CONTACT INFORMATION	368 Litton Reaves Hall 175 West Campus Drive Virginia Tech Blacksburg, Virginia 24061 USA	*E-mail:* morota@vt.edu *Phone:* (540)-231-XXXX *WWW:* morotalab.org

RESEARCH INTERESTS

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

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
- Available at UW-Madison Libraries

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 POSITIONS

Department of Animal and Poultry Sciences
Virginia Polytechnic Institute and State University, Blacksburg, Virginia USA

Assistant Professor of Quantitative Genetics (70% Research & 30% Teaching)	**08/2018 - Present**

Laboratory of Biometry and Bioinformatics
Department of Agricultural and Environmental Biology
Graduate School of Agriculture and Life Science
The University of Tokyo, Bunkyo, Tokyo, Japan

JST-CREST Oversea Research Fellow	**09/2018 - 12/2018**

Department of Animal Science
University of Nebraska-Lincoln, Lincoln, Nebraska USA
Assistant Professor of Theoretical Quantitative Genetics   **08/2014 - 07/2018**
(70% Research & 30% Teaching)

<table>
<tr><td>WORK
EXPERIENCE</td><td>Department of Animal Sciences
University of Wisconsin-Madison, Madison, Wisconsin USA
Graduate Research Assistant</td><td>**06/2011 - 05/2014**</td></tr>
</table>

Animal Genetics Research & Development Group
Zoetis, Inc., Kalamazoo, Michigan USA
Quantitative Geneticist (student internship)   **06/2013 - 11/2013**

PROFESSIONAL
SOCIETY
MEMBERSHIPS

- The Japanese Society of Breeding. 2018 - Present

- The Genetics Society of America. 2016 - Present

- The Japanese Society of Animal Science. 2016 - Present

- The American Society of Animal Science. 2014 - Present

- The International Biometric Society (ENAR). 2012 - Present

EDITORIAL
ACTIVITIES

Editorial Board

- Journal of Animal Science, July 2017 - July 2020

Reviewed for

- Animal (1), Animal Genetics (1), Animal Production Science (2), Animal Science Journal (1), BMC Bioinformatics (1), BMC Genetics (5), BMC Genomics (1), BMC Plant Biology (1), Computers and Electronics in Agriculture (1), DNA Research (1), Functional & Integrative Genomics (1), Frontiers in Genetics (1), G3: Genes, Genomes, Genetics (1), Genetics (2), Genetics Selection Evolution (3), Heredity (1), Journal of Agricultural, Biological, and Environmental Statistics (1), Journal of Animal Breeding and Genetics (6), Journal of Animal Science (5), Journal of Animal Science and Biotechnology (2), Livestock Science (3), New Phytologist (1), PLoS ONE (2), Poultry Science (1), Scientia Agricola (3)

- Number of reviewed papers: 2012 (1), 2013 (1), 2014 (6), 2015 (10), 2016 (10), 2017 (20)

PREPRINTS

27. Momen M, Mehrgardi AA, Roudbar MA, Kranis A, Pinto RM, Valente BD, **<u>Morota G</u>**, Rosa GJM, and Gianola D. Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation models. bioRxiv. doi: 10.1101/251421

PEER REVIEWED
JOURNAL PAPERS

10 first author, 13 co-author, and 3 senior author

2018

26. Yu H, Spangler ML, Lewis RM, and **Morota G**. 2018. Do stronger measures of genomic connectedness enhance prediction accuracies across management units? *Journal of Animal Science.* Forthcoming.

25. Momen M, Mehrgardi AA, Sheikhy ASA, Kranis A, Tusell L, **Morota G**, Rosa GJM, and Gianola D. 2018. Predictive ability of genome-assisted statistical models under various forms of gene action. *Scientific Reports.* Forthcoming.

24. Campbell MT, Walia H, and **Morota G**. 2018. Utilizing random regression models for genomic prediction of a longitudinal trait derived from high-throughput phenotyping. *Plant Direct.* Forthcoming.

