Gota Morota **April 2023**

CONTACT INFORMATION

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RESEARCH INTERESTS

I am a quantitative geneticist interested in incorporating statistics, machine learning, bioinformatics, and high-throughput phenotyping data to the study of animal and plant genetics in the omics era. The core line of my research is connecting the theory of statistical quantitative genetics to currently available molecular information. I am particularly interested in statistical methods for prediction of complex traits using whole-genome molecular markers. Because phenotypic data collection is paramount in quantitative genetics, I integrate precision agriculture and high-throughput phenotyping into my research program to collect a wide range of phenotypes.

EDUCATION

University of Wisconsin-Madison, Madison, Wisconsin USA

Ph.D., Animal Sciences, August 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 by Simulation and Real Data"
- Advisor: Prof. Dr. Mitsuyoshi Suzuki

PROFESSIONAL POSITIONS

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

Associate Professor of Quantitative Genetics (with tenure) **08/2022 - Present**
Principal Investigator
FTE: 70% Research & 30% Teaching

School of Animal Sciences (merger with the Department of Dairy Science)
Virginia Polytechnic Institute and State University, Blacksburg, Virginia USA

Assistant Professor of Quantitative Genetics **07/2022 - 08/2022**
Principal Investigator

FTE: 70% Research & 30% Teaching

Department of Animal and Poultry Sciences
Virginia Polytechnic Institute and State University, Blacksburg, Virginia USA
Assistant Professor of Quantitative Genetics **08/2018 - 06/2022**
Principal Investigator
FTE: 70% Research & 30% Teaching

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

Affiliated Positions

Virginia Polytechnic Institute and State University, Blacksburg, Virginia USA

- Center for Advanced Innovation in Agriculture Affiliated Executive Committee Member **4/2023 - Present**
- Translational Plant Sciences Center Faculty Member **03/2021 - Present**
- Center for Advanced Innovation in Agriculture Affiliated Faculty Member **12/2020 - Present**
- The Fralin Life Science Institute Affiliated Faculty Member **3/2020 - Present**
- Genetics, Bioinformatics, and Computational Biology Program Faculty Member **11/2019 - Present**
- Translational Plant Sciences Program Faculty Member **3/2019 - 3/2021**

Visiting & Temporary Positions

Department of Animal Science
University of Nebraska-Lincoln, Lincoln, Nebraska USA
Adjunct Professor **09/2018 - 12/2019**

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 International Visiting Research Fellow **09/2018 - 12/2018**
Host: Dr. Hiroyoshi Iwata

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**

Professional society memberships

- American Association for the Advancement of Science. 2023 - Present
- American Dairy Science Association. 2020 - Present
- Crop Science Society of America. 2019 - Present
- American Statistical Association. 2018 - Present
- Japanese Society of Breeding. 2018 - Present
- North American Plant Phenotyping Network. 2018 - Present
- Genetics Society of America. 2016 - Present
- Japanese Society of Animal Science. 2016 - Present
- American Society of Animal Science. 2014 - Present
- International Biometric Society (ENAR). 2012 - Present

Awards and Recognition

2022

- Industrial and Systems Engineering (ISE) Senior Symposium 2022 Advisory Board Award, Grado Department of Industrial and Systems Engineering, Virginia Tech

Editorial Activities

Section Editor

- **Journal of Animal Science** **October 2021 - Present**
  - Number of manuscripts handled: 2022 (36), 2021 (5)

Associate Editor

- **Brazilian Journal of Biometrics** **January 2023 - Present**
  - Number of manuscripts handled:
- **BMC Genomics** **January 2021 - Present**
  - Number of manuscripts handled: 2022 (0), 2021 (1)
- **Frontiers in Animal Science** **September 2020 - Present**
  Precision Livestock Farming specialty section

- Number of manuscripts handled: 2022 (0), 2021 (1), 2020 (0)

- **BMC Genetics** **September 2019 - December 2020**
  - Number of manuscripts handled: 2020 (3), 2019 (1)

Guest Associate Editor

- **Frontiers in Genetics** **July 2019 - December 2020**
  Livestock Genomics specialty section
  Research Topic: High-throughput phenotyping in the genomic improvement of livestock
  - Number of manuscripts handled: 2019 (1)

Overall Summary

- Total number of manuscripts handled as a section/associate editor per year: 2022 (36), 2021 (7), 2020 (3), 2019 (2)

Editorial Board

- **Journal of Animal Science** **July 2017 - July 2020**

Ad Hoc Reviewer

- Number of manuscripts reviewed per journal (revised versions are not counted): Animal (2), Animal Genetics (5), Animal Production Science (3), Animal Science Journal (1), Bioinformatics (4), BMC Bioinformatics (3), BMC Genetics (6), BMC Genomics (3), BMC Genomic Data (1), BMC Plant Biology (1), Computers and Electronics in Agriculture (2), Crop Science (2), DNA Research (1), Euphytica (1), Functional & Integrative Genomics (1), Frontiers in Animal Science (2), Frontiers in Genetics (8), Frontiers in Plant Science (2), G3: Genes, Genomes, Genetics (4), Genetics (3), Genetics Selection Evolution (9), Heredity (3), Journal of Agricultural, Biological, and Environmental Statistics (1), Journal of Animal Breeding and Genetics (8), Journal of Animal Science (27), Journal of Animal Science and Biotechnology (3), Journal of Dairy Science (9), Journal of the Royal Statistical Society (1), Livestock Science (7), Meat Science (1), Nature Communications (1), New Phytologist (1), PeerJ (1), Plant Breeding (1), Plant Communications (1), PLOS ONE (6), Poultry Science (3), Rice Science (1), Scientia Agricola (3), Scientific Reports (2), Statistics in Medicine (1), Theoretical and Applied Genetics (10), The Crop Journal (1), Theoretical Population Biology (1), The Plant Genome (1), Translational Animal Science (1)
- Number of manuscripts reviewed per year (revised versions are not counted): 2022 (18), 2021 (28), 2020 (19), 2019 (27), 2018 (19), 2017 (20), 2016 (10), 2015 (10), 2014 (6), 2013 (1), 2012 (1)

Preprints

2. Bi Y, Campos LM, Wang J, Yu H, Hanigan MD, and **Morota G**. Depth video data-enabled predictions of longitudinal dairy cow body weight using thresholding and Mask R-CNN algorithms. arXiv. doi: 10.48550/arXiv.2307.01383

1. Silva CM, Mezzomo, HC, Ribeiro JPO, Signorini VS, Lima GW, Torres Vieira EF, Portes MF, **Morota G**, Corredo LP, and Nardino M. Insights on multi-spectral vegetation indices derived

from UAV-based high-throughput phenotyping for indirect selection in tropical wheat breeding. Research Square. doi: 10.21203/rs.3.rs-3111326/v1 w

Publications

	First/Senior/Corresponding author	Co-author	Total
Book chapters	1	0	1
Editorials	0	1	1
Peer-reviewed research journal articles	35	33	68
Peer-reviewed review journal articles	3	2	5
Peer-reviewed conference proceedings	2	6	8
Outreach publications	0	1	1
Total	41	43	84

