CONTACT INFORMATION	A218f Animal Science Building Department of Animal Science University of Nebraska-Lincoln Lincoln, NE 68583-0908 USA	*E-mail:* morota@unl.edu *Phone:* TBA *WWW:* morotalab.org

RESEARCH INTERESTS

I am a quantitative geneticist interested in incorporating statistics, machine learning, and bioinformatics to the study of animal genetics in the omics era. The core line of my research is connecting the quantitative genetics and animal breeding theories to currently available molecular information. I am particularly interested in statistical methods for prediction of complex traits using whole-genome molecular markers.

PROFESSIONAL POSITIONS

Department of Animal Science
University of Nebraska-Lincoln, Lincoln, Nebraska USA

Assistant Professor (70% Research & 30% Teaching)   **Start date: 08/2014**

WORK EXPERIENCE

Department of Animal Sciences
University of Wisconsin-Madison, Madison, Wisconsin USA

Graduate Research Assistant   **06/2011 - 05/2014**

Animal Genetics Research & Development Group
Zoetis, Inc., Kalamazoo, Michigan USA

Quantitative Geneticist (student internship)   **06/2013 - 11/2013**

EDUCATION

University of Wisconsin-Madison, Madison, Wisconsin USA

Ph.D., Animal Sciences, May 2014

- Dissertation: "Whole-genome Prediction of Complex Traits Using Kernel Methods."
- Advisor: Prof. Dr. Daniel Gianola
- Committee: Drs. Corinne D. Engelman, Guilherme J. M. Rosa, Grace Wahba and Kent A. Weigel

University of Wisconsin-Madison, Madison, Wisconsin USA

M.S., Dairy Science, December 2011

- Thesis: "Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants."
- Advisor: Prof. Dr. Daniel Gianola
- Committee: Drs. Guilherme J. M. Rosa and Kent A. Weigel

Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido Japan

B.S., Agricultural Science, March 2008

- Thesis: "Genetic Analysis of Threshold Traits."
- Advisor: Prof. Dr. Mitsuyoshi Suzuki

PROFESSIONAL SOCIETY MEMBERSHIPS	• American Society of Animal Science 2014 - Present • Japanese Society of Animal Breeding and Genetics 2013 - Present • The International Biometric Society (ENAR) 2012 -
EDITORIAL ACTIVITIES	Ad hoc Reviewer for: Computers and Electronics in Agriculture, DNA Research, Scientia Agricola Number of reviewed papers: 2012 (1), 2013 (1), 2014 (1)
MANUSCRIPTS IN PREP	**9**. **Morota G** and Gianola D. Kernel-based whole-genome prediction of complex quantitative traits. In prep. **8**. Valente BD, **Morota G**, Rosa GJM, Gianola D, and Weigel KA. The causal meaning of genomic predictors and how it affects the construction and comparison of genome-enabled selection models. In prep. *BioRxiv doi: 10.1101/001511* , *arXiv: http://arxiv.org/abs/1401.1165*
PEER REVIEWED JOURNAL PAPERS	As of March 2014, 10 citations total, h-index of 2, i10-index of 0 on Google Scholar and 6 citations total, h-index of 2 according to Web of Science.
2014	**7**. **Morota G**, Boddhireddy P, Vukasinovic N, Gianola D and DeNise S. Kernel-based variance components estimation and whole-genome prediction of pre-corrected phenotypes and progeny tests for dairy cow health traits. *Frontiers in Genetics.* **5**:56 . **6**. **Morota G**, Abdollahi-Arpanahi R, Kranis A and Gianola D. (2014) Genome-enabled prediction of broiler traits in chickens using genomic annotation. *BMC Genomics.* **15**:109 ⋆ **Highly accessed.** **5**. Abdollahi-Arpanahi R, Pakdel A, Nejati-Javaremi A, Moradi-Shahrbabak M, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. (2014) Dissection of additive genetic variability for quantitative traits in chickens using SNP markers. *Journal of Animal Breeding and Genetics.* doi: 10.1111/jbg.12079 **4**. Abdollahi-Arpanahi R, Nejati-Javaremi A, Pakdel A, Moradi-Shahrbabak M, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D (2014). Effect of allele frequencies, effect sizes and number of markers on prediction of quantitative traits in chickens. *Journal of Animal Breeding and Genetics.* doi: 10.1111/jbg.12075
2013	**3**. **Morota G**, Koyama M, Rosa GJM, Weigel KA, and Gianola D. (2013) Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. *Genetics Selection Evolution.* **45**:17. ⋆ **Highly accessed.** **2**. **Morota G** and Gianola D. (2013) Evaluation of linkage disequilibrium in wheat with an L1 regularized sparse Markov network. *Theoretical and Applied Genetics.* **126**(8):1991-2002.

