Draft Program
Symposia and Oral Presentations
Monday, August 18, 2014

Plenary Speaker – Monday
Chairs: E. John Pollak, USDA, ARS, U.S. Meat Animal Research Center and Filippo Miglior,
Canadian Dairy Network and University of Guelph
Bayshore Grand Ballroom

8:30 AM  Plenary 1  Animal Breeding in the Next-Generation Sequencing Era.
J. F. Taylor*, University of Missouri, Columbia

Bioinformatics: New Tools and Approaches
Chair: Paul Stothard, University of Alberta
Bayshore Grand Ballroom A

E. L. Nicolazzi1, N. Nazzicari1, A. Caprera1, I. Fojadelli1, F. Strozzi1, R. D. Schnabel2, C. Lawley1, A. Pirani1, F. Brew3, C. Soans1, H. Jorjani6, G. Evans7, B. Simpson1, J. L. Williams1 and A. Stella10, 1 Fondazione Parco Tecnologico Padano, Lodì, Italy, 2 University of Missouri, Columbia, 3 Illumina Inc., San Diego, CA, 4 Affymetrix Inc., Santa Clara, CA, 5 Affymetrix UK Ltd., High Wycombe, United Kingdom, 6 Interbull Centre, Uppsala, Sweden, 7 GeneSeek, a Neogen Company, Auchenruive, Ayr, Scotland, 8 GeneSeek, a Neogen Company, Lincoln, NE, 9 IBBA CNR, Lodì, Italy

C. Wang1, D. Prakapenka2, H. B. Runesha2 and Y. Da1*, 1 Department of Animal Science, University of Minnesota, Saint Paul, 2 Research Computing Center, The University of Chicago, Chicago, IL

11:00 AM  159  A Computationally Efficient Algorithm for Genomic Prediction using a Bayesian Model.
T. Wang1,2*, Y. P. P. Chen4, M. E. Goddard6, T. H. E. Meuwissen8 and B. J. Hayes5, 1 Biosciences Research Division, Department of Primary Industries, Melbourne, Australia, 2 Dairy Futures Cooperative Research Centre, Melbourne, Australia, 3 Faculty of Science, Technology and Engineering, La Trobe University, Melbourne, Australia, 4 Faculty of Science, Technology and Engineering, La Trobe University, Melbourne, CA, USA, 5 The Department of Environment and Primary Industries, Bundoora, Australia, 6 Norwegian University of Life Sciences, Ås, Norway

11:15 AM  160  Selection of SNP Panels for Parentage Testing.
C. Gondro1, E. M. Stracken1, H. K. Lee2, K. D. Song2 and S. W. Lee1, 1 University of New England, Armidale, Australia, 2 Hankyong National University, Anseong, South Korea, 3 Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea

J. B. van Kaam1 and R. Finocchiaro, Anafi, Cremona, Italy

11:45 AM  162  QS@breeding – A Virtual Appliance for Quality Control in BLUP Genetic Evaluation.
E. Groeneveld1*, U. Müller2, C. V. Truong3 and S. Krostitz4, 1 Institute of Farm Animal Genetics (FLI), Mariensee, Germany, 2 Saxon State Agency for Environment, Agriculture and Geology, Kölletsch, Germany

Breeding in Aquaculture Species – Salmonids
Chair: Thomas Moen, AquaGen AS
Cypress Room

10:30 AM  261  RNA-seq Analysis of Transcriptome Response to VHS-V Infection in Two Target Tissues of Resistant vs Susceptible Trout Clonal Lines.
C. Genet1, E. R. Verrier2, C. Ciobotaru1, C. Klopp1, D. Esquerre3, D. Laloe2, P. Boudinot2 and E. Quillet1, 1 INRA
10:45 AM 262 Genetic Variation in Resistance to Pancreas Disease in Atlantic Salmon.
S. Gonen1, A. Norris2, P. Arnexen1, S. C. Bishop1 and R. D. Houston1, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Marine Harvest, Sandviksboder 78a, Bergen, Norway

11:00 AM 263 Development of a 200K SNP Array for Atlantic Salmon: Exploiting Across Continents Genetic Variation.
J. M. Yañez1,2, S. Naswa1, M. E. López1, L. Bassini1,2, M. E. Cabrejos, J. Gilbey2, L. Bernatchez3, A. Norris4, C. Soto4, J. Eisenhart5, B. Simpson1, R. Neira6,7, J. P. Lhorente2, P. Schnable4,10,11, S. Newman1, A. Mileham2 and N. Deeb3, 1University of Chile, Santiago, Chile, 2Aquainnovo, Puerto Montt, Chile, 3Genus, plc, Hendersonville, TN, 4Marine Scotland Science, Perth, United Kingdom, 5Université Laval, Québec, QC, Canada, 6Marine Harvest, Dublin, Ireland, 7Camanchaca, Puerto Montt, Chile, 8GeneSeek, a Neogen Company, Lincoln, NE, 9University of Chile, Aquainnovo, Santiago, Chile, 10Data2Bio LLC, Ames, IA, 11Iowa State University, Ames, 2Genus plc, DeForest, WI

J. J. Tosh1, R. V. Ventura2,3, K. P. Ang1, J. A. K. Elliott1, M. P. Kent1, S. Lien1, E. G. Boullding1, and L. R. Schaeffer1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Beef Improvement Opportunities, Guelph, ON, Canada, 3Cooke Aquaculture, Blacks Harbour, NB, Canada, 4Centre for Integrative Genetics, Norwegian University of Life Sciences, Ås, Norway, 5Department of Integrative Biology, University of Guelph, Guelph, ON, Canada

11:30 AM 265 Genome Wide Association Analysis for Resistance to Sea Lice in Atlantic Salmon: Application of a Dense SNP Array.
R. D. Houston1, S. C. Bishop1, D. R. Guy2, A. E. Tinch2, J. B. Taggart1, J. E. Bron1, A. Downing1, M. J. Stear2, K. Garbit1 and A. Hamilton1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Landcatch Natural Selection, Stirling, United Kingdom, 3Institute of Aquaculture, School of Natural Sciences, University of Stirling, Stirling, United Kingdom, 4Edinburgh Genomics, University of Edinburgh, Edinburgh, United Kingdom, 5University of Glasgow, Glasgow, United Kingdom

11:45 AM 266 RAD-Seq Mapping of Spontaneous Masculinization in XX Doubled Haploid Rainbow Trout Lines.

Breeding Objectives and Economics of Breeding Schemes
Chair: Jack C. M. Dekkers, Iowa State University
Bayshore Grand Ballroom B-C

10:30 AM 001 How to Select the Best Bulls Worldwide for a Particular National Market.
C. Patry1 and V. Ducrocq4, 1INRA, UMR 1313 GABI, Jouy-en-Josas, France, 2INRA, UMR 1313 GABI, Jouy-en-Josas, France

10:45 AM 002 Factors Affecting Ratings of Dairy Bulls across New Zealand Dairy Farm Systems.
B. Santos1, T. Byrne1, B. Visser1, J. Bryant1 and P. Amer1, 1AbacusBio Limited, Dunedin, New Zealand, 2DairyNZ, Hamilton, New Zealand

11:00 AM 003 Economic Breeding Objectives for Canadian Lamb.
C. D. Quinton1, D. Kennedy2, K. Stachowicz1,3 and S. P. Miller4, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Ontario Ministry of Agriculture and Food, Guelph, ON, Canada, 3AbacusBio Limited, Dunedin, New Zealand, 4AgResearch, Invermay, Mosgiel, New Zealand

11:15 AM 004 Optimal Breeding Strategies for Sheep should consider Variation in Feed Availability.
G. Rose1,2, H. A. Mulder1, J. van der Werf1 and J. A. M. van Arendonk1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Sheep CRC, Armidale, Australia, 3Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 4University of New England, Armidale, Australia
Multiple Regression and Mediator Variables can be used to Avoid Double Counting when Economic Values are Derived using Stochastic Herd Simulation.
S. Østergaard1, J. Ettema2,3, L. Hjortø1, J. Pedersen1 and M. K. Sørensen1,3, 1Aarhus University, Tjele, Denmark, 2SimHerd Inc., Tjele, Denmark, 3Knowledge Centre for Agriculture, Aarhus, Denmark

S. M. Mbuku1, I. S. Kosgey2, O. Mwai3 and A. K. Kahi4, 1Kenya Agricultural Research Institute, National Beef Research Centre, Nakuru, Kenya, 2Laikipia University, Nyahururu, Kenya, 3International Livestock Research Institute, Nairobi, Kenya, 4Egerton University, Njoro, Kenya

Symposium: Leveraging the Poultry Genome Assembly
Chair: Hans H. Cheng, USDA, ARS, ADOL
Bayshore Grand Ballroom D

Allele-Specific Expression Screening Demonstrates that Variation in Genetic Resistance to Marek's Disease in Chicken is Mainly Controlled at the Transcriptional Level.
H. H. Cheng1, USDA, ARS, ADOL, East Lansing, MI

mRNAseq-based Functional and Pathway Analysis in Chicken is Sensitive to the Method Used to Construct the Reference Transcriptome.
L. Preeyanon1, H. H. Cheng2 and C. T. Brown2,1, 1Michigan State University, East Lansing, 2USDA, ARS, ADOL, East Lansing, MI

Whole Transcriptome Sequencing in Reciprocal Crosses Suggests Parent-of-Origin Effects on Gene Expression in the Chicken Genome.
F. Lopes Pinto1, A. M. Molin1, E. R. Gilbert2, C. Honaker2, P. B. Siegel2, G. Andersson3, L. Andersson3 and D. J. de Koning4, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2Virginia Polytechnic Institute and State University, Blacksburg, 3Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden

Symposium: Management of Animal Genetic Resources
Chair: Harvey D. Blackburn, USDA-ARS-National Animal Germplasm Program
Bayshore Grand Ballroom E-F

The Global Plan of Action for Animal Genetic Resources: its History and Future.
P. Boettcher1, I. Hoffmann, R. Bauning, D. Pilling, M. Wieczorek and B. Scherf, Food and Agriculture Organization of the United Nations, Rome, Italy

Status and Gaps in Characterization of Animal Genetic Resources.
M. Tixier-Boichard1, INRA, AgroParisTech, Jouy-en-Josas, France

Conservation of Animal Genetic Resources (AnGR): the Next Decade.
S. R. Paiva1, C. M. Pimentel2 and H. D. Blackbum1, 1Embrapa - Labex - Secretariat International Affairs, Brasilia, Brazil, 2Università de Brasilia, Brasilia, Brazil, 3USDA-ARS-National Animal Germplasm Program, Fort Collins, CO

Symposium: Statistical Methods for Genomic Prediction
Chair: Roel F. Veerkamp, Wageningen University
Stanley Park Ballroom