23. Alvarenga AB, Rovadoscki GA, Petrini J, Coutinho LL, **Morota G**, Spangler ML, Pinto LFB, Carvalho GGP, and Mourão GB. 2018. Linkage disequilibrium in Brazilian Santa Inês breed, Ovis aries. *Scientific Reports.* **8**:8851. doi: 10.1038/s41598-018-27259-7

22. Rovadoscki GA, Pertille SFN, Alvarenga AB, Cesar ASM, Pértille F, Petrini J, Franzo V, Soares WVB, **Morota G**, Spangler ML, Pinto LFB, de Carvalho GGP, Lanna DPD, Coutinho LL, and Mourão GB. 2018. Estimates of genomic heritability and genome-wide association study for fatty acids profile in Santa Inês sheep. *BMC Genomics.* **19**:375. doi: 10.1186/s12864-018-4777-8

21. **Morota G**, Ventura RV, Silva FF, Koyama M, and Fernando SC. 2018. Machine learning and data mining advance predictive big data analysis in precision animal agriculture. *Journal of Animal Science.* **96**:1540-1550. doi: 10.1093/jas/sky014

20. He J, Xu J, Wu XL, Bauck S, Lee J, **Morota G**, Kachman SD, and Spangler ML. 2018. Comparing strategies for selection of low-density SNPs for imputation-mediated genomic prediction in U.S. Holsteins. *Genetica.* **146**:137-149. doi: 10.1007/s10709-017-0004-9

2017

19. **Morota G**. 2017. ShinyGPAS: Interactive genomic prediction accuracy simulator based on deterministic formulas. *Genetics Selection Evolution.* **49**:91. doi: 10.1186/s12711-017-0368-4.

18. Abdollahi-Arpanahi R, **Morota G**, and Peñagaricano F. 2017. Predicting bull fertility using genomic data and biological information. *Journal of Dairy Science.* **100**:9656-9666. doi: 10.3168/jds.2017-13288.

17. Yu H, Spangler ML, Lewis RM, and **Morota G**. 2017. Genomic relatedness strengthens genetic connectedness across management units. *G3: Genes, Genomes, Genetics.* **10**:3543-3556. doi: 10.1534/g3.117.300151.

16. Beissinger TM and **Morota G**. 2017. Medical subject heading (MeSH) annotations illuminate maize genetics and evolution. *Plant Methods.* **13**:8. doi: 10.1186/s13007-017-0159-5.

2016

15. **Morota G**, Beissinger TM, and Peñagaricano F. 2016. MeSH-informed enrichment analysis and MeSH-guided semantic similarity among functional terms and gene products in chicken. *G3: Genes, Genomes, Genetics.* **6**:2447-2453. doi: 10.1534/g3.116.031096.

14. Abdollahi-Arpanahi R, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. 2016. Differential contribution of genomic regions to marked genetic variation and prediction of quantitative traits in broiler chickens. *Genetics Selection Evolution.* **48**:10. doi: 10.1186/s12711-016-0187-z.

2015   **13**. Hu Y, **Morota G**, Rosa GJM, and Gianola D. 2015. Prediction of plant height in Arabidopsis thaliana from DNA methylation data. *Genetics.* **201**:779-793. doi: 10.1534/genetics.115.177204.

12. Valente BD, **Morota G**, Peñagaricano F, Gianola D, Weigel KA, and Rosa GJM. 2015. The causal meaning of genomic predictors and how it affects construction and comparison of genome-enabled selection models. *Genetics.* **200**:483-494. doi: 10.1534/genetics.114.169490.

11. **Morota G**, Peñagaricano F, Petersen JL, Ciobanu DC, Tsuyuzaki K, and Nikaido I. 2015. An application of MeSH enrichment analysis in livestock. *Animal Genetics.* **46**:381-387. doi: 10.1111/age.12307.

10. Abdollahi-Arpanahi R, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. 2015. Assessment of bagging GBLUP for whole-genome prediction of broiler chicken traits. *Journal of Animal Breeding and Genetics.* **132**:218-228. doi: 10.1111/jbg.12131.

