Centers Annual Symposium, Montreal, Canada
 Department of Chemistry & Biochemistry, University of North Carolina Greensboro, Greensboro, NC
 Plenary Speaker, “Evolution, of Cells, Genomes and Proteins” Workshop, Nanyang Technological University, Singapore
- 2015** Plenary Speaker, Society of Systematic Biologists Standalone Meeting, Ann Arbor, MI
 Plenary Speaker, “Phylogeny meets genomics” workshop, Center for Advanced Studies (CAS), Ludwig-Maximilians-University, Munich, Germany
 Plenary Speaker, “Genomes to Secondary Metabolites”, GSC-17 Satellite Workshop, DOE Joint Genome Institute, Walnut Creek, CA
 Plenary Speaker, “Genomics of Energy and the Environment” meeting, DOE Joint Genome Institute, Walnut Creek, CA
 March of Dimes Prematurity Research Centers Annual Symposium, San Francisco, CA

- 2014** Plenary Speaker, Comparative and Functional Genomics of Fungal Pathogens, Current Trends in Biomedicine Series, International University of Andalusia, Baeza, Spain
 Evolution Seminar Series, University of Wisconsin-Madison, WI
 Department of Genetics, University of Wisconsin-Madison, WI
 Center for Bioinformatics Research, Indiana University, IN
 Session Chair and Discussion Leader, Cellular and Molecular Fungal Biology Gordon Research Conference, Holderness, NH
 Plenary Speaker, XVI International Congress on Molecular Plant-Microbe Interactions, Rhodes, Greece
 Plenary Speaker, Protein Structure and Protein Evolution Symposium, Royal Swedish Academy of Sciences
 Organismic and Evolutionary Biology Seminar Series, Univ. Massachusetts–Amherst, MA
 Plenary Speaker, 12th European Conference on Fungal Genetics, Seville, Spain
- 2013** Department of Plant Pathology, North Carolina State University, Raleigh, NC
 American Museum of Natural History, New York, NY
 Department of Plant Pathology, ETH Zurich, Switzerland
 European Bioinformatics Institute, Hinxton, UK
 Plenary Speaker, Italian Zoological Association Spring School on “Metazoan Phylogeny and Evolution”, Venice, Italy
 Plenary Speaker, 27TH Fungal Genetics Meeting, Asilomar, CA
 Plenary Speaker, 10TH International *Aspergillus* Meeting, Asilomar, CA
 Cornell Center for Comparative and Population Genomics, Cornell University, NY
 Department of Ecology and Evolutionary Biology, Yale University, CT
- 2007 – 2012 (Invited talks as Assistant Professor)**
 (2012) Department of Genetics, University of Georgia, GA
 (2012) Plenary Speaker, The 13th Annual Vanderbilt Genetics Symposium on “Evolution and the Genetic Basis for Human Disease”, Vanderbilt University, TN
 (2012) Plenary Speaker, Graduate Research School in Genomic Ecology Summer Meeting, Lund, Sweden
 (2012) Plenary Speaker, Cellular and Molecular Fungal Biology Gordon Research Conference, Holderness, NH
 (2012) Plenary Speaker, HHMI Bioinformatics Workshop for Student-Scientist Partnerships, Chevy Chase, MD
 (2012) Institute for Molecular Biology and Biotechnology, University of Crete, Greece
 (2012) Plenary Speaker, 5TH Advances Against Aspergillosis Meeting, Istanbul, Turkey
 (2012) Department of Biological Sciences, University of Alabama, AL
 (2011) Department of Entomology, University of Maryland, MD
 (2011) Department of Biological Science, University of Pittsburgh, PA
 (2011) Plenary Speaker, Smithsonian Initiative in Biodiversity Genomics Lectures, Washington, DC
 (2011) Plenary Speaker, 26TH Fungal Genetics Meeting, Asilomar, CA
 (2010) Department of Ecology and Evolutionary Biology, University of Tennessee-Knoxville, TN
 (2010) Department of Parasitology and Mycology, Institut Pasteur, Paris, France
 (2010) Department of Biological and Environmental Sciences, University of Tennessee-Chattanooga, TN
