Gota Morota **January 2026**

CONTACT INFORMATION

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RESEARCH INTERESTS

I am a quantitative geneticist interested in bringing 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 to combine the theory of statistical quantitative genetics with currently available molecular information. I am particularly interested in statistical methods for prediction of complex traits using whole-genome molecular markers. Since phenotypic data collection is paramount in quantitative genetics, I integrate phenomics into my research program to collect a wide range of phenotypes.

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 by Simulation and Real Data"
- Advisor: Prof. Dr. Mitsuyoshi Suzuki

PROFESSIONAL POSITIONS

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

Associate Professor (with tenure) **01/2025 - Present**
Principal Investigator

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

Associate Professor of Quantitative Genetics (with tenure) **08/2022 - 12/2024**

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

- Translational Plant Sciences Center Faculty Member **03/2021 - 12/2024**
- Center for Advanced Innovation in Agriculture Affiliated Faculty Member **12/2020 - 12/2024**
- The Fralin Life Science Institute Affiliated Faculty Member **3/2020 - 12/2024**
- Genetics, Bioinformatics, and Computational Biology Program Faculty Member **11/2019 - 12/2024**
- 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 Assistant 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
- Japanese Society of Breeding. 2018 - Present
- Japanese Society of Animal Science. 2016 - Present
- American Society of Animal Science. 2014 - Present
- American Statistical Association. 2018 - 2024
- Genetics Society of America. 2016 - 2024
- International Biometric Society (ENAR). 2012 - 2024

Awards and Recognition

2025

- 2024 The Plant Phenome Journal Editor's Citation for Excellence Award (2024 The Plant Phenome Journal Outstanding Reviewer Award). ASA-CSSA-SSSA (American Society of Agronomy, Crop Science Society of America, Soil Science Society of America). WWW1 WWW2

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 - December 2024**
  - Number of manuscripts handled: 2024 (39), 2023 (51), 2022 (36), 2021 (5)

Associate Editor

- **G3: Genes, Genomes, Genetics** **January 2026 - 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: 2024 (39), 2023 (51), 2022 (36), 2021 (7), 2020 (3), 2019 (2)

Editorial Board

- **Brazilian Journal of Biometrics** **January 2023 - December 2026**
- **Journal of Animal Science** **July 2017 - July 2020**

Ad Hoc Reviewer

- Number of manuscripts reviewed per journal (revised versions are not counted): Agronomy Journal (1), Animal (3), Animal Genetics (7), Animal Production Science (3), Animal Science Journal (3), Bioinformatics (5), Bioinformatics Advance (1), BMC Bioinformatics (3), BMC Genetics (6), BMC Genomics (3), BMC Genomic Data (1), BMC Plant Biology (1), Computers and Electronics in Agriculture (3), Crop Science (3), 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 (6), Genetics (3), Genetics Selection Evolution (11), Genome (1), Heredity (3), Horticulture Research (2), JDS Communications (3), Journal of Agricultural, Biological, and Environmental Statistics (1), Journal of Animal Breeding and Genetics (11), Journal of Animal Science (29), Journal of Animal Science and Biotechnology (3), Journal of Dairy Science (18), Journal of the Royal Statistical Society (1), Livestock Science (7), Meat Science (2), Nature Communications (1), New Phytologist (1), PeerJ (1), Plant Breeding (1), Plant Communications (1), PLOS ONE (6), Poultry Science (3), Preventive Veterinary Medicine (1), Rice Science (1), Scientia Agricola (3), Scientific Reports (2), Statistics in Medicine (1), Theoretical and Applied Genetics (12), The Crop Journal (1), Theoretical Population Biology (1), The Plant Genome (3), The Plant Journal (1), The Plant Phenome Journal (4), The R Journal (1), Translational Animal Science (2)

- Number of manuscripts reviewed per year (revised versions are not counted): 2025 (11), 2024 (20), 2023 (16), 2022 (18), 2021 (28), 2020 (19), 2019 (27), 2018 (19), 2017 (20), 2016 (10), 2015 (10), 2014 (6), 2013 (1), 2012 (1)

Preprints

2. Wang J, De Castro A, Zhang Y, Borsatto LB, Guo Y, Primo VB, Bernardino ABM, **Morota G**, Chebel RC, and Yu H. Evaluating transfer learning strategies for improving dairy cattle body weight prediction in small farms using depth-image and point-cloud data. *arXiv* doi: 10.48550/arXiv.2601.010

1. Bi Y, Huang Y, Yu H, and **Morota G**. Impact of trait measurement error on quantitative genetic analysis of computer vision derived traits. *bioRxiv*. doi: 10.1101/2025.06.02.657462

Publications

	First/Senior/Corresponding author	Co-author	Total
Book chapters	1	0	1
Editorials	0	1	1
Peer-reviewed research journal articles	42	51	93
Peer-reviewed review journal articles	5	2	7
Peer-reviewed conference proceedings	1	12	13
Outreach publications	0	1	1
Total	49	667	116

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

2026

93. Silva CM, Signorini VS, Mezzomo HC, Ribeiro JPO, Lima GW, Portes MF, Corredo LP, Olivoto T, **Morota G**, and Nardino M. 2026. Optimizing indirect selection of tropical wheat genotypes using high-throughput longitudinal phenotyping and trait relationships. *Remote Sensing Applications: Society and Environment*. In press.

