Timothy M. Beissinger

| Contact Information | Carl-Sprengel-Weg 1 Georg-August-Universität 37075 Göttingen, Germany | +49 551 3924369 beissinger@gwdg.de http://uni- goettingen.de/plantbreeding | |
|--------------------------|--|---|--|
| Education | The University of Wisconsin at Madison, Madison, Ph.D., Statistical and Quantitative Genetics Advisors: Natalia de Leon and Daniel Gianola M.S., Statistics B.S., Mathematics and Geography | Wisconsin USA 2014 2011 2009 | |
| Current Appointments | Professor and Chair, Plant Breeding Methodology Division of Plant Breeding Methodology Center for Integrated Breeding Research (CiBreed) Georg-August-Universität, Göttingen | 2018 - Present | |
| Previous Appointments | Research Geneticist USDA-ARS, Plant Genetics Research Unit University of Missouri Columbia | 2015 - 2018 | |
| | Adjunct Assistant Professor University of Missouri, Columbia Division of Plant Sciences | 2015 - 2018 | |
| | Postdoctoral Research Associate Mentored by Professor Jeff Ross-Ibarra Department of Plant Sciences | 2014 - 2015 | |
| | Visiting Scientist Mentored by Professor Henner Simianer Department of Animal Breeding and Genetics | 2014 | |
| | Georg-August Universitat, Gottingen, Germany Research Assistant Department of Agronomy University of Wisconsin, Madison | 2009 - 2014 | |
| Publications | Gyawali, A., Shrestha, V., Guill, K.E., Flint-Garcia, S., and Beissinger, T.M., 2019. Single Plants GWAS coupled with bulk segregant analysis Allows rapid identification and plant-height candidate SNPs, BMC Plant Biology. In Press. | | |
| | Sekhon, RS, Saski, C., Kumar, R., Flinn, B., Luo, F., Beissinger, T.M. , Ackerman, A.J., Breitzman, M.W., Bridges, W.C., de Leon, N., Kaeppler, S.M., 2019. Integrated genome-scale analysis identifies novel genes and networks underlying senescence in maize. The Plant Cell, DOI: https://doi.org/10.1105/tpc.18.00930. | | |
| | Petrowski, P.F. , King, E.G. , Beissinger, T.M. 2019. An R Framework for the Partitioning of Linkage Disequilibrium between and Within Populations. Journal of Open Research Software. DOI: http://doi.org/10.5334/jors.250. | | |

*Beissinger, T.M., Kruppa, J., Cavero, D., Ha, N., Erbe, M., Simianer, H. 2018. A simple test identifies selection on complex traits. Genetics. 209(1). DOI: 10.1534/genetics.118.300857.

*Selected as a highlighted article of the issue and subsequently as a 2018 *Spotlight* article indicating it stood out as one of the most impactful Genetics articles of the year.

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. Genome Biology. https://doi.org/10.1186/s13059-017-1346-4

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., Gi- anola, 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 | Turner-Hissong, S. , Mabry, M., Beissinger, T.M. , Ross-Ibarra, J., Pires, J. Evo- lutionary insights into plant breeding. AgriXiv Preprint: https://agrixiv.org/akdt8 | |
| | 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.https://www.biorxiv.org/content/10.1101/272047v1.abstract | |
| Software | Ghat: Quantifying Evolution and Selection on Complex Traits An R package to test for selection on measured phenotypes, using whole-genome marker data. https://cran.r-project.org/web/packages/Ghat/index.html | |
| | 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 | |
| | ohtastats: Tomoko Ohta's D Statistics An R package to Calculate Tomoka Ohta's partitioning of linkage disequilibrium between and within populations. https://cran.r-project.org/web/packages/ohtadstats/index.html | |
| Grants and Funding | 2018, USDA-NIFA AFRI award Title: Leveraging Genomic Prediction And Exploiting Exotic Alleles For Maize Nutritional Quality. Award of approximately \$500,000 USD was declined due to professional relocation to Germany. | |
| | 2017, Midwest Big Data Spoke Project. Seed grant to develop an online QTL database for maize. Initial source of funds was NSF. | |
| | 2015-2018 , USDA-ARS . Project Number 3622-21000-034-00D. Revolving funds. Budget supported 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

