

Curriculum Vitae

Gavin C. Conant

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Education:

B.S. Biology *summa cum laude*, 1998, The University of New Mexico. Thesis title: “Effects of nucleotide composition bias on the success of the parsimony criterion in phylogenetic inference.” Advisor: Prof. Paul Lewis

Ph. D. Biology, with distinction, 2004, The University of New Mexico. Dissertation title: “Functional divergence at the molecular level: Robustness, asymmetry, and convergence.” Advisor: Prof. Andreas Wagner.

Positions Held:

January 2017-present: Associate Professor, Department of Biological Sciences, North Carolina State University, Raleigh, NC.

January 2017-2020: Adjunct Professor, Division of Animal Sciences, University of Missouri, Columbia, Missouri.

September 2014-December 2016: Associate Professor, Division of Animal Sciences and Informatics Institute, University of Missouri, Columbia, Missouri.

March 2014-December 2016: Associate Director for Education, Missouri Informatics Institute, University of Missouri, Columbia, Missouri.

September 2008-August 2014: Assistant Professor, Division of Animal Sciences and Informatics Institute, University of Missouri, Columbia, Missouri.

January 2005-July 2008: Post-doctoral fellow, Smurfit Institute of Genetics, Trinity College, Dublin, Ireland. Supervisor: Prof. Kenneth Wolfe.

June-Dec. 2004: Post-doctoral fellow, Lehrstuhl für Bioinformatik, Universität Leipzig, Leipzig, Germany. Supervisor: Prof. Peter Stadler.

Albuquerque High Performance Computing Center, Research Assistant (1998-2000)

Funding and awards

Department of Energy Computational Sciences Graduate Fellowship (2000-2004). Included research practicum at Sandia National Laboratories, Summer 2002.

Phi Beta Kappa, The University of New Mexico, 1998

- USDA: “Improving Profitability and Sustainability of Sheep Production.” U. Wyoming subcontract to MU. Kristi Cammack P. I., W. Lamberson and **G. Conant**, Co-Is.
- European Research Council: “GplusE— Genotype and Environment contributing to the sustainability of dairy cow production systems through the optimal integration of genomic selection and novel management protocols based on the development.” University College, Dublin subcontract to MU. Mark Crowe, PI, **G. Conant**, C. Elsik, M. Lucy and J. Taylor, MU co-Is.
- National Science Foundation: “REU: Educating for the grand challenges at the intersection of biocomplexity and high-performance computing.” **G. C. Conant, P.I.**, C.-R. Shyu, M. Becchi and D. Korkin, Co-I.
- National Science Foundation: “SHF: Small: Collaborative Research: The Automata Programming Paradigm for Genomic Analysis.” M. Becchi, PI, J. Bakos and **G. C. Conant**, CoIs.
- National Science Foundation: “Polyploidy and Plasticity in the Crop Brassicas,” J. C. Pires, M. Barker, **G. C. Conant** and E. Lyons, CoIs.
- National Science Foundation: “Inferring the gene coevolution network from deep comparative genomics,” **G. Conant, P.I.**

Representative Publications:

- An, H., J. C. Pires and G. C. Conant. (2024) Gene expression bias between the subgenomes of allopolyploid hybrids is an emergent property of the kinetics of expression. *PLoS Computational Biology*, *in press*.
- Hao, Y., J. Fleming, J. Petterson, E. Lyons, P. P. Edger, J. C. Pires, J. L. Thorne, and **G. C. Conant**. (2022) Convergent evolution of polyploid genomes from across the eukaryotic tree of life. *G3: Genes, Genomes, Genetics*, **12**: jkac094.
- Hao Y, M. E. Mabry, P. Edger, M. Freeling, C. Zheng, L. Jin, R. VanBuren, M. Colle, H. An, R. S. Abrahams, J. D. Washburn, X. Qi, K. Barry, C. Daum, S. Shu, J. Schmutz, D. Sankoff, M. S. Barker, E. Lyons, J. C. Pires and **G. C. Conant**. (2021) The contributions of the allopolyploid parents of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. *Genome Research* **31**:799–810.
- Emery, M., M. M. S. Willis, Y. Hao, K. Barry, K. Oakgrove, Y. Peng, J. Schmutz, E. Lyons, J. C. Pires, P. P. Edger, and **G. C. Conant**. (2018). Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. *PLoS Genetics*, **14**: e1007267.
- Pires, J. C. and **G. C. Conant**. (2016) Robust yet fragile: Expression noise, protein misfolding and gene dosage in the evolution of genomes, *Annual Review of Genetics*, **50**: 113-131.
- Taxis, T. M., S. Wolff, S. J. Gregg, N. O. Minton, C. Zhang, J. Dai, R. D. Schnabel, J. F. Taylor, M. S. Kerley, J. C. Pires, W. R. Lamberson and **G. C. Conant**. (2015) The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity, *Nucleic Acids Research*, **43**: 9600-9612.
- Conant, G. C.** (2014) Comparative genomics as a time machine: How relative gene dosage and metabolic requirements shaped the time-dependent resolution of yeast polyploidy, *Molecular Biology and Evolution*, **31**: 3184-3193.