2025

92. Yoshioka H, **Morota G**, and Iwata H. 2025. Reciprocal BLUP: A predictability-guided multi-omics framework for plant phenotype prediction. *Plants*. **15**:17. doi: 10.3390/plants15010017

91. Habimana V, Ekine-Dzivenu CC, Nguluma AS, Nziku ZC, **Morota G**, Chenyambuga SW, and Mrode R. 2025. Estimation of genetic parameters for physiological and milk production traits of Holstein Friesian crossbreds reared in Tanzania. *International Journal of Livestock Production*. **16**:9-18. doi: 10.3168/10.5897/IJLP2025.0874

90. Morales AG, Amorim ST, Lizana C, Pulido RG, Hanigan MD, Cockrum RR, and **Morota G**. 2025. Incorporating heterosis effects enhances genetic evaluations for milk production and functional traits in Chilean crossbred dairy cows. *Journal of Dairy Science*. **108**:13565-13576. doi: 10.3168/jds.2025-26445

89. Suela MM, Azevedo CF, Nascimento ACC, **Morota G**, Lopes da Silva F, Nizio GM Giasson F, and Nascimento M. 2025. Using Structural Equation Models to Interpret Genome-Wide Association Studies for Morphological and Productive Traits in Soybean [Glycine max (L.) Merr.]. *Plants*. **14**:3015. doi: 10.3390/plants14193015

88. Silva CM, Kunduru B, Bokros N, Tabaracci K, Oduntan Y, Brar MS, Kumar R, Stubbs CJ, Nardino M, McMahan CS, DeBolt S, Robertson DJ, Sekhon RS, and **Morota G**. 2025. Genomic prediction of stalk lodging resistance and the associated intermediate phenotypes in maize using whole-genome resequence and multi-environmental data. *The Plant Genome*. **18**:e70125. doi: 10.1002/tpg2.70125

87. Bi Y, Huang Y, Xuan J, and **Morota G**. 2025. Industry-scale prediction of video-derived pig body weight using efficient convolutional neural networks and vision transformers. *Biosystems Engineering*. **257**:104243. doi: https://doi.org/10.1016/j.biosystemseng.2025.104243

86. Gonçalves MTV, Dias KODG, da Silva Pereira G, Ferreira PHS, Barbosa MHP, **Morota G**, and Peternelli LA. 2025. Single-step genomic best linear unbiased predictions of sugarcane genotype performance. *Euphytica*. **221**:131. doi: 10.1007/s10681-025-03577-6

85. Suela MM, Azevedo CF, Nascimento ACC, Caixeta ET, de Oliveira ACB, **Morota G**, Nascimento M. 2025. Structural equation modeling and genome-wide selection for multiple traits to enhance Arabica coffee breeding programs. *Agronomy*. **15**:1686. doi: 10.3390/agronomy15071686

84. Amorim ST, Retallick KJ, Garcia A, Noelia Ibañez-Escriche N, and **Morota G**. 2025. Genetic heterogeneity of residual variance for foot score traits in American Angus cattle. *Journal of Animal Breeding and Genetics*. **143**:68-78. doi: 10.1111/jbg.12949

83. Fletcher EB, Rosso ML, Walker T, Huang H, **Morota G**, and Zhang B. 2025. Near-infrared reflectance spectroscopy calibration for trypsin inhibitor in soybean seed and meal. *Agriculture*. **15**:1062. doi: 10.3390/agriculture15101062

82. Liao M, **Morota G**, Bi Y, and Cockrum RR. 2025. Predicting dairy calf body weight from depth images using deep learning (YOLOv8) and threshold segmentation with cross-validation and longitudinal analysis. *Animals*. **15**:868. doi: 10.3390/ani15060868

81. Sahoo MM, Tarshish R, Tubul Y, Sabag I, Gadri Y, **Morota G**, Peleg Z, Alchanatis V, and Herrmanna I. 2025. Multimodal ensemble of UAV-borne hyperspectral, thermal, and RGB imagery to identify combined nitrogen and water deficiencies in field-grown sesame. *ISPRS Journal of Photogrammetry and Remote Sensing*. **222**:33-53. doi: 10.1016/j.isprsjprs.2025.02.011

80. Habimana V, Nguluma AS, Nziku ZC, Ekine-Dzivenu CC, **Morota G**, Mrode R, and Chenyambuga SW. 2025. An HPLC-MS/MS method for the quantification of heat stress-related milk

metabolites in milk from Holstein-Friesian cross-bred cows in Tanzania. *South African Journal of Animal Science*. **55**:154-172. doi: 10.4314/sajas.v55i3.07

