Timothy M. Beissinger

CONTACT
INFORMATION

Department of Plant Sciences
University of California, Davis
Davis, CA 95616

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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

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. Genetics Selection Evolution. *In Press.*

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. Genes Genomes Genetics. 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., 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.

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.*

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. *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., 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 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., Vaillancourt, 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

Tutoring

Statistics	Fall 2010 - Spring 2011

Advanced Placement Statistics

Calculus	Fall 2006- Spring 2007

Advanced Placement Calculus AB

REVIEWED FOR	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
	Pittspburgh, PA	
	Scholarship to attend Open Science Grid Summer School	2010
	Madison, WI	
	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

LANGUAGES	English: Mother tongue
	Spansih: Basic abilities

COMPUTER ABILITIES	Software	
	R, Linux/Unix, SAS, Latex, Condor, Java, Perl	
	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 |