Table 1: Summary of my publications

Book chapters

2022

1. **Morota G**, Jarquin D, Campbell MT, and Iwata H. 2022. Statistical methods for the quantitative genetic analysis of high-throughput phenotyping data. *In High Throughput Plant Phenotyping: Methods and Protocols*. Molecular Biology Series, Springer, New York. **2539**:269-296. doi: 10.1007/978-1-0716-2537-8_21

Editorials

2021

1. Silva FF, **Morota G**, and Rosa GJM. 2021. Editorial: High-throughput phenotyping in the genomic improvement of livestock. *Frontiers in Genetics*. **12**:707343. doi: 10.3389/fgene.2021.707343

Peer-reviewed research journal articles

2023

68. Suela MM, Azevedo CF, Nascimento ACC, Momen M, Caixeta ET, **Morota G**, and Nascimento M. 2023. Genome-wide association study for morphological, physiological, and productive traits in Coffea arabica using structural equation models. *Tree Genetics and Genomes*. **19**:23. doi: 10.1007/s11295-023-01597-8

67. Baba T, **Morota G**, Kawakami J, Goto Y, Oka T, Masuda Y, Brito LF, Cockrum RR, and Kawahara T. 2023. Longitudinal genome-wide association analysis using a single-step random regression model for height in Japanese Holstein cattle. *JDS Communications*. Early view. doi: 10.3168/jdsc2022-0347

66. Yassue RM, Galli G, Chen CJ, Fritsche-Neto R, and **Morota G**. Genome-wide association analysis of hyperspectral reflectance data to dissect the genetic architecture of growth-related

traits in maize under plant growth-promoting bacteria inoculation. *Plant Direct*. **7**:e492. doi: 10.1002/pld3.492

65. Bi Y, Yassue RM, Paul P, Dhatt BK, Sandhu J, Do PT, Walia H, Obata T, and **Morota G**. 2023. Evaluating metabolic and genomic data for predicting grain traits under high night temperature stress in rice. *G3: Genes, Genomes, Genetics*. **13**:5. doi: 10.1093/g3journal/jkad052

64. Sabag I, Bi Y, Peleg Z, and **Morota G**. 2023. Multi-environment analysis enhances genomic prediction accuracy of agronomic traits in sesame. *Frontiers in Genetics*. **14**:1108416. doi: 10.3389/fgene.2023.1108416

63. Wang Z, Yu D, **Morota G**, Dhakal K, Singer W, Lord N, Huang H, Chen P, Mozzoni L, Li S, and Zhang B. 2023. Genome-wide association analysis of sucrose and alanine contents in edamame bean. *Frontiers in Plant Science*. **13**:1086007. doi: 10.3389/fpls.2022.1086007

62. Kadlec R, Indest S, Castro K, Waqar S, Campos LM, Amorim ST, Bi Y, Hanigan MD, and **Morota G**. 2023. Automated acquisition of top-view dairy cow depth image data using an RGB-D sensor camera. *Translational Animal Science*. **6**:1-6. doi: 10.1093/tas/txac163

61. Yassue RM, Galli G, Fritsche-Neto R, and **Morota G**. 2023. Classification of plant growth-promoting bacteria inoculation status and prediction of growth-related traits in tropical maize using hyperspectral image and genomic data. *Crop Science*. **63**:88-100. doi: 10.1002/csc2.20836

2022

60. de Novais FJ, Yu H, Cesar ASM, Momen M, Poleti MD, Petry B, Mourão GB, de Almeida Regitano LC, **Morota G**, and Coutinho LL. 2022. Multi-omic data integration for the study of production, carcass, and meat quality traits in Nellore cattle. *Frontiers in Genetics*. **13**:948240. doi: 10.3389/fgene.2022.948240

59. Chandaran AK, Sandhu J, Irvin L, Paul P, Hussain W, Gao T, Staswick P, Yu H, **Morota G**, and Walia H. 2022. Rice Chalky Grain 5 regulates natural variation for grain quality under heat stress. *Frontiers in Plant Science*. **13**:1026472. doi: 10.3389/fpls.2022.1026472

58. Alghamdi S, Zhao Z, Ha DS, **Morota G**, and Ha SS. 2022. Improved pig behavior analysis by optimizing window sizes for individual behaviors on acceleration and angular velocity data. *Journal of Animal Science*. **100**:1–9. doi: 10.1093/jas/skac293

57. Murphy MD, Fernandes SB, **Morota G**, and Lipka AE. 2022. Assessment of two statistical approaches for variance genome-wide association studies in plants. *Heredity*. **129**:93–102. doi: 10.1038/s41437-022-00541-1

56. Notter DR, Heidaritabar M, Burke JM, Shirali M, Murdoch BM, Morgan JLM, **Morota G**, Sonstegard TS, Becker GM, Spangler GL, MacNeil MD, and Miller JE. 2022. Single nucleotide polymorphism effects on lamb fecal egg count estimated breeding values in progeny-tested Katahdin sires. *Frontiers in Genetics*. **13**:866176. doi: 10.3389/fgene.2022.866176

55. Qu J, **Morota G**, and Cheng H. 2022. A Bayesian random regression method using mixture priors for genome-enabled analysis of time-series high-throughput phenotyping data. *The Plant Genome*. **15**:e20228. 10.1002/tpg2.20228

54. Chen CJ, **Morota G**, Lee K, Zhang Z, and Cheng H. 2022. VTag: a semi-supervised pipeline for tracking pig activity with a single top-view camera. *Journal of Animal Science*. **100**1–10. doi: 10.1093/jas/skac147

53. Yassue RM, Galli G, Borsato Junior R, Cheng H, **Morota G**, and Fritsche-Neto R. 2022. A low-cost greenhouse-based high-throughput phenotyping platform for genetic studies: A case study in maize under inoculation with plant growth-promoting bacteria. *The Plant Phenome Journal*. **5**:e20043. doi: 10.1002/ppj2.20043

52. Amorim ST, Tsuyuzaki K, Nikaido I, and **Morota G**. 2022. Improved MeSH analysis software tools for farm animals. *Animal Genetics*. **53**:171-172. doi: 10.1111/age.13159

2021

51. Sabag I, **Morota G**, and Peleg Z. 2021. Genome-wide association analysis uncovers the genetic architecture of tradeoff between flowering date and yield components in sesame. *BMC Plant Biology*. **21**:549. doi: 10.1186/s12870-021-03328-4

50. Mota LFM, Pegolo S, Baba T, **Morota G**, Peñagaricano F, Bittante G, and Cecchinato A. 2021. Comparison of single-breed and multi-breed training population for infrared predictions of novel phenotypes in Holstein cows. *Animals*. **11**:1993. doi: 10.3390/ani11071993