9. Tsuyuzaki K, **Morota G**, Ishii M, Nakazato T, Miyazaki S, and Nikaido I. 2015. MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. *BMC Bioinformatics.* **16**:45. doi: 10.1186/s12859-015-0453-z.

2014   **8**. **Morota G** and Gianola D. 2014. Kernel-based whole-genome prediction of complex traits: a review. *Frontiers in Genetics.* **5**:363. doi: 10.3389/fgene.2014.00363.

7. **Morota G**, Boddhireddy P, Vukasinovic N, Gianola D, and DeNise S. 2014. 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. doi: 10.3389/fgene.2014.00056.

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. doi: 10.1186/1471-2164-15-109.

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.* **131**:183-193. 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.* **131**:123-133. 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. doi: 10.1186/1297-9686-45-17.

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**:1991-2002. doi: 10.1007/s00122-013-2112-y.

2012   **1**. **Morota G**, 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**:474-487. doi: 10.1111/jbg.12002.

PAPERS IN
PROCEEDINGS

2018   **6.** Yu H, Spangler ML, Lewis RM, and **<u>Morota G</u>**. 2018. Stronger measures of genomic connectedness enhance prediction accuracies across management units. In: *Proceedings, 11th World Congress of Genetics Applied to Livestock Production.* 11:406. February 11-16, Auckland, New Zealand. PDF.

               5. Abdollahi-Arpanahi R, **<u>Morota G</u>**, and Penagaricano F. Predicting bull fertility using biologically informed genomic models. Proceedings, 11th World Congress of Genetics Applied to Livestock Production. 11:683. February 11-16. Auckland, New Zealand. PDF.

               4. Mamani GC, Santana BF, Oliveira Junior GA, Mattos E, Ventura RV, Eler JP, **<u>Morota G</u>**, and Ferraz JBS. Proceedings, 11th World Congress of Genetics Applied to Livestock Production. 11:855. February 11-16. Auckland, New Zealand. PDF.

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? In: *Proceedings, 10th World Congress of Genetics Applied to Livestock Production.* August 17-22, Vancouver, BC, Canada. PDF.

               2. Valente BD, **<u>Morota G</u>**, Rosa GJM, Gianola D, and Weigel KA. 2014. Causal meaning of genomic predictors: Implication on genome-enabled selection modeling. In: *Proceedings, 10th World Congress of Genetics Applied to Livestock Production.* August 17-22, Vancouver, BC, Canada. PDF.

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. In: *BMC Proceedings.* **5**(Suppl 9):S93. DOI: 10.1186/1753-6561-5-S9-S93. *equal contribution.

INVITED
PRESENTATIONS   9 domestic and 3 international
                    My PDF presentation slides are available on SlideShare (http://www.slideshare.net/chikudaisei/).

2018   **12**. Do structural equation models advance genome-wide association analysis? Special seminar. School of Veterinary Medicine and Animal Science (FMVZ), University of São Paulo. May 28.

               11. Statistical and computational quantitative genetic analyses for genetic improvement of agricultural species. Special seminar. Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University. February 23.

               10. Do stronger measures of genomic connectedness enhance prediction accuracies across management units? Genomic Selection and Genome-Wide Association Studies Workshop. The Plant and Animal Genome XXVI Conference. Town and Country Hotel, San Diego, CA. January 13-17.

2017   **9**. Genomic connectedness across management units. The 62nd RBras (The Brazilian Region of the International Biometric Society) and 17th SEAGRO (Symposium on Statistics Applied to Agricultural Experimentation) Meeting. University of Lavras, Lavras, MG, Brazil. July 24-28.

8. Applications of data mining and prediction methods to animal sciences. Symposium on Big Data Analytics and Precision Animal Agriculture. ASAS-CSAS Annual Meeting. Baltimore Convention Center, Baltimore, MD. July 8-12.

2016   **7**. Phenome-wide genetic mean effect and variance heterogeneity association analysis. Biological Sciences Graduate Seminar. School of Biological Sciences, University of Nebraska-Lincoln. September 23.