 (2010) Department of Ecology and Evolution, Michigan University, Ann Arbor, MI
 (2009) Plenary Speaker, 100th International Titisee Conference on “Genome evolution and the origin of novel gene functions”, Lake Titisee, Germany
 (2009) Plenary Speaker, IGERT Deep Genomics Symposium, Arizona University, Tucson, AZ
 (2009) Plenary Speaker, “Evolutionary Biology: 150 Years After *The Origin*”, University of Michigan Life Sciences Institute Eighth Annual Symposium, Ann Arbor, MI
 (2009) Department of Biology, IGERT Seminar Series, Indiana University, Bloomington, IN

- (2009) Plenary Speaker, International Symposium on Deep Metazoan Phylogeny, Berlin, Germany
(2009) Department of Integrative Biology, University of Guelph, Ontario, Canada
- (2008) Plenary Speaker, Entomological Society of America Annual Meeting, Reno, NV
(2008) Department of Genetics, Washington University in St. Louis, MO
(2008) Plenary Speaker, XII International Congress of Mycology, Istanbul, Turkey
(2008) Plenary Speaker, 33rd FEBS Congress / 11th IUBMB Conference, Athens, Greece
(2008) Plenary Speaker, Society of Molecular Biology and Evolution Annual Meeting, Barcelona, Spain
(2008) Infectious Disease Rounds, Vanderbilt University Medical Center, Nashville, TN
- 2000 – 2007 (Invited talks as graduate student, postdoc, or research scientist)**
- (2007) Plenary Speaker, Comparative Genomics of Eukaryotic Microorganisms ESF-EMBO Symposium, San Feliu de Guixols, Spain
(2007) Department of Plant Pathology, Pennsylvania State University, PA
(2007) Plenary Speaker, “*Aspergillus* systematics in the genomics era” Symposium, CBS Fungal Biodiversity Centre, Utrecht, The Netherlands
(2007) Plenary Speaker, “Tree of Life” Symposium, University of Iowa, IA
(2007) Department of Biology, Johns Hopkins University, MD
(2007) Department of Biology, Boston College, MA
(2007) Department of Biology, Georgetown University, DC
(2006) Department of Earth & Planetary Sciences, Harvard University, MA
(2006) Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, MA
(2006) Department of Biological Sciences, Vanderbilt University, TN
(2006) Department of Biology, Clark University, MA
(2006) Department of Biology, Duke University, NC
(2006) Plenary Speaker, IXTH International Fungal Biology Conference & 16TH New Phytologist Symposium on “Impact of Genomics on Fungal Biology”, Nancy, France
(2006) Plenary Speaker, Joint meeting of American Phytopathological Society, Canadian Phytopathological Society & Mycological Society of America, Symposium on “Gene Clustering as a Mechanism for Microbial Innovation”, Quebec City, Canada
(2006) Department of Earth, Atmospheric and Planetary Sciences, MIT, MA
(2006) Darwin Day Speaker, Department of Biology, St. John’s University, NY
(2005) Plenary Speaker, Phylogeography and Phylogenetics Workshop, Mathematical Biosciences Institute, Ohio State University, OH
(2005) The Broad Institute of MIT & Harvard, MA
(2004) Department of Biology, New York University, NY
(2004) Department of Biology, Boston College, MA
(2004) Plenary Speaker, Mycological Society of America, Symposium on “Phyloinformatics”, Asheville, NC
(2004) Plenary Speaker, Royal Netherlands Academy of Arts and Sciences, Colloquium on “Fungal Phylogenomics”, Amsterdam, The Netherlands
(2004) Plenary Speaker, Workshop Research School on “Phylogenomics of Fungi”, Utrecht, The Netherlands
(2003) Department of Entomology, University of Wisconsin-Madison, WI
(2002) Department of Ecology and Evolutionary Biology, University of Kansas, KS
(2000) Department of Zoology, Reading University, U.K.