79. De Castro A, Wang J, Bonney-King JG, **Morota G**, Miller-Cushon EK, and Yu H. 2025. AnimalMotionViz: an interactive software tool for tracking and visualizing animal motion patterns using computer vision. *JDS Communications*. **6**:416-421. doi: 10.3168/jdsc.2024-0706

78. Bi Y, Walia H, Obata T, and **Morota G**. 2025. Genomic prediction of metabolic content in rice grain in response to warmer night conditions. *Crop Science*. **65**:e21435. doi: 10.1002/csc2.21435

2024

77. Sabag I, Pnini S, **Morota G**, and Peleg Z. 2024. Refining flowering date enhances sesame yield independently of day-length. *BMC Plant Biology*. **24**:711. doi: 10.1186/s12870-024-05431-8

76. Kravitz A, Liao M, **Morota G**, Tyler R, Cockrum RR, Manohar BM, Ronald BSM, Collins MT, and Sriranganathan N. 2024. Retrospective single nucleotide polymorphism analysis of host resistance and susceptibility to ovine Johne's disease using restored FFPE DNA. *International Journal of Molecular Sciences*. **25**:7748. doi: 10.3390/ijms25147748

75. Habimana V, Nguluma AS, Nziku ZC, Ekine-Dzivenu CC, **Morota G**, Mrode R, and Chenyambuga SW. 2024. Heat stress effects on physiological and milk yield traits of lactating Holstein Friesian crossbreds reared in Tanga region, Tanzania. *Animals*. **14**:1914. doi: 10.3390/ani14131914

74. Sabag I, Bi, Y, Sahoo MM, Herrmann I, **Morota G**, and Peleg Z. 2024. Leveraging genomics and temporal high-throughput phenotyping to enhance association mapping and yield prediction in sesame. *The Plant Genome*. **17**:e20481. doi: 10.1002/tpg2.20481

73. Sandhu J, Irvin L, Chandaran AK, Oguro S, Paul P, Dhatt B, Hussain W, Cunningham SS, Quinones CO, Lorence A, Adviento-Borbe MA, Staswick P, **Morota G**, and Walia H. 2024. Natural variation in *LONELY GUY-like 1* regulates rice grain weight under warmer night conditions. *Plant Physiology*. **196**:164-180. doi: 10.1093/plphys/kiae313

72. Maurer JJ, Cheng Y, Pedroso A, Thompson KK, Akter S, Kwan T, **Morota G**, Kinstler S, Porwollik S, McClelland M, Escalante-Semerena JC, and Lee MD. 2024. Peeling back the many layers of competitive exclusion. *Frontiers in Microbiology*. **15**:1342887. doi: 10.3389/fmicb.2024.1342887

71. Silva CM, Mezzomo, HC, Ribeiro JPO, Signorini VS, Lima GW, Torres Vieira EF, Portes MF, **Morota G**, Corredo LP, and Nardino M. 2024. Insights on multi-spectral vegetation indices derived from UAV-based high-throughput phenotyping for indirect selection in tropical wheat breeding. *Euphytica*. **220**:35. doi: 10.1007/s10681-024-03299-1

70. Wang J, Hu Y, Xiang L, **Morota G**, Brooks SA, Wickens CL Miller-Cushon EK, and Yu H. 2024. Technical note: ShinyAnimalCV: open-source cloud-based web application for object detection, segmentation, and three-dimensional visualization of animals using computer vision. *Journal of Animal Science*. **102**:1-6. doi: 10.1093/jas/skad416

2023

69. Bi Y, Campos LM, Wang J, Yu H, Hanigan MD, and **Morota G**. 2023. Depth video data-enabled predictions of longitudinal dairy cow body weight using thresholding and Mask R-CNN algorithms. *Smart Agricultural Technology*. **6**:100352. doi: 10.1016/j.atech.2023.100352

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*. **4**:363-368. 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. 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

61. Kadlec R, Indest S, Castro K, Waqar S, Campos LM, Amorim ST, Bi Y, Hanigan MD, and **Morota G**. 2022. 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

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 methods 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

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2018

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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

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2017

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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

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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

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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

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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

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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

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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

2026

7. **Morota G**, Lee, HJ, Lee SH, Park HB, and Onogi A. 2026. Artificial intelligence in animal breeding and genetics: applications, opportunities, and challenges. *Animal Frontiers*. Early view. doi: 10.1093/af/vfaf058

2024

6. Aydin KB, Bi Y, Brito LF, Ulutaş Z, and **Morota G**. 2024. Review of sheep breeding and genetic research in Türkiye. *Frontiers in Genetics*. **15**:1308113. doi: 10.3389/fgene.2024.1308113

2023

5. Habimana V, Nguluma AS, Nziku ZC, Ekine-Dzivenu CC, **Morota G**, Mrode R, and Chenyambuga SW. 2023. 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 papers