6. MeSH annotation of the chicken genome. Poultry 2 Workshop. The Plant and Animal Genome XXIV Conference. Town and Country Hotel, San Diego, CA. January 9-13.

2015   **5**. Inferring the impact of population stratification on genomic heritability using a reparameterized genomic best linear unbiased prediction model. Statistics Seminars. Department of Statistics, University of Nebraska-Lincoln. September 23.

4. Quantitative genetics in the functional genomics era. Animal Breeding & Genetics Seminars. Department of Animal Science, Iowa State University. March 3.

2014   **3**. Quantitative genetics in the functional genomics era. Special Seminar. PIC, Inc., Hendersonville, TN. November 12.

2013   **2**. Whole-genome prediction of complex traits using kernel methods. Department of Animal Science, University of Nebraska-Lincoln. December 19.

2011   **1**. Obihiro GCOE Animal Global Health Seminars. Obihiro University of Agriculture and Veterinary Medicine. January 7.

CONTRIBUTED
PRESENTATIONS

2018   **9**. Investigating the relationship between microbial community and carcass traits in beef cattle. The 124th Japanese Society of Animal Science Meeting. The University of Tokyo, Yayoi Bunkyo-ku, Tokyo, Japan. March 27-30.

9. Stronger measures of genomic connectedness enhance prediction accuracies across management units. The 11th World Congress of Genetics Applied to Livestock Production. Aotea Centre, Auckland, New Zealand. February 11-16.

2017   **8**. ShinyGPAS: Interactive genomic prediction accuracy simulator based on deterministic formulas. NCERA-225 Meeting. Stanley Stout Livestock Marketing Center, Manhattan, KS. October 18-19.

7. Genomic connectedness across management units. The 123rd Japanese Society of Animal Science Meeting. Shinshu University, Kamiina, Nagano, Japan. September 4-8.

2015   **6**. Quantitative genetics in the functional genomics era. Special Seminar. The National Institute of Agrobiological Sciences, Tsukuba, Japan. November 12.

5. Quantitative genetics in the functional genomics era. Special Seminar. Laboratory of Biometry and Bioinformatics, The University of Tokyo. November 6.

4. The impact of population stratification on genomic heritability. NCERA-225 Meeting. North Dakota State University. October 22-23.

3. An application of MeSH enrichment analysis in livestock. ADSA-ASAS Joint Annual Meeting. Rosen Shingle Creek, Orlando FL. July 12-16.

2. Prediction of complex quantitative traits using functional annotations and bootstrap aggregating. Special Seminar. National Livestock Breeding Center, Shirakawa, Japan. January 10.

2012   **1**. Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants. 26th International Biometric Conference. Kobe International Conference Center, Kobe Japan. August 26-31. http://secretariat.ne.jp/ibc2012/30Aug.html#aug-30-14:00-Contributed36.   ⋆**Second Oral Prize Winners**.

POSTERS

2015
- Population stratification contribution to genomic heritability. Probabilistic Modeling in Genomics. Cold Spring Harbor Laboratory, NY. October 14 - 17.

- Estimating genomic heritability in the presence of population stratification. NGS Field 4th Meeting. Tsukuba International Congress Center, Tsukuba, Japan. July 1-3.

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, WA. https://secure.bioconductor.org/BioC2013/posters.php#8.

- 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, WA. https://secure.bioconductor.org/BioC2013/posters.php#7.

INTRAMURAL SEMINARS

2017
- Monthly Brown Bag Series on Plant Phenotyping. University of Nebraska-Lincoln. March 31.

2015
- Animal Breeding & Genetics Seminars. Department of Animal Science, University of Nebraska-Lincoln. September 15.

2014
- Animal Breeding & Genetics Seminars. Department of Animal Science, University of Nebraska-Lincoln. September 18.

- Ph.D. Thesis Defense. Department of Animal Sciences, University of Wisconsin-Madison. May 12.

- Dairy Science Graduate Seminars. Department of Dairy Science, University of Wisconsin-Madison. February 14.

