

Timothy M. Beissinger

CONTACT INFORMATION	Department of Plant Sciences University of California, Davis Davis, CA 95616	(608) 320-1913 beissinger@ucdavis.edu
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
EMPLOYMENT	Postdoctoral Research Associate	June 2014 - Present
	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	
	Research Assistant	2009 - 2014
	Department of Agronomy University of Wisconsin, Madison	
PUBLICATIONS	In peer reviewed journals	
	Haase, N.J., Beissinger, T.M. , Hirsch, C.N., Vaillancourt, B., Deshpande, S., Barry, K., Buell, C.R., Kaeppler, S., de Leon, N. 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. 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. 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 (<i>Zea mays L.</i>). <i>Theoretical and Applied Genetics</i> . DOI: 10.1007/s00122-014-2451-3.	
	Hirsch, C.N., Flint-Garcia, S.A., Beissinger, T.M. , Eichten, S.R., Deshpande, S., Barry, K., 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. <i>Genetics</i> . 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.

Submitted

Beissinger, T.M., Gholami, M., Erbe, M., Weigend, S., Weigend, A., de Leon, N., Gianola, D., Simianer, H. Using the variability of linkage disequilibrium between subpopulations to scan for selection in a diverse panel of chickens. *Submitted*.

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. [Department of Botany and Plant Sciences](#)

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 Universität](#)
February 2014

Beissinger, T. [Center of Life and Food Sciences, Technische Universität München](#)
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
Diego, CA, January 10-14, 2015.

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., Vaillancourt, B., Buell, R.C., Kaeppler, S., Gianola, D.,
de Leon, N. Maize Genetics Conference. St. Charles, IL, March 14-17, 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., Vail-
lancourt, B., Buell, C.R., Kaeppler, S., de Leon, N. Maize Genetics Conference.
Portland, OR, March 15-18, 2012.

Beissinger, T., de Leon, N., Kaeppler, S. Maize Genetics Conference. St Charles,

IL, March 17-20, 2011.

TEACHING EXPERIENCE	Co-instructor	
	Intoduction to Linux and High Throughput Computing	Fall 2010
	University of Wisconsin, Madison Department of Animal Sciences	
	Teaching assistant	
	Biometrical Procedures in Plant Breeding	Fall 2011, 2013
	University of Wisconsin, Madison Department of Agronomy	
	Experimental Design	Spring 2013
	University of Wisconsin, Madison Department of Agronomy	
	Advanced Plant Breeding	Spring 2012
	University of Wisconsin, Madison Department of Agronomy	
REVIEWED FOR	Tutoring	
	Statistics	Fall 2010 - Spring 2011
	Advanced Placement Statistics	
	Calculus	Fall 2006- Spring 2007
	Advanced Placement Calculus AB	
	PeerJ	
	BMC Evolutionary Biology	
AWARDS AND SCHOLARSHIPS	Monsanto fellowship recipient	2009-2014
	Scholarship to attend Summer Institute in Statistical Genetics	2012
	University of Washington, Seattle	
	Scholarship to attend TeraGrid Conference	2010
	Pittsburgh, PA	
	Scholarship to attend Open Science Grid Summer School	2010
	Madison, WI	
ACADEMIC AND PROFESSIONAL DEVELOPMENT	Undergraduate deans list	All semesters 2007-2009
	Susan B. Hotchkiss memorial scholarship	2005
	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
LANGUAGES	University of Wisconsin Plant Breeding Internship	Summer 2008
COMPUTER ABILITIES	English: Mother tongue	
	Spansih: Basic abilities	
	Software	
	R, Linux/Unix, SAS, Latex, Condor, Java, Perl	
	Linux workstation system administrator	2010 - 2014

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