

Timothy M. Beissinger

CONTACT INFORMATION	302 Curtis Hall University of Missouri Columbia, MO 65211	(608) 320-1913 beissinger@missouri.edu http://beissingerlab.org
EDUCATION	The University of Wisconsin at Madison , Madison, Wisconsin USA	
	Ph.D., Statistical and Quantitative Genetics	May 2014
	Departments: Agronomy and Animal Science Advisors: Professors Natalia de Leon and Daniel Gianola	
	M.S., Statistics	May 2011
	B.S., Mathematics and Geography	May 2009
APPOINTMENTS	Research Geneticist	2015 - Present
	USDA-ARS, Plant Genetics Research Unit University of Missouri, Columbia	
	Adjuct Assistant Professor	2015 - Present
	Division of Plant Sciences University of Missouri, Columbia	
	Postdoctoral Research Associate	2014 - 2015
	Mentored by Professor Jeff Ross-Ibarra Department of Plant Sciences University of California, Davis	
	Visiting Scientist	Jan - Apr 2014
	Mentored by Professor Henner Simianer Department of Animal Breeding and Genetics Georg-August Universität, Göttingen, Germany	
PUBLICATIONS	Beissinger, T.M. , Gholami, M., Erbe, M., Weigend, S., Weigend, A., de Leon, N., Gianola, D., Simianer, H. 2015. Using the variability of linkage disequilibrium between subpopulations to scan for selection in a diverse panel of chickens. <i>Heredity</i> . DOI: 10.1038/hdy.2015.81.	
	Haase, N.J., Beissinger, T.M. , Hirsch, C.N., Vaillancourt, B., Deshpande, S., Barry, K., Buell, C.R., Kaeppler, S., de Leon, N. 2015. Genetic Dissection of quantitative traits using a bulked segregant analysis (BSA)-sequencing method on a large segregating population of maize. <i>Genes Genomes Genetics</i> . DOI: 10.1534/g3.115.017665.	
	Beissinger, T.M. , Rosa, J.G.M., Kaeppler, S.M., de Leon, N., Gianola, D. 2015. Defining window-boundaries for genomic analyses using smoothing spline techniques. <i>Genetics Selection Evolution</i> . 47(30). DOI: 10.1186/s12711-015-0105-9.	
	Lorenz, A. J., Beissinger, T.M. , Rodrigues, R., de Leon, N. 2015. Selection for silage yield and composition did not affect genomic diversity within the Wisconsin Quality Synthetic maize population. <i>Genes Genomes Genetics</i> . DOI: 10.1534/g3.114.015263.	

Foerster, J.M., **Beissinger, T.M.**, de Leon, N., Kaeppler, S.M. 2015. Large effect QTL explain natural phenotypic variation for the developmental timing of vegetative phase change in maize (*Zea mays L.*). Theoretical and Applied Genetics. DOI: 10.1007/s00122-014-2451-3.

Hirsch, C.N., Flint-Garcia, S.A., **Beissinger, T.M.**, Eichten, S.R., Deshpande, S., Barry, K., McMullen, M.D., Holland, J.B., Buckler, E.S., Springer, N.M., Buell, C.R., de Leon, N., Kappler, S.M. 2014. Insights into the effects of long-term artificial selection on seed size in maize. Genetics. 198(1): 409-421.

Beissinger, T.M., Hirsch, C.N., Vaillancourt, B., Deshpande, S., Barry, K., Buell, C. R., Kaeppler, S. M., Gianola, D., de Leon, N. 2014. A genome-wide scan for evidence of selection in a maize population under long-term artificial selection for ear number. Genetics. 196(3): 829-840.

***Beissinger, T.M.**, Hirsch, C.N., Sekhon, R.S., Foerster, J.M., Johnson, J.M., Muttoni, G., Vaillancourt, B., Buell, C.R., Kaeppler, S.M., de Leon, N. 2013. Marker density and read-depth for genotyping populations using genotyping-by-sequencing. Genetics. 193: 1073-1081.

* Selected as a highlighted article by the editorial board.

Wu, X., Chuanyu, S., **Beissinger, T.M.**, Rosa, G., Weigel, K., de Leon, N., Gianola, D. 2012. Parallel Markov chain Monte Carlo - bridging the gap to high performance Bayesian computation in animal breeding and genetics. Genet Sel Evol. 44:29.

Wu, X., **Beissinger, T.M.**, Bauck, S., Woodward, B., Rosa, G., Weigel, K., de Leon, N., Gianola, D. 2011. A primer on high-throughput computing for genomic selection. Frontiers in Genetics. 2, 4.

PREPRINTS

Morota, G., **Beissinger, T.M.**, Peñagaricano, F. 2015. MeSH annotation of the chicken genome: MeSH-informed enrichment analysis and MeSH-guided semantic similarity among functional terms and gene products. BioRxiv. (in revision)

Beissinger, T.M., Wang, L., Crosby, C., Durvasula, A., Hufford, M.B., Ross-Ibarra, J. 2015. Recent demography drives changes in linked selection across the maize genome. BioRxiv. (in revision)

SOFTWARE

GenWin: Spline Based Window Boundaries for Genomic Analyses

An R package for analyzing genetic data across distinct bins.

