

Spencer Vance Muse
Bioinformatics Research Center and
Department of Statistics
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North Carolina State University
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Positions Held

- 1998– Assistant, Associate, Full Professor
 Department of Statistics
 North Carolina State University
- 1996–1998 Assistant Professor
 Division of Biological Sciences
 University of Missouri-Columbia
- 2011–present Director, NCSU Bioinformatics Graduate Program
- 2013-present Director of Undergraduate Programs, NCSU Dept. of Statistics

Education and Training

- 1993–1996 Postdoctoral Research
 Institute of Molecular Evolutionary Genetics
 Department of Biology
 Pennsylvania State University
 Supervisor: Dr. Andrew G. Clark
- 1989–1993 Ph.D. Statistics and Genetics
 Departments of Statistics and Genetics
 North Carolina State University
 Advisor: Dr. Bruce S. Weir
- 1985–1989 B.S. (Honors) Statistics (Minor: Mathematics)
 Department of Statistics
 North Carolina State University

Honors and Awards

- 1995–1996 NIA Postdoctoral Fellowship
- 1995 NSF US-Japan Workshop on Molecular Evolution (Young Investigator Award)
- 1993–1995 NIH Postdoctoral Fellowship
- 1990–1993 NSF Graduate Fellowship
- 1990–1993 Gertrude Cox Fellowship
- 1989 Outstanding Graduating Senior in Statistics

Teaching and Training Activities

Courses Taught: ST 301* Statistical Inference I, ST 302* Statistical Inference II, ST 305** Statistical Methods, ST 311 Introduction to Statistics, ST 370 Statistics for Engineers, ST 372 Introduction to Statistical Inference and Regression, ST 590A** Introduction to Bioinformatics, ST 590C Bioinformatics II, ST 590D* Statistics for Molecular Biology, ST 590G** Probability Applications in Genetics, ST 810A* Preparation for Research in Statistics, ST 810E** Responsible Practice of Statistics, ST/GN 756 Computational Molecular Evolution, PP 810 Genomics Journal Club

* indicates a course I redesigned; ** indicates a new course that I developed.

Training Grants: PI and Program Director for predoctoral training grants from UNC Office of the President (2005-2010) and NIH (2007-present) (see **Funding** below).

Short Courses and Workshops: Marine Biological Lab, Wood's Hole MA (1998); University of Canterbury, Christchurch NZ (2001); University of Arizona (2002); SRCIS (2004); University of Texas (2005); ENAR (2005); Duke University (2005); National Evolutionary Synthesis Center (2007, 2008); George Washington University (2009); Summer Institute in Statistical Genetics, NCSU and U. Washington (1996-2010); NIH Grantsmanship Workshops, NCSU (2014, 2015); NCSU Building Future Faculty Grant Writing Workshop (2015)

Doctoral Students: Jun Lu (Bioinformatics, 2002), Wenli Tao (Biomathematics, 2002), Kejun Liu (Bioinformatics, 2004), Frank Mannino (Bioinformatics, 2006), Errol Strain (Bioinformatics, 2006), Samuel Wilson (Statistics, 2016), Sarah Wisotsky (Bioinformatics, current)

Postdoctoral Associates Chunguang Du (1999-2002) Professor, Montclair State University

Funding (all are as PI unless otherwise noted)

- 2017-2019 NCSU Game-Changing Research Program (GRIP): *The NCSU/RTI Program In Genetic Discovery and Prediction*. \$573,264. (co-investigator; PI F.A. Wright)
- 2015-2019 NIH: *HyPhy: Comprehensive, fast, and user-friendly software for evolutionary analysis*. \$1,381,878.
- 2010-2015 NIH: *HyPhy: Molecular Evolutionary Analysis*. \$1,112,934.
- 2007-2117 NIH: *Biostatistics Training in the Omics Era*. (Current year funding level \$217,458).
- 2005-2010 UNC Office of the President: *Graduate Training in Statistical Genetics*. (\$270,000).
- 2003-2008 NSF, via subcontract to University of New Mexico: *Building the Tree of Life: A National Resource for Phyloinformatics and Computational Phylogenetics* (\$175,000).
- 2002-2003 Research Triangle Institute: *Bioinformatics Graduate Industrial Traineeship* (\$36,000)
- 2002-2003 SAS Institute: *Bioinformatics Graduate Industrial Traineeship* (\$41,122)
- 2002-2003 Paradigm Genetics: *Bioinformatics Graduate Industrial Traineeship* (\$28,921)
- 2001-2002 National Science Foundation: *Purchase of an oligonucleotide-based microarray system* (\$222,309) Co-PIs Linda Hanley-Bowden, Steve Clouse
- 1999-2004 National Science Foundation: *Statistical Methods for Plant Genomic Sciences* (\$1,122,660) Co-PI Bruce S. Weir
- 1997-2000 National Science Foundation: *Statistical Methods for Multilocus Molecular Evolutionary Analyses* (\$104,938)
- 1997-2000 NSF/Alfred P. Sloan Foundation Young Investigator Award in Molecular Studies of Evolution (\$100,000)
- 1997-1998 University of Missouri Research Board (\$30,000)