2025

13. Sahoo, MM Tarshish R, Sabag I, Gadri Y, **Morota G**, Peleg Z, Alchanatis V, and Herrmann I. 2025. Sesame yield prediction using UAV-borne hyperspectral imagery, crop traits and genotype category. 15th European Conference on Precision Agriculture (ECPA). Polytechnic University of Catalonia, Barcelona, Spain. June 29 – July 3. doi: 10.1163/9789004725232_071

12. Bharadwaj S, Ranjan P, Pei Y, Yim J, Bi Y, Ha D, **Morota G**, and Shin S. 2025. Non-invasive pig weight prediction using SAM-enhanced deep learning and depth imaging. SoutheastCon25. Embassy Suites Concord, Concord, NC, USA. March 22-23. doi: 10.1109/SoutheastCon56624.2025.10971513

2024

11. Ranjan P, Ha DS, **Morota G**, and Shin S. 2024. Multi-input deep learning models for weight forecasting of pigs using depth images. IEEE 36th International Conference on Tools with Artificial Intelligence (ICTAI). 1048-1055. Herndon, VA, USA. October 28-30. doi: 10.1109/ICTAI62512.2024.00149

10. Ranjan P, Bharadwaj S, Pei Y, Aydin KB, Ha DS, **Morota G**, and Shin S. 2024. Improved pig behavior analysis through strategic data preprocessing framework in machine learning. IEEE 36th International Conference on Tools with Artificial Intelligence (ICTAI). 984-991. Herndon, VA, USA. October 28-30. 10.1109/ICTAI62512.2024.00141

9. Zhang Z, Abraham S, Lee A, Li Y, **Morota G**, Ha DS, and Shin S. 2024. SegIt: Empowering sensor data labeling with enhanced efficiency and security. *MLMI 2024: Proceedings of the 2024 7th International Conference on Machine Learning and Machine Intelligence (MLMI)*. 97-103. Osaka, Japan. August 2-4. doi: 10.1145/3696271.3696287

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

29 domestic and 25 international

2025

54. Evaluating the impact of trait measurement error on genetic analysis of computer vision-based phenotypes. Advances in statistics and ML for breeding studies: From trait analysis to genomic prediction saession. The 19th International Joint Conference on Computational and Financial Econometrics (CFE) and Computational and Methodological Statistics (CMStatistics) (CFE-CMStatistics 2025). Birkbeck, University of London, London, UK. December 13-15, 2025.

53. Evaluating the impact of trait measurement error on genetic analysis of computer vision-based phenotypes. Methods and Practice in Agricultural Analytics. Biometrics in the Bush Capital (BIBC2025). The Australasian Region Biometrics Conference. National Film and Sound Archive of Australia, Canberra, Australia. November 24-28. 2025,

52. Current status and prospects of breeding in animal science. Webinar on Breeding Science. Division of Breeding Science, Science Council of Japan. Online. October 24, 2025.

51. Digital innovations in quantitative genetic analysis of image-derived traits. Animal Bio Bigdata Session. Chungnam National University Conference of Advanced Technology (CCAT). Chungnam National University, Daejeon, South Korea. September 25, 2025.

50. A Journey to reconsider what we take for granted: The value of experiencing minority status abroad. Diversity & Inclusion (D&I) Promotion Seminar. The 148th Japanese Society of Breeding Meeting. Sapporo Convention Center, Sapporo, Hokkaido, Japan. September 10-11. 2025.

49. Trait measurement error and its impact on genetic analysis of computer vision-based phenotypes. Statistical methodologies shaping the future of plant and animal breeding session. The 8th International Conference on Econometrics and Statistics (EcoSta 2025). Waseda University, Shinjuku, Tokyo, Japan. August 21-23. 2025.

48. Addressing challenges in agricultural biology through biometric approaches. Research Center for Agricultural Information Technology, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki, Japan. July 7. 2025.

47. Animal Breeding & Genetics x Data Science / AI. Special Seminar. Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki, Japan. April 14. 2025.

2024

46. Interactive (re)visualization for animal phenomics. Invited Session: Interactive visualisation for effective decision-making in agricultural and environmental sciences. The 32nd International Biometric Conference (IBC2024). Atlanta Marriott Marquis, Atlanta, GA, USA. December 8-13. 2024.

45. The cutting edge of phenotyping. The 2024 American Wagyu Association Conference. Williamsburg Lodge, Williamsburg, VA, USA. September 11-14. 2024.

44. Quantitative genetic analysis of metabolite accumulation in rice. The 21st International Symposium of Rice Functional Genomics Meeting (ISRFG2024). Little Rock/Stuttgart, AR, USA. September 9-11. 2024.

43. Phenomics-enabled quantitative genetic modeling of complex traits. Animal Breeding and Genetics Symposium. 2024 ASAS Midwest Annual Meeting. Monona Terrace Community and Convention Center, Madison, WI, USA. March 10-13. 2024.

42. Quantitative genetic modeling of rice grain metabolite accumulation under warmer nights. Breeding for Changing Weather Conditions Workshop. The Plant and Animal Genome Conference (PAG 31). Town & Country Resort and Conference Center, San Diego, CA, USA. January 12-17. 2024.