49. Mota LFM, Pegolo S, Baba T, Peñagaricano F, **Morota G**, Bittante G, and Cecchinato A. 2021. Evaluating the performance of machine learning and variable selection methods for predicting difficult-to-measure traits in Holstein dairy cattle using milk infrared spectral data. *Journal of Dairy Science*. **104**:8107-8121. doi: 10.3168/jds.2020-19861

48. Baba T, Pegolo S, Mota LFM, Peñagaricano F, Bittante G, Cecchinato A, and **Morota G**. 2021. Integrating genomic and infrared spectral data improves the prediction of milk proteins in dairy cattle. *Genetics Selection Evolution*. **53**:29. doi: 10.1186/s12711-021-00620-7

47. Gonçalves MTV, **Morota G**, Almeida Costa PM, Vidigal PMP, Barbosa MHP, and Peternelli LA. 2021. Near-infrared spectroscopy outperforms genomics for predicting sugarcane feedstock quality traits. *PLOS ONE*. **16**(3): e0236853. doi: 10.1371/journal.pone.0236853

46. Yu H and **Morota G**. 2021. GCA: An R package for genetic connectedness analysis using pedigree and genomic data. *BMC Genomics*. **22**:119. doi: 10.1186/s12864-021-07414-7

45. Yu H, Lee K, and **Morota G**. 2021. Forecasting dynamic body weight of non-restrained pigs from images using an RGB-D sensor camera. *Translational Animal Science*. **5**:1-9. doi: 10.1093/tas/txab006

44. Pegolo S, Yu H, **Morota G**, Bisutti V, Rosa GJM, Bittante G, and Cecchinato A. 2021. Structural equation modelling for unravelling the multivariate genomic architecture of milk proteins in dairy cattle. *Journal of Dairy Science*. **104**:5705-5718. doi: 10.3168/jds.2020-18321

43. Zhu F, Paul P, Hussain W, Wallman K, Dhatt BK, Sandhu J, Irvin L, **Morota G**, Yu H, and Walia H. 2021. SeedExtractor: an open-source GUI for seed image analysis. *Frontiers in Plant Science*. **11**:581546. doi: 10.3389/fpls.2020.581546

42. Momen M, Bhatta M, Hussain W, Yu H, and **Morota G**. 2021. Modeling multiple phenotypes in wheat using data-driven genomic exploratory factor analysis and Bayesian network learning. *Plant Direct*. **5**:e00304. doi: 10.1002/pld3.304

41. Dhatt B, Paul P, Sandhu J, Hussain W, Irvin L, Zhu F, Adviento-Borbe M, Lorence A, Staswick P, Yu H, **Morota G**, and Walia H. 2021. Allelic variation in rice *Fertilization independent endosperm 1* contributes to grain width under high night temperature stress. *New Phytologist*. **229**:335-350. doi: 10.1111/nph.16897

2020

40. Wang Z, Chapman D, **Morota G**, and Cheng H. 2020. A Multiple-trait Bayesian variable selection regression method for integrating phenotypic causal networks in genome-wide association studies. *G3: Genes, Genomes, Genetics*. **10**:4439-4448. doi: 10.1534/g3.120.401618

39. Amorim ST, Yu H, Momen M, de Albuquerque, LG, Pereira, ASC, Baldi F, and **Morota G**. 2020. An assessment of genomic connectedness measures in Nellore cattle. *Journal of Animal Science*. **98**:1-12. doi: 10.1093/jas/skaa289

38. Campbell MT, Grondin A, Walia H, and **Morota G**. 2020. Leveraging genome-enabled growth models to study shoot growth responses to water deficit in rice (*Oryza sativa*). *Journal of Experimental Botany*. **71**:5669-5679. doi: 10.1093/jxb/eraa280

37. Yu H, **Morota G**, Celestino Jr. EF, Dahlen CR, Wagner SA, Riley DG, and Hulsman Hanna LL. 2020. Deciphering cattle temperament measures derived from a four-platform standing scale using genetic factor analytic modeling. *Frontiers in Genetics*. **11**:599. doi: 10.3389/fgene.2020.00599

36. Pegolo S, Momen M, **Morota G**, Rosa GJM, Gianola G, Bittante G, and Cecchinato A. 2020. Structural equation modeling for investigating multi-trait genetic architecture of udder health in dairy cattle. *Scientific Reports*. **10**:7751. doi: 10.1038/s41598-020-64575-3.

35. Roudbar MA, Mohammadabadi MR, Mehrgardi AA, Abdollahi-Arpanahi R, Momen M, **Morota G**, Lopes FB, Gianola D, and Rosa GJM. 2020. Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. *Heredity*. **124**:658-674. doi: 10.1038/s41437-020-0301-4

34. Hussain W, Campbell MT, Jarquin D, Walia H, and **Morota G**. 2020. Variance heterogeneity genome-wide mapping for cadmium in bread wheat reveals novel genomic loci and epistatic interactions. *The Plant Genome*. **13**:e20011. doi: 10.1002/tpg2.20011

33. Baba T, Momen M, Campbell, MT, Walia H, and **Morota G**. 2020. Multi-trait random regression models increase genomic prediction accuracy for a temporal physiological trait derived from high-throughput phenotyping. *PLOS ONE*. **15**(2):e0228118. doi: 10.1371/journal.pone.0228118

32. Paul P, Dhatt B, Sandhu J, Hussain W, Irvin L, **Morota G**, Staswick P, and Walia H. 2020. Divergent phenotypic response of rice accessions to transient heat stress during early seed development. *Plant Direct*. **4**:1-13. doi: 10.1002/pld3.196

2019

31. Momen M, Campbell MT, Walia H, and **Morota G**. 2019. Utilizing trait networks and structural equation models as tools to interpret multi-trait genome-wide association studies. *Plant Methods*. **15**:107. doi: 10.1186/s13007-019-0493-x

30. Momen M, Campbell MT, Walia H, and **Morota G**. 2019. Predicting longitudinal traits derived from high-throughput phenomics in contrasting environments using genomic Legendre polynomials and B-splines. *G3: Genes, Genomes, Genetics*. **9**:3369-3380. doi: 10.1534/g3.119.400346

29. Yu H, Campbell MT, Zhang Q, Walia H, and **Morota G**. 2019. Genomic Bayesian confirmatory factor analysis and Bayesian network to characterize a wide spectrum of rice phenotypes. *G3: Genes, Genomes, Genetics*. **9**:1975-1986. doi: 10.1534/g3.119.400154

28. Campbell MT, Momen M, Walia H, and **Morota G**. 2019. Leveraging breeding values obtained from random regression models for genetic inference of longitudinal traits. *The Plant Genome*. **12**:180075. doi: 10.3835/plantgenome2018.10.0075

2018

27. Hussain W, Campbell MT, Walia H, and **Morota G**. 2018. ShinyAIM: Shiny-based application of interactive Manhattan plots for longitudinal genome-wide association studies. *Plant Direct*. **2**:1-4. doi: 10.1002/pld3.91