Professional Service

Journals

- Associate Editor, *Genetics* (2005-2010)
- Associate Editor, *Molecular Biology and Evolution* (2003-2010)
- Associate Editor, *Journal of Experimental Zoology* (2005-2012)
- Editorial Board, *Systematic Biology* (1999-2004)

Funding Agencies

NIH Study Sections

- Research

BD2K Biomedical Big Data Software and Analysis (2014, 2016)
NIDCR FaceBase 2: Dataset, Tool and Resource Development (2013)
Microbiome Multi-Omic Data in Human Health and Disease (2013)
NIAID Omics Technologies for Predictive Models of Disease (2013)
NIAID Systems Approaches to Immunity and Inflammation (2010, 2012, 2014, 2015)
NIH Special Emphasis Panels (2009-2010, five panels, Chair for three)
Clinical and Translational Science Awards, (2009)
Continued Maintenance and Support of Software (2007, 2008, 2009-Chair)
Charter Member Biodata Management and Analysis (BDMA) (2003-2006)
Genomics, Computational Biology, and Technology (GCAT) (2007)

- Training and Mentoring

BD2K Biomedical Big Data Career Development Awards (2016)
NINDS Training Grants (2013-2016)
NIAID Career Development Awards (2015, 2016)
NIMH BRAIN Initiative: Short Courses in Research Tools and Methods (2015)
NHLBI AIDS Training Grants (2014)
NIGMS Training and Workforce Development (2009-2014, 3 training grant panels per year)

NSF Panels

NSF Mathematical Biology (2007)
NSF Statistics CAREER (2003)
NSF Population Biology Doctoral Dissertation Improvement Grant Program (2002)
Site Visit Team Member, NSF Plant Genome Program

Department and University

Department of Statistics Advisory Committee (2011-present)
Department of Statistics Basic Exam Committee (2000)
Department of Statistics Written Prelim Committee (2002, 2006-Chair, 2010-Chair, 2013)
Department of Statistics Faculty Search Committee (2002, 2004, 2007-Chair, 2008, 2012, 2016)
Department of Statistics Department Head Search Committee (2017)
Department of Statistics Course and Curriculum Committee (2011- present)
Department of Statistics Post-tenure Review Committee (2012-2014, Chair, 2014)
Department of Statistics Administrative Team (2013-present)
College of Sciences Undergraduate Course and Curriculum Committee (2013-present)
College of Sciences Graduate Course and Curriculum Committee (2011-present)
NCSU Administrative Board of the Graduate School (2011-2014, 2016-present)
NCSU Graduate Operations Council (2016-present)
NCSU Chancellor's Excellence Faculty Cluster Hire Search Committee, Bioinformatics (2014)
NCSU Genomic Sciences Admissions Committee
NCSU Genomic Sciences Steering Committee

Miscellaneous

Program Committee, 2003 SMCBE annual meeting

Session Chair, Bioinformatics and DNA Computing. Gordon Research Conference in Computational Biology, T

Member, NSF Plant Genome Bioinformatics Working Group (2002)

Member, NSF Evolution Synthesis Center Working Group (2002)

Advisory Board, Rochester Institute of Technology Bioinformatics Program

Major Software Projects

HyPhy: Hypothesis Testing Using Phylogenies. Kosakovsky Pond, S.L., and S.V. Muse. The primary focus of my current research, HyPhy is a high-level programming language designed for general likelihood-based analyses of the evolution of molecular sequences. A full-featured graphical interface has also been developed: <http://www.hyphy.org>. Since its publication in 2005, HyPhy has been registered over 10,000 times and been cited in over 1,700 publications. Datamonkey, its graphical front end and web server, has been cited in over 1,600 more.

PowerMarker. Liu, K., B.S. Weir, and S.V. Muse. PowerMarker is an integrative package for managing and analyzing population genetic data based on molecular markers, with specific emphasis on SSR data. <http://statgen.ncsu.edu/powermarker>. Since its publication in 2005, PowerMarker has been cited in over 2,500 publications.