2012	**1**. <u>**Morota G**</u>, Valente BD, Rosa GJM, Weigel KA, and Gianola D. (2012) An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. *Journal of Animal Breeding and Genetics.* **129**(6):474-487. ⋆ **Highlighted in the Genomic Selection Virtual Issue.**

PAPERS IN PROCEEDINGS

2014	**3.** Gianola D, <u>**Morota G**</u>, and Crossa J. (2014) Genome-enabled Prediction of Complex Traits with Kernel Methods: What Have We Learned? Proceedings, 10th World Congress of Genetics Applied to Livestock Production. August 17-22, Vancouver, BC, Canada.
	2. Valente BD, <u>**Morota G**</u>, Rosa GJM and Gianola D and Weigel KA (2014) The causal meaning of genomic predictors and how it affects the construction and comparison of genome-enabled selection models. Proceedings, 10th World Congress of Genetics Applied to Livestock Production. August 17-22, Vancouver, BC, Canada.
2011	**1.** Bueno Filho JS*, <u>**Morota G**</u>*, Tran Q, Maenner MJ, Vera-Cala LM, Engelman CD, and Meyers KJ. (2011) Analysis of human mini-exome sequencing data from Genetic & Analysis Workshop 17 using a Bayesian hierarchical mixture model. *BMC Proceedings,* **5**(Suppl 9):S93. *equal contribution

INVITED PRESENTATIONS

My PDF presentation slides are available on SlideShare (http://www.slideshare.net/chikudaisei/).

2013	**2.** Department of Animal Science, University of Nebraska-Lincoln, Nebraska, USA.
2011	**1.** OBIHIRO GCOE Animal Global Health Seminar. Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido Japan

CONFERENCE ABSTRACTS

Contributed

2012	• <u>**Morota G**</u>, Rosa GJM, Weigel KA, and Gianola D. (2012) Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants. 26th International Biometric Conference. August 26-31, Kobe, Japan. http://secretariat.ne.jp/ibc2012/30Aug.html#aug-30-14:00-Contributed36. ⋆ **Second Oral Prize Winners.**

Posters

2013	• <u>**Morota G**</u>, Tsuyuzaki K, and Nikaido I. (2013) MeSHR: R/Bioconductor package for finding statistically overrepresented MeSH terms in a set of genes. Annual Bioconductor Conference BioC 2013. July 18-19, Seattle, USA. https://secure.bioconductor.org/BioC2013/posters.php#8.
	• <u>**Morota G**</u>. (2013) Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. Annual Bioconductor Conference BioC 2013. July 18-19, Seattle, USA. https://secure.bioconductor.org/BioC2013/posters.php#7.

2014
- Ph.D. Thesis Defense. University of Wisconsin-Madison.
- Dairy Science Graduate Seminar. University of Wisconsin-Madison.

2013
- Special Seminar. Zoetis, Inc., Kalamazoo, Michigan USA.

2012
- Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.

2011
- Master's Thesis Defense. University of Wisconsin-Madison.

2010
- Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.

2008
- Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.

Participation in
conferences and
workshops

2014
- Short course: "Evolutionary Quantitative Genetics". University of Wisconsin-Madison. May 19-23. Taught by Bruce Walsh.

2013
- Short course: "Statistical methods for prediction of complex traits using whole-genome molecular markers". University of Wisconsin-Madison. May 27-31. Taught by Daniel Gianola and Gustavo de los Campos.

2012
- Short course: "Introduction to genome-enabled selection & Inferring causal phenotype networks using structural equation models". Kyoto University. August 31. Taught by Guilherme J.M. Rosa.

- Short course: "Identifying Genes for Complex and Mendelian Traits Using Next Generation Sequence Data". 26th International Biometric Conference. August 26. Taught by Suzanne Leal.

- Short course: "Programming and computer algorithms with focus on genomic selection in animal breeding". University of Georgia. May 15 - June 1. Taught by Ignacy Misztal, Shogo Tsuruta, Ignacio Aguilar, Zulma Vitezica, and Andres Legarra.

2009
- Symposium: "Statistical Genetics of Livestock for the Post-Genomic Era (SGLPGE)". University of Wisconsin-Madison. May 4-6.