Representative Publications (continued):

- Conant, G. C.**, J. A. Birchler, and J. C. Pires. (2014) Dosage, Duplication, and Diploidization: Clarifying the interplay of multiple models for duplicate gene evolution over time, *Current Opinion in Plant Biology*, **19**: 91-98.
- Bekaert, M., P. P. Edger, C. M. Hudson, J. C. Pires, and **G. C. Conant**, (2012) Metabolic and evolutionary costs of herbivory defense: Systems biology of glucosinolate synthesis, *The New Phytologist*, **196**:596-605.
- Conant, G. C.** and K. H. Wolfe, (2008) Turning a hobby into a job: How duplicated genes find new functions, *Nature Reviews Genetics*, **9**: 938-950.
- Conant, G. C.** and K. H. Wolfe, (2007) Increased glycolytic flux as an outcome of whole-genome duplication in yeast, *Molecular Systems Biology*, **3**: 129.
- Conant, G. C.** and A. Wagner, (2003) Asymmetric sequence divergence of duplicate genes, *Genome Research*, **13**: 2052-2058.
- Conant, G. C.** and A. Wagner, (2003) Convergent evolution of gene circuits, *Nature Genetics*, **34**: 264-266.

All Publications (82 total):

- An, H., J. C. Pires and G. C. Conant. (2024) Gene expression bias between the subgenomes of allopolyploid hybrids is an emergent property of the kinetics of expression. *PLoS Computational Biology*, in press.
- Mabry, M. E., R. S. Abrahams, I. A. Al-Shehbaz, W. J. Baker, S. Barak, M. S. Barker, R. L. Barrett, A. Beric, S. Bhattacharya, S. B. Carey, **G. C. Conant**, J.G. Conran, M. Dassanayake, P.P. Edger, J. C. Hall, Y. Hao, K.P. Hendriks, J.M. Hibberd, G.J. King, D.J. Kliebenstein, M.A. Koch, I.J. Leitch, F. Lens, M.A. Lysak, A.C. McAlvay, M.T.W. McKibben, F. Mercati, R.C. Moore, K. Mummenhoff, D.J. Murphy, L.A. Nikolov, M. Piasias, E.H. Roalson, M.E. Schranz, S.K. Thomas, Q. Yu, A. Yocca, J. C. Pires & A. E. Harkess (2023) Complementing model species with model clades. *The Plant Cell*, in press. <https://doi.org/10.1093/plcell/koad260>.
- Siddiqui, M. and **G. C. Conant**. (2023) POInT_{browse}: Orthology prediction and synteny exploration for paleopolyploid genomes. *BMC Bioinformatics*, **24**: 174.
- Assis R, **G. Conant**, B. Holland, D. A. Liberles, M. M. O'Reilly and A. E.. Wilson Models for the retention of duplicate genes and their biological underpinnings. *F1000Research* 2023, **12**:1400.
- Yang, Y., T. Xu, **G. Conant**, H. Kishino, J. L. Thorne and X. Ji. (2023) Interlocus gene conversion, natural selection, and paralog homogenization. *Molecular Biology and Evolution*, **40**: msad198.
- McRae, L., A. Beric and **G. C. Conant**. (2022) Hybridization order is not the driving factor behind biases in duplicate gene losses among the hexaploid Solanaceae. *Proceedings of the Royal Society, Biological Sciences*, **289**: 20221810.
- Hao, Y., J. Fleming, J. Petterson, E. Lyons, P. P. Edger, J. C. Pires, J. L. Thorne, and **G. C. Conant**. (2022) Convergent evolution of polyploid genomes from across the eukaryotic tree of life. *G3: Genes, Genomes, Genetics*, **12**: jkac094.

Publications (continued):