Panzea Panzea was a database system designed to store and distribute data from the NSF project *Evolutionary Genomics of Maize* (Project Director John Doebley, Univ. Wisconsin). The work on this project was subsequently used as a core component of the MaizeGDB comprehensive maize database resource, <http://www.maizegdb.org>

Publications

- [1] Muse, S.V., and B.S. Weir. 1992. Testing for equality of evolutionary rates. *Genetics* **132**:269–276.
- [2] Gaut, B.S., S.V. Muse, W.D. Clark, and M.T. Clegg. 1992. Relative rates of nucleotide substitution at the *rbcL* locus in monocotyledonous plants. *J. Mol. Evol.* **35**:292–303.
- [3] Gaut, B.S., S.V. Muse, and M.T. Clegg. 1993. Relative rates of nucleotide substitution in the chloroplast genome. *Mol. Phylo. Evol.* **2**:89–96.
- [4] Muse, S.V., and B.S. Gaut. 1994. A likelihood approach for comparing synonymous and nonsynonymous nucleotide substitution rates with application to the chloroplast genome. *Mol. Biol. Evol.* **11**:715–724.
- [5] Muse, S.V. 1995. Evolutionary analyses of DNA sequences subject to constraints on secondary structure. *Genetics* **139**:1429–1439.
- [6] Leicht, B.G., S.V. Muse, M. Hanczyc, and A.G. Clark. 1995. Constraints on intron evolution in the gene encoding the myosin alkali light chain in *Drosophila*. *Genetics* **139**:299–308.
- [7] Kirby, D.A., S.V. Muse, and W. Stephan. 1995. Maintenance of pre-mRNA secondary structure by epistatic selection. *Proc. Natl. Acad. Sci. USA* **92**:9047–9051.
- [8] Muse, S.V. 1996. Evolutionary analyses when nucleotides do not evolve independently. In M. Nei and N. Takahata (Eds.), *Current Topics of Molecular Evolution* 115–124.
- [9] Muse, S.V. 1996. Estimating synonymous and nonsynonymous nucleotide substitution rates. *Mol. Biol. Evol.* **13**:105–114.
- [10] Clark, A.G., B.G. Leicht, and S.V. Muse. 1996. Length variation and secondary structure of introns in the *Mlc1* gene in six species of *Drosophila*. *Mol. Biol. Evol.* **13**:471–482.
- [11] Muse, S.V., A.G. Clark, and G.H. Thomas. 1997. Comparisons of the process of nucleotide substitution among repeated segments of the α - and β -spectrin genes. *J. Mol. Evol.* **44**:492–500.
- [12] Muse, S.V., and B.S. Gaut. 1997. Comparing patterns of nucleotide substitution rates among chloroplast loci using the relative ratio test. *Genetics* **146**:393–399.
- [13] Gaut, B.S., L.G. Clark, J.F. Wendel, and S.V. Muse. 1997. Comparisons of the molecular evolutionary process at *rbcL* and *ndhF* in the grass family (Poaceae). *Mol. Biol. Evol.* **14**:769–777.
- [14] Thomas, G.H., C. Newbern, C.C. Korte, M.A. Bales, S.V. Muse, A.G. Clark, and D.P. Kiehart. 1997. Intragenic duplication and divergence in the spectrin superfamily of proteins. *Mol. Biol. Evol.* **14**:1285–1295.
- [15] Lin, Qing, E.S. Buckler IV, S.V. Muse, and J.C. Walker. 1999. Molecular evolution of type one serine/threonine protein phosphatases. *Mol. Phylo. Evol.* **12**:57–66.
- [16] Muse, S.V. 1999. Modeling the molecular evolution of HIV sequences. pp. 122–152 In K.A. Crandall (Ed.), *The Evolution of HIV*. The Johns Hopkins University Press, Baltimore.