26. Momen M, Mehrgardi AA, Roudbar MA, Kranis A, Pinto RM, Valente BD, **Morota G**, Rosa GJM, and Gianola D. 2018. Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation models. *Frontiers in Genetics*. **9**:455. doi: 10.3389/fgene.2018.00455

25. Momen M and **Morota G**. 2018. Quantifying genomic connectedness and prediction accuracy from additive and non-additive gene actions. *Genetics Selection Evolution*. **50**:45. doi: 10.1186/s12711-018-0415-9

24. 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*. **96**:4490-4500. doi: 10.1093/jas/sky316

23. 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*. **8**:12309. doi: 10.1038/s41598-018-30089-2

22. 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*. **2**:1-11. doi: 10.1002/pld3.80

21. 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

20. 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

19. 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

18. **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

17. 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

16. 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

15. 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

14. **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

13. 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

12. 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

11. 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

10. **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

9. 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

8. 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

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

Peer-reviewed review journal articles

2023

5. Habimana V, Nguluma AS, Nziku ZC, Ekine-Dzivenu CC, **Morota G**, Mrode R, and Chenyambuga SW. Heat stress effects on milk yield traits and metabolites and mitigation strategies for dairy cattle breeds reared in tropical and sub-tropical countries. *Frontiers in Veterinary Science*. **10**:1121499. doi: 10.3389/fvets.2023.1121499

4. Habimana V, Ekine-Dzivenu C, Nguluma AS, Nziku ZC, **Morota G**, Chenyambuga SW, and Mrode R. 2023. Genes and models for estimating genetic parameters for heat tolerance in dairy cattle. *Frontiers in Genetics*. **14**:1127175. doi: 10.3389/fgene.2023.1127175

2021

3. **Morota G**, Cheng H, Cook D, and Tanaka E. 2021. ASAS-NANP SYMPOSIUM: Prospects for interactive and dynamic graphics in the era of data-rich animal science. *Journal of Animal Science*. **99**:1-17. doi: 10.1093/jas/skaa402

2016

2. **Morota G**, Ventura RV, Silva FF, Koyama M, and Fernando SC. 2018. BIG DATA ANALYTICS AND PRECISION ANIMAL AGRICULTURE SYMPOSIUM: 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

2014

1. **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

Peer-reviewed conference proceedings

2022

8. Chen CJ, **Morota G**, and Cheng H. 2022. VTag: automatic pipeline to annotate video data for pig phenomics studies. In: *Proceedings, 12th World Congress of Genetics Applied to Livestock Production*. **12**:545-548. Rotterdam, The Netherlands. July 3-8. doi: 10.3920/978-90-8686-940-4_124

2019

7. Atagi Y, **Morota G**, Onogi A, Osawa T, Yasumori T, Adachi K, Yamaguchi S, Aihara M, Goto H, Togashi K, and Iwata H. 2019. Consideration of heat stress in multiple lactation test–day models for dairy production traits. *Interbull Bulletin*. **55**:81-87. HTML

2018

6. Yu H, Spangler ML, Lewis RM, and **Morota G**. 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. Auckland, New Zealand. February 11-16. PDF

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

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

2014

3. Gianola D, **Morota G**, 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*. Vancouver, BC, Canada. August 17-22. PDF

2. Valente BD, **Morota G**, 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*. Vancouver, BC, Canada. August 17-22. PDF

2011

1. Bueno Filho JS*, **Morota G***, 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.

Outreach publications

1. **Morota G** and Ha SS. 2023. Pig monitoring is feasible. Using wireless sensor nodes and machine learning. *National Hog Farmer*. url: https://informamarkets.turtl.co/story/national-hog-farmer-marchapril-2023/page/3

bioRxived manuscripts

2. Vidigal PMP, Momen M, Costa PMA, Barbosa MHP, **Morota G**, and Peternelli LA. Regional genomic heritability mapping for agronomic traits in sugarcane. *bioRxiv*. doi: 10.1101/2020.04.16.045310

1. Campbell MT, Yu H, Momen M, and **Morota G**. Examining the relationships between phenotypic plasticity and local environments with genomic structural equation models. *bioRxiv*. doi: 10.1101/2019.12.11.873257

Invited Presentations

19 domestic and 19 international

2023

38. Quantitative genetic analysis of metabolites in rice. Emerging statistical approaches to improve the development of cultivars. The 6th International Conference on Econometrics and Statistics (EcoSta 2023). Waseda University, Tokyo, Japan. August 1-3.

37. Data science in precision livestock farming. Symposium on spaced-based effective production for beef. Online. February 22.

2022

36. Data science and high-throughput phenotyping in animal science. Symposium on the role of technology and breeding for the future of animal agriculture. The 23rd Japanese Society of Animal Breeding and Genetics Meeting. Online. November 27.

35. Machine learning-enabled pig activity monitoring. Session 3: Enhance rigor and reproducibility in animal research by managing extrinsic factors (nonhuman primates/swine). NIH/ORIP workshop. Online. September 30.

34. How can artificial intelligence accelerate phenotyping efforts in animal breeding? Animal Breeding and Genetics Symposium I: New Insights on Artificial Intelligence Applied to Precision Animal Breeding. ASAS-CSAS Annual Meeting. Oklahoma City Convention Center, Oklahoma City, OK. June 26-30.

33. Genome-enabled analysis of time-series high-throughput phenotyping data. Emerging statistical approaches to improve the development of cultivars session. The 5th International Conference on Econometrics and Statistics (EcoSta 2022). Online. June 4-6.

2021

32. Statistical methods for quantitative genetic analysis of image-derived traits from high-throughput phenotyping. Center for Mathematics and Applications, NOVA School of Science and Technology. NOVA University Lisbon, Caparica, Portugal. October 27.

31. High-throughput phenotyping driven quantitative genetics. Centre for Genetic Improvement of Livestock Seminar. Department of Animal Biosciences. University of Guelph. Online. September 17.

2020

30. High-throughput phenotyping and precision agriculture in animals and plants. Current Topics in Genomics Seminar. Department of Animal Sciences. Purdue University. Online. October 20.

29. Statistical methods for quantitative genetic analysis of longitudinal traits derived from high-throughput plant phenotyping. Crop Science Seminar. Department of Crop Sciences. University of Illinois Urbana-Champaign. Online. September 17.

28. Statistical graphics and interactive visualization in animal science. Mathematical Modeling in Animal Nutrition: Training the Future Generation in Data and Predictive Analytics for a Sustainable Development. NANP Symposium. ASAS Annual Meeting Pre-Conference. Online. July 19.

27. Interactive visualization for animal and plant breeding. Invited Session: Interactive visualization for effective decision-making in agricultural sciences. The 30th International Biometric Conference (2020IBC). Seoul, South Korea. July 5-10. Canceled due to COVID-19.

26. Variance heterogeneity genome-wide mapping for cadmium in bread wheat reveals novel genomic loci and epistatic interactions. Plant Molecular Breeding Workshop. The Plant and Animal Genome XXVIII Conference. Town and Country Hotel, San Diego, CA. January 11-15.