- Hao Y, M. E. Mabry, P. Edger, M. Freeling, C. Zheng, L. Jin, R. VanBuren, M. Colle, H. An, R. S. Abrahams, J. D. Washburn, X. Qi, K. Barry, C. Daum, S. Shu, J. Schmutz, D. Sankoff, M. S. Barker, E. Lyons, J. C. Pires and **G. C. Conant**. (2021) The contributions of the allopolyploid parents of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. *Genome Research* **31**:799–810.
- Washburn, J. D., J. Strable, P. Dickinson, S. S. Kothapalli, J. M. Brose, S. Covshoff, **G. C. Conant**, J. M. Hibberd and J. C. Pires (2021) Distinct C4 sub-types and C3 bundle sheath isolation in the Paniceae grasses. *Plant Direct*, **5**:e373.
- Patil, R. D., M. J. Ellison, K. J. Austin, W. R. Lamberson, K. M. Cammack and **G. C. Conant**. (2021) A metagenomic analysis of the effect of antibiotic feed additives on the ovine rumen metabolism. *Small Ruminant Research*, **205**: 106539.
- Beric, A., M. E. Mabry, A. E. Harkess, J. Brose, M. E. Schranz, **G. C. Conant**, P. P. Edger, B. C. Meyers, and J. C. Pires. (2021) Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). *G3: Genes, Genomes, Genetics*, **11**: jkab140.
- Qi, X., H. An, T. E. Hall, C. Di, P. D. Blischak, M. T. W. McKibben, Y. Hao, **G. C. Conant**, J. C. Pires and M. S. Barker. (2021) Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in *Brassica rapa*. *New Phytologist*, **230**: 372-386.
- Conant, G. C.** (2020) The lasting after-effects of an ancient polyploidy on the genomes of teleosts. *PLoS ONE*, **15**: e0231356.
- Hao, Y. H. J. Lee, M. Baraboo, K. Burch, T. Maurer, J.A. Somarelli and **G. C. Conant**. (2020) Baby genomics: tracing the evolutionary changes that gave rise to placentation. *Genome Biology and Evolution*, **12**: 35-37.
- Mabry, M. E., J. M. Brose, P. D. Blischak, B. Sutherland, W. T. Dismukes, C. A. Bottoms, P. P. Edger, J. D. Washburn, H. An, J. C. Hall, M. R. McKain, I. Al-Shehbaz, M. S. Barker, M. E. Schranz, **G. C. Conant** and J. C. Pires. (2020) Phylogeny and multiple independent whole-genome duplication events in the Brassicales. *American Journal of Botany*, **107**: 1148–1164.
- Schoonmaker, A., Y. Hao, D. M. McK Bird and **G. C. Conant**. (2020) A single, shared triploidy in three species of parasitic nematodes. *G3: Genes, Genomes, Genetics*, **10**: 225-233.
- Shamimuzzaman, M., J. J. Le Tourneau, D. R. Unni, C. M. Diesh, D. A. Triant, A. T. Walsh, A. Tayal, **G. C. Conant**, D. E. Hagen and C. G. Elsik. (2019) Bovine Genome Database: new annotation tools for a new reference genome. *Nucleic Acids Research*, **48**: D676-D681.
- An, H., X.i Qi, M. Gaynor, Y. Hao, S. Gebken, M. Mabry, A. McAlvay, G. Teakle, **G. C. Conant**, M. Barker, T. Fu, B. Yi, and J. C. Pires. (2019) Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid *Brassica napus*. *Nature Communications*, **10**: 2878.
- Osman, E. Y., M. R. Bolding, E. Villalón, K. Kaifer, Z. C. Lorson, S. Tisdale, Y. Hao, **G. C. Conant**, J. C. Pires, L. Pellizzoni and C. Lorson. (2019) Functional characterization of SMN evolution in mouse models of SMA. *Scientific Reports*, **9**: 9472.
- Ellison, M. J., **G. C. Conant**, W. R. Lamberson, K. J. Austin, E. van Kirk, H. C. Cunningham, D. C. Rule and K. M. Cammack. (2019) Predicting residual feed intake status using rumen microbial profiles in ewe lambs. *Journal of Animal Science*, **97**: 2844–2854.

Publications (continued):