- [17] Muse, S.V. 2000. Rates and patterns of nucleotide substitution in plants. pp. 25–43 In B.S. Gaut and J.J. Doyle (Eds.), *Plant Molecular Evolution*. Kluwer Academic Publishers, Dordrecht, The Netherlands.
- [18] Muse, S.V. 2000. Rates and patterns of nucleotide substitution in plants. *Plant Mol. Biol.* **42**:25–43.
- [19] Gibson, G. and S.V. Muse. 2001. *A Primer of Genome Science*. Sinauer and Associates, Inc. Sunderland, MA.
- [20] Buckler, E., J.F. Doebley, B.S. Gaut, M.M. Goodman, S. Kresovich, S.V. Muse, and B.S. Weir. 2002. Evolutionary genomics of maize. *Maize Cooperation Newsletter* **76**:86–88.
- [21] Lu, J., S. Hardy, W. Tao, S.V. Muse, B.S. Weir, and S. Spruill. 2002. Classical statistical approaches to molecular classification of cancer from gene expression profiling. pp. 97–108 in S.M. Lin and K.F. Johnson (Eds.), *Methods of Microarray Data Analysis*. Kluwer Academic Publishers, Boston.
- [22] Israel, R.L., S.L. Kosakovsky Pond, S.V. Muse, and L.A. Katz 2002. Evolution of duplicated alpha-tubulin genes in ciliates. *Evolution* **56**:1110–1122.
- [23] Muse, S.V. 2002. Review of *Statistical Methods in Bioinformatics* by W.J. Ewens and G.R. Grant (invited book review). *Theor. Pop. Biol.*
- [24] Du, C.G., E. Buckler, and S.V. Muse 2003. Development of a maize molecular evolutionary database. *Comparative and Functional Genomics* **4**:246–249.
- [25] Liu, K.J., M.M. Goodman, S.V. Muse, J.S. Smith, E. Buckler, and J.F. Doebley 2003. Genetic structure and diversity among maize inbred lines as inferred from DNA microsatellites. *Genetics* **165**:2117–2128.
- [26] Gibson, G. and S.V. Muse. 2004. *A Primer of Genome Science, 2nd ed.*. Sinauer and Associates, Inc. Sunderland, MA.
- [27] Katz, L.A., J.G. Bornstein, E. Lasek-Nesselquist, and S.V. Muse 2004. Dramatic diversity of ciliate histone H4 genes revealed by comparisons of patterns of substitutions and paralog divergences among eukaryotes. *Mol. Biol. Evol.* **21**:555–62.
- [28] Kosakovsky Pond, S.L. and S.V. Muse 2004. Column ordering: rapid calculation of the phylogenetic likelihood function. *Syst. Biol.* **53**:685–692.
- [29] Kosakovsky Pond, S.L., S.D. Frost, and S.V. Muse 2005. HyPhy: A platform for molecular evolutionary analysis. *Bioinformatics* **21**:676–679.
- [30] Kosakovsky Pond, S.L. and S.V. Muse 2005. HyPhy: Hypothesis testing using phylogenies. In R. Nielsen (Ed.), *Statistical Methods in Molecular Evolution*. Springer.
- [31] Liu, K.J. and S.V. Muse 2005. PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics* **21**:2128–2129.
- [32] Kosakovsky Pond, S.L. and S.V. Muse 2005. Modeling heterogeneity of synonymous and nonsynonymous substitution rates across sites. *Mol. Biol. Evol.* **22**:2375–2385.

- [33] Strain, E., and S. V. Muse 2005. Positively selected sites in the Arabidopsis receptor-like kinase gene family. *J. Mol. Evol.* **60**:1–9.
- [34] Zufall, R.A., C.I. McGrath, S.V. Muse, and L.A. Katz. 2006. Genome architecture drives protein evolution in ciliates. *Mol. Biol. Evol.* **23**: 1681–1687
- [35] Kosakovsky Pond, S.L. F.V. Mannino, M.B. Gravenor, S.V. Muse, and S.D.W. Frost. 2007. Evolutionary model selection with a genetic algorithm: A case study using stem RNA. *Mol. Biol. Evol.* **24**: 159–170.
- [36] Strain, E.A., L. Kelly, S. Schultz-Cherry, S.V. Muse, and M. Koci. 2008. Genetic analysis of closely related Astroviruses. *J. Virology* **82**: 5099-5103.
- [37] Gibson, G.G. and S.V. Muse. 2009. *A Primer of Genome Science, 3rd ed.*. Sinauer and Associates, Inc. Sunderland, MA.
- [38] Delpont, W., K. Scheffler, G. Botha, M.B. Gravenor, S.V. Muse, and S.L. Kosakovsky Pond 2010. CodonTest: Modeling amino acid substitution preferences in coding sequences. *PLoS Comput. Biol.* **19**: e1000885.
- [39] Kosakovsky Pond, S.L., W. Delpont, S.V. Muse, and K. Scheffler 2010. Correcting the bias of empirical frequency parameter estimators in codon models. *PLoS ONE* **5**: e11230.
- [40] Delpont, W., K. Scheffler, M.B. Gravenor, S.V. Muse, and S.L. Kosakovsky Pond 2010. Benchmarking multi-rate codon models. *PLoS ONE* **5**: e11587.
- [41] Katz, L.A., J. DeBerardinis, M.S. Hall, A.M. Kovner, M. Dunthorn, and S.V. Muse 2011. Heterogeneous Rates of Molecular Evolution Among Cryptic Species of the Ciliate Morphospecies *Chilodonella uncinata*. *J. Mol. Evol.* **73**:266-272.
- [42] Pattin, K.A., A.C. Green, R.B. Altman, K.B. Cohen, E. Wethington, C. Gorg, L.E. Hunter, S.V. Muse, P.D. Radivojac, and J.H. Moore 2015. Training the next generation of quantitative scientists in the era of big data. *Pac. Symp. Biocomput.* 2015 **20**:488-492.