2006
- Short course: "Estimation of Variance Conponents in Animal Breeding". Obihiro University of Agriculture and Veterinary Medicine. November. Taught by Shogo Tsuruta.

TEACHING	**University of Wisconsin-Madison**, Madison, Wisconsin USA

Teaching Assistant
ANSCI/DYSCI 363: "Principles of Animal Breeding"   **Spring, 2011**

Teaching Assistant
ANSCI/DYSCI 361: "Introduction to Animal and Veterinary Genetics"   **Spring, 2011**

OSS CONTRIBUTIONS	R packages

- dkDNA: http://cran.r-project.org/web/packages/dkDNA/index.html

Bioconductor packages
- meshr

- MeSH.db

- MeSH.AOR.db

- MeSH.PCR.db

- org.MeSH.XXX.db (120 packages)

- org.MeSH.Aca.db
- org.MeSH.Aga.PEST.db
- org.MeSH.Ame.db
- org.MeSH.Aml.db
- org.MeSH.Ana.db
- org.MeSH.Ani.FGSC.db
- org.MeSH.Ath.db
- org.MeSH.Atu.K84.db
- org.MeSH.Bfl.db
- org.MeSH.Bsu.168.db
- org.MeSH.Bsu.Bsn5.db
- org.MeSH.Bsu.RONN1.db
- org.MeSH.Bsu.TUB10.db
- org.MeSH.Bsu.W23.db
- org.MeSH.Bta.db
- org.MeSH.Cal.SC5314.db
- org.MeSH.Cbr.db
- org.MeSH.Cel.db
- org.MeSH.Cfa.db
- org.MeSH.Cin.db
- org.MeSH.Cja.db
- org.MeSH.Cpo.db
- org.MeSH.Cre.db
- org.MeSH.Dan.db
- org.MeSH.Dda.3937.db

- org.MeSH.Ddi.AX4.db
- org.MeSH.Der.db
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- org.MeSH.Eco.55989.db
- org.MeSH.Eco.APEC01.db
- org.MeSH.Eco.B.REL606.db
- org.MeSH.Eco.BW2952.db
- org.MeSH.Eco.CFT073.db
- org.MeSH.Eco.E24377A.db
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- org.MeSH.Eco.O103.H2.12009.db

- org.MeSH.Eco.O111.H.11128.db
- org.MeSH.Eco.O127.H6.E2348.69.db
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- org.MeSH.Ocu.db
- org.MeSH.Oni.db
- org.MeSH.Osa.db
- org.MeSH.Pab.db
- org.MeSH.Pae.LESB58.db
- org.MeSH.Pae.PA14.db
- org.MeSH.Pae.PA7.db
- org.MeSH.Pae.PAO1.db
- org.MeSH.Pfa.3D7.db
- org.MeSH.Pto.db
- org.MeSH.Ptr.db
- org.MeSH.Rno.db
- org.MeSH.Sau.COL.db
- org.MeSH.Sau.ED98.db
- org.MeSH.Sau.M013.db
- org.MeSH.Sau.MRSA252.db
- org.MeSH.Sau.MSHR1132.db
- org.MeSH.Sau.MSSA476.db
- org.MeSH.Sau.Mu3.db
- org.MeSH.Sau.Mu50.db
- org.MeSH.Sau.MW2.db
- org.MeSH.Sau.N315.db
- org.MeSH.Sau.Newman.db
- org.MeSH.Sau.RF122.db
- org.MeSH.Sau.USA300FPR3757.db
- org.MeSH.Sau.USA300TCH1516.db
- org.MeSH.Sau.VC40.db
- org.MeSH.Sce.S288c.db
- org.MeSH.Sco.A32.db
- org.MeSH.Sil.db
- org.MeSH.Spo.972h.db
- org.MeSH.Spu.db
- org.MeSH.Ssc.db
- org.MeSH.Syn.db
- org.MeSH.Tbr.9274.db
- org.MeSH.Tgo.ME49.db
- org.MeSH.Tgu.db
- org.MeSH.Vvi.db
- org.MeSH.Xla.db
- org.MeSH.Xtr.db
- org.MeSH.Zma.db

Github
- https://github.com/morota

COMPUTER SKILLS
- Programming Languages: Python, Fortran
- Statistical/Numerical Computational Tools: R, Octave

- Content-description Languages: XML, XHTML, CSS, LaTeX

- Operating Systems: Linux and Mac OS X

MISCELLANEOUS

- Languages: English and Japanese

REFERENCES   References and additional information available upon request.