| Selection Theory Sp University of Göttingen, Interdisciplinary Plant and Animal I | ring/Summer 2019 Breeding | | | |
|--|------------------------------|--|--|--|
| Co-instructor | - | | | |
| Population and Quantitative Genetics Fall/ | Winter 2018 - 2019 | | | |
| University of Göttingen. Interdisciplinary Plant and Animal | Breeding | | | |
| Genome Analysis and Application of Markers in Plant Breeding Fall/Winter 2019 | | | | |
| University of Göttingen, Division of Plant Breeding | , | | | |
| Breeding Schemes Sp | ring/Summer 2019 | | | |
| University of Göttingen. Interdisciplinary Plant and Animal Breeding | | | | |
| 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 Scie | ences | | | |
| Guest Lectures | | | | |
| Advanced Plant Genetics | December 2016 | | | |
| Lecture on Plant Population Genetics MU Division of Biolog | vical Sciences | | | |
| Applied Quantitative and Statistical Genetics | December 2015 | | | |
| Two lectures on Genomic Prediction MU Division of Plant Sciences | | | | |
| | | | | |
| Teaching assistant | E 11 0011 0010 | | | |
| Biometrical Procedures in Plant Breeding | Fall 2011, 2013 | | | |
| University of Wisconsin, Madison Department of Agronomy | G | | | |
| Experimental Design | Spring 2013 | | | |
| University of Wisconsin, Madison Department of Agronomy | G · 0010 | | | |
| Advanced Plant Breeding | Spring 2012 | | | |
| University of Wisconsin, Madison Department of Agronomy | | | | |

Direct Supervising & Advising

Current

Instructor

| Senior scientists: 2 |
|------------------------------------|
| Lecturers: 2 |
| PostDocs: 2 |
| PhD Students: 2 |
| PhD examination committees: 4 |
| Technicians: 1 |
| Administrative personnel: 2 |
| Previous |
| Senior scientists: 1 |
| Postdocs: 2 |
| PhD Students: 2 |
| PhD examination committees: 8 |
| Masters students and committees: 2 |

Technicians: 1

| Academic and Professional Service | Center for Integrated Plant and Animal Breeding (CiBREED)Executive board member201 | | | |
|---|---|--|---|--|
| DERVICE | MU Informatics Institute Core faculty member | | 2016 - 2018 | |
| | Editorial Boards Associate Editor, Crop Science | t | erm runs 2018 - 2021 | |
| | Conference and Workshop Organizing Chair of Predictive Breeding Session at GPZ 2020 Digital Breeding Meeting2020Organizer of 2019 CiBREED Workshop2019 | | | |
| | Faculty advisor for student-organized MU Plant Sciences Symposium 2016 - 2018 Funded by Pioneer Hi-Bred | | | |
| | "Detox" Evolutionary Genetics Discussion Group Faculty organizer and host of extracurricular journal club Fall 2015 - Present | | | |
| | Journal reviews | | | |
| | Nature Nature Genetics Genetics BMC Evolutionary Biology PLoS Computational Biology PLoS Biology BMC Genomics | Genes Genomes C Heredity PeerJ The Plant Genom Theoretical and A Crop Science Plants | Genetics (G3) ne Applied Genetics | |
| | Ad-hoc grant and accreditation reviewsUniversity of Illinois GWAS Accreditation for universitiesin developing countries2017, 2019 | | | |
| | USDA-NIFA, Plant Breeding for Ag University of Missouri Research Boa | ricultural Production ard | | |
| Awards and Scholarships | USDA Group Platinum Hall of Fame For contributions to Feds Feed Families Campaign | | 2016 | |
| | 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 Gr. Madison, WI | id Summer School | 2010 | |
| | Undergraduate deans list | All | l semesters 2007-2009 | |
| | Susan B. Hotchkiss memorial scholarsh | ip | 2005 | |

INVITED Julius Kühn Institute (JKI) PRESENTATIONS (LAST 3 YEARS) Quedlingburg, Germany October, 2019

University fo Giessen Giessen, Germany June, 2019

Leibniz Institute for Plant Genetics (IPK) Gatersleben, Germany May, 2019

CiBREED Kick-off Conference: Plants and Animals – Bridging the Gap in Breeding Research University of Göttingen Göttingen, Germany October, 2018 Link to video of talk

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, USA May, 2017

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

Danforth Center for Plant Science St. Louis, Missouri, USA March, 2017

Department of Plant Breeding and Genetics Cornell University, USA February, 2017

Pioneer Hi-Bred Ankeny, Iowa, USA 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, USA November, 2016

Department of Crop Sciences University of Illinois, USA October, 2016

Division of Biological Sciences University of Missouri, Columbia, USA 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, USA March 2016

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