Bayesian Prediction Combining Genotyped and Non-Genotyped Individuals.
D. J. Garrick1, J. C. M. Dekkers2, B. L. Golden3 and R. L. Fernando2,1, 1Iowa State University, Ames, 2Calpoly, San Luis Obispo, CA
11:00 AM 054 Genomic Evaluation using QTL Information.
V. Ducrocq, P. Croiseau, A. Baur, R. Santillan, S. Fritz, and D. Boichard, INRA, UMR1313 GABI, Jouy-en-Josas, France, INRA UMR 1313 GABI, Jouy-en-Josas, France

11:30 AM 055 Genomic Heritability: What Is It?.
G. de los Campos, D. A. Sorensen and D. Gianola, University of Alabama at Birmingham, Birmingham, AL, Aarhus University, Tjele, Denmark, University of Wisconsin, Madison

Adaptation and Selection in Harsh Environments
Chair: Susan J. Lamont, Iowa State University
Cypress Room

1:30 PM 030 Genotype x Climate Interactions for Protein Yield using Four European Holstein populations.
H. Hammami, M. J. Carabaño, B. Logar, M. L. Vanrobaey and N. Gengler, University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium, National Fund for Scientific Research, Brussels, Belgium, INIA, Madrid, Spain, Agricultural Institute of Slovenia, Ljubljana, Slovenia

1:45 PM 031 Phenotypic Analysis of Pulmonary Arterial Pressure and Feed Intake Data in Angus Cattle.
R. J. Boldt, M. M. Culbertson, N. F. Berge, M. G. Thomas, T. N. Holt, S. E. Speidel and R. M. Enns, Colorado State University, Department of Animal Sciences, Fort Collins, Colorado State University, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO

2:00 PM 032 Breeding Objectives for Red Maasai and Dorper Sheep in Kenya – a Participatory Approach.

2:15 PM 033 Selection Criteria for Heat Tolerance in Dairy Cattle Production.
M. J. Carabaño, K. Bachaghia, M. Ramón and C. J. Díaz, INIA, Madrid, Spain, CERSYRA, Valdepeñas, Spain

2:30 PM 034 A Running Breeding Program for Indigenous Chickens in Ethiopia: Evaluation of Success.
W. E. Woldegiorgis, ILRI-Addis, Addis Ababa, Ethiopia; Wageningen University, Wageningen, Netherlands

2:45 PM 035 Genetic Improvement of Meat Production in Reindeer.
K. Muuttoranta, O. Holand, K. H. Roed, M. Nieminen and A. Mäki-Tanila, MTT Agrifood Research Finland, Jokioinen, Finland, Norwegian University of Life Sciences, Ås, Norway, Norwegian University of Life Sciences, Oslo, Norway, Finnish Game and Fisheries Research Institute, Inari, Finland, MTT Agrifood Research, Jokioinen, Finland

Alternative Methods for Analysis of Disease Phenotypes
Chair: Stephen C. Bishop, The Roslin Institute and University of Edinburgh
Bayshore Grand Ballroom E-F

1:30 PM 088 Genetic Selection for Disease Resistance and Tolerance in Pigs using Reproduction Records.

1:45 PM 089 Genome Wide Association Analysis of Lung Lesions in Cattle using Sample Pooling.

2:00 PM 090 Definition and Utilization of Among Hosts Heritable Variation in Reproduction Ratio R0 for Infectious Diseases.
M. Anche, M. C. M. de Jong and P. Bijma, Animal Breeding and Genomics Centre, Quantitative Veterinary Epidemiology Group, Wageningen University, Wageningen, Netherlands, Quantitative Veterinary Epidemiology
2:15 PM 091 Dynamic and Genetic Signatures of Resistance and Tolerance of Pigs to PRRS.  
G. Lough1, I. Kyriazakis1, S. Forni2 and A. Doeschl-Wilson3, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Newcastle University, Newcastle upon Tyne, United Kingdom, 3Genus Plc, Hendersonville, TN

2:30 PM 092 Mediation Analysis of Milk Losses Associated With Clinical Mastitis.  
J. Detilleux1*, J. P. Kastelic2 and H. Barkema2, 1University of Liege, Liege, Belgium, 2Agriculture & Agri-Food Canada, Calgary, AB, Canada, 3University of Calgary, Calgary, AL, Canada

2:45 PM 093 Simultaneous Inference of Genetic Parameters Underlying Susceptibility and Infectivity of Livestock from Epidemiological Data.  
O. Anacleto1, D. Lipschutz-Powell1, L. A. García-Cortés2, J. A. Woolliams1 and A. Doeschl-Wilson1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2SGIT - INIA, Ministerio de Ciencia e Innovación, Madrid, Spain

Improving Difficult Traits in Beef Cattle  
Chair: Stephen P. Miller, AgResearch  
Bayshore Grand Ballroom B-C

1:30 PM 232 Selection Enhanced Estimates of μ-Calpain, Calpastatin, and Dacetylgluceral O-Acyltransferase 1 Genetic Effects on Pre-weaning Performance, Carcass Quality Traits, and Residual Variance of Tenderness in Composite MARC III Beef Cattle.  

1:45 PM 233 Genetic Correlations Between Carcass and Meat Quality Traits of Adult Cows and Similar Traits of Young Bulls in French Charolais Beef Cattle.  
C. Aviles1, A. Vinet1, R. Saintilan1, B. Picard1, D. Maupetit1 and G. Renand2, 1Universidad de Córdoba, Cordoba, Spain, 2INRA, UMR1313 GABI, Jouy en Josas, France, 3UNCEA, Jouy-en-Josas, France, 4INRA, Thieix, France, 5INRA, Bourges, France, 6INRA, Jouy en Josas, France

2:00 PM 234 Phenotypic and Genetic Analysis of Meat Eating Quality Traits in Irish Cattle.  
F. Kearney1, A. P. Moloney1, R. Prendiville2, P. Allen1, B. Meredith1 and S. Conroy2, 1Irish Cattle Breeding Federation, Cork, Ireland, 2TEAGASC, Dunsany, Meath, Ireland, 3Teagasc, Grange, Co. Meath, Ireland, 4Teagasc, Ashstown, Dublin 15, Ireland, 5Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland

2:15 PM 235 Genomic Wide-Selection for Tick Resistance in Hereford and Brahford Cattle via Reaction Norm Models.  
R. R. Mota1,2, R. J. Tempelman3, F. F. Cardoso1, I. Aguilar2 and P. S. Lopes1, 1Universidade Federal de Viçosa, Viçosa, Minas Gerais State, Brazil, 2Michigan State University, East Lansing, 3Embrapa Southern Region Animal Husbandry, Bage, Brazil, 4INIA, Las Brujas, Uruguay, 5Universidade Federal de Viçosa, Viçosa, Brazil

2:30 PM 236 Angus Cattle at High Altitude: Genetic Relationships and Initial Genome-Wide Association Analyses of Pulmonary Arterial Pressure.  
R. R. Cockrum1,2, X. Zeng3, N. F. Berge1, J. M. Neary1, F. B. Garry1, T. N. Holt4, H. D. Blackburn5, S. P. Thomas5, S. E. Speidel1, D. J. Garrick6, R. M. Enns2 and M. G. Thomas2, 1Virginia Polytechnic Institute and State University, Blacksburg, 2Colorado State University, Department of Animal Sciences, Fort Collins, 3Colorado State University, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO, 4Colorado State University, Fort Collins, 5USDA-ARS-National Animal Germplasm Program, Fort Collins, CO, 6Iowa State University, Ames

2:45 PM 237 A Haplotype Diagnostic for Polled in Australian Beef Cattle.  
E. K. Piper*, The University of Queensland, School of Veterinary Science, Gatton, Australia
Symposium: Genomic Selection in Sheep

Chair: Julius H.J. van der Werf, CRC for Sheep Industry Innovation

Bayshore Grand Ballroom A

1:30 PM 332 Toward Genomic Breeding Programs in French Dairy Sheep and Goats.
H. Larroque1,2, F. Barillet1, G. Balocchi1, J. M. Astruc2, D. Buisson1, F. Shumbusho1,2, V. Clément2, G. Lagriﬀfout2, I. Palhière1, R. Rupp1, C. Carillier1, C. Robert-Granié1 and A. Legarra1, 1Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy, 2Institut de l’Elevage, Castanet-Tolosan, France, 3Institut de l’Elevage, Castanet-Tolosan, France

2:00 PM 333 Genomic Selection in New Zealand Dual Purpose Sheep.
K. G. Dodds1, B. Auveray2, M. A. Lee2, S. A. N. Newman1 and J. C. McEwan2, 1AgResearch, Mosgiel, New Zealand, 2AgResearch, Invermay, New Zealand

2:30 PM 334 Genomic Evaluations in the Australian Sheep Industry.
A. A. Swan1, D. Brown1, H. D. Daetwyler2, M. J. Kelly3, B. J. Hayes4, N. Moghaddar1 and J. van der Werf5, 1Animal Genetics and Breeding Unit, Armidale, Australia, 2CRC for Sheep Industry Innovation, Armidale, Australia, 3The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia, 4Department of Environment and Primary Industries, Bundoora, Australia, 5Cooperative Research Centre for Sheep Industry Innovation, Armidale, Australia, 6School of Environmental & Rural Science, University of New England, Armidale, Australia

Symposium: Improving Nutrient Utilization and Reducing the Environmental Impact of Dairy Operations through Genetic or Genomic Selection

Statistical and Genomic Tools for Mapping QTL and Genes (Swine, Poultry, Sheep and Mice)

Chair: Michel Georges, University of Liège

Bayshore Grand Ballroom D

1:30 PM 184 Mapping Resolution in Single and Multiple Porcine F2 Populations using Genome Sequence Marker Panels.
J. Bennewitz1 and R. Wellmann, Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

1:45 PM 185 Meta-Analysis of Genome Wide Association Studies for Pork Quality Traits.
Y. L. Bernal Rubio1,2, J. L. Gualdrón Duarte3, R. O. Bates4, C. W. Ernst1, D. Nonneman1, G. A. Rohrer1, D. A. King1, S. D. Shackelford1, T. L. Wheeler3, R. J. C. Canter1 and J. P. Steibel3, 1Michigan State University, East Lansing, 2Department of Animal Science, University of Buenos Aires, Buenos Aires, Argentina, 3USDA/ARS, Clay Center, NE

2:00 PM 186 The Collaborative Cross – A Next Generation Mouse Genetic Resource Population for Precision Agriculture through Deep Genetic Analysis.
M. Soller1, H. Abu-Toamih-Atamni2 and F. Iraqi3, 1Hebrew University of Jerusalem, Jerusalem, Israel, 2Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel

M. G. Usai1,2, S. Casu, T. Sechi, S. Miari, G. Mulas, G. B. Congiu, S. Sechi, S. L. Salaris and A. Carta, Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy

2:30 PM 188 Investigating a Highly Significant QTL for Milk Protein Content Segregating in Sarda Sheep Breed Close to the Caseins Cluster Region by Whole Genome Re-Sequencing of Target Animals.
S. Casu1,2, T. Sechi1, M. G. Usai1, S. Miari1, M. Casula1, G. Mulas1, R. Giannico1, B. Lazzari1, A. Stella1,2 and A. Carta1, 1Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy, 2Fondazione Parco Tecnologico Padano, Lodi, Italy, 3IBBA CNR, Lodi, Italy

2:45 PM 189 Footprints of Parallel Selection Revealed by Direct Sequencing in Egg Laying Chicken.
S. Qanbari1, T. Sechi1, M. G. Usai1, S. Miari1, M. Casula1, G. Mulas1, R. Giannico1, B. Lazzari1, A. Stella1,2 and A. Carta1, 1Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy, 2Fondazione Parco Tecnologico Padano, Lodi, Italy, 3IBBA CNR, Lodi, Italy

Symposium: Genomic Selection in Sheep

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Bayshore Grand Ballroom D

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Symposium: Genomic Selection in Sheep

Chair: Julius H.J. van der Werf, CRC for Sheep Industry Innovation

Bayshore Grand Ballroom A

1:30 PM 332 Toward Genomic Breeding Programs in French Dairy Sheep and Goats.
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Symposium: Improving Nutrient Utilization and Reducing the Environmental Impact of Dairy Operations through Genetic or Genomic Selection
Chair: Kent A. Weigel, University of Wisconsin
Stanley Park Ballroom

1:30 PM 285 Improving Biological and Economic Aspects of Production Efficiency through Genetic Selection and Genome-Guided Replacement Management.
K. A. Weigel1, C. Yao1, P. C. Hoffman1, L. E. Armentano1, D. M. Spurlock2, R. J. Tempelman2 and M. J. VandeHaar2,
1University of Wisconsin, Madison, 2Iowa State University, Ames, 3Michigan State University, East Lansing

2:00 PM 286 Genetic and genomic solutions to improve feed efficiency and reduce environmental impact of dairy cattle.
Y. de Haas1, J. E. Pryce1, D. P. Berry1 and R. F. Veerkamp1, Animal Breeding and Genomics Centre, Wageningen UR
Livestock Research, Wageningen, Netherlands, 2Biosciences Research Division, Department of Environment and
Primary Industries, Victoria, Australia, 3Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark,
Fermoy, Co. Cork, Ireland, 4Animal Breeding and Genomics Centre, Wageningen University, Wageningen,
Netherlands

2:30 PM 287 Genetic Architecture and Temporal Basis of Feed Efficiency in Dairy Cattle.
D. M. Spurlock1, R. J. Tempelman2, K. A. Weigel1, L. E. Armentano1, G. R. Wiggins3, R. F. Veerkamp2, Y. de Haas4, M.
P. Coffey1, E. E. Connor5, M. D. Hanigan5, C. R. Staples6 and M. J. VandeHaar2, 1University of Wisconsin, Madison,
2Animal Improvement Programs Laboratory, Agricultural Experimental Station, USDA, Beltsville, MD, 3Animal Breeding and Genomics Centre,
Wageningen University, Wageningen, Netherlands, 4Animal Breeding and Genomics Centre, Wageningen UR Livestock
Research, Wageningen, Netherlands, 5SRUC, Edinburgh, United Kingdom, 6USDA-ARS, Bovine Functional Genomics
Laboratory, Beltsville, MD, 7Virginia Polytechnic Institute and State University, Blacksburg, 8Dept. of Animal
Sciences, University of Florida, Gainesville

Genetics of Trait Complexes: Growth and Development
Chair: Michael D. MacNeil, Delta G
Bayshore Grand Ballroom A

4:00 PM 126 Muscle Transcriptomic Investigation of Late Fetal Development and Determinism of Maturity at Birth in Two
Extreme Breeds: Meishan and Large White.
V. Voillet1, M. San Cristobal1,2, Y. Lippi1, P. Martin1, N. Iannuccelli1, Y. Billon1, L. Canario1 and L. Liaubet1,
1INRA, Castanet Tolosan, France, 2INSA - IMT, Toulouse, France, 3INRA, Toulouse, France, 4INRA UE1372, F-17700
Surgères, France

L. J. Kogelman1, D. V. Zhernakova2, H. J. Westra2, S. Cirera2, M. Fredholm1, L. Franke3 and H. N. Kadarimdeent3,
1Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of
Copenhagen, Copenhagen, Denmark, 2Department of Genetics, University Medical Center Groningen, Groningen,
Netherlands

4:30 PM 128 Transcriptomic Prediction of Piglet Vitality from Umbilical Cord Blood of Purebreds and Crossbreds born in
the Same Litter – Comparison of Meishan and Large White Sows.
L. Canario1, V. Voillet2, N. Iannuccelli2, Y. Lippi2, P. Martin2, Y. Billon2, M. San Cristobal2 and L. Liaubet2,
1INRA UMR1388, F-3126 Castanet-Tolosan, France, 2INRA, Castanet-Tolosan, France, 3INRA, Toulouse, France,
4INRA, Toulouse, France, 5INRA UE1372, F-17700 Surgères, France, 6INSA - IMT, Toulouse, France

4:45 PM 129 The First Whole Transcriptome Profiling of Fibro/adipogenic Progenitor Cells and Discovery of Essential Genes
Potentially Favorable to either Myogenesis or Adipogenesis in Muscle.
R. Li1, S. Dayal2, X. Zhou1, X. Fu1, J. J. Michal1, W. Khan1, M. Du1 and Z. Jiang1, 1Washington State University,
Pullman, 2ICAR Research Complex for Eastern Region, Bihar, India, 3University of Sargodha, Sargodha, Pakistan

5:00 PM 130 Genomic Imprinting as a Potential Source of Missing Heritability of Mouse Body Mass Index.
Y. Hu1, G. J. M. Rosa and D. Gianola, University of Wisconsin, Madison

5:15 PM 131 A Comprehensive Expression Profile of MicroRNAs in Porcine Developing Thyroid.
Y. Shen1, College of Animal Science, Zhejiang University, Hangzhou, China
5:30 PM 132 The Minipig Genome Harbors Regions of Selection for Growth.  
C. H. U. W. Reimer\textsuperscript{1}\textsuperscript{*}, C. J. Rubin\textsuperscript{1}, S. Weigend\textsuperscript{2}, K. H. Waldmann\textsuperscript{1}, O. Distl\textsuperscript{1} and H. Simianer\textsuperscript{1}, \textsuperscript{1}Georg-August-University, Göttingen, Germany, \textsuperscript{2}Uppsala University, Uppsala, Sweden, \textsuperscript{1}Institute of Farm Animal Genetics of the Friedrich-Loeffer-Institute, Neustadt-Mariensee, Germany, \textsuperscript{1}University of Veterinary Medicine, Hannover, Germany

5:45 PM 133 Searching for Causal Networks Involving Latent Variables in Complex Traits: An Application to Growth, Carcass, and Meat Quality Traits in Pig.  
F. Peñagaricano\textsuperscript{1}\textsuperscript{*}, B. D. Valente\textsuperscript{1}, J. P. Steibel\textsuperscript{2}, R. O. Bates\textsuperscript{2}, C. W. Ernst\textsuperscript{2}, H. Khatibi\textsuperscript{1} and G. J. M. Rosa\textsuperscript{1}, \textsuperscript{1}University of Wisconsin, Madison, \textsuperscript{2}Michigan State University, East Lansing

Improving Accuracy of Genomic Prediction  
Chair: Dorian J. Garrick, Iowa State University
Bayshore Grand Ballroom D

4:00 PM 056 Joint Genomic Evaluation of Cows and Bulls with BayesD for Prediction of Genotypic Values and Dominance Deviations.  
R. Wellmann\textsuperscript{1}\textsuperscript{*}, J. Ertl\textsuperscript{2}, R. Emmerling\textsuperscript{2}, C. Edel\textsuperscript{2}, K. U. Götz\textsuperscript{2} and J. Bennewitz\textsuperscript{1}, \textsuperscript{1}Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany, \textsuperscript{2}Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Grub, Germany

4:15 PM 057 Size of Required Reference Population Updates to Achieve Constant Genomic Prediction Accuracy Across Generations.  
M. Pszczola\textsuperscript{1}, T. Strabel\textsuperscript{1} and M. P. L. Calus\textsuperscript{2}, \textsuperscript{1}Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poznan, Poland, \textsuperscript{2}Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

4:30 PM 058 Genomic Selection of Pork pH in Purebred Pigs for Crossbred Performance.  
Y. Miar\textsuperscript{1}, G. Plastow\textsuperscript{1}, H. Bruce\textsuperscript{2}, R. Kemp\textsuperscript{2}, P. Charugu\textsuperscript{1}, C. Zhang\textsuperscript{1}, A. Huisman\textsuperscript{1} and Z. Wang\textsuperscript{1}, \textsuperscript{1}University of Alberta, Edmonton, AB, Canada, \textsuperscript{2}Genesis Genetics Inc., Oakville, MB, Canada, \textsuperscript{1}Hypor Inc, Regina, SK, Canada, \textsuperscript{1}Hendrix Genetics, Boxmeer, Netherlands

4:45 PM 059 Prediction of Heterosis in White Leghorn Crossbreds using Paternal 60K SNP Genotypes.  
E. N. Amuzu-Aweh\textsuperscript{1}\textsuperscript{2}\textsuperscript{*}, H. Bovenhuis\textsuperscript{3}, D. J. de Koning\textsuperscript{3} and P. Bijma\textsuperscript{1}, \textsuperscript{1}Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, \textsuperscript{2}Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

5:00 PM 060 Improving Genomic Prediction for Danish Jersey using a Joint Danish-US Reference Population.  
G. Su\textsuperscript{1}, U. S. Nielsen\textsuperscript{1}, G. R. Wiggans\textsuperscript{2}, G. P. Aamand\textsuperscript{2}, B. Guldbrandtsen\textsuperscript{3} and M. S. Lund\textsuperscript{4}, \textsuperscript{1}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, \textsuperscript{2}Knowledge Center for Agriculture, Aarhus, Denmark, \textsuperscript{3}Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, \textsuperscript{4}Nordic Cattle Genetic Evaluation, Aarhus, Denmark