2013	• Special Seminar. Zoetis, Inc., Kalamazoo, MI. August 8.
2012	• Animal Breeding & Genomics Seminars. Department of Animal Sciences, University of Wisconsin-Madison. April 10.
2011	• Master's Thesis Defense. Department of Dairy Science, University of Wisconsin-Madison. December 5.
2010	• Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison. November 30.
	• Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison. March 23.
2008	• Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison. November 25.

TEACHING

University of Nebraska-Lincoln, Lincoln, Nebraska, USA

<u>Lead Instructor</u>

- ASCI 944 / STAT 844 Quantitative Methods for Genomics of Complex Traits [WWW] **Spring, 2018**
- ASCI 896 Statistical Genomics [WWW] **Spring, 2017**
- ASCI 896 Statistical Genomics [WWW] **Spring, 2016**

<u>Co-Instructor</u>

- STAT 892-004 Integrative Data Science for Plant Phenomics [WWW] **Spring, 2018**
- ASCI 431/831 Advanced Animal Breeding [WWW] **Spring, 2018**
- LIFE 891-002 Integrating Quantitative and Computational Biology into Life Sciences Research [WWW] **Spring, 2018**
- ASCI 431/831 Advanced Animal Breeding [WWW] **Spring, 2017**

<u>Guest Instructor</u>

- ASCI 432/832 Genome Analysis - April 21 **Spring, 2017**
- ASCI/AGRO 931 Population Genetics - November 2 **Fall, 2016**
- ASCI 432/832 Genome Analysis - April 15 **Spring, 2016**
- ASCI 432/832 Genome Analysis - April 16 **Spring, 2015**

University of Wisconsin-Madison, Madison, Wisconsin, USA

<u>Teaching Assistant</u>

- ANSCI/DYSCI 363: Principles of Animal Breeding **Spring, 2011**
- ANSCI/DYSCI 361: Introduction to Animal and Veterinary Genetics **Spring, 2011**

SHORT COURSES

University of São Paulo / ESALQ, Piracicaba, São Paulo, Brazil

Co-Instructor
Quantitative Genetics and Genomics Workshop - [WWW] **May 21-25, 2018**
55 students

Co-Instructor
Quantitative Genetics and Genomics Workshop - [WWW]   **May 16-20, 2016**
35 students

RESEARCH SUPPORT

External Funding

- Food Safety Challenge Area: Effective Mitigation Strategies for Antimicrobial Resistance -
  $773,607.00   USDA-NIFA
  PI: Samodha Fernando   **February 15, 2018 - February 14, 2022**
  Proposal: Investigating mobile genetic elements and resistance gene reservoirs towards under-
  standing the emergence and ecology of antimicrobial resistance in beef cattle production systems
  Role: Co-Principal Investigator

- Animal Health and Production and Animal Products: Improved Nutritional Performance, Growth,
  and Lactation of Animals - $500,000.00   USDA-NIFA
  PI: Samodha Fernando   **March 1, 2018 - February 28, 2022**
  Proposal: Moving beyond rumen microbiota composition to identify interactions between host
  genotype and rumen function towards identifying genetic markers and microbial functions that
  influence feed efficiency
  Role: Co-Principal Investigator

- NEDED - $21,472.00   NuGUT LLC
  PI: Gota Morota   **September 1, 2017 - August 31, 2018**
  Proposal: Development of Statistical Software for Detecting Fetal Aneuploidy in Livestock
  Species
  Role: Principal Investigator

- EPSCoR Research Infrastructure Improvement Program - $5,783,738.00   NSF
  PI: Harkamal Walia   **August 1, 2017 - July 31, 2021**
  Proposal: Comparative genomics and phenomics approach to discover genes underlying heat
  stress resilience in cereals (RII Track-2 FEC)
  Award number: 1736192
  Role: Co-Principal Investigator

Internal Funding

- IANR Travel Funds - $800.00   UNL
  PI: Gota Morota   **February 11, 2018 - February 16, 2018**
  Proposal: Participating in the World Congress on Genetics Applied to Livestock Production
  Role: Principal Investigator