2023

41. Use of data science and big data in animal breeding. Special Seminar. Animal Breeding and Genetics Division at the National Institute of Animal Science, Cheonan, Chungnam, South Korea. December 19. 2023.

40. Phenomics-driven quantitative genetic modeling of complex traits in animals and plants. Interdisciplinary Convergence Symposium on Digital Breeding in Animals and Plants. Kongju National University, Yesan, Chungnam, South Korea. December 18. 2023.

39. Animal data science applied to digital data. Special Seminar. Smithfield Premium Genetics. Rose Hill, NC, USA. August 14. 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. 2023.

37. Data science in precision livestock farming. Symposium on spaced-based effective production for beef. X-Nihonbashi Tower, Chuo-city, Tokyo, Japan. Online. February 22. 2023.

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. 2022.

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. 2022.

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, USA. June 26-30. 2022.

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. 2022.

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. 2021.

31. High-throughput phenotyping driven quantitative genetics. Centre for Genetic Improvement of Livestock Seminar. Department of Animal Biosciences. University of Guelph. Online. September 17. 2021.

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. 2020.

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. 2020.

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. 2020.

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. 2020. 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, USA. January 11-15. 2020.

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. 2019.

24. Variance heterogeneity association analysis in wheat reveals 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. 2019.

23. Statistical methods for quantitative genetic analysis of high-throughput phenotyping data. University of Florida Genetics Institute Seminar. University of Florida, Gainesville, FL, USA. October 10. 2019.

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. 2019.

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. 2019.

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. 2019.

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, USA. March 11-13. 2019.

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, USA. January 12-16. 2019.

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. 2018.

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. 2018.

15. How big data, machine learning and bioinformatics are impacting genetic selection. Poultry Tech Summit. Georgia Tech Hotel & Conference Center, Atlanta, GA, USA. November 5-7. 2018.

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. 2018.

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. 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, Pirassununga, São Paulo, Brazil. May 28. 2018.

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, USA. February 23. 2018.

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, USA. January 13-17. 2018.

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. 2017.

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, USA. July 8-12. 2017.

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, USA. September 23. 2016.

6. MeSH annotation of the chicken genome. Poultry 2 Workshop. The Plant and Animal Genome XXIV Conference. Town and Country Hotel, San Diego, CA, USA. January 9-13. 2016.

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, USA. September 23. 2015.

4. Quantitative genetics in the functional genomics era. Animal Breeding & Genetics Seminars. Department of Animal Science, Iowa State University, Ames, IA, USA. March 3. 2015.

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

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

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

Contributed Presentations

2025

22. From cornfields to the red gate. Agricultural and Environmental Biology Special Seminar. Graduate School of Agricultural and Life Sciences, The University of Tokyo, Bunkyo, Tokyo, Japan. October 22, 2025.

21. Trait measurement error and its impact on genetic analysis of computer vision-based phenotypes. The 133rd Annual Meeting of Japanese Society of Animal Science Meeting. Gifu University, Gifu, Gifu, Japan. September 12-15. 2025.

20. Single-step genomic best linear unbiased predictions in sugarcane. The 148th Japanese Society of Breeding Meeting. Sapporo Convention Center, Sapporo, Hokkaido, Japan. September 10-11. 2025.

19. Public plant breeding programs in the USA. Sustainable agriculture and its future. 2025 The University of Tokyo Sarabetsu Satellite Campus Public Seminar. SaraPark Hall, Sarabetsu, Hokkaido, Japan. June 10, 2025.

18. Genomic prediction of stalk lodging resistance and the associated intermediate phenotypes in maize. The 147th Japanese Society of Breeding Meeting. Tohoku University, Sendai, Miyagi, Japan. March 20-21. 2025.

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. 2020. Canceled due to COVID-19.

16. The use of milk-infrared spectroscopy data to improve milk protein phenotype predictions. The 127th Annual Meeting of Japanese Society of Animal Science Meeting. Kyoto University, Kyoto, Kyoto, Japan. March 25-28. 2020. 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. 2018.

14. Multivariate analyses for longitudinal phenotypes and genome-wide association studies in plants and animals. Special seminar. Crop Science Laboratory, Faculty of Agriculture, Iwate University, Ueda, Morioka, Iwate, Japan. November 21. 2018.

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. 2018.

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. 2018.

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

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. 2018.

2017

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

8. Genomic connectedness across management units. The 123rd Annual Meeting of Japanese Society of Animal Science Meeting. Shinshu University, Kamiina, Nagano, Japan. September 4-8. 2017.

2015

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

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. 2015.

5. The impact of population stratification on genomic heritability. NCERA-225 Meeting. North Dakota State University, Fargo, ND, USA. October 22-23. 2015.

4. An application of MeSH enrichment analysis in livestock. ADSA-ASAS Joint Annual Meeting. Rosen Shingle Creek, Orlando FL, USA. July 12-16. 2015.