5:15 PM 061 Maximizing Crossbred Performance through Purebred Genomic Selection.  
H. Esfandyari\textsuperscript{1}\textsuperscript{2}\textsuperscript{*}, A. C. Sørensen\textsuperscript{1} and P. Bijma\textsuperscript{1}, \textsuperscript{1}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, \textsuperscript{2}Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, \textsuperscript{1}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

5:30 PM 062 Genomic Estimation of Additive and Dominance Genetic Variance and their Effect on the Accuracy of Genomic Prediction of Sheep.  
N. Moghaddar\textsuperscript{1}\textsuperscript{2} and J. van der Werf\textsuperscript{3}, \textsuperscript{1}School of Environmental & Rural Science, University of New England, Armidale, Australia, \textsuperscript{2}Sheep-CRC, Armidale, Australia, \textsuperscript{3}University of New England, Armidale, Australia

5:45 PM 063 Genomic Prediction using QTL Derived from Whole Genome Sequence Data.  
R. F. Brøndum\textsuperscript{1}, G. Su, L. Janss, G. Sahana and M. S. Lund, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark
Sheep and Goats Breeding (1)
Chair: John C. McCowan, AgResearch
Cypress Room

4:00 PM 335 Genomic Selection Experiment in Lacaune Dairy Sheep: Progeny Test Results of Rams Initially Selected either on Parent Average or on Genomic Prediction.
G. Baloche1, J. M. Astruc2, P. Boulenc3, B. Giral-Viala1, P. Guibert4, P. Panis5, A. Legarra7 and F. Barillet5, 1INRA, Toulouse, France, 2Institut de l’Elevage, Castanet-Tolosan, France, 3Ovitec, Rodez, France, 4Confédération Générale de Roquefort, Millau, France, 5INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France

4:15 PM 336 Genome-Wide Scan for Carcass Composition as Assessed by X-Ray Computed Tomography (CT) in Scottish Blackface Lambs.
O. Matika1, M. Anselme-Moizan2, V. Riggio1 and S. C. Bishop1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2INP, Ecole Nationale Vétérinaire, Toulouse, France

C. Carillier*, H. Larroque and C. Robert-Granié, INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France

4:45 PM 338 Estimation of Genomic Breeding Values for Milk Yield in UK Dairy Goats.
S. Mucha1, R. Mrode, M. Coffey and J. Conington, Scotland’s Rural College, Easter Bush, United Kingdom

5:00 PM 339 Exploring the Genetic Variation between Sarda and Lacaune Dairy Sheep Breeds by Genome Wide Association Study on Economic Traits.
A. Carta1, M. G. Usai1, T. Sechi1, S. Miari1, S. Sechi1, S. L. Salaris1, G. Mulas1, F. Bariller1, J. M. Elsen3 and S. Casu1, 1Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy, 2INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, 3INRA, UMR1388 GenPhySE, Castanet-Tolosan, France

5:15 PM 340 Genomic Wide Association for Heat Stress Tolerance/Susceptibility in Florida Dairy Goats.
A. Zidi1, H. Abo-Shady1, A. Molina1, A. Menéndez-Buxadera1, M. Sánchez-Rodríguez2, C. J. Díaz2, M. J. Carabaño2 and J. M. Serradilla2, 1Universidad de Córdoba, Córdoba, Spain, 2INIA, Madrid, Spain

5:30 PM 341 Expression of the Ovine Hippocampal Glucocorticoid Receptor (GR) and Mineralocorticoid Receptor, and Adrenal Melanocortin 2 Receptor and GR Genes in Offspring Born to Ewes Supplemented with Fishmeal and Challenged with Endotoxin During Late Pregnancy.
R. E. Fisher1, M. Or’Rashid1, O. AlZahal1, M. Quinton1, B. W. McBride1, H. J. Boermans2 and N. A. Karrow1, 1Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, 2Department of Biomedical Sciences, University of Guelph, Guelph, ON, Canada

5:45 PM 342 Mitochondrial DNA Diversity in Nepalese Goats.
N. A. Gorkhali*, Nepal Agriculture Research Council, Kathmandu, Nepal; Chinese Academy of Agriculture Sciences, Beijing, China

Symposium: Genetics of Trait Complexes - Feed Intake and Efficiency
Chair: Donagh P. Berry, Teagasc, Moorepark
Stanley Park Ballroom

4:00 PM 109 Feed Efficiency in Growing and Mature Animals.
D. P. Berry1 and J. E. Pryce2, 1Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia

4:30 PM 110 Lessons Learnt from 25 Years of Feed Efficiency Research in Australia.
P. F. Arthur1, *J. E. Pryce2 and R. M. Herd3, 1NSW Department of Primary Industries, Narellan, NSW, Australia, 2Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, 3NSW Department of Primary Industries, Armidale, Australia
5:00 PM  111  Selection for Improved Efficiency in Poultry, Progress To-Date and Challenges for the Future.
  B. J. Wood¹ ² and O. W. Willems³, ³Hybrid Turkeys, Kitchener, ON, Canada, ²Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

5:30 PM  112  An Alternative Approach to Modeling Genetic Merit of Feed Efficiency in Dairy Cattle.
  Y. Lu*, Michigan State University, East Lansing

5:45 PM  113  Increasing the Accuracy of Genomic Predictions for RFI in Dairy Cattle through using Genomic Information from Beef Breeds.
  M. Khansifid¹ ², J. E. Pryce¹, S. Bolormad¹, S. P. Miller³, Z. Wang¹, C. Li² and M. E. Goddard³, ³The University of Melbourne, Melbourne, Australia, ²Department of Environment and Primary Industries, Melbourne, Australia, ³Dairy Futures Cooperative Research Centre (CRC), Melbourne, Australia, ³Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, ³CRC for Sheep Industry Innovation, Armidale, Australia, ³Centre for Genetic Improvement of Livestock - University of Guelph, Guelph, ON, Canada, ³University of Alberta, Edmonton, AB, Canada, ³The Department of Environment and Primary Industries, Bundoora, Australia

Symposium: Omics and Swine
Chair: Graham S. Plastow, University of Alberta
Bayshore Grand Ballroom B-C

4:00 PM  355  New Strategies Accelerating Progress from QTL to QTN: Example of the Identification of Causal Variants underlying Three Complex Traits in Pigs.
  L. Huang*, Jiangxi Agricultural University, NanChang, China

4:30 PM  356  SNP Effects Depend on Genetic and Environmental Context.
  J. W. M. Bastiaansen¹, H. Bovenhuis¹, M. S. Lopes¹ ², F. F. Silva¹, H. J. Megens¹, M. P. L. Calus¹, ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²TOPIGS Research Center IPG, Beuningen, Netherlands, ³Universidade Federal de Viçosa, Viçosa, Brazil, ¹Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

5:00 PM  357  Beyond Genomic Selection.
  B. P. Kinghorn¹, University of New England, Armidale, Australia

5:30 PM  358  The Influence of Host’s Genetics on the Gut Microbiota Composition in Pigs and its Links with Immunity Traits.
  J. Estellé¹, N. Machª², Y. Ramayo-Calda², F. Levenez², G. Lemonnier¹, C. Denis¹, J. Dorè¹, C. Larzi², P. Lepea² and C. Rogel-Gaillard², ¹INRA, UMR1313 GABI, Jouy-en-Josas, France, ²INRA, UMR1319 MICALIS, Jouy-en-Josas, France

5:45 PM  359  Genome Wide Perspective of Genetic Variation in Pig Metabolism and Production Traits.
  L. Fontanesi³, S. Bovo¹, G. Mazzoni¹, A. B. Samorè¹, G. Schiavi¹, E. Scotti¹, F. Fanelli², F. Bertolini¹, M. Gallo¹, L. Buttazzoni³, G. Galimberti³, D. G. Calò³, M. Mezzullo³, P. L. Martelli³, R. Casadio³, U. Pagotto³, V. Russo³ and S. Dall’Olio³, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ²Department of Surgical and Medical Sciences, Endocrinology Unit, University of Bologna, Bologna, Italy, ³ANAS, Roma, Italy, ³Consiglio per la Ricerca e la Sperimentazione in Agricoltura - Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Roma, Italy, ³Department of Statistical Sciences “Paolo Fortunati”, University of Bologna, Bologna, Italy, ²Biocomputing Group, University of Bologna, Bologna, Italy

Symposium: Statistical Methods - Linear and Nonlinear Models: Inference
Chair: Daniel Gianola, University of Wisconsin
Bayshore Grand Ballroom E-F

4:00 PM  202  Statistical Problems in Livestock Population Genomics.
  H. Simianer¹, Y. Ma² and S. Qambari¹, ¹Georg-August-University, Göttingen, Germany, ²China Agricultural University, Beijing, China, ¹Georg-August University, Göttingen, Germany
New Methods for Capturing Unidentified Genetic Variation underlying Infectious Disease in Livestock Populations.
A. Doeschl-Wilson, D. Lipschutz-Powell, O. Anacleto, L. A. García-Cortés, G. Lough, A. Lengeling, S. Bergmann and J. A. Woolliams, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2SGIT - INIA, Ministerio de Ciencia e Innovación, Madrid, Spain, 3Helmholtz Centre for Infection Research, Braunschweig, Germany

My P Value is Lower than Your P Value! Beyond GWAS in Livestock Genomics.
J. Szyda, M. Fraszczak, R. Giannico, S. Kaminski, M. Mielczarek, G. Minozzi, E. L. Nicolazzi, T. Suchocki, K. Wojdak-Maksymiec and A. Zarnecki, 1Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, 2National Research Institute of Animal Production, Cracow-Balice, Poland, 3Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, 4Fondazione Parco Tecnologico Padano, Lodi, Italy, 5University of Warmia and Mazury, Olsztyn, Poland, 6Parco Tecnologico Padano, Lodi, Italy, 7West Pomeranian University of Technology, Szczecin, Poland

Heritability of Complex Human Diseases in the UK Biobank.
M. Muñoz, R. Pong-Wong, C. Haley and A. Tenesa, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Roslin, United Kingdom, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 3MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, 4The Roslin Institute and R(D)SVS & The MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine, University of Edinburgh, Midlothian, United Kingdom
Tuesday, August 19, 2014

Plenary Speaker - Tuesday

Chairs: E. John Pollak, USDA, ARS, U.S. Meat Animal Research Center and Filippo Miglior, Canadian Dairy Network and University of Guelph

Bayshore Grand Ballroom

8:30 AM  Plenary 2  Bridging the Gap Between Scientific Facts and Societal Perceptions about Agriculture.
 M. Lohuis*, Monsanto, St. Louis, MO

Genetics of Trait Complexes - Feed Intake and Efficiency (Cattle)
Chair: Donagh P. Berry, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark

Bayshore Grand Ballroom B-C

10:30 AM  114  Mid-Infrared Spectroscopy to Predict Feed Intake and Efficiency in Lactating Dairy Cows.
 S. McParland1, E. Kennedy1, S. Butler2, M. O'Donovan1, B. McCarthy1, J. E. Pryce3 and D. P. Berry2, 1Teagasc, Moorepark, Co. Cork, Ireland, 2Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 3Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia

10:45 AM  115  Breeding Value for Dry Matter Intake for Dutch Bulls based on DGV for DMI and BV for Predictors.
 R. F. Veerkamp1, M. P. L. Calus1, G. de Jong2, R. van der Linde1 and Y. de Haas1, 1Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 2CRV, Arnhem, Netherlands, 3CRV BV, Arnhem, Netherlands

11:00 AM  116  Deriving Genomic Breeding Values for Residual Feed Intake from Covariance Functions of Random Regression Models.
 A. B. Strathe1,2, T. Mark1, B. Nielsen1, D. N. Do1, H. N. Kadarmideen1 and J. Jensen1, 1Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 2Danish Agriculture & Food Council, Pig Research Centre, Copenhagen, Denmark, 3Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

11:15 AM  117  Collation of Data and Genetic Parameter Estimation in Different Experimental Canadian Beef Cattle Populations Measured for Feed Efficiency.
 J. Crowley*, University of Alberta, Edmonton, AB, Canada

 J. B. S. Ferraz1, M. H. A. Santana1, G. A. Oliveira Jr1, F. M. Rezende2, H. Fukumasa1, P. A. Alexandre1, A. S. M. Cesar2, M. E. Carvalho1, L. L. Coutinho1, J. P. Eler1, E. C. Mattos1, F. Baldi1 and D. J. Garrick6, 1NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 2Federal University of Uberlandia, Patos de Minas, Brazil, 3LZT/ESALQ/University of Sao Paulo, Piracicaba, Brazil, 4Universidade de Sao Paulo/Esalq, Piracicaba, Brazil, 5Universidade Estadual Paulista “Julio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 6Iowa State University, Ames

11:45 AM  119  Genome Wide Association Study for Feed Efficiency Traits in Beef Cattle using CNV.
 G. C. Márquez1, J. W. Keele2, L. A. Kuehn1, H. C. Freely2, A. K. Lindholm-Perry2 and R. M. Lewis2, 1ABS Global, DeForest, WI, 2USDA-ARS, Clay Center, NE, 3USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 4USDA, ARS, US MARC, Clay Center, NE, 5University of Nebraska, Lincoln, NE

Methods and Tools - Genome Sequencing
Chair: Ben J. Hayes, Department of Environment and Primary Industries

Bayshore Grand Ballroom D
10:30 AM 175 Identification and Comparison of MicroRNAs from Mammary Glands from Two Porcine Breeds using Solexa Deep-Sequencing technology.
J. Peng*1, College of Animal Sciences, Zhejiang University, Hangzhou, China

10:45 AM 176 Polymorphism and Mobilization of Ransposons in Bos taurus.
B. Guldbrandsen*, G. Sahana and M. S. Lund, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

11:00 AM 177 Consequences of Splitting Sequencing Effort over Multiple Breeds on Imputation Accuracy.
A. C. Bouwman*1 and R. F. Veerkamp, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

11:15 AM 178 Genomic Predictions using Whole Genome Sequence Data and Multi-breed Reference Populations.
O. O. M. Iheshiulor1, J. A. Woolliams2, X. Yu1, R. Wellmann1 and T. H. E. Meuwissen1, 1Norwegian University of Life Sciences, Ås, Norway, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 3Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

11:30 AM 179 Fast Imputation using Medium- or Low-Coverage Sequence Data.
P. M. VanRaden*1 and C. Sun2, 1Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, 2National Association of Animal Breeders, Columbia, MO

11:45 AM 180 A Gene Expression Atlas From Bovine RNAseq Data.

Linear and Nonlinear Models: Prediction
Chair: Marco C.A.M. Bink, Wageningen University
Bayshore Grand Ballroom A

10:30 AM 206 Using Random Forests (RF) To Prescreen Candidate Genes: A New Prospective for GWAS.
Y. Li1, J. Kijas1, J. M. Henshall2, S. A. Lehnert3, R. McCulloch4 and A. Reverter-Gomez4, 1CSIRO Animal, Food and Health Sciences, Brisbane, Australia, 2Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Armidale, Australia, 3CSIRO Food Futures Flagship, Brisbane, Australia, 4Pharmatics Limited, Edinburgh, United Kingdom

10:45 AM 207 Genomic Prediction of Health Traits in Humans: Demonstrating the Value of Marker Selection.
M. L. Bermingham1, R. Pong-Wong2, A. Spiliopoulou1, C. Hayward1, I. Rudan1, H. Campbell3, A. F. Wright1, J. F. Wilson1, F. V. Agakov1, P. Navarro2 and C. Haley1, 1MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 3Centre for Population Health Sciences, University of Edinburgh, Edinburgh, United Kingdom

11:00 AM 208 Extreme Learning Machine: A New Approach for Genomic Prediction of Complex Traits.
A. Ehret1, D. Hochstuhl2 and G. Thaller1, 1Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany, 2Institute for Theoretical Physics and Astrophysics, University Kiel, Kiel, Germany

11:15 AM 209 Improved Accuracy of Genomic Prediction for Traits with Rare QTL by Fitting Haplotypes.
X. Sun1, R. L. Fernando, D. J. Garrick and J. C. M. Dekkers, Iowa State University, Ames

11:30 AM 210 Correcting For Unequal Sampling in Principal Component Analysis of Genetic Data.
W. O. Burgos-Paz1, S. E. Ramos-Onsins2, M. Perez-Enciso2 and L. Ferretti2, 1Centre for Research in Agricultural Genomics, Bellaterra, Spain, 2Universitat Autònoma de Barcelona, Bellaterra, Spain, 3UMR 7138, UPMC and CIRB, College de France, Paris, France

11:45 AM 211 Evaluation of Antedependence Model Performance and Genomic Prediction for Growth in Danish Pigs.
L. Wang1, D. Edwards and L. Janss, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark
Symposium: Breeding of Companion Animals  
Chair: Sheila M. Schmutz, University of Saskatchewan  
Cypress Room

10:30 AM 276 Genomic Signatures of Selection in the Modern Horse.  
J. R. Mickelson*, J. L. Petersen, S. J. Valberg and M. E. McCue, University of Minnesota, Saint Paul

11:00 AM 277 Cat Domestication & Breed Development.  
L. A. Lyons*, Department of Veterinary Medicine & Surgery, College of Veterinary Medicine, University of Missouri - Columbia, Columbia, MO

11:30 AM 278 Genetic Interactions Among Three Pigmentation Loci in Domestic Dogs.  
S. M. Schmutz* and D. L. Dreger, University of Saskatchewan, Saskatoon, SK, Canada

Symposium: Genetics of Trait Complexes - Lactation  
Chair: Juan F. Medrano, University of California  
Bayshore Grand Ballroom E-F

10:30 AM 137 RNA Sequencing for the Analysis of Complex Traits in Milk: Detection of Bacteria.  
J. F. Medrano1, A. Canovas2 and A. Islas-Trejo2, 1University of California, Davis, 2University of California, Davis, CA

11:00 AM 138 Functional Variation in the Prolactin Receptor of Pigs.  
R. C. Hovey1, A. Schennink, M. K. VanKlompenberg, R. Manjarin and J. F. Trott, University of California, Davis, Davis, CA

11:30 AM 139 Rare Genetic Variants and the Regulation of Bovine Milk Composition.  
S. Davis* and M. Littlejohn, Livestock Improvement Corporation, Hamilton, New Zealand

Symposium: Genomic Tools for Mapping QTL and Genes  
Chair: Michel Georges, University of Liège  
Stanley Park Ballroom

10:30 AM 190 NGS-based Reverse Genetic Screen Reveals Loss-of-Function Variants Compromising Fertility in Cattle.  
M. Georges1, C. Charlier2, W. Li3, C. Harland2, M. Littlejohn2, F. Creagh4, M. D. Keehan4, T. Drue1, W. Coppie2 and R. Spelman4, 1University of Liège, Liège, Belgium, 2University of Liège, Liège, Belgium, 3Livestock Improvement Corporation, Hamilton, New Zealand, 4LIC, Hamilton, New Zealand

11:00 AM 191 Exploiting Whole Genome Sequence Data for the Identification of Causal Trait Variants in Cattle.  
H. Pausch2, C. Warnser1, C. Edel2, R. Emmerling2, K. U. Götz2 and R. Fries1, 1Chair of Animal Breeding, Technische Universität Muenchen, Freising, Germany, 2Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Grub, Germany

11:30 AM 192 Cis and Trans-Acting eQTL Mapping from RNAseq Data in Swine Populations.  
J. P. Steibel2, Michigan State University, East Lansing

Developments in Beef Cattle Genetics  
Chair: David Johnston, University of New England  
Bayshore Grand Ballroom A

1:30 PM 238 The Genetics of Brahman Cow Weight in Northern Australia and its Relationship with Female Reproductive Performance.  
M. L. Wolcott*, Animal Genetics and Breeding Unit, Armidale, Australia
Genetic Parameter Estimates for Calving Difficulty and Birth Weight in a Multi-breed Population.
C. M. Ahlberg, L. A. Kuehn, R. M. Thallman, S. D. Kachman and M. L. Spangler, University of Nebraska, Lincoln, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, University of Nebraska, Lincoln

Estimation of Breed-Specific Heterosis Effects for Birth, Weaning and Yearling Weight in Cattle.
L. N. Schiermiester, University of Nebraska, Lincoln

Estimated Additive and Non-additive Breed Effects and Genetic Parameters for Ultrasound Scanned Traits of a Multi-breed Beef Population in Tropical Australia.
G. M. Jeyaruban, Animal Genetics and Breeding Unit, Armidale, Australia

Quantifying Differences in Genetic Merit Between Australian Angus Seedstock Herds.
S. J. Lee, J. K. Naeburg and W. S. Pitchford, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, 5371, Australia

Analysis of US Cow-Calf Producer Survey Data to Assess Knowledge, Awareness and Attitudes Related to Genetic Improvement of Feed Efficiency.
R. L. Weaber, Kansas State University, Manhattan

Selection for Reduced Environmental Impact
Chair: Hutton V. Oddy, NSW Department of Primary Industries
Bayshore Grand Ballroom D

Progress with Genetic Selection for Low Methane Traits in Dairy Cows.
J. Lassen, P. C. Garnsworthy, M. G. Chagunda, E. Negussie, P. Løvendahl and Y. de Haas, Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, The University of Nottingham, Loughborough, United Kingdom, Scottish Rural University College (SRUC), Edinburgh, United Kingdom, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

Animal Wise Variation in Enteric Methane Output Traits and its Relationship with Feed Efficiency in Dairy Cattle: A Longitudinal Model Analysis.
E. Negussie, P. Mäntysaari, E. A. Mäntysaari and M. H. Lidauer, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, MTT Agrifood Research Finland, Animal Production Research, Jokioinen, Finland

Genetic Variation for Methane Traits in Beef Cattle.
P. F. Arthur, R. M. Herd, S. S. Bird, K. A. Donoghue and R. S. Hegarty, NSW Department of Primary Industries, Narellan, NSW, Australia, NSW Department of Primary Industries, Armidale, Australia, NSW Department of Primary Industries, Trangie, Australia, University of New England, Armidale, Australia

Rumen Differences between Sheep Identified as Being Low or High Methane Emitters.
W. E. Bain, L. Bezuidenhout, N. B. Jopson, C. S. Pinares-Patino and J. C. McEwan, AgResearch Invermay, Dunedin, New Zealand, AgResearch, Palmerston North, New Zealand, AgResearch, Invermay, New Zealand

Consequences of Selection for Environmental Impact Traits in Dairy Cows.