- SPRINT 4th Edition - $18,300.00   UNL/FAPESP
  PI: Gota Morota   **June 1, 2017 - May 31, 2019**
  Proposal: Integration of genomic resources in beef cattle breeding program - a collaborative effort
  between UNL and ESALQ
  Role: Principal Investigator

- ARD Plant Phenotyping Seed Grant - $100,000.00   UNL
  PI: Gota Morota   **January 1, 2017 - June 30, 2018**
  Proposal: Development of imaging-informed dynamic subgenome specific co-expression gene networks in wheat
  Role: Principal Investigator

- Research Council Interdisciplinary Grant - $20,000.00   UNL
  PI: Gota Morota   **January 1, 2017 - December 31, 2017**
  Proposal: Advancing plant phenomics through leveraging an image-based longitudinal quantitative genetics model and a gene annotation tool
  Role: Principal Investigator

- IANR International Impact Award - $3,000.00   UNL
  PI: Gota Morota   **May 16, 2016 - May 20, 2016**
  Proposal: Delivering a graduate training program at University of São Paulo / ESALQ
  Role: Principal Investigator

- ORED Layman Seed Award - $9,910.00   UNL
  PI: Gota Morota   **June 1, 2015 - May 31, 2016**
  Proposal: Cracking the blackbox of whole-genome prediction: Genome partitioning of predictive ability
  Role: Principal Investigator

ADVISEES AND TRAINEES

<u>Visiting Scholars</u>

- Jun He, Hunan Agricultural University (jointly with Matt Spangler & Steve Kachman), 8/2015 - 2/2016

<u>Visiting Postdoctoral Scholars</u>

- Juliana Petrini [WWW], University of Sao Paulo, 4/16/2018 - 5/4/2018

<u>Visiting Students</u>

- Gerardo Mamani [WWW], University of Sao Paulo, 4/12/2017 - 12/31/2017

<u>Postdoctoral Scholars</u>

- Waseem Hussain 3/2018 [WWW] -

- Malachy T. Campbell (jointly with Harkamal Walia), 9/2017 [WWW] -

<u>Ph.D. Students</u>

- Haipeng Yu [WWW], 8/2016 -

- Reza Nabavi [WWW], 8/2017 -

Service Activities

Ad hoc Review of Proposals

- BBSRC grant proposal reviewer (2014)

Animal Breeding & Genetics Group

- Animal Breeding & Genetics Seminars organizer
  Department of Animal Science, University of Nebraska-Lincoln **Spring 2016**

- Animal Breeding & Genetics Seminars organizer
  Department of Animal Science, University of Nebraska-Lincoln **Fall 2015**

OSS CONTRIBUTIONS

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

Shiny Applications
- ShinyAIM - https://chikudaisei.shinyapps.io/shinyaim/

- ShinyGPAS - https://chikudaisei.shinyapps.io/shinygpas/

Bioconductor packages
- meshr

- MeSH.db

- MeSH.AOR.db

- MeSH.PCR.db

- MeSH.XXX.eg.db (84 packages)

  - MeSH.Aca.eg.db
  - MeSH.Aga.PEST.eg.db
  - MeSH.Ame.eg.db
  - MeSH.Aml.eg.db
  - MeSH.Ana.eg.db
  - MeSH.Ani.FGSC.eg.db
  - MeSH.Ath.eg.db
  - MeSH.Bfl.eg.db
  - MeSH.Bsu.168.eg.db
  - MeSH.Bsu.TUB10.eg.db
  - MeSH.Bta.eg.db
  - MeSH.Cal.SC5314.eg.db
  - MeSH.Cbr.eg.db
  - MeSH.Cel.eg.db
  - MeSH.Cfa.eg.db
  - MeSH.Cin.eg.db
  - MeSH.Cja.eg.db
  - MeSH.Cpo.eg.db
  - MeSH.Cre.eg.db
  - MeSH.Dan.eg.db
  - MeSH.Dda.3937.eg.db
  - MeSH.Ddi.AX4.eg.db
  - MeSH.Der.eg.db
  - MeSH.Dgr.eg.db
  - MeSH.Dme.eg.db