2019

25. Do structural equation models advance multi-trait genome-wide association analysis? Special Seminar. Bioscience and Biotechnology Center, Nagoya University, Nagoya, Japan. October 25.

24. Variance heterogeneity association analysis in wheat reveal novel genomic loci and epistatic interactions. Symposium on Statistical and Data Scientific Methods for Omics-data Analysis in Agricultural and Life Sciences. TKP Ochanomizu Conference Center, Tokyo, Japan. October

15.

23. Statistical methods for quantitative genetic analysis of high-throughput phenotyping data. University of Florida Genetics Institute Seminar. University of Florida, Gainesville, FL. October 10.

22. Big data statistical techniques applied to precision animal nutrition and production. The 6th EAAP International Symposium on Energy and Protein Metabolism and Nutrition. Ouro Minas Palace Hotel, Belo Horizonte, MT, Brazil. September 9-12.

21. Statistical quantitative genetic modeling for image-based high-throughput phenotyping data. The 64th RBras (The Brazilian Region of the International Biometric Society) and 18th SEAGRO (Symposium on Statistics Applied to Agricultural Experimentation) Meeting. Centro de Eventos do Pantanal, Cuiabá, MT, Brazil. July 29 - August 2.

20. Statistical methods for quantitative genetic analysis of high-throughput phenotyping data. Special seminar. Department of Statistics. Federal University of Viçosa, Viçosa, MG, Brazil. July 25.

19. Multi-omic data integration in quantitative genetics. Breeding and Genetics Symposium: FAANG. ASAS-ADSA Midwest Joint Annual Meeting. CHI Health Center Convention, Omaha, NE. March 11-13.

18. Recent advances in Medical Subject Headings (MeSH) analysis. Cattle/Sheep/Goat 2 Workshop. The Plant and Animal Genome XXVII Conference. Town and Country Hotel, San Diego, CA. January 12-16.

2018

17. The role of interactive visualization in big data analysis and its application to plant breeding. The 8th Agrigenomic Industry Workshop. Co-working space Kayabacho Co-Edo, Chuo-ku, Tokyo, Japan. December 21.

16. Quantifying genomic connectedness and whole-genome prediction accuracy using bootstrap aggregation sampling. The 11th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics 2018). University of Pisa, Pisa, Italy. December 14-16.

15. How big data, machine learning and bioinformatics are impacting genetic selection. Poultry Tech Summit. Georgia Tech Hotel & Conference Center, Atlanta, GA. November 5-7.

14. Statistical learning in animal and plant breeding using multi-omic data. IX International Symposium on Genetics and Breeding (IX SIGM) / DuPont Plant Sciences Symposium. Federal University of Viçosa, Viçosa, MG, Brazil. October 24-25.

13. Bayesian genomic factor analysis and Bayesian network to characterize high-throughput phenotyping data. T-PIRC Symposium: Innovation for global food production towards sustainable future. The 2018 Tsukuba Global Science Week. Tsukuba International Congress Center, Tsukuba, Ibaraki, Japan. September 20-22.

12. Do structural equation models advance genome-wide association analysis? Special seminar. School of Veterinary Medicine and Animal Science (FMVZ), University of São Paulo, Pirassununga, São Paulo, Brazil. 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, Blacksburg, VA. 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. Federal 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, Lincoln, NE. 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, Lincoln, NE. September 23.

4. Quantitative genetics in the functional genomics era. Animal Breeding & Genetics Seminars. Department of Animal Science, Iowa State University, Ames, IA. 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, Lincoln, NE. December 19.

2011

1. Obihiro GCOE Animal Global Health Seminars. Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan. January 7.

Contributed Presentations

2020

17. A new statistical model for integrating trait networks with multi-trait genome-wide association studies. The 137th Japanese Society of Breeding Meeting. The University of Tokyo, Bunkyo-ku, Tokyo, Japan. March 28-29. Canceled due to COVID-19.

16. The use of milk-infrared spectroscopy data to improve milk protein phenotype predictions. The 127th Japanese Society of Animal Science Meeting. Kyoto University, Kyoto, Kyoto, Japan. March 25-28. Canceled due to COVID-19.

2018

15. Longitudinal genomic prediction of image-derived phenotypes and interactive visualization tools. Special seminar. Breeding Unit, Division of Apple Research, Institute of Fruit Tree and Tea Science, Shimo-kuriyagawa, Morioka, Iwate, Japan. November 22.

14. Multivariate analyses for longitudinal phenotypes and genome-wide association studies in plant and animals. Special seminar. Crop Science Laboratory, Faculty of Agriculture, Iwate University, Ueda, Morioka, Iwate, Japan. November 21.

13. Longitudinal genomic prediction of image-derived phenotypes in rice using a random regression model. The 8th Rice Genetics Symposium (RG8), The International Rice Research Conference 2018 (IRRC 2018). Marina Bay Sands, Singapore. October 15-17.

12. Genome-enabled prediction and genome-wide association analysis for longitudinal image-based data in rice. The 134th Japanese Society of Breeding Meeting. Okayama University, Kita Ward, Okayama, Japan. September 22-23.

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

10. 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

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

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

2015

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

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

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

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

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

2012

2. 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**.

2007

1. The impact of missing information in continuous and threshold trait analyses under a linear mixed model framework. The 62nd Hokkaido Animal Science and Agriculture Society Meeting. Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan. September 5-6.

Posters

2015

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

3. **Morota G**. 2015. Estimating genomic heritability in the presence of population stratification. NGS Field 4th Meeting. Tsukuba International Congress Center, Tsukuba, Japan. July 1-3.

2013

2. **Morota G**. 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.

1. **Morota G**. 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, WA. https://secure.bioconductor.org/BioC2013/posters.php#7.

Intramural Seminars

2021

18. High-throughput animal phenotyping. Animal Science Seminar. Department of Animal and Poultry Sciences. Virginia Polytechnic Institute and State University, Blacksburg, VA. September 13.

17. High-throughput phenotyping driven quantitative genetics. Translational Plant Sciences Program Orientation Week. Virginia Polytechnic Institute and State University, Blacksburg, VA. August 18.

16. Application of Computer Vision Systems for High-throughput Phenotyping in Agriculture. Virginia Tech Genetics, Bioinformatics, and Computational Biology Program Seminar. Virginia Polytechnic Institute and State University. Online. March 24.

15. Can computer vision systems help animal phenotyping and monitoring? CAIA Lightning Talk Session. Artificial Intelligence in Agriculture and Life Sciences – VT and Beyond. Virginia Polytechnic Institute and State University. Online. February 24.

2019

14. Statistical methods for quantitative genetic analysis of high-throughput phenotyping data. Translational Plant Sciences Discussion Group. Virginia Polytechnic Institute and State University, Blacksburg, VA. September 26.

13. What is quantitative genetics? Translational Plant Sciences Program Orientation Week. Virginia Polytechnic Institute and State University, Blacksburg, VA. August 21.

12. Statistical learning for multi-omic data. Reproductive Biology Club. Virginia Polytechnic Institute and State University, Blacksburg, VA. April 19.