- Blischak, P. D., M. E. Mabry, **G. C. Conant** and J. C. Pires. (2018) Integrating networks, phylogenomics, and population genomics for the study of polyploidy. *Annual Review of Ecology, Evolution, and Systematics*, **49**:253–278.
- Emery, M., M. M. S. Willis, Y. Hao, K. Barry, K. Oakgrove, Y. Peng, J. Schmutz, E. Lyons, J. C. Pires, P. P. Edger, and **G. C. Conant**. (2018). Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. *PLoS Genetics*, **14**: e1007267.
- Hao, Y., J. D. Washburn, J. Rosenthal, B. Nielsen, E. Lyons, P. P. Edger, J. C. Pires, and **G. C. Conant**. 2018. Patterns of population variation in two paleopolyploid eudicot lineages suggest that dosage-based selection on homeologs is long-lived. *Genome Biology and Evolution* **10**: 999-1011.
- Patil, R. D., M. J. Ellison, S. M. Wolff, C. Shearer, A. M. Wright, R. R. Cockrum, K. J. Austin, W. R. Lamberson, K. M. Cammack, and **G. C. Conant**. (2018). Poor feed efficiency in sheep is associated with several structural abnormalities in the community metabolic network of their ruminal microbes. *Journal of Animal Sciences*, **96**: 2113-2124.
- Cammack, K. M. K.J. Austin, W.R. Lamberson, **G.C. Conant**, H.C. Cunningham. (2018). Tiny but mighty: The role of the rumen microbes in livestock production, *Journal of Animal Science*, **96**: 752–770.
- Washburn, J. D., J. C. Schnable, **G. C. Conant**, T. P. Brutnell, Y. Shao, Y. Zhang, M. Ludwig, G. Davidse and J. C. Pires. (2017) Genome-guided phylo-transcriptomic methods and the nuclear phylogenetic tree of the Paniceae grasses, *Scientific Reports*, **7**: 13528.
- Ellison, M.J., **G.C. Conant**, W.R. Lamberson, R.R. Cockrum, K.J. Austin, D.C. Rule, and K.M. Cammack. (2017) Diet and feed efficiency status affect rumen microbial profiles of sheep, *Small Ruminant Research*, **156**: 12-19.
- Wolff, S. M., M. J. Ellison, Y. Hao, R. R. Cockrum, K. J. Austin, M. Baraboo, K. Burch, H. J. Lee, T. Maurer, R. Patil, A. Ravelo, T. M. Tasis, H. Truong, W. R. Lamberson, K. M. Cammack and **G. C. Conant**. (2017) Diet shifts provoke complex and variable changes in the metabolic networks of the ruminal microbiome, *Microbiome*, **5**: 60.
- Pires, J. C. and **G. C. Conant**. (2016) Robust yet fragile: Expression noise, protein misfolding and gene dosage in the evolution of genomes, *Annual Review of Genetics*, **50**: 113-131.
- Washburn, J. D., K.A. Bird, **G.C. Conant** and J.C. Pires. (2016) Convergent evolution and the origin of complex phenotypes in the age of systems biology, *International Journal of Plant Sciences* **177**: 305-318.
- Mordhorst, B. R., M. L. Wilson and **G. C. Conant**. (2016) Some assembly required: evolutionary and systems perspectives on the mammalian reproductive system, *Cell and Tissue Research*, **363**: 267-278.
- Scienski, K., J. C. Fay, and **G. C. Conant**. (2015) Patterns of gene conversion in duplicated yeast histones suggests strong selection on a co-adapted macromolecular complex, *Genome Biology and Evolution*, **7**: 3249-3258.
- Taxis, T. M., S. Wolff, S. J. Gregg, N. O. Minton, C. Zhang, J. Dai, R. D. Schnabel, J. F. Taylor, M. S. Kerley, J. C. Pires, W. R. Lamberson and **G. C. Conant**. (2015) The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity, *Nucleic Acids Research*, **43**: 9600-9612.

Publications (continued):

- Edger, P. P., H. M. Heidele-Fischer, M. Bekaert, J. Rota, G. Glöckner, A. E. Platts, D. G. Heckel, J. P. Der, E. K. Wafula, M. Tang, J. A. Hofberger, A. Smithson, J. C. Hall, M. Blanchette, T. E. Bureau, S. I. Wright, M. E. Schranz, M. S. Barker, **G. C. Conant**, N. Wahlberg, H. Vogel, J. C. Pires and C. W. Wheat. (2015) The butterfly plant arms-race escalated by gene and genome duplications, *Proceedings of the National Academy of Sciences, U.S.A.*, **112**: 8362-8366
- Conant, G. C.** (2014) Comparative genomics as a time machine: How relative gene dosage and metabolic requirements shaped the time-dependent resolution of yeast polyploidy, *Molecular Biology and Evolution*, **31**: 3184-3193.
- Dhroso, A., D. Korkin and **G. C. Conant**. (2014) The yeast protein interaction network has a capacity for self-organization, *The FEBS Journal*, **281**: 3420-3432.
- Edger, P. P., M. Tang, K. A. Bird, D. R. Mayfield, **G. Conant**, K. Mummenhoff, M. A. Koch, J. C. Pires. (2014) Secondary Structure Analyses of the Nuclear rRNA Internal Transcribed Spacers and Assessment of Its Phylogenetic Utility across the Brassicaceae (Mustards), *PLoS ONE*, **9**: e101341.
- Truong, H., D. Li, K. Sajjapongse, **G. Conant** and M. Becchi. (2014) Large-Scale pairwise alignments on GPU clusters: Exploring the implementation space, *Journal of Signal Processing Systems*, **77**: 131-149.
- Conant, G. C.**, J. A. Birchler, and J. C. Pires. (2014) Dosage, Duplication, and Diploidization: Clarifying the interplay of multiple models for duplicate gene evolution over time, *Current Opinion in Plant Biology*, **19**: 91-98.
- Bekaert, M. and **G. C. Conant**. (2014) Gene duplication and phenotypic changes in the evolution of mammalian metabolic networks, *PLoS ONE*, **9**: e87115.
- Zimmerman, S. W. Y.-J. Yi, M. Sutovsky, F. W. van Leeuwen, **G. Conant** and P. Sutovsky. (2014) Identification and characterization of RING-finger ubiquitin 5 ligase UBR7 in mammalian spermatozoa, *Cell and Tissue Research*, **356**:261-278.
- Ellison, M., **G. C. Conant**, R. Cockrum, K. Austin, M. Becchi, H. Truong, W. Lamberson, and K. Cammack. (2014) Diet alters both the structure and taxonomy of the ovine gut microbial ecosystem, *DNA Research*, **21**: 115-125.
- Warren, S., X.-F. Wan, **G. C. Conant**, and D. Korkin. (2013) Extreme evolutionary conservation of functionally important regions in H1N1 influenza proteome. *PLoS ONE*, **8**: e81027.
- Mayfield-Jones, D. J. D. Washburn, T. Arias, P. P. Edger, J. C. Pires and **G. C. Conant**, (2013) Watching the grin fade: Tracing the effects of polyploidy on different evolutionary time scales, *Seminars in Cell and Developmental Biology*, **24**: 320-331.
- Pérez-Bercoff, Á., C. M. Hudson and **G. C. Conant**, (2013) A Conserved Mammalian Protein Interaction Network, *PLoS ONE*, **8**: e52581.
- Bekaert, M., P. P. Edger, C. M. Hudson, J. C. Pires, and **G. C. Conant**, (2012) Metabolic and evolutionary costs of herbivory defense: Systems biology of glucosinolate synthesis, *The New Phytologist*, **196**:596-605.
- Casola, C., **G. C. Conant** and M. W. Hahn, (2012) Very low rate of gene conversion in the yeast genome, *Molecular Biology and Evolution*, **29**: 3817-3826.
- Huminięcki, L. and **G. C. Conant**, (2012) Polyploidy and the evolution of complex traits, *International Journal of Evolutionary Biology*, **2012**: 292068.