- MeSH.Dmo.eg.db
- MeSH.Dpe.eg.db
- MeSH.Dre.eg.db
- MeSH.Dse.eg.db
- MeSH.Dsi.eg.db
- MeSH.Dvi.eg.db
- MeSH.Dya.eg.db
- MeSH.Eco.55989.eg.db
- MeSH.Eco.CFT073.eg.db
- MeSH.Eco.ED1a.eg.db
- MeSH.Eco.HS.eg.db
- MeSH.Eco.IAI1.eg.db
- MeSH.Eco.IAI39.eg.db
- MeSH.Eco.K12.DH10B.eg.db
- MeSH.Eco.K12.MG1655.eg.db
- MeSH.Eco.O127.H6.E2348.69.eg.db
- MeSH.Eco.O157.H7.EDL933.eg.db
- MeSH.Eco.O157.H7.Sakai.eg.db
- MeSH.Eco.S88.eg.db
- MeSH.Eco.UMN026.eg.db
- MeSH.Eqc.eg.db
- MeSH.Gga.eg.db
- MeSH.Gma.eg.db
- MeSH.Hsa.eg.db
- MeSH.Laf.eg.db
- MeSH.Lma.eg.db
- MeSH.Mdo.eg.db
- MeSH.Mes.eg.db
- MeSH.Mga.eg.db
- MeSH.Miy.eg.db
- MeSH.Mml.eg.db
- MeSH.Mmu.eg.db
- MeSH.Mtr.eg.db
- MeSH.Nle.eg.db
- MeSH.Oan.eg.db
- MeSH.Ocu.eg.db
- MeSH.Oni.eg.db
- MeSH.Osa.eg.db
- MeSH.Pab.eg.db
- MeSH.Pae.PAO1.eg.db
- MeSH.Pfa.3D7.eg.db
- MeSH.Pto.eg.db
- MeSH.Ptr.eg.db
- MeSH.Rno.eg.db
- MeSH.Sau.USA300TCH1516.eg.db
- MeSH.Sce.S288c.eg.db
- MeSH.Sco.A32.eg.db
- MeSH.Sil.eg.db
- MeSH.Spo.972h.eg.db
- MeSH.Spu.eg.db
- MeSH.Ssc.eg.db
- MeSH.Syn.eg.db
- MeSH.Tbr.9274.eg.db
- MeSH.Tgo.ME49.eg.db
- MeSH.Tgu.eg.db
- MeSH.Vvi.eg.db
- MeSH.Xla.eg.db
- MeSH.Xtr.eg.db
- MeSH.Zma.eg.db

Github
- https://github.com/morota

ADDITIONAL
TRAINING

2014-2015
- Participant of the Research Development Fellows Program (RDFP)

2014
- Participant of Fall 2014 Adopting Research Based Instructional Strategies for Enhancing (ARISE) Professional Development Programs - Just in Time Teaching (JiTT)

2018

- UNL Plant Phenomics Symposium. Cather Dining Complex, University of Nebraska-Lincoln. April 2.

2017

- EPSCoR 2017 Track 2 Kickoff Meeting. National Science Foundation, Alexandria, VA. October 3.

- The 15th International Symposium on Rice Functional Genomics. Gyeonggi Small and Medium Business Support Center, Suwon, Gyeonggi, South Korea. September 25-28.

2016

- NCERA-225 Meeting. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Stoney Creek Hotel, St. Joseph, MO. October 27-28.

- The 5th International Conference on Quantitative Genetics. Monona Terrace Community and Convention Center, Madison, WI. June 12-17.

- Next Generation Plant and Animal Breeding Programs. University of Nebraska-Lincoln. March 21-25. Taught by John Hickey, Gregor Gorjanc, and Chris Gaynor.

2015

- The 29th International Mammalian Genome Conference. Yokohama Port Opening Memorial Hall, Yokohama, Japan. November 8-11.