2017 **11**. Predictomics in Quantitative Genetics. Monthly Brown Bag Series on Plant Phenotyping. University of Nebraska-Lincoln, Lincoln, NE. March 31.

2015 **10**. Quantifying the contribution of population stratification to genomic heritability. Animal Breeding & Genetics Seminars. Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE. September 15.

2014 **9**. Prediction of complex quantitative traits using non-additive genomic relationship kernels and bootstrap aggregating. Animal Breeding & Genetics Seminars. Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE. September 18.

8. Whole-genome prediction of complex traits using kernel methods. Ph.D. Thesis Defense. Department of Animal Sciences, University of Wisconsin-Madison, Madison, WI. May 12.

7. Is internship experience beneficial for obtaining a TT job? Dairy Science Graduate Seminar. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI. February 14.

2013 **6**. Kernel-based whole-genome enabled prediction of complex traits. Special Seminar. Zoetis, Inc., Kalamazoo, MI. August 8.

2012 **5**. Diffusion kernels on SNP data embedded in a non-Euclidean metric space. Animal Breeding & Genomics Seminars. Department of Animal Sciences, University of Wisconsin-Madison, Madison, WI. April 10.

2011 **4**. Application of Bayesian and sparse network models for assessing linkage disequilibrium in Animals and Plants. Master's Thesis Defense. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI. December 5.

2010 **3**. Allele frequencies as stochastic processes: Mathematical & statistical approaches. Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI. November 30.

2. Hierarchical Bayesian logistic regression. Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI. March 23.

2008 **1**. Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI. November 25.

Teaching

Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA

Lead Instructor

- ALS 3104 Animal Breeding and Genetics [WWW] **Spring, 2023**
  115 participants
- GRAD 5515 Molecular Plant Science Laboratory Rotation **Spring, 2023**
  1 participant
- ALS 3104 Animal Breeding and Genetics [WWW] **Spring, 2022**
  91 participants
- ALS 5984 High-Throughput Phenotyping in Agriculture [WWW] **Spring, 2021**
  10 participants
- APSC 4004 Contemporary Issues in APSC - Recitation section [WWW] **Spring, 2021**
  16 participants
- APSC 5984 Complex Trait Genomics [WWW] **Spring, 2020**
  10 participants
- GRAD 5515 Molecular Plant Science Laboratory Rotation **Fall, 2019**
  1 participant

Guest Instructor

- FREC 5164 Population Genomics - April 14 **Spring, 2022**
  Genomic prediction
- ALS 3104 Animal Breeding and Genetics - September 27 and 29 **Fall, 2021**
  Hybrid Vigor
- FREC 5164 Population Genomics - April 7 **Spring, 2020**
  Genomic prediction

Helper

- Programming with R Software Carpentry Workshop - August 20 **Fall, 2020**
  10 participants

University of Nebraska-Lincoln, Lincoln, Nebraska, USA

Lead Instructor

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

14 participants

Co-Instructor

- STAT 892-004 Integrative Data Science for Plant Phenomics [WWW] **Spring, 2018**
  15 participants

- ASCI 431/831 Advanced Animal Breeding [WWW] **Spring, 2018**
  11 participants

- LIFE 891-002 Integrating Quantitative and Computational Biology into Life Sciences Research [WWW] **Spring, 2018**
  5 participants

- ASCI 431/831 Advanced Animal Breeding [WWW] **Spring, 2017**
  3 participants

Guest Instructor

- ASCI 432/832 Genome Analysis - April 21 **Spring, 2017**
  Statistical methods for whole-genome regression

- ASCI/AGRO 931 Population Genetics - November 2 **Fall, 2016**
  Response to selection

- ASCI 432/832 Genome Analysis - April 15 **Spring, 2016**
  Statistical methods for whole-genome regression

- ASCI 432/832 Genome Analysis - April 16 **Spring, 2015**
  Statistical methods for whole-genome regression

The University of Tokyo, Bunkyo-ku, Tokyo, Japan

Guest Instructor

- Special Lecture on Agricultural and Environmental Biology. Graduate School of Agricultural and Life Sciences - November 3 **Fall, 2022**
  Data Science in Agriculture

- Biometrics. Faculty of Agriculture - November 26 **Fall, 2018**
  Introduction to Genome to Phenome

University of Wisconsin-Madison, Madison, Wisconsin, USA

Teaching Assistant

- ANSCI/DYSCI 363: Principles of Animal Breeding **Spring, 2011**

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

Short Courses

2022 **Satellite Course at the 10th Workshop on Modelling Nutrient Digestion and Utilization in Farm Animals**, Alghero, Sardinia, Italy.

Lead Instructor
Statistical graphics, interactive visualization, and computer vision in animal science - [WWW] **September 21, 2022**
40 participants

2021 **IRRI Virtual Training Program: Breeding Innovation for Crop Improvement to Enhance Genetic Gains**, Online

Lead Instructor
Structural equation model GWAS - [WWW] **November 12, 2021**
40 participants

NOVA University Lisbon, Caparica, Portugal

Lead Instructor
High-throughput phenotyping driven quantitative genetics Workshop - [WWW] **October 20 and 22, 2021**
30 participants

ASAS-NANP Symposium: Mathematical Modeling in Animal Nutrition, Online

Lead Instructor
Application of Computer Vision Systems for High-throughput Phenotyping in Animal Science - [WWW] **July 14, 2021**
45 participants

2019 **Federal University of Viçosa**, Viçosa, MG, Brazil

Lead Instructor
Quantitative Genetics Workshop - [WWW] **November 18-26, 2019**
15 participants

The 64th RBras and 18th SEAGRO Meeting, Cuiabá, MT, Brazil

Lead Instructor
Quantitative Genetics Short Courses - [WWW] **July 29 - August 2, 2019**
20 participants

Virginia Polytechnic Institute and State University, Blacksburg, VA, USA

Co-Instructor
GWAS Workshop - [WWW] **June 24-26, 2019**
20 participants

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

Co-Instructor
Quantitative Genetics and Genomics Workshop - [WWW] **May 20-24, 2019**

20 participants

The Hebrew University of Jerusalem, Rehovot, Israel

Co-Instructor
Bridging the Gap: From Phenomics to Functional Genetics - [WWW] **April 1-3, 2019**
20 participants

2018 **The University of Tokyo**, Bunkyo-ku, Tokyo, Japan

Co-Instructor
Statistical Methods for Omics-assisted Breeding Workshop - [WWW] **November 12-15, 2018**
50 participants

Federal University of Viçosa, Viçosa, MG, Brazil

Co-Instructor
Linear Mixed Model Workshop - [WWW] **October 26, 2018**
20 participants

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

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

2016 **University of São Paulo / ESALQ**, Piracicaba, São Paulo, Brazil

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

Research Support

External Funding

- Pre-Tenure Faculty 4-VA Collaborative Research Grant - $14,500.00 4-VA
  PI: Azahar Ali **March 1, 2023 - June 30, 2023**
  Proposal: Machine learning assisted 3D printed biomedical sensors for on-farm diagnosis of sub-clinical mastitis in dairy cows.
  Role: Co-Principal Investigator