3. Prediction of complex quantitative traits using functional annotations and bootstrap aggregating. Special Seminar. National Livestock Breeding Center, Shirakawa, Japan. January 10. 2015.

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. 2012. 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. 2007.

Posters

2015

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

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

2013

2. **Morota G**. MeSHR: R/Bioconductor package for finding statistically overrepresented MeSH terms in a set of genes. Annual Bioconductor Conference BioC 2013. Seattle, WA, USA. July 18-19. 2013.
https://secure.bioconductor.org/BioC2013/posters.php#8.

1. **Morota G**. Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. Annual Bioconductor Conference BioC 2013. Seattle, WA, USA. July 18-19. 2013. https://secure.bioconductor.org/BioC2013/posters.php#7.

Intramural Seminars

2026

2025

20. Year-end summary updates. Seminar in Agricultural Biology. Laboratory of Biometry and Bioinformatics. Department of Agricultural and Environmental Biology. The University of Tokyo, Bunkyo, Tokyo, Japan. December 17. 2025.

19. What can be done with Agricultural Biology x Data Science/AI? Agricultural Biology Major Lunch Seminar. The University of Tokyo, Meguro, Tokyo, Japan. April 28. 2025.

2021

18. High-throughput animal phenotyping. Animal Science Seminar. Department of Animal and Poultry Sciences. Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. September 13. 2021.

17. High-throughput phenotyping driven quantitative genetics. Translational Plant Sciences Program Orientation Week. Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. August 18. 2021.

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, Blacksburg, VA, USA. Online. March 24. 2021.

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, Blacksburg, VA, USA. Online. February 24. 2021.

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, USA. September 26. 2019.

13. What is quantitative genetics? Translational Plant Sciences Program Orientation Week. Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. August 21. 2019.

12. Statistical learning for multi-omic data. Reproductive Biology Club. Virginia Polytechnic Institute and State University, Blacksburg, VA, USA. April 19. 2019.

2017

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

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, USA. September 15. 2015.

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, USA. September 18. 2014.

8. Whole-genome prediction of complex traits using kernel methods. Ph.D. Dissertation Defense. Department of Animal Sciences, University of Wisconsin-Madison, Madison, WI, USA. May 12. 2014.

7. Is internship experience beneficial for obtaining a TT job? Dairy Science Graduate Seminar. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI, USA. February 14. 2014.

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

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, USA. April 10. 2012.

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, USA. December 5. 2011.

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

2. Hierarchical Bayesian logistic regression. Animal Breeding & Genomics Seminars. Department of Dairy Science, University of Wisconsin-Madison, Madison, WI, USA. March 23. 2010.

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

Teaching

The University of Tokyo, Bunkyo, Tokyo, Japan

Lead Instructor

- Biometrics **A Semester, 2025**
  Faculty of Agriculture & Faculty of Science

Co-Instructor

- Play and Learn! Exploring Genetics and Data Science with the Genome Breeding Game **A1 Term, 2025**
  College of Arts and Sciences
  13 participants

- Introduction to Agricultural and Environmental Biology - 11/20 **A Semester, 2025**
  Graduate School of Agricultural and Life Sciences
  Topic: Decoding mixed model equations

- Experiments in Advanced Applied Biology - 10/2, 10/3, 10/9, 10/10 **A Semester, 2025**
  Faculty of Agriculture
  Topics: Deep learning for image analysis and Plant breeding simulation game

- Practice in Intensive Field Agrobiology **S Semester, 2025**
  Faculty of Agriculture
  Location: Obihiro Hokkaido, Japan

- Advanced Biometrics **S Semester, 2025**
  Graduate School of Agricultural and Life Sciences
  Book: Falconer, D. S., and T. F. C. Mackay, 1996 Introduction to Quantitative Genetics, Ed 4. Longmans Green, Harlow, Essex, UK.

- Mathematical Sciences in Agriculture - July 11 **S Semester, 2025**
  Graduate School of Agricultural and Life Sciences & Faculty of Agriculture
  Topic: Quantitative genetics modeling as a basis of animal and plant breeding

- Practice in Basic Field Agrobiology - April 16 **S Semester, 2025**
  Faculty of Agriculture
  Topic: Design of experiments

- Experiments in Applied Biology I - 5/16, 5/22, 5/29 **S Semester, 2025**
  Faculty of Agriculture
  Topic: Image analysis, QTL mapping, and GWAS

Guest Instructor

- Biometrics - Janauary 20 **A Semester, 2024**
  Faculty of Agriculture & Faculty of Science
  Topic: Practical applications of effective data-driven breeding

- Special Lecture on Agricultural and Environmental Biology - November 3 **A Semester, 2022**
  Graduate School of Agricultural and Life Sciences
  Topic: Data science in agriculture

- Biometrics - November 26 **A Semester, 2018**
  Faculty of Agriculture & Faculty of Science
  Topic: Introduction to genome to phenome

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

Lead Instructor

- ALS 3104 Animal Breeding and Genetics [WWW] **Spring, 2024**
  118 participants

