

## Timothy M. Beissinger

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CONTACT INFORMATION	302 Curtis Hall University of Missouri Columbia, MO 65211	(608) 320-1913 <a href="mailto:beissinger@missouri.edu">beissinger@missouri.edu</a> <a href="http://beissingerlab.org">http://beissingerlab.org</a>
EDUCATION	<b>The University of Wisconsin at Madison</b> , Madison, Wisconsin USA	
	Ph.D., <b>Statistical and Quantitative Genetics</b>	May 2014
	Departments: Agronomy and Animal Science Advisors: Professors Natalia de Leon and Daniel Gianola	
	M.S., <b>Statistics</b>	May 2011
	B.S., <b>Mathematics and Geography</b>	May 2009
APPOINTMENTS	<b>Research Geneticist &amp; Adjunct Assistant Professor</b> USDA-ARS, Plant Genetics Research Unit Division of Plant Sciences University of Missouri, Columbia	2015 - Present
	<b>Postdoctoral Research Associate</b> Mentored by Professor Jeff Ross-Ibarra Department of Plant Sciences University of California, Davis	2014 - 2015
	<b>Visiting Scientist</b> Mentored by Professor Henner Simianer Department of Animal Breeding and Genetics Georg-August Universität, Göttingen, Germany	Jan - Apr 2014
PUBLICATIONS	<b>Beissinger, T.M.</b> , 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., <b>Beissinger, T.M.</b> , 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.	
	<b>Beissinger, T.M.</b> , 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., <b>Beissinger, T.M.</b> , 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., <b>Beissinger, T.M.</b> , 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.

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

#### 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. [Plant and Animal Genome Conference 24](#)  
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](#)  
March, 2015

Beissinger, T. [Plant and Animal Genome Conference 23](#)  
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](#)  
February 2014

Beissinger, T. [Center of Life and Food Sciences, Technische Universitat Munchen](#)  
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, February, 2013.

**Contributed**

Beissinger, T. Bay Area Population Genomics Meeting XI. Davis, CA, December, 2014.

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

Beissinger, T., Hansey, C., Sekhon, R., Vaillancourt, B., Buell, C.R., Kaeppler, S., de Leon, N. North Central Regional Corn Breeding Research Meeting. Portland, OR, March, 2012.

POSTER  
ABSTRACTS

Beissinger, T. and Ross Ibarra, J. [Plant and Animal Genome Conference 23.](#) San



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 <a href="#">Open Science Grid Summer School</a>	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	