- Virginia Agricultural Council Research Program - $13,250.00 Virginia Agricultural Council
  PI: Rebecca Cockrum **July 1, 2022 - June 30, 2023**
  Proposal: Use of precision technology to predict pathogenic diarrhea in pre-weaned diary heifers.
  Role: Co-Principal Investigator

- BARD Research Program - $310,000.00 US-Israel Binational Agricultural Research and Development Fund (IS-5400-21)
  PIs: Gota Morota (USA) and Zvi Peleg (Israel) **October 1, 2021 - September 30, 2024**

Proposal: Leveraging genomics and temporal high-throughput phenotyping to enhance association mapping and yield prediction of sesame
Role: Principal Investigator

- Exploratory Research Program - $200,000.00 USDA-NIFA (2020-67030-31339)
  PI: Gota Morota **June 1, 2020 - May 31, 2023**
  Proposal: Wireless monitoring and assess system to improve productivity and animal welfare in swine
  Role: Principal Investigator

- 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 understanding 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

- EPSCoR Research Infrastructure Improvement Program - $5,783,738.00 NSF (1736192)
  PI: Harkamal Walia **August 1, 2017 - July 31, 2023**
  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

- Pratt Equipment Fund - $21,500 VT
  PI: Azahar Ali **November 7, 2022 - June 15, 2023**
  Proposal: Machine learning-assisted nutrition management of dairy cows by enabling 3D printed metabolite sensors
  Role: Co-Principal Investigator

- CALS Integrated Internal Competitive Grants Program - $30,000 VT
  PI: Nicholas Santantonio **March 1, 2021 - June 30, 2022**
  Proposal: High-throughput phenotyping for malt quality
  Role: Co-Principal Investigator

- CALS Integrated Internal Competitive Grants Program - $46,689 VT
  PI: Mark Hanigan **March 1, 2021 - June 30, 2022**
  Proposal: SL-Dairy: Precision Feeding and Diagnostics
  Role: Co-Principal Investigator

- John Lee Pratt Animal Nutrition Program - $104,500 VT
  PI: Gota Morota **October 1, 2020 - June 30, 2024**
  Proposal: Establishing a 3D cow body surface imaging system for data-driven body condition monitoring
  Role: Principal Investigator

- John Lee Pratt Animal Nutrition Program - $125,000 VT
  PI: Rebecca Cockrum **October 1, 2020 - June 30, 2024**
  Proposal: Integration of early dietary supplementation and automated feeding systems to mitigate post-weaning slump in dairy heifers
  Role: Co-Principal Investigator

- SmartFarm Innovation Network - $349,150.00 VT
  PI: Robin White / Vitor Mercadante **October 1, 2019 - September 30, 2021**
  Proposal: Establishment of SmartFarm innovation network nodes at Middleburg and Shenandoah Valley Agricultural Research and Extension Centers
  Role: Co-Principal Investigator

- Hebrew University of Jerusalem - Virginia Tech Joint Travel Grant - $500.00 HUJI-VT
  PI: Zvi Peleg **August 25, 2019 - August 30, 2019**
  Proposal: Deciphering the genetic architecture of wheat root system
  Role: Co-Principal Investigator

- ICAT SEAD Grant - $25,000.00 VT
  PI: Koeun Choi **July 15, 2019 - June 30, 2020**
  Proposal: Mobile learning across the life span: Processing and learning information from mobile media technology in children, young adults, and older adults
  Role: Co-Principal Investigator

- New Faculty Mentoring Project Grant - $1,500.00 VT
  PI: Gota Morota **January 11, 2020 - January 15, 2020**
  Proposal: Participating in the Plant & Animal Genome Conference XXVIII
  Role: Principal Investigator

- 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

Postdoctoral Scholars

3. Mehdi Momen [WWW] 11/27/2018 - 11/26/2019
   - Current position: Postdoctoral Scholar, University of Wisconsin-Madison

2. Waseem Hussain [WWW] 3/9/2018 - 7/26/2019
   - Current position: Research Scientist, International Rice Research Institute

1. Malachy T. Campbell [WWW] 9/1/2017 - 9/30/2019
   - Current position: Postdoctoral Scholar, Cornell University

Ph.D. Students

5. Ye Bi [WWW] 8/10/2021 -

4. Sabrina T. Amorim [WWW] 8/10/2021 -

3. Kenan Burak Aydin [WWW] 8/24/2020 -

2. Idan Sabag (jointly with Zvi Peleg) [WWW] 10/24/2019 -
    - Committee members: Zvi Peleg (co-chair), Gota Morota (co-chair), Amit Gur, and Ittai Herrmann

1. Haipeng Yu [WWW] 8/22/2016 - 5/15/2020
    - Committee members: Gota Morota (chair), Heather Bradford, Ina Hoeschele, Dave R. Notter, and M. A. Saghai-Maroof

Visiting Scholars

3. Luiz A. Peternelli, Federal University of Viçosa [WWW] 12/9/2019 - 2/28/2020

2. Toshimi Baba, Hokkaido Holstein Agricultural Association [WWW] 4/22/2019 - 5/8/2020

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

Visiting Postdoctoral Scholars

2. Sara Pegolo, University of Padova [WWW] 1/21/2019 - 2/1/2019

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

Visiting Ph.D. Students

4. Mateus Teles Vital Gonçalves, Federal University of Viçosa [WWW] 9/1/2022 - 2/28/2023

3. Rafael M. Yassue, University of Sao Paulo [WWW] 11/1/2021 - 4/30/2022

2. Francisco José de Novais, University of Sao Paulo [WWW] 9/3/2019 - 2/29/2020

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

Visiting M.S. Students

1. Sabrina T. Amorim, Sao Paulo State University [WWW] 5/28/2019 - 11/27/2019

Thesis Committees

Ph.D Thesis Committees

9. Mingsi Liao — 2022 -
   School of Animal Sciences, Virginia Tech
   Major advisor: Rebecca R. Cockrum

8. Tommy Phannareth — 2020 -
   Department of Forest Resources and Environmental Conservation, Virginia Tech
   Major advisor: Jason Holliday

7. Mackenzie Marrella — 2021 -
   School of Animal Sciences, Virginia Tech
   Major advisor: Fernando H. Biase

6. Letícia Marra Campos — 2019 -
   School of Animal Sciences, Virginia Tech
   Major advisor: Mark Hanigan

5. Amanda Kravitz — 2023
   Virginia-Maryland College of Veterinary Medicine, Virginia Tech
   Major advisor: Nammalwar Sriranganathan

4. Matthew Murphy — 2023
   Department of Crop Sciences, University of Illinois at Urbana-Champaign
   Major advisor: Alexander E. Lipka