Publications (continued):

- Wang, S., **G. C. Conant**, R. Ou, B. T. Beerntsen (2012) Cloning and characterization of the peptidoglycan recognition protein genes in the mosquito, *Armigeres subalbatus* (Diptera: Culicidae), *Journal of Medical Entomology*, **49**: 656-671.
- Reneker, J., E. Lyons, **G. C. Conant** J. C. Pires, M. Freeling, C.-R. Shyu, and D. Korkin, (2012) Long identical multispecies elements in plant and animal genomes, *Proceedings of the National Academy of Sciences, U.S.A.*, **109**: E1183-E1191.
- Tang, H., M. R. Woodhouse, F. Cheng, J. C. Schnable, B. S. Pedersen, **G. C. Conant**, X. Wang, M. Freeling and J. Chris Pires, (2012) Altered Patterns of Fractionation and Exon Deletions in *Brassica rapa* Support a Two-step Model of Paleohexaploidy, *Genetics*, **190**:1563-74.
- Hudson, C. M., E. E. Puckett, M. Bekaert, J. C. Pires and **G. C. Conant**, (2011) Selection for higher gene copy number after different types of plant gene duplications, *Genome Biology and Evolution*, **3**: 1369-1380.
- Pérez-Bercoff, Á., A. McLysaght and **G. C. Conant**, (2011) Patterns of indirect protein interactions suggest a spatial organization to metabolism, *Molecular BioSystems*, **7**: 3056 - 3064.
- Wang, X., H. Wang, J. Wang, R. Sun, J. Wu, S. Liu, Y. Bai, J. H. Mun, I. Bancroft, F. Cheng, S. Huang, X. Li, W. Hua, M. Freeling, J. C. Pires, A. H. Paterson, B. Chalhoub, B. Wang, A. Hayward, A. G. Sharpe, B. S. Park, B. Weisshaar, B. Liu, B. Li, C. Tong, C. Song, C. Duran, C. Peng, C. Geng, C. Koh, C. Lin, D. Edwards, D. Mu, D. Shen, E. Soumpourou, F. Li, F. Fraser, **G. Conant**, G. Lassalle, G. J. King, G. Bonnema, H. Tang, H. Belcram, H. Zhou, H. Hirakawa, H. Abe, H. Guo, H. Jin, I. A. Parkin, J. Batley, J. S. Kim, J. Just, J. Li, J. Xu, J. Deng, J. A. Kim, J. Yu, J. Meng, J. Min, J. Poulain, K. Hatakeyama, K. Wu, L. Wang, L. Fang, M. Trick, M. G. Links, M. Zhao, M. Jin, N. Ramchiary, N. Drou, P. J. Berkman, Q. Cai, Q. Huang, R. Li, S. Tabata, S. Cheng, S. Zhang, S. Sato, S. Sun, S. J. Kwon, S. R. Choi, T. H. Lee, W. Fan, X. Zhao, X. Tan, X. Xu, Y. Wang, Y. Qiu, Y. Yin, Y. Li, Y. Du, Y. Liao, Y. Lim, Y. Narusaka, Z. Wang, Z. Li, Z. Xiong, and Z. Zhang, (2011) The genome of the mesopolyploid crop species *Brassica rapa*, *Nature Genetics*, **43**: 1035–1039.
- Bekaert, M. and **G. C. Conant**, (2011) Transcriptional robustness and protein interactions are associated in yeast, *BMC Systems Biology*, **5**:62.
- Bekaert, M., P. P. Edger, J. C. Pires and **G. C. Conant**, (2011) Two-phase resolution of polyploidy in the *Arabidopsis* metabolic network gives rise to relative and absolute dosage constraints, *The Plant Cell*, **23**: 1719-1728.
- Hudson, C. M. and **G. C. Conant**, (2011) Expression level, cellular compartment and metabolic network position all influence the average selective constraint on mammalian enzymes, *BMC Evolutionary Biology*, **11**: 89.
- Bekaert, M. and **G. C. Conant**, (2011) Copy number alterations among mammalian enzymes cluster in the metabolic network, *Molecular Biology and Evolution*, **28**: 1111-1121.
- Evangelisti, A. M. and **G. C. Conant**, (2010) Non-random survival of gene conversions among yeast ribosomal proteins duplicated through genome doubling, *Genome Biology and Evolution*, **2**:826-834. *Recognized by the Faculty of 1000*
- Foy, N., B. Jester , **G. C. Conant** and K. M. Devine, (2010) The T box regulatory element controlling expression of the class I lysyl-tRNA synthetase of *Bacillus cereus* strain 14579 is functional and can be partially induced by reduced charging of asparaginyl-tRNAAsn, *BMC Microbiology*, **10**: 196.
- Conant, G. C.**, (2010) Rapid reorganization of the transcriptional regulatory network after genome duplication in yeast, *Proceedings of the Royal Society, Biological Sciences*, **277**: 869-876.