- DNA Technology: Where we've been, where we are, and where we're headed. The US Meat Animal Research Center, Clay Center, NE. October 19.

- GO-FAANG Workshop. National Academy of Sciences Building, Washington, DC. October 7-8.

2014

- Sheep Genomics Workshop. University of Nebraska-Lincoln. November 13-14.

- NCERA-225 Meeting. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Bozeman, MT. October 23-24.

- 19th Summer Institute in Statistical Genetics: "Module 23: Advanced Quantitative Genetics ". University of Washington. July 23-25. Taught by Mike Goddard and Peter Visscher.

- 19th Summer Institute in Statistical Genetics: "Module 19: Statistical & Quantitative Genetics of Disease". University of Washington. July 21-23. Taught by John Witte and Naomi Wray.

- UC Davis Bioinformatics Training Program: "Using Galaxy for Analysis of High Throughput Sequence Data". University of California, Davis. June 16-20. Taught by the Bioinformatics Core.

- 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.

2008
- The 109th Japanese Society of Animal Science Meeting. Tokiwa University, Mito, Ibaraki, Japan. March 27-29.

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

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

- Courses taken for credits at the University of Wisconsin-Madison
  - Spring 2012
    - Animal Sciences 875-004: Topics in Analysis of Quantitative Genomic Data (Daniel Gianola)
    - Dairy Science 875-005: Parallel Programming & High Performance Computing (Xiao-Lin Nick Wu)
  - Fall 2011
    - Dairy Science 875-005: Molecular Aspects of Animal Breeding (Hasan Khatib)
    - Statistics 840: Statistical Model Building and Learning (Grace Wahba)
  - Spring 2011
    - Mathematics 609: Mathematical Methods in Systems Biology (Gheorghe Craciun)
    - Statistics 610: Introduction to Statistical Inference (Chunming Zhang)
    - Statistics 992-001: Statistical Methods for QTL Mapping (Karl Broman)
  - Fall 2010

- – Statistics 609: Mathematical Statistics I (Chunming Zhang)
- – Statistics 701: Applied Time Series Analysis, Forecasting & Control I (Yazhen Wang)
- – Statistics 775: Introduction to Bayesian Decision & Control (Kam-Wah Tsui)
- Summer 2010
  - – Population Health Sciences 904: Analytic Methods in Genetic Epidemiology (Corinne Engelman, Karl Broman, Bret Payseur, Kristin Meyers)
- Spring 2010
  - – Animal Sciences 875: Linear Models with Applications in Biology and Agriculture (Daniel Gianola)
  - – Statistics 850: Theory & Application of Regression and Analysis of Variance II (Wei-Yin Loh)
- Fall 2009
  - – Computer Science 576: Introduction to Bioinformatics (Colin Dewey)
  - – Dairy Science 875-006: Design & Analysis of Microarray Experiments in Agriculture (Guilherme J. M. Rosa)
  - – Dairy Science 875-011: Introduction to Bayesian Data Analysis with R (Xiao-Lin Nick Wu)
  - – Genetics 629: Evolutionary Genetics (John Doebley, Bret Larget, Bret Payseur)
  - – Statistics 849: Theory & Application of Regression and Analysis of Variance I (Sunduz Keles)
- Summer 2009
  - – Computer Science 367: Introduction to Data Structure
- Spring 2009
  - – Agronomy 771: Experimental Design (Mike Casler)
  - – Agronomy 772: Applications in ANOVA (Mike Casler)
  - – Mathematics 222: Calculus and Analytic Geometry
  - – Statistics 771: Statistical Computing (Michael Newton)
- Fall 2008
  - – Statistics 424: Statistical Experimental Design for Engineers (Peter Z. G. Qian)
  - – Statistics 541: Introduction to Biostatistics (Ismor Fischer)
  - – Zoology 645: Modeling in Population Genetics & Evolution (Andrew Peters)
- Summer 2008
  - – Computer Science 302: Introduction to Programming
  - – Mathematics 431: Introduction to the Theory of Probability

REFERENCES   References and additional information available upon request.