3. Kshitiz Dhakal — 2023
   School of Plant and Environmental Sciences, Virginia Tech
   Major advisor: Song Li

2. Kosuke Hamazaki — 2023
   Department of Agricultural and Environmental Biology, The University of Tokyo
   Major advisor: Hiroyoshi Iwata

1. Amanda B. Alvarenga — 2022
   Department of Animal Sciences, Purdue University
   Major advisor: Luiz F. Brito

M.S. Thesis Committees

2. Stephen Pietruszka — 2022 -
   Translational Plant Sciences, Virginia Tech
   Major advisor: Bingyu Zhao

1. Mateus Teles Vital Gonçalves — 2019
   Genetics and Plant Breeding Program, Federal University of Viçosa
   Major advisor: Luiz A. Peternelli

Visitors hosted

- Daniel Gianola, University of Wisconsin-Madison — September 2019
- Zvi Peleg, Hebrew University of Jerusalem — August 2019
- Yutaka Masuda, University of Georgia — April 2019
- Luiz A. Peternelli, Federal University of Viçosa — July 2018
- Hiroyoshi Iwata, University of Tokyo — March 2018
- Luiz L. Coutinho, University of Sao Paulo / ESALQ — August 2017

Service Activities

Proposal review panel

- BARD US-Israel Agricultural Research and Development Fund **2022**
- BARD US-Israel Agricultural Research and Development Fund **2021**

Ad hoc review of proposals

- USDA ARS Research Project Plan **2023**
- Biotechnology and Biological Sciences Research Council (BBSRC) **2014**

Internal review of proposals

- Virginia Tech Hatch Project **2023**
- Virginia Tech Hatch Project **2021**
- Virginia Tech Hatch Project **2019**

Multistate research activities

- NCERA-225: Implementation and Strategies for National Beef Cattle Genetic Evaluation
  University of Nebraska-Lincoln representative **2015 - 2018**

National

- Annual Meeting Program Committee - Animal Breeding and Genetics
  American Society of Animal Science **2022-2024**

Center

- Translational Plant Sciences Center Seed Grant committee
  Virginia Polytechnic Institute and State University **2022 Fall**

- Translational Plant Sciences Center Seed Grant committee
  Virginia Polytechnic Institute and State University **2022 Spring**

- Translational Plant Sciences Center Website Committee
  Virginia Polytechnic Institute and State University **2021**

- Translational Plant Sciences Program Graduate Student Recruitment Committee
  Virginia Polytechnic Institute and State University **2019-2020**

- Translational Plant Sciences Program Website Committee
  Virginia Polytechnic Institute and State University **2019**

Departmental

- Faculty Search Committee (Chair)
  Department of Animal and Poultry Sciences
  Virginia Polytechnic Institute and State University **2021**

- Faculty Search Committee
  Department of Animal and Poultry Sciences
  Virginia Polytechnic Institute and State University **2021**

- Promotion and Tenure Committee (non-voting observer)
  Department of Animal and Poultry Sciences
  Virginia Polytechnic Institute and State University **2020-2021**

- Graduate Programs Committee
  Department of Animal and Poultry Sciences
  Virginia Polytechnic Institute and State University **2019-2023**

- Research Programs Committee
  Department of Animal and Poultry Sciences
  Virginia Polytechnic Institute and State University **2019-2021**

Research Area

- 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**

Software tools

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/

Image/Video analysis
- Automated depth data collection - https://github.com/codeandstuf/CattleDepthCollection

Bioconductor packages
- meshr
- MeSH.db
- MeSH.AOR.db
- MeSH.PCR.db
- MeSH.XXX.eg.db (84 packages available through the AnnotationHub package)
  - 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

Participation in meetings, symposiums, and workshops

2023
- ASAS-CSAS-WSASAS Annual Meeting. Albuquerque Convention Center, Albuquerque, NM. July 16-20.
- Leveraging High-Throughput Phenotyping Techniques to Study Complex Traits. Quantitative Genetics and Genomics Gordon Research Conference. Four Points Sheraton/Holiday Inn Express, Ventura, CA. February 12-17.

2022
- The 12th World Congress of Genetics Applied to Livestock Production. De Doelen International Conference Center Rotterdam, Rotterdam, The Netherlands. July 3-8.
- CAIA/CCI SWVA Agricultural Cyber Field Day. Virginia Tech, Blacksburg, VA. April 28.
- CAIA's Big Event. Inn at Virginia Tech, Blacksburg, VA. March 28.
- The 141th Japanese Society of Breeding Meeting. Online. March 20-21.

2021
- The 140th Japanese Society of Breeding Meeting. Online. September 23-25.
- The National Association of Plant Breeders (NAPB) 2021 Annual Meeting. Online. August 15-19.
- The 128th Japanese Society of Animal Science Meeting. Online. March 27-30.
- The 139th Japanese Society of Breeding Meeting. Online. March 19-21.
- 2021 North American Plant Phenotyping Network (NAPPN) Annual Conference. Online. February 16-19.

2020
- The 6th International Conference of Quantitative Genetics. Online. November 2-12.
- The 138th Japanese Society of Breeding Meeting. Online. October 10-11.
- The 2020 European Conference on Computer Vision (ECCV 2020). Online. August 24-28.
- MIRU 2020. The 23rd Meeting on Image Recognition and Understanding. Online. August 2-5.

2019
- NCERA-225 Meeting. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Alphin Stuart Livestock Arena, Blacksburg, VA. October 10-11.
- Phenome 2019. El Conquistador Tucson, A Hilton Resort, Tucson, AZ. February 6-9.

2018
- Agrigenomic Industry Workshop. Co-working space Kayabacho Co-Edo, Chuo-ku, Tokyo, Japan. September 14
- UNL Plant Phenomics Symposium. Cather Dining Complex, University of Nebraska-Lincoln, Lincoln, NE. 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.

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.

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.

Additional training

2019
- Quantitative and Statisitical Genetics. The University of Tokyo, Bunkyo-ku, Tokyo, Japan. October 17-18. Taught by Daniel Gianola.
- Phenome Digital Phenotyping Workshop. Phenome 2019. El Conquistador Tucson, A Hilton Resort, Tucson, AZ. February 6. Taught by Malia Gehan, Noah Fahlgren, Joshua Peschel, Sierra Young, Magdalena Julkowska and Alina Zare.

2016
- Next Generation Plant and Animal Breeding Programs Workshop. University of Nebraska-Lincoln. March 21-25. Taught by John Hickey, Gregor Gorjanc, and Chris Gaynor.

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)
- 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. Kobe International Conference Center, Kobe Japan. 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.

2006

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

Miscellaneous

- Languages: English and Japanese

- Computer skills
  - Statistical/Numerical computational tools: R and Octave
  - Computer vision and image processing: Python and MATLAB
  - Content-description languages: XML, XHTML, CSS, LaTeX, and Markdown
  - Operating systems: Linux and Mac OS X

- Number of new papers read: 2022 (60), 2021 (60), 2020 (130), 2019 (95), 2018 (125), 2017 (130), 2016 (142), 2015 (148)

- 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.