Publications (continued):

- Conant, G. C.**, (2009) Neutral evolution on mammalian protein surfaces, *Trends in Genetics*, **25**: 377-381.
- Decker, J. E., J. C. Pires, **G. C. Conant**, S. D. McKay, M. P. Heaton, K. Chen, A. Cooper, J. Vilkki, C. M. Seabury, A. R. Caetano, G. S. Johnson, R. A. Brenneman, O. Hanotte, L. S. Eggert, P. Wiener, J.-J. Kim, K. Suk Kim, T. S. Sonstegard, C. P. Van Tassell, H. L. Neibergs, J. C. McEwan, R. Brauning, L. L. Coutinho, M. E. Babar, G. A. Wilson, M. C. McClure, M. M. Rolf, J. Kim, R. D. Schnabel, and J. F. Taylor, (2009) Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics, *Proceedings of the National Academy of Sciences, U.S.A.*, **106**:18644-18649.
- Conant, G. C.** and P. F. Stadler, (2009) Solvent exposure imparts similar selective pressures across a range of yeast proteins, *Molecular Biology and Evolution*, **26**: 1155-1161.
- Conant, G. C.** and K. H. Wolfe, (2008) Turning a hobby into a job: How duplicated genes find new functions, *Nature Reviews Genetics*, **9**: 938-950.
- Conant, G. C.** and K. H. Wolfe, (2008) Probabilistic cross-species inference of orthologous genomic regions created by whole-genome duplication in yeast, *Genetics*, **179**: 1681-1692.
- Powell, A. J., **G. C. Conant**, D. E. Brown, I. Carbone and R. A. Dean, (2008) Altered patterns of gene duplication and differential gene gain and loss in fungal pathogens, *BMC Genomics*, **9**: 147.
- Conant, G. C.** and K. H. Wolfe, (2008) GenomeVx: Simple web-based creation of editable circular chromosome maps, *Bioinformatics*, **24**: 861-862.
- Conant, G. C.** and K. H. Wolfe, (2007) Increased glycolytic flux as an outcome of whole-genome duplication in yeast, *Molecular Systems Biology*, **3**: 129.
- Scannell, D. R., A. C. Frank, **G. C. Conant**, K. P. Byrne, M. Woolfit and K. H. Wolfe, (2007) Independent sorting-out of thousands of duplicated gene pairs in two yeast species descended from a whole-genome duplication, *Proceedings of the National Academy of Sciences, U.S.A.*, **104**: 8397-8402.
- Conant, G. C.**, G. P. Wagner, and P. F. Stadler, (2007) Modeling amino acid substitution patterns in orthologous and paralogous genes, *Molecular Phylogenetics and Evolution*, **42**: 298-307.
- Conant, G. C.** and K. H. Wolfe, (2006) Functional partitioning of yeast co-expression networks after genome duplication, *PLoS Biology*, **4**:e109.
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- Hahn, M. W., **G. C. Conant**, and A. Wagner, (2004) Molecular evolution in large genetic networks: Does connectivity equal constraint? *Journal of Molecular Evolution*, **58**: 203-211.
- Conant, G. C.** and A. Wagner, (2004) A fast algorithm for determining the best combination of local alignments to a query sequence, *BMC Bioinformatics*, **5**: 62.
- Conant, G. C.** and A. Wagner, (2004) Duplicate genes and robustness to transient gene knockouts in *Caenorhabditis elegans*, *Proceedings of the Royal Society, Biological Sciences*, **271**: 89-96.
- Conant, G. C.** and A. Wagner, (2003) Asymmetric sequence divergence of duplicate genes, *Genome Research*, **13**: 2052-2058.