Symposium: Breeding in Aquaculture Species
Chair: William S. Davidson, Simon Fraser University
Cypress Room
Genomics in Selective Breeding of Atlantic Salmon.
T. Moen and J. Ødegård, AquaGen AS, Trondheim, Norway

The Development and Characterization of a 57K SNP Chip for Rainbow Trout.
Y. Palti, G. Gao, T. Moen, S. Liu, M. P. Kent, S. Lien, M. R. Miller and C. E. Rexroad,
NCCWA-ARS-USDA, Kearneysville, WV, AquaGen, Aas, Norway

Evolution of Coho Salmon (Oncorhynchus kisutch) Breeding Programs.
R. Neira, University of Chile, Aquainnovo, Santiago, Chile

Symposium: Genomic Prediction Across Populations
Chair: Esa A. Mäntysaari, MTT Agrifood Research Finland
Stanley Park Ballroom

(A)cross-Breed Genomic Prediction.
Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands,
Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands,
Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Lelystad, Netherlands,
Hendrix Genetics, Boxmeer, Netherlands

Across Breed Genomic Predictions in Beef Cattle.
M. Saatchi and D. J. Garrick, Iowa State University, Ames, Massey University, Palmerston North, New Zealand

Across-Breed Genomic Prediction in Dairy Cattle.
B. L. Harris, LIC, Hamilton, New Zealand

Symposium: Genomics of Disease in Swine
Chair: Graham S. Plastow, University of Alberta
Bayshore Grand Ballroom B-C

Genome-Wide Analysis of the Differential Response to Experimental Challenges with Porcine Circovirus 2b.
T. Engle, E. Jobman, T. Moural, A. McKnite, S. Barnes, E. Davis, J. Qiu, J. Bundy, T. Johnson,
M. F. Rothschild, J. Galeota, R. K. Johnson, G. Plastow, S. D. Kachman and D. C. Ciobanu,
University of Nebraska, Lincoln, Iowa State University, Ames, University of Nebraska, Lincoln,
University of Alberta, Edmonton, AB, Canada

Strategies for using Genomics to Improve Swine Resistance to PRRS.
L. R. Schaeffer, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Improving Pig Genetic Resistance and Muscle Production through Molecular Biology.
Q. Kang, Y. Hu, Y. Zou, W. Hu, L. Li, F. Chang, Y. Li, D. Lu, Z. Sun, R. Zhang, X. Hu, Q. Li, Y. Dai and N. Li,
State Key Laboratory for Agrobiotechnology, China Agricultural University, Beijing, China

Symposium: Variance Components and Indicators of Disease Resistance
Chair: Nathalie Mandonnet, INRA-UR0143, INRA Antilles-Guyane
Bayshore Grand Ballroom E-F

A Genome-Wide Association Study of Immune Response in Holstein Bulls.
K. A. Thompson-Crispi, M. Sargolzaei, F. Miglior, F. S. Schenkel and B. Mallard,
Dept Pathobiology, University of Guelph, Guelph, ON, Canada,
Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,
The Semex Alliance, Guelph, ON, Canada,
Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,
Canadian Dairy Network, Guelph, ON, Canada
Longitudinal Analysis of Somatic Cell Count for Joint Genetic Evaluation of Mastitis and Recovery Liability.
B. G. Welderafetal, D. J. D. Koning†, L. Jans†, J. Franzen† and W. F. Fikset, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Department of Statistics, Stockholm University, Stockholm, Sweden

Genetics of Tolerance and Resistance to Nematode Infection in Sheep.
H. Rashidi†, H. A. Mulder†, J. A. M. van Arendonk†, M. C. M. de Jong† and M. J. Stear†, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Quantitative Veterinary Epidemiology Group, Wageningen University, Wageningen, Netherlands, 3Veterinary School, Glasgow University, Glasgow, United Kingdom

Variance Components and Genome Wide Association Analysis of Mycobacterium bovis Infection in Dairy and Beef Cattle.
I. Richardson†, H. Wiencko†, D. Bradley†, S. J. More†, I. M. Higgins† and D. P. Berry†, 1Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Trinity College Dublin, Dublin 2, Ireland, 3Department of Genetics, Trinity College Dublin, Dublin, Ireland, 4University College Dublin, Dublin, Ireland

Plasma Components as Traits for Resistance to Coccioidiosis in Chicken.
E. Hanzic†, B. Bed Hom†, H. Jun†, R. Hawken†, M. S. Abrahamsson†, J. M. Elsen†, B. Servin†, M. H. Pinard-van der Laan† and O. Demeure**†, 1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2AgroParisTech, UMR1313 GABI, Paris, France, 3Department of Molecular Biology and Genetics, Aarhus University, Foulum, Denmark, 4INRA UMR1313 GABI, Jouy-en-Josas, France, 5INRA, UE1206 EASM, Surgères, France, 6Cobb-Vantress Inc., Siloam Springs, AR, 7INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 8INRA, Castanet-Tolosan, France, 9Agrocampus Ouest, UMR1348 PEGASE, Rennes, France, 10INRA, UMR1348 PEGASE, Saint-Gilles, France

Genetic Parameters for Resistance to Parasites in Nellore Cattle through Random Regression.

Genetics of Trait Complexes - Reproduction
Chair: Jennie E. Pryce, Department of Environment and Primary Industries
Bayshore Grand Ballroom D

A 660-Kb Deletion with Antagonistic Effects on Fertility and Milk Production Segregates at High Frequency in Nordic Red Cattle: Additional Evidence for the Common Occurrence of Balancing Selection in Livestock.
N. K. Kadri1,2, G. Sahana1, C. Chartier1, I. T. Terhi1, B. Gulbrandsen1, L. Karin1, U. S. Nielsen2, F. Punizz2, G. P. Aamand2, N. Schultmann1, M. Georges1, J. Vilkkil, M. S. Lund1 and T. Druet1, 1University of Liège, Liège, Belgium, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 4Knowledge Center for Agriculture, Aarhus, Denmark, 5Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 6Nordic Cattle Genetic Evaluation, Aarhus, Denmark

A Gene Network Inferred from Genome-wide Association: Prioritization of QTLs Associated with Tropical Cattle Reproduction.
L. R. Porto-Neto1, M. R. Fortes2, M. J. Kelly1, S. A. Lehnert1 and A. Reverter-Gomez1, 1CSIRO Food Futures Flagship, Brisbane, Australia, 2The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 3The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia

Using Genome-Wide Data for Detecting Inbreeding Depression in Eeproductive Traits in Iberian pigs.
B. Villanueva1, M. Saura1, A. Fernandez2, L. Varona1, A. Fernandez1, A. de Cara1 and C. Barraquen1, 1INIA, Madrid, Spain, 2Universidad de Zaragoza, Zaragoza, Spain, 3Museum National d’Histoire Naturelle, Paris, France

Effect of Selection for Residual Variance of Litter Size on Components of Litter Size in Rabbits.
M. J. Argente1, M. D. L. L. Garcia2 and A. Blasco2, 1Universidad Miguel Hernández de Elche, Orihuela, Spain, 2Universidad Politecnica De Valencia, Valencia, Spain
5:00 PM 150 Evaluating Genetic Variance of Reproductive Traits across Ten Years of Selection in the Turkey (Meleagris gallopavo).
J. Proulx¹, O. W. Willems¹ and B. J. Wood², ¹Centre for the Genetic Improvement of Livestock, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, ²Hybrid Turkeys, Kitchener, ON, Canada

5:15 PM 151 Genetic Parameters for Endocrine Fertility Traits from In-line Milk Progesterone Records in Dairy Cows.
A. M. M. Tenghe¹,², A. C. Bouwman¹, B. Berglund¹, E. Strandberg¹ and R. F. Veerkamp¹,², ¹Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ³Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

5:30 PM 152 Causal Relationships Between Milk Yield, Body Condition Score and Fertility in Italian Holstein Friesian Dairy Cattle.
M. Battagin¹, F. Tiezzi², M. Cassandro¹ and C. Maltecca², ¹Italian Holstein Friesian Cattle Breeders Association, Cremona, Italy, ²North Carolina State University, Raleigh, ³Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Legnaro, Italy

5:45 PM 153 Genetic Relationships of Fertility Disorders with Reproductive Traits in Canadian Holsteins.
A. Koeck¹, F. Miglior², J. Jamrozik³, D. F. Kelton¹ and F. S. Schenkel², ¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³Canadian Dairy Network, Guelph, ON, Canada, ⁴Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada

Integrating the Discovery and Usage of Functional Mutations into Dairy Genomic selection Programs for Complex Traits
Chair: Hermann Swalve, Martin Luther University Halle-Wittenberg
Bayshore Grand Ballroom A

4:00 PM 288 CEACAM18 as Candidate for the Holstein Calving QTL on BTA18.
X. Mao¹, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

4:15 PM 289 Using Haplotypes to Unravel the Inheritance of Holstein Coat Color.
T. J. Lawlor¹, Holstein Association USA Inc., Brattleboro, VT

4:30 PM 290 Performance of Single Markers vs. Haplotypes to Identify Genomic Loci Associated With Mastitis Resistance in German Holstein Cattle.
H. Abdel-Shafy¹,², R. H. Bortfeldt¹, J. Tetens¹, G. Thaller¹ and G. A. Brockmann², ¹Department of Animal Production, Faculty of Agriculture, Cairo University, Cairo, Egypt, ²Department for Crop and Animal Sciences, Humboldt-Universität zu Berlin, Berlin, Germany, ³Institute of Animal Breeding and Husbandry, Christian-Albrechts-Universität zu Kiel, Kiel, Germany, ⁴Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany

4:45 PM 291 Increasing Predictive Ability using Dominance in Genomic Selection.
C. Sun¹,², P. M. VanRaden², J. B. Cole¹ and J. O'Connell³, ¹National Association of Animal Breeders, Columbia, MO, ²Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, ³Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, ⁴University of Maryland School of Medicine, Baltimore, MD

5:00 PM 292 Prenatal Maternal Genetic, Permanent Environmental And Paternal Epigenetic Effects In New Zealand Dairy Cattle.
B. Gudex¹,², D. Johnson¹, C. Gondro¹ and K. Singh⁴, ¹LIC, Hamilton, New Zealand, ²University of New England, Armidale, Australia, ³School of Environmental & Rural Science, University of New England, Armidale, Australia, ⁴AgResearch Ltd, Ruakura Research Centre, Hamilton, New Zealand

5:15 PM 293 Laminitis-Related Claw Disorders in Dairy Cattle: A Genome-Wide Association Study.
D. Van der Spek¹, J. A. M. van Arendonk and H. Bovenhuis, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands
5:30 PM  294  Genetic Evaluation of Survival Traits in German Holstein Dairy Cattle using a Six-Trait Linear Model.  
J. Wiebelitz*, Vereinigte Informationssysteme Tierhaltung w.V. (vii), Verden, Germany

5:45 PM  295  Genetic Analysis of Longevity in Dutch Dairy Cattle using Random Regression.  
M. L. van Pelt*1,2 and R. F. Veerkamp*, 1Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 2CRV, Arnhem, Netherlands

Sheep and Goats Breeding (2)  
Chair: Julius H.J. van der Werf, CRC for Sheep Industry Innovation  
Cypress Room

4:00 PM  343  Production Benefits of Breeding for Worm Resistance in Merino sheep in a Mediterranean Environment.  
J. Greeff*, Department of Agriculture and Food Western Australia, Perth, Australia

4:15 PM  344  Assessment of Changes in Estimated Breeding Values Caused by Varying Genetic Connectedness between Two Flocks.  
B. Visser*, AbacausBio Limited, Dunedin, New Zealand

4:30 PM  345  Genetic Parameters Revisited for Ultrasound Scanning Traits in Australian Sheep.  
S. Mortimer*, NSW DPI, Trangie, Australia

4:45 PM  346  Is Variation in Growth Trajectories genetically correlated with Meat quality Traits in Australian Terminal Lambs?.  
C. A. de Hollander*1,2, N. Moghaddar2,3, K. R. Kelman2,4, G. E. Gardner2,5 and J. van der Werf4, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Cooperative Research Centre for Sheep Industry Innovation, Armidale, Australia, 3School of Environmental and Rural Science, University of New England, Armidale, Australia, 4Murdoc University, School of Veterinary and Life Sciences, Western Australia, Australia, 5School of Veterinary and Biomedical Science, Murdoch University, Murdoch, Australia, 6University of New England, Armidale, Australia

5:00 PM  347  Exploring Genotype x Environment Interaction and Heritabilities for a Reproduction Trait in Merino Sheep using Three Approaches.  
S. Dominik*1, J. E. Newton2, B. J. Hayes1 and J. van der Werf3, 1CSIRO Animal Food and Health Sciences, Armidale, Australia, 2Animal Genetics and Breeding Unit, UNE, Armidale, Australia, 3The Department of Environment and Primary Industries, Bundooora, Australia, 4University of New England, Armidale, Australia

5:15 PM  348  Evaluating Sires from Commercial Progeny Data using Pooled DNA.  
A. M. Bell1, J. M. Henshall1, R. McCulloch1 and J. Kijas4, 1CSIRO Animal, Health and Food Sciences, Armidale, Australia, 2Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Armidale, Australia, 3Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Brisbane, Australia, 4CSIRO Animal, Food and Health Sciences, Brisbane, Australia

5:30 PM  349  Introgression of Wool-Shedding Genes into the Romane Breed Sheep.  
D. Allain1, B. Penet1, D. Fouliquet2, Y. Bourdillion1 and D. François3, 1INRA, UMR1388 GenPhysSE, Toulouse, France, 2INRA UEO3321, La Fage, France, 3INRA UE0322, La Sapinière, Bourges, France, 4INRA UMR1388 GenPhysSE, Toulouse, France

5:45 PM  350  Genetic Analysis of Lamb Survival in a Crossbred Population.  
V. Cardoso Ferreira1, G. J. M. Rosa1 and D. L. Thomas2, 1University of Wisconsin, Madison, 2University of Wisconsin-Madison, Department of Animal Sciences, Madison, WI

Symposium: Breeding Objectives and Economics of Breeding Schemes  
Chair: Jack C. M. Dekkers, Iowa State University  
Stanley Park Ballroom
4:00 PM 007 Pig Breeding Goals in Competitive Markets.
P. W. Knap, Genus-PIC, Schleswig, Germany

4:30 PM 008 Breeding Goals and Phenotyping Programs for Multi-Trait Improvement in the Genomics Era.
J. C. M. Dekkers¹ and J. van der Werf², ¹Iowa State University, Ames, ²School of Environmental & Rural Science, University of New England, Armidale, Australia

5:00 PM 009 Who Benefits from Genetic Improvement?.
R. Banks*, University of New England, Armidale, Australia

5:30 PM 010 Comparison of Different Methods to Calculate a Total Merit Index - Results of a Simulation Study.
C. Fuerst¹, C. Pfeiffer², H. Schwarzenbacher³, F. Steininger⁴ and B. Fuerst-Waltl⁵, ¹ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria, ²University of Natural Resources and Life Sciences, Vienna, Austria, ³University of Natural Resources and Life Sciences (BOKU), Vienna, Austria

5:45 PM 011 Economic and Environmental Impacts of Improving Growth Rate and Feed Efficiency in Fish Farming Depend on Nitrogen and Density Limitation.
M. Besson¹,²,³, H. Komen¹, M. Vandeputte³, J. Aubin¹, I. de Boer¹,² and J. A. M. van Arendonk¹, ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²AgroParisTech, Paris, France, ³INRA, Jouy en Josas, France

Symposium: Developments in Beef Cattle Genetics
Chair: Stephen P. Miller, AgResearch
Bayshore Grand Ballroom B-C

4:00 PM 244 Developments in Genetic Prediction of Carcase Merit in Limousin Beef Cattle in the UK.
K. Moore¹, T. Pritchard, S. Wilkinson, R. Mrode, F. Pearsonst, K. Kaseja, E. Wall and M. P. Coffey, SRUC, Edinburgh, United Kingdom

4:30 PM 245 Large Effects on Birth Weight Follow Inheritance Pattern Consistent with Gametic Imprinting and X Chromosome.
R. M. Thallman¹, J. A. Dillon², J. O. Sanders³, A. D. Herring¹ and D. G. Riley¹, ¹USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, ²Department of Animal Science, Pennsylvania State University, University Park, ³Texas A&M University, College Station

5:00 PM 246 Genetic Improvement of Reproduction in Beef Cattle.
D. Johnston¹, Animal Genetics and Breeding Unit, University of New England, Armidale, Australia

5:30 PM 247 Partitioning of Multiple-Trait Model Parameters with Respect to Phenotypic Recursion: Case Study of Birth Weight and Calving Ease in Canadian Simmentals.
J. Jamrozik¹, Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

5:45 PM 248 Benefits of Interbeef International Genetic Evaluations for Weaning Weight.
E. Venot¹, T. Pabion², E. Hjerpe³, M. Niforooshan², A. Launay² and B. Wickham³, ¹INRA UMR 1313 GABI, Jouy-en-Josas, France, ²Irish Cattle Breeding Federation, Cork, Ireland, ³Interbull center, Uppsala, Sweden, ⁴Institut de l'Elevage, Paris, France, ⁵ConsultWickham, Clonakilty, Ireland

Symposium: Statistical Methods - Linear and Nonlinear Models: Prediction
Chair: Marco C.A.M. Bink, Wageningen University
Bayshore Grand Ballroom E-F

4:00 PM 212 Genome-enabled Prediction of Complex Traits with Kernel Methods: What Have We Learned?.
D. Gianola¹, G. Morota¹ and J. Crossa¹, ¹University of Wisconsin, Madison, ²CIMMYT, El Batan, Mexico
4:30 PM 213 Integration of Multi-Layer Omic Data for Prediction of Disease Risk in Humans.
A. I. Vazquez*, H. W. Wiener, S. Shrestha, H. K. Tiwari and G. de los Campos, University of Alabama at Birmingham, Birmingham, AL

5:00 PM 214 Disentangling Pleiotropy along the Genome using Sparse Latent Variable Models.
L. Janss*, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

5:30 PM 215 Efficiency of Variable Selection in Genome-Wide Prediction for Traits of Different Genetic Architecture.
C. C. Schoen1 and V. Wimmer2, 1Technical University Munich, Freising, Germany, 2KWS SAAT AG, Einbeck, Germany
Wednesday, August 20, 2014

Plenary Speaker - Wednesday

Chairs: E. John Pollak, USDA, ARS, U.S. Meat Animal Research Center and Filippo Miglior, Canadian Dairy Network and University of Guelph
Bayshore Grand Ballroom

8:30 AM  Plenary 3  Phylogenies Meet Quantitative Genetics: Some Attempts to Extrapolate.
  J. Felsenstein*, Department of Genome Sciences and Department of Biology, University of Washington, Seattle, WA

Developing Effective Dairy Genomic Selection Programs for Traits or Breeds that Lack Massive Reference Populations
Chair: Christian Maltecca, North Carolina State University
Bayshore Grand Ballroom E-F

10:30 AM  On the Value of the Phenotypes in the Genomic Era.
  O. Gonzalez-Recio¹, M. Coffey² and J. E. Pryce³, ¹Department of Environment and Primary Industries, Bundoora, Australia, ²Scotland’s Rural College, Easter Bush, United Kingdom, ³Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia

10:45 AM  Are Evaluations on Young Genotyped Dairy Bulls Benefiting from the Past Generations?
  D. Lourenço¹, J. M. P. Tsuruta¹, I. Aguilar² and I. Aguilar³, ¹INIA, Las Brujas, Uruguay, ²Holstein Association USA Inc., Brattleboro, VT, ³ARO, The Volcani Center, Bet Dagan, Israel

11:00 AM  Analyses of Functional Traits with Indicator Traits to improve genomic reliability in Australian Holstein Cattle using Domestic Daughter Deviation or De-Regressed Proofs as Response Variable.
  M. M. Haile-Mariam¹, J. E. Pryce² and B. J. Hayes¹, ¹Biosciences Research Division, Bundoora, Australia, ²Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, ³Department of Environment and Primary Industries, Bundoora, Australia

