Timothy M. Beissinger

CONTACT INFORMATION	203 Curtis Hall University of Missouri Columbia, MO 65211	(608) 320-1913 beissingert@missouri.edu http://beissingerlab.org

EDUCATION

The University of Wisconsin at Madison, Madison, Wisconsin USA
- Ph.D., **Statistical and Quantitative Genetics** — 2014
  - Advisors: Natalia de Leon and Daniel Gianola
- M.S., **Statistics** — 2011
- B.S., **Mathematics and Geography** — 2009

CURRENT APPOINTMENTS

Research Geneticist — 2015 - Present
USDA-ARS, Plant Genetics Research Unit
University of Missouri, Columbia

Adjunct Assistant Professor University of Missouri, Columbia
- Division of Plant Sciences — 2015 - Present
- Division of Biological Sciences — 2016 - Present

PREVIOUS APPOINTMENTS

Postdoctoral Research Associate — 2014 - 2015
Mentored by Professor Jeff Ross-Ibarra
- Department of Plant Sciences
- University of California, Davis

Visiting Scientist — 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

ADVISING

Direct advisees
- PostDocs
  - NSF Postdoc (NSF Plant Genome Fellowship) (1)
- PhD Students
  - Division of Biological Sciences (1)
  - MU Informatics Institute (1)
- Undergraduate student researchers (2)

PhD Committees
- Division of Animal Sciences (2)
- Division of Biological Sciences (3)
- Division of Plant Sciences (1)
- MU Informatics Institute (1)

MSc Committees
- Division of Animal Sciences (1)

PUBLICATIONS

Wang, L., **Beissinger, T.M.**, Lorant, A., Ross-Ibarra, C., Ross-Ibarra, J., Hufford, M. 2017. The interplay of demography and selection during maize domestication and expansion. *In Press* at Genome Biology. http://biorxiv.org/content/early/2017/03/07/114579

Beissinger, T.M., Morota, G. 2017. Medical subject heading (MeSH) annotations illuminate maize genetics and evolution. Plant Methods. 13(8). DOI: 10.1186/s13007-017-0159-5.

Morota, G., **Beissinger, T.M.**, Peñagaricano, F. 2016. MeSH annotation of the chicken genome: MeSH-informed enrichment analysis and MeSH-guided semantic similarity among functional terms and gene products. Genes Genomes Genetics. DOI: 10.1534/g3.116.031096.

Beissinger, T.M., Wang, L., Crosby, C., Durvasula, A., Hufford, M.B., Ross-Ibarra, J. 2017. Recent demography drives changes in linked selection across the maize genome. Nature Plants. 2(16084). DOI:10.1038/nplants.2016.84.

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. Heredity. 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. Genes Genomes Genetics. 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. Genetics Selection Evolution. 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. 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., 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 per-

formance 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 AND MANUSCRIPTS UNDER REVIEW

Beissinger, T.M., Kruppa, J., Cavero, D., Ha, N., Erbe, M., Simianer, H., A simple test identifies selection on complex traits in breeding and experimentally-evolved populations. bioRxiv. DOI: 10.1101/238295

Bird, K., **Beissinger, T.M.**, Angelovici, R.A., Subset-based genomic prediction provides insights into the genetic architecture of free amino acid levels in dry Arabidopsis thaliana seeds. *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 AND FUNDING

2018, USDA NIFA, Agriculture and food research initiative,foundational program. Exploiting exotic alleles for the Nutritional Enhancement of Maize. Recommended for funding in the amount of $490,000. Declined due to pending institional change.

2017, Midwest Big Data Spoke Project. Seed grant to develop an online QTL database for maize. Initial source of funds is NSF.

2015-Present, USDA-ARS. Project Number 3622-21000-034-00D. Revolving funds. Budget supports a technician, student employees, supplies, equipment, and space.

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. Funding supported the first University of Wisconsin Pioneer Plant Sciences Symposium.

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

TEACHING

Co-instructor

Genetics of Populations	Fall 2016
University of Missouri, Division of Animal Sciences	
Systems Biology Reading Group	Spring 2016
University of Missouri, Division of Biological Sciences	
Intoduction to Linux and High Throughput Computing	Fall 2010
University of Wisconsin, Madison Department of Animal Sciences	

Guest Lectures

Advanced Plant Genetics	December 2016
Lecture on Plant Population Genetics, MU Division of Biological Sciences	

	Applied Quantitative and Statistical Genetics	December 2015

Applied Quantitative and Statistical Genetics   December 2015
Two lectures on Genomic Prediction, MU Division of Plant 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

ACADEMIC AND PROFESSIONAL SERVICE

MU Informatics Institute

Core faculty member   2016 - Present

Editorial Boards

Associate Editor, Crop Science   2018 - 2021

Faculty advisor for student-organized MU Plant Sciences Symposium

Building the Bridge from Fundamental Research to Improving
Tomorrows Crops
Funded by Pioneer Hi-Bred   2016 - Present

"Detox" Evolutionary Genetics Discussion Group

Faculty organizer and host of extracurricular journal club   Fall 2015 - Present

Journal reviews

Nature	Genes Genomes Genetics (G3)
Nature Genetics	Heredity
Genetics	PeerJ
BMC Evolutionary Biology	The Plant Genome
PLoS Computational Biology	Theoretical and Applied Genetics
BMC Genomics	Crop Science

Ad-hoc grant reviews

USDA-NIFA, Plant Breeding for Agricultural Production
University of Missouri Research Board

AWARDS AND SCHOLARSHIPS

USDA Group Platinum Hall of Fame   2016
For contributions to Feds Feed Families Campaign

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

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

COMPUTING
EXPERTISE

R, Linux/Unix, SAS, Latex, Condor, Java, Perl, Python	
Linux workstation system administrator	2010 - 2014
Participated in Open Science Grid Summer School	July 2010

INVITED
PRESENTATIONS
(LAST 4 YEARS)

Georg-August-Universität
Göttingen, Germany
November, 2017

Universidade Federal de Lavras
Lavras, Brazil
November, 2017

Korea Rural Development Administration
Daejeon, South Korea
June, 2017

Seoul National University
Seoul, South Korea
June, 2017

Asian Crop Science Association Conference
Jeju, South Korea
June, 2017

Department of Ecology and Evolutionary Biology
University of Oregon
May, 2017

Department of Ecology and Evolutionary Biology
University of Kansas
March, 2017

Department of Plant Breeding and Genetics
Cornell University
February, 2017

Pioneer Hi-Bred
Ankeny, Iowa
February, 2017

Advances in Plant Breeding Workshop
CiBreed, Georg-August-Universität, Göttingen, Germany
January, 2017

Seminar for Evolution, Ecology, and Population Biology Program

Washington University in St. Louis, Missouri
November, 2016

Department of Crop Sciences
University of Illinois
October, 2016

Division of Biological Sciences
University of Missouri, Columbia
October, 2016

Department of Crop Sciences, Chungnam National University
Deajeon, South Korea.
July, 2016

KWS Seed Company
Einbeck, Germany
April, 2016

Advanced Seminar for Statistical Genetics
Department of Animal Breeding and Genetics, Georg-August Universitat,
Göttingen, Germany
April 2016

Corn Breeding Research Meeting
Jacksonville, FL
March 2016

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

Division of Plant Sciences, University of Missouri
Columbia, Missouri
November, 2015

Department of Botany and Plant Sciences
University of California, Riverside
April, 2015

USDA-ARS Plant Genetics Research Unit
University of Missouri
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

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