Publications (continued):

- Conant, G. C.**, S. J. Plimpton, W. Old, A. Wagner, P. R. Fain, T. R. Pacheco, and G. Heffelfinger. (2003). Parallel GeneHunter: Implementation of a linkage analysis package for distributed-memory architectures, *Journal of Parallel and Distributed Computing*, **63**: 674-682.
- Conant, G. C.** and A. Wagner, (2003) Convergent evolution of gene circuits, *Nature Genetics*, **34**: 264-266.
- Conant, G. C.** and A. Wagner. (2002) GenomeHistory: A software tool and its application to fully sequenced genomes, *Nucleic Acids Research*, **30**: 3378-3386.
- Conant, G. C.** and P. O. Lewis. (2001) Effects of nucleotide composition bias on the success of the parsimony criterion in phylogenetic inference, *Molecular Biology and Evolution*, **18**: 1024-1033.

Book Chapters:

- G. C. Conant** (2023) POInT: Modeling Polyploidy in the Era of Ubiquitous Genomics. In *Polyploidy: Methods and Protocols*. Edited by Y. Van de Peer: Springer; 77-90.
- Hao Y. and **G. C. Conant** (2022) POInT: A Tool for Modeling Ancient Polyploidies Using Multiple Polyploid Genomes. In *Plant Comparative Genomics*. Edited by A. Pereira-Santana, S. D. Gamboa-Tuz, Rodríguez-Zapata L.C.: Springer; 81-91.
- Conant G.C.** (2015) Structure, Interaction, and Evolution: Reflections on the Natural History of Proteins. In *Evolutionary Biology: Biodiversification from Genotype to Phenotype*. Edited by Pontarotti P.: Springer; 187-201.
- Hudson C.M. and **G. C. Conant** (2012) Yeast as a window into changes in genome complexity due to polyploidization. In *Polyploidy and genome evolution*. Edited by P. S. Soltis, Soltis D.E.: Springer; 293-308.

Web servers:

GenomeVx: <http://wolfe.ucd.ie/GenomeVx/>

POInT_{browse}: <https://wgd.statgen.ncsu.edu>

QBio@NCSU: <http://qbio.statgen.ncsu.edu>

Invited Seminars:

“Hybrid conflict, biased gene losses and developmental innovation.” University of North Carolina, Charlotte, Oct. 2019.

“Hybrid conflict, biased gene losses and developmental innovation.” Plant and Animal Genome XXVII, San Diego, CA 2019.

“Combining bioinformatics and statistical modeling to understand the ecology of the rumen microbial ecosystem in sheep.” Plant and Animal Genome XXII, San Diego, CA 2014.

“Genome duplication and the evolution of complex innovations in yeast.” Department of Biology, Saint Louis University, St. Louis, MO, 2013

“Evolution of novel traits in the plant metabolic network through gene and genome duplication.” Donald Danforth Center for Plant Sciences, St. Louis, MO, 2013.

“Evolution of novel traits in the plant metabolic network through gene and genome duplication.” Plant Genome Evolution, Amsterdam, 2013.

“Dosage and interaction in the structure and evolution of metabolism.” Department of Agronomy & Horticulture, University of Nebraska, Lincoln, NE, 2012.

“Dosage and interaction in the structure and evolution of metabolism.” Department of Biomedical Sciences, University of Missouri, 2012.

“Dosage and interaction in the structure and evolution of metabolism.” Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS, 2011.

“The role of interactions between genes in the evolution and function of metabolism.” Department of Biology, Indiana University, Bloomington, IN, 2010.

“Ohno revisited – contribution of genome duplication to innovation in baker’s yeast.” Boehringer Ingelheim Fonds 100th Titisee Conference: Genome evolution and the origin of novel gene functions, Titisee, Germany, 2009.

“Modeling gene order evolution after a genome duplication in yeast.” Department of Plant Systems Biology, Ghent University, Ghent Belgium, 2006.

“Implications of whole-genome duplication on the ecological niche of *Saccharomyces cerevisiae*.” Biological Networks III: Modularity and Genome Evolution, Bertinoro Italy, 2006.

Seminars:

“Comparative genomics as a time machine: How relative gene dosage and metabolic requirements shaped the time-dependent resolution of yeast polyploidy.” 18th Evolutionary Biology Meeting at Marseilles, France, Sept. 2014.

“Self-organization in the cellular structure of metabolism.” 3rd International Conference on Proteomics and Bioinformatics, Philadelphia, PA, 2013

“Protein interactions and the spatial structure of metabolism.” Informatics Day, University of Missouri. Columbia, MO 2011.

“Gene conversion among duplicated yeast ribosomal proteins does not extend to upstream regulatory regions.” Society for Molecular Biology and Evolution, Lyon, France, 2010.

“Appearance of regulatory novelty after genome duplication in yeast.” Society for Molecular Biology and Evolution, Iowa City, IA, 2009.