- 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

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

2025 **Niigata University**, Niigata city, Niigata, Japan

Co-Instructor
Advanced Agricultural Technologies - [WWW] **November 10-12, 2025**
8 participants

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

- Virginia Soybean Board Funding - $63,818.00 Virginia Soybean Board
  PI: Bo Zhang **April 1, 2024 - May 24, 2025**
  Proposal: Advance the soybean breeding scheme by integrating traditional selection and modern prediction methods
  Role: Co-Principal Investigator

- Inter-Disciplinary Engagement in Animal Systems (IDEAS) - $1,150,000.00 USDA-NIFA
  PI: Mark Hanigan **September 1, 2024 - August 31, 2028**
  Proposal: Optimizing individualized feeding to increase production and profit, and minimize environmental impacts of dairy farms
  Role: Co-Principal Investigator

- National Needs Graduate and Postgraduate Fellowship Grant - $499,949.00 USDA-NIFA
  PI: Fernando Biase **November 15, 2023 - November 14, 2028**
  Proposal: Bridging Genomes to Phenomes: Fostering interdisciplinary expertise to advance animal production (2024-38420-41540)
  Role: Co-Principal Investigator

- 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 - December 31, 2024**
  Proposal: Use of precision technology to predict pathogenic diarrhea in pre-weaned dairy heifers
  Role: Co-Principal Investigator

- BARD Research Program - $310,000.00 US-Israel Binational Agricultural Research and Development Fund
  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 (IS-5400-21)
  Role: Principal Investigator

- Exploratory Research Program - $200,000.00 USDA-NIFA
  PI: Gota Morota **June 1, 2020 - May 31, 2023**
  Proposal: Wireless monitoring and assess system to improve productivity and animal welfare in swine (2020-67030-31339)
  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
  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) (1736192)
  Role: Co-Principal Investigator

Internal Funding

- Pratt Equipment Fund - $21,500.00 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 - $30,000.00 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 - $46,689.00 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 - $104,500.00 VT
  PI: Gota Morota **May 1, 2021 - 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 - $125,000.00 VT
  PI: Rebecca Cockrum **May 1, 2021 - 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

6. Kenan Burak Aydin [WWW] 8/2020 - 8/2025
    - Committee members: Fernando Biase, Luiz Brito, and Scott Greiner

5. Ye Bi [WWW] 8/2021 - 12/2024
    - Committee members: Mark Hanigan, Ismini Lourentzou, and Nicholas Santantono

4. Mateus Teles Vital Gonçalves (jointly with Luiz A. Peternelli and Márcio Henrique Pereira Barbosa) [WWW] 1/2020 - 9/2024
    - Committee members: Lucas de Paula Corrêdo, Matheus Ferreira, Hélcio Duarte Pereira, Guilherme Silva Pereira, and Rafael Massahiro Yassue

3. Sabrina T. Amorim [WWW] 8/2021 - 8/2024
    - Committee members: C. P. James Chen, Jason Holliday, and Johan Osorio

2. Idan Sabag (jointly with Zvi Peleg) [WWW] 10/2019 - 5/2024
    - Committee members: Amit Gur, and Ittai Herrmann

1. Haipeng Yu [WWW] 8/22/2016 - 5/15/2020
    - Committee members: 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

5. Caique Machado e Silva, Federal University of Viçosa [WWW] 9/1/2023 - 2/28/2024

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

Dissertation Committees

Ph.D Dissertation Evaluation Committees

7. Fangming Zhu 2026
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisors: Hiroyoshi Iwata / Masaru Fujimoto

6. Hayato Yoshioka 2026
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisor: Hiroyoshi Iwata

5. Sylvain Grison 2026
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisor: Wei Guo

4. Hideto Mochizuki 2026
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisor: Hiroyoshi Iwata

3. Mashiro Okada 2025
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisor: Hiroyoshi Iwata

2. Kengo Sakurai 2025
   Department of Agricultural and Environmental Biology, University of Tokyo
   Major advisor: Hiroyoshi Iwata

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

Ph.D Advisory Committees

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

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

8. Elizabeth B. Fletcher — 2025
School of Plant and Environmental Sciences, Virginia Tech
Major advisor: Bo Zhang

7. Patrick Bewick — 2025
School of Plant and Environmental Sciences, Virginia Tech
Major advisor: Bo Zhang

6. Letícia Marra Campos — 2024
School of Animal Sciences, Virginia Tech
Major advisor: Mark Hanigan

5. Mackenzie Marrella — 2024
School of Animal Sciences, Virginia Tech
Major advisor: Fernando H. Biase

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

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

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

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

M.S. Advisory Committees

3. Pranjal Ranjan — 2024
The Bradley Department of Electrical and Computer Engineering, Virginia Tech
Major advisor: Sook Shin Ha

2. Stephen Pietruszka (Non-thesis option) — 2024
School of Plant and Environmental 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

- Hee-Bok Park, Kongju National University — January 2024
- 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