<http://cran.r-project.org/web/packages/GenWin/index.html>

GRANTS

2012, University of Wisconsin Graduate School. Awarded one year of funding and supplies to support dissertation research.

2012, DuPont-Pioneer and UW Associated Students of Madison. Co-authored grant to support the first University of Wisconsin Plant Sciences Symposium.

2011, DuPont-Pioneer. Awarded funding to genotyping 240 samples with the Pioneer Public SNP array.

CONFERENCE,
WEBINAR, AND
DEPARTMENTAL
PRESENTATIONS

Invited

Beissinger, T. KWS seed company, Einbeck, Germany
April, 2016

Beissinger, T. Department of Animal Breeding and Genetics & Session in 'Scaling Problems in Statistics', Georg-August Universitat, Göttingen, Germany
April 2016

Beissinger, T. Corn Breeding Research Meeting, Jacksonville, FL
March 2016

Beissinger, T. Plant and Animal Genome Conference 24, San Diego, CA
Maize workshop
January, 2016

Beissinger, T. Division of Plant Sciences, University of Missouri
November, 2015

Beissinger, T. Department of Botany and Plant Sciences, University fo California, Riverside
April, 2015

Beissinger, T. USDA-ARS Plant Genetics Research Unit, University of Missouri, Columbia
March, 2015

Beissinger, T., Wang, L., Durvasula, A., Crosby, K., Hufford, M., and Ross-Ibarra, J. 57th annual Maize Genetics Conference, St. Charles, IL
March, 2015

Beissinger, T. Plant and Animal Genome Conference 23, San Diego, CA
Genomic selection and genome-wide association studies workshop
January 2015

Beissinger, T. Department of Animal Science, University of California, Davis
August, 2014

Beissinger, T. Department of Animal Breeding and Genetics,
Georg-August Universitat, Göttingen, Germany
February 2014

Beissinger, T. Center of Life and Food Sciences, Technische Universitat Munchen, Munich, Germany
April 2014

Beissinger, T. Animal Science Department, University of Nebraska, Lincoln
December, 2013

Beissinger, T., Hirsch, C., Buell, R.C., Kaeppler, S., Gianola, D., de Leon, N. Gordon Research Seminar in Quantitative Genetics and Genomics. Galveston, TX

Contributed

Beissinger, T. Corn Breeding Webinar Series, hosted by Dr. Rex Bernardo at the University of Minnesota. December, 2012.

POSTER ABSTRACTS

Beissinger, T., Gianola, D., de Leon, N. Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics Conference. Seattle, WA, November 23-26, 2013.

Beissinger, T., Hirsch, C., Buell, R.C., Kaeppler, S., Gianola, D., de Leon, N. Gordon Research Seminar in Quantitative Genetics and Genomics. Galveston, TX, February 16-17, 2013.

Beissinger, T., Hansey, C., Foerster, J., Sekhon, R., Johnson, J., Muttoni, G., Vailancourt, B., Buell, C.R., Kaeppler, S., de Leon, N. Maize Genetics Conference. Portland, OR, March 15-18, 2012.

TEACHING

Co-instructor

Guest Lectures

Teaching assistant

Experimental Design
University of Wisconsin, Madison Department of Agronomy

Advanced Plant Breeding Spring 2012
University of Wisconsin, Madison Department of Agronomy

	Tutoring	
	Statistics	Fall 2010 - Spring 2011
	Advanced Placement Statistics	
	Calculus	Fall 2006- Spring 2007
	Advanced Placement Calculus AB	
REVIEWED FOR	BMC Evolutionary Biology BMC Genomics Crop Science Genes Genomes Genetics (G3) Heredity PeerJ The Plant Genome Theoretical and Applied Genetics	
AWARDS AND SCHOLARSHIPS	Monsanto fellowship recipient	2009-2014
	Scholarship to attend Summer Institute in Statistical Genetics University of Washington, Seattle	2012
	Scholarship to attend TeraGrid Conference Pittsburgh, PA	2010
	Scholarship to attend Open Science Grid Summer School Madison, WI	2010
	Undergraduate deans list	All semesters 2007-2009
	Susan B. Hotchkiss memorial scholarship	2005
ACADEMIC AND PROFESSIONAL DEVELOPMENT	Monsanto Fellows Professional Development Program	September 2012
	17th Summer Institute in Statistical Genetics	July 2012
	Monsanto Fellows Professional Development Program	September 2011
	Monsanto Fellows Professional Development Program	September 2010
	Monsanto Fellows Professional Development Program	September 2009
	University of Wisconsin Plant Breeding Internship	Summer 2008
COMPUTER ABILITIES	Software R, Linux/Unix, SAS, Latex, Condor, Java, Perl, Python	
	Linux workstation system administrator	2010 - 2014
	Participated in Open Science Grid Summer School	July 2010
STATISTICAL EXPERTISE	Bayesian analysis, estimation of functions from data, mixed models, mathematical statistics, statistical inference, linear regression and analysis of variance	
MATHEMATICAL EXPERTISE	Real and complex analysis, combinatorics, topology, number theory, modern algebra, cellular automata	