“Patterns of amino acid substitution in orthologous and paralogous genes.” VIBE Meeting, Dublin City University, Dublin Ireland, 2005.

“Parallel Genehunter: Implementation of a linkage analysis package for distributed-memory architectures.” First Workshop on High Performance Computational Biology, 16th IPDPS, Ft. Lauderdale, FL, 2002.

Conference Posters:

Conant, G., S. Plimpton, W. Old, W., A. Wagner, P. Fain, and G. Heffelfinger, "Parallel Genehunter: Implementation of a Linkage Analysis Package for Distributed-Memory Architectures," The Conference on High Speed Computing, Gleneden Beach, OR, 2002, and Supercomputing 2003, Krell Institute Booth, Phoenix AZ, 2003.

Conant, G. and A. Wagner, “The rarity of evolutionary innovation by gene shuffling,” German Conference on Bioinformatics, Bielefeld Germany, 2004.

Conant, G. and K. Wolfe, “Network subfunctionalization after whole-genome duplication in yeast,” RECOMB Workshop on Comparative Genomics, Dublin, Ireland 2005 and Wenner-Gren Foundation Symposium on Mutation, Selection and Genome Evolution, Stockholm Sweden, 2006.

Bekaert, M., C. Hudson, P. Edger, E. Puckett, C. Pires and G. Conant “Evolution of novel traits in the plant metabolic network through gene and genome duplication,” Society for Molecular Biology and Evolution, Dublin, Ireland, 2012.

Bekaert, M. and G. C. Conant, “Predicting longevity and body temperature from the genetics of mammalian metabolic networks,” 33rd Conference of the International Society for Animal Genetics, Cairns Australia, 2012.

Bekaert, M., Å. Pérez-Bercoff, C. Hudson and G. Conant, “Conserved mammalian biological networks suggest common underlying mechanisms in trait evolution,” Society for Molecular Biology and Evolution, Chicago, IL 2013.

Student Contributed Seminars:

Hudson, C. E. Puckett, M. Bekaert, J. C. Pires and G. Conant, “Selection for higher gene copy number is active after different types of plant gene duplications,” *Evolution* 2011, Norman OK, 2011.

Bekaert, M, and G. Conant, “Gene duplication and loss in mammalian metabolic networks is associated with changes in longevity and body temperature,” *Evolution* 2011, Norman OK, 2011.

Service:

Software packages distributed: GenomeHistory, parallel Genehunter, find_max_cover, GenomeVx, POInT, POInT_{browse}

Reviewer for *Advances in Complex Systems*, *Anaerobe*, *Animal Behavior*, *Bioinformatics*, *Annals of the New York Academy of Sciences*, *BMC Bioinformatics*, *BMC Biology*, *BMC Evolutionary Biology*, *BMC Genomics*, *BMC Systems Biology*, *BMC Veterinary Research*,

Current Biology, Current Opinion in Plant Biology, Database, eLife, Evolutionary Bioinformatics, Frontiers in Genetics, Frontiers in Microbiology, Frontiers in Plant Science, G3, Genetics, Genome Biology, Genome Biology and Evolution, Genome Research, Journal of Bioinformatics and Computational Biology, Journal of Integrative Agriculture, Journal of Mathematical Biology, Journal of Theoretical Biology, Mammalian Genome, Molecular Biology and Evolution, Molecular and Developmental Biology, Molecular Systems Biology, New Phytologist, Nature Communications, Nature Genetics, Nature Ecology and Evolution, Nucleic Acids Research, Oncogene, Peer Journal, Plant Communications, The Plant Cell, The Plant Journal, Peer Journal, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PLoS ONE, Proceedings of the National Academy of Sciences, U.S.A., Science Advances, Scientific Reports, Small Ruminant Research, Systematic Biology, Theory in Biosciences, Toxin, Trends in Genetics, Trends in Microbiology, and the Workshops on High-Performance Computational Biology.

Panel member, National Research Council of Romania, October 2012.

External specialist reviewer for the LABEX program of the French national research agency (ANR), January 2011.

Ad hoc reviewer for Fonds National de la Recherche, Luxembourg.

Ad hoc reviewer for the Netherlands Organisation for Scientific Research's Innovational Research Incentives Scheme (2012)

Ad hoc reviewer for Israeli Science Foundation (2020)

Ad hoc reviewer for Cancer Research Trust New Zealand (2020)

Ad hoc reviewer of Research Foundation Flanders (FWO) (2012, 2013, 2017)

Ad hoc reviewer for the Czech Science Foundation (2013,2021-2022)

Ad hoc reviewer for US-Israel Bi-national Agricultural Research and Development Fund (2019,2022)

Ad hoc reviewer for Canada First Research Excellence Fund (2015, 2016)

Ad hoc reviewer for the Austrian National Science Foundation (2018-2019)

Ad hoc reviewer for the Swiss National Science Foundation (2020)

Panelist and ad hoc reviewer for the US National Science Foundation (2015-2023).

Panelist for USDA ARS (2014-2015).