External proposal review panels

- BARD US-Israel Agricultural Research and Development Fund **2023**
- BARD US-Israel Agricultural Research and Development Fund **2022**
- BARD US-Israel Agricultural Research and Development Fund **2021**

Ad hoc review of external proposals

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

Societies

- JSB Representative to the Association of Japanese Agricultural Scientific Societies
  Executive Committee
  Japanese Society of Breeding **2026 - Present**
- Press Announcement/Press Release Coordinator
  Executive Committee
  Japanese Society of Breeding **2026 - Present**

- Annual Meeting Program Committee - Breeding and Genetics
  American Dairy Science Association **2024-2026**

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

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

Center

- Center for Advanced Innovation in Agriculture Affiliated Executive Committee Member
  Virginia Polytechnic Institute and State University **2023-2024**

- 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**

Graduate School

- Information Ethics Committee
  Graduate School of Agricultural and Life Sciences
  The University of Tokyo **2025-Present**

Departmental

- Undergraduate Education Committee
  Agricultural Biology Major, Faculty of Agriculture
  The University of Tokyo **2026-2027**

- Practice in Intensive Field Agrobiology Committee
  Agricultural Biology Major, Faculty of Agriculture
  The University of Tokyo **2025**

- Undergraduate Curriculum Committee
  School of Animal Sciences
  Virginia Polytechnic Institute and State University **2023-2024**

- Virginia Tech Hatch Project Proposal Reviewer
  Virginia Polytechnic Institute and State University **2023**

- Graduate Education Committee
  School of Animal Sciences
  Virginia Polytechnic Institute and State University **2019-2023**

- 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**

- Virginia Tech Hatch Project Proposal Reviewer
  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**

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

- Virginia Tech Hatch Project Proposal Reviewer
  Virginia Polytechnic Institute and State University **2019**

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

- GCA - https://github.com/QGresources/GCA
- dkDNA - http://cran.r-project.org/web/packages/dkDNA/index.html

Shiny Applications

- ShinyAnimalCV - https://shinyanimalcv.rc.ufl.edu/
- 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

2026
- The 149th Japanese Society of Breeding Meeting. Ibaraki University, Mito, Ibaraki, Japan. March 21-22, 2026.

2025
- Seventh International Workshop on Machine Learning for Cyber-Agricultural Systems (ML-CAS2025). The University of Tokyo, Bunkyo, Tokyo, Japan. August 5-6, 2025

2024
- ASAS-CSAS-WSASAS Annual Meeting. Calgary TELUS Convention Centre, Calgary, Alberta, Canada. July 21-25, 2024.
- ADSA 2024 Annual Meeting. Palm Beach County Convention Center, West Palm Beach, FL, USA. June 16–19, 2024.

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

2022
- The 12th World Congress of Genetics Applied to Livestock Production. De Doelen International Conference Center Rotterdam, Rotterdam, The Netherlands. July 3-8, 2022.

- CAIA/CCI SWVA Agricultural Cyber Field Day. Virginia Tech, Blacksburg, VA, USA. April 28, 2022.
- CAIA's Big Event. Inn at Virginia Tech, Blacksburg, VA, USA. March 28, 2022.
- The 141th Japanese Society of Breeding Meeting. Online. March 20-21, 2022.

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

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

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

2018
- Agrigenomic Industry Workshop. Co-working space Kayabacho Co-Edo, Chuo-ku, Tokyo, Japan. September 14, 2018.
- UNL Plant Phenomics Symposium. Cather Dining Complex, University of Nebraska-Lincoln, Lincoln, NE, USA. April 2, 2018.

2017
- EPSCoR 2017 Track 2 Kickoff Meeting. National Science Foundation, Alexandria, VA, USA. October 3, 2017.
- The 15th International Symposium on Rice Functional Genomics. Gyeonggi Small and Medium Business Support Center, Suwon, Gyeonggi, South Korea. September 25-28, 2017.

2016
- NCERA-225 Meeting. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Stoney Creek Hotel, St. Joseph, MO, USA. October 27-28, 2016.

- The 5th International Conference on Quantitative Genetics. Monona Terrace Community and Convention Center, Madison, WI, USA. June 12-17, 2016.

2015

- The 29th International Mammalian Genome Conference. Yokohama Port Opening Memorial Hall, Yokohama, Japan. November 8-11, 2015.
- DNA Technology: Where we've been, where we are, and where we're headed. The US Meat Animal Research Center, Clay Center, NE, USA. October 19, 2015.
- GO-FAANG Workshop. National Academy of Sciences Building, Washington, DC, USA. October 7-8, 2015.

2014

- Sheep Genomics Workshop. University of Nebraska-Lincoln, Lincoln, NE, USA. November 13-14, 2014.
- NCERA-225 Meeting. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Bozeman, MT, USA. October 23-24, 2014.

2009

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

2008

- The 109th Annual Meeting of Japanese Society of Animal Science Meeting. Tokiwa University, Mito, Ibaraki, Japan. March 27-29, 2009.

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: 2023 (145), 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.