11:15 AM  Integrate Cow and Bull Data in a Genomic Evaluation for Conformation Traits and Claw Health.
  G. C. B. Schopen¹, P. J. A. Vessies¹, M. P. L. Calus¹, C. Schrooten¹ and S. A. P. W. de Roos¹, ¹CRV, Arnhem, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

11:30 AM  Predictive Ability of Genomic Breeding Values for Corkscrew Claw in Norwegian Red.
  C. Ødegård¹,², M. Svendsen¹ and B. Heringstad¹,², ¹Geno, Ås, Norway, ²Norwegian University of Life Sciences, Ås, Norway

11:45 AM  Increasing the Number of Single Nucleotide Polymorphisms Used in Genomic Evaluations of Dairy Cattle.
  G. R. Wiggans¹, T. A. Cooper¹, D. J. Null² and P. M. VanRaden¹, ¹Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, ²Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD

Poultry Breeding (1)
Chair: Hans H. Cheng, USDA, ARS, ADOL
Cypress Room

10:30 AM  Comparison of Empirical and Theoretical Responses to Selection Against Mortality due to Cannibalism in Layers.
  E. D. Ellen¹, J. Visscher¹ and P. Bijma¹, ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Institut de Sélection Animale B.V., Hendrix Genetics, Boxmeer, Netherlands

11:00 AM 319 Genetic Parameters for Feather Pecking and Aggressive Behavior in Laying Hens using Poisson and Linear Models.
V. Grams, W. Bessel, H. P. Piepho and J. Bennewitz, Institute of Animal Husbandry and Breeding, University Hohenheim, Hohenheim, Germany, Institute of Crop Science, University of Hohenheim, Hohenheim, Germany, Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

11:15 AM 320 A Genome Wide Association Analysis Confirms a Complex, Polygenic Determinism of Resistance to Salmonella Carrier-State in Chicken.
F. Calenge, A. Vignal, B. Bed’Hom, P. Kaiser, P. Menanteau, P. Velge and C. Beaumont, INRA UMR1313 GABI, Jouy-en-Josas, France, INRA UMR1388 GenPhySe, Castanet-Tolosan, France, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, INRA UMR1282 ISP, Nouzilly, France, INRA UR083 URA, Nouzilly, France

11:30 AM 321 Identification of SNP Markers for Resistance to Salmonella and IBDV in Indigenous Ethiopian Chickens.
A. Psifidi, G. Banos, O. Matika, T. Dessie, R. Christley, P. Wigley, J. Bettridge, O. Hanotte, T. Desta and P. Kaiser, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, Scotland’s Rural College, Edinburgh, United Kingdom, International Livestock Research Institute, Addis Abeba, Ethiopia, Institute of Infection & Global Health, University of Liverpool, Liverpool, United Kingdom, School of life Sciences, University of Nottingham, Nottingham, United Kingdom

11:45 AM 322 Genomic Evaluation for Egg Weight in Crossbred Layers Receiving Various Diets.

Statistical Methods for Genomic Prediction
Chair: Roel F. Veerkamp, Wageningen University
Bayshore Grand Ballroom B-C

10:30 AM 067 Genomic Prediction using a Weighted Relationship Matrix to Account for Trait Architecture in US Holstein Cattle.
F. Tiezzi and C. Maltecca, North Carolina State University, Raleigh

10:45 AM 068 Hierarchical Quantitative Genetic Model using Genomic Information.
G. Gorjanc, J. A. Wolliams and J. M. Hickey, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

11:00 AM 069 Comparison of Some Equivalent Equations to Solve Single-Step GBLUP.
I. Strandén and E. A. Mäntysaari, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, MTT Agrifood Research Finland, Jokioinen, Finland

11:15 AM 070 Semi-Supervised Learning Combining Phenotyped and Non-Phenotyped Individuals for Enhancing Prediction in Residual Feed Intake.
C. Yao, X. Zhu and K. A. Weigel, University of Wisconsin, Madison, Department of Computer Science University of Wisconsin, Madison

11:30 AM 071 A Single Step SNP Model Applied to Test-Day Data of Dairy Cows.
Z. Liu, vit Germany, Verden, Germany
11:45 AM 072 Haplotype Based Genome-Enabled Prediction of Traits Across Nordic Red Cattle Breeds.
B. Castro Dias Cayabana¹, Aarhus University, Tjelle, Denmark

Swine Breeding (1)
Chair: Brian P. Kinghorn, University of New England
Bayshore Grand Ballroom D

10:30 AM 363 Consequences of Selection for Indirect Genetic Effect for Growth in Pigs on Behavior and Production.
I. Camerlink¹, N. Duijvesteijn², W. W. Ursinus¹, J. E. Bolhuis¹ and P. Bijma⁴, Wageningen University, Wageningen, Netherlands, ²TOPIGS Research Center IPG B.V., Beuningen, Netherlands, ³Wageningen UR Livestock Research, Lelystad, Netherlands, ⁴Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

10:45 AM 364 Genetic Analysis of Skin Lesion Traits in Pigs and their Relationship with Growth Traits.
S. Desire¹, S. P. Turner¹, C. R. G. Lewis², R. B. D'Eath¹, A. Doeschl-Wilson¹ and R. Roehe¹, ¹SRUC, Edinburgh, United Kingdom, ²PIC Europe, Nantwich, United Kingdom, ³The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

11:00 AM 365 Genetic Relationships between Measures of Sexual Development, Boar Taint, Health and Aggressiveness in Pigs.
S. Parois¹, A. Prunier¹, M. J. Mercar², N. Muller¹, E. Merlot³ and C. Larzelère⁴, INRA, Saint-Gilles, France, ²IFIP, Le Rheu, France, ³INRA, Le Rheu, France, ⁴INRA UMR1313 GABI, Jouy-en-Josas, France

11:15 AM 366 Genetic Control of Skatole in Intact Boars is Dependent on the Actual Androstenedione Level.
J. ten Napel¹, P. K. Mathur¹, H. A. Mulder² and E. F. Knol³, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Lelystad, Netherlands, ²TOPIGS Research Center IPG, Beuningen, Netherlands, ³Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

11:30 AM 367 Maternal Genetic Effects for Lifetime Growth Should be Considered More in Pig Breeding.
S. Hermesch¹, C. R. Parke¹, M. M. Bauer² and H. Gilbert³, AGBU - University of New England, Armidale, NSW, Australia, ²University of Queensland, Gatton QLD, Australia, ³INRA UMR1388, F-31326 Castanet-Tolosan, France

11:45 AM 368 Nurse Capacity in Crossbred Sows and Genetic Correlation to Purebred Fertility.
B. Nielsen¹, J. Velander¹, T. Ottersen¹, M. A. Henryson¹ and O. F. Christensen², ¹Pig Research Centre, Copenhagen, Denmark, ²Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjelle, Denmark

Symposium: Education and Training
Chair: Ronald M. Lewis, University of Nebraska
Bayshore Grand Ballroom A

10:30 AM 222 Filling the Knowledge Gap: Integrating Quantitative Genetics and Genomics in Graduate Education and Outreach.
R. M. Lewis¹, M. L. Spangler¹, B. B. Lockee², R. M. Enns³, K. J. Enns³, J. C. M. Dekkers⁴, C. Maltecca⁵, J. P. Cassady⁶, M. D. MacNeil⁷, C. A. Gould⁸, D. L. Boggs⁹, I. Miszta³ and E. J. Pollak¹², ¹Virginia Tech, Blacksburg, VA, ²University of Nebraska, Lincoln, ³University of Nebraska, Lincoln, ⁴Virginia Tech, Blacksburg, ⁵Colorado State University, Fort Collins, ⁶Iowa State University, Ames, ⁷North Carolina State University, Raleigh, ⁸South Dakota State University, Brookings, ⁹Delta G, Montana, MT, ¹⁰Kansas State University, Manhattan, ¹¹University of Georgia, Athens, ¹²USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

11:00 AM 223 Interdisciplinarity, Internationalization, Interculturality: Three Challenges of Training in Animal Breeding and Genetics in Europe.
E. Verrier¹ and H. Thomas², INRA UMR 1313 GABI, Jouy en Josas, France, ²AgroParisTech, Paris, France

11:30 AM 224 Training and Human Capacity Development in Australasia, S. and S.E. Asia and Sub-Saharan Africa.
J. Gibson¹, E. O. Rege² and M. G. Chaganda¹, ¹University of New England, Armidale, Australia, ²PICO- Eastern Africa, Nairobi, Kenya, ³Scottish Rural University College (SRUC), Edinburgh, United Kingdom
Symposium: Selection for Reduced Environmental Impact Chair: Paul Boettcher, FAO
Stanley Park Ballroom

10:30 AM 041 Breeding Ruminants that Emit Less Methane – The Role of International Collaboration.
H. V. Oddy*, Y. de Haas*, J. A. Basarab*, K. M. Cammack*, B. J. Hayes*, R. S. Hegarty*, J. Lassen*, J. C. McEwan*, S. P. Miller*, C. S. Pinares-Patino*, G. Shackell*, P. Vercoe**, and N. K. Pickering1, 1NSW Department of Primary Industries, Armidale, NSW, Australia, 2Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 3Alberta Agriculture and Rural Development, Lacombe, AB, Canada, 4Department of Animal Science, University of Wyoming, Laramie, WY, 5Department of Environment and Primary Industries, Bundoora, Australia, 6University of New England, Armidale, NSW, Australia, 7Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, 8AgResearch, Invermay, New Zealand, 9AgResearch, Palmerston North, New Zealand, 10University of Western Australia, Perth, WA, Australia, 11AgResearch, Mosgiel, New Zealand

11:00 AM 042 Genetic Improvement Options for the Cost Effective Reduction of Greenhouse Gas Emissions from Ruminant Production Systems.
E. Wall*, V. Eory, M. MacLeod and D. Moran, SRUC, Edinburgh, United Kingdom

11:30 AM 043 Genomic Selection as a Tool to Decrease Greenhouse Gas Emission from Dual Purpose New Zealand Sheep.
Thursday, August 21, 2014

Plenary Speaker - Thursday

Chairs: E. John Pollak, USDA, ARS, U.S. Meat Animal Research Center and Filippo Miglior, Canadian Dairy Network and University of Guelph

Bayshore Grand Ballroom

8:30 AM  Plenary 4  Quantitative Genetics of Complex Traits in Human Populations.

Chair: Ronald M. Lewis, University of Nebraska

Cypress Room

10:30 AM  225  Research Trainee Participation is a Bonus to Teaching Aims in the Bovine Respiratory Disease Complex Coordinated Agricultural Project.

M. G. Thomas, N. F. Berge, R. M. Enns, R. Hagevoort, T. T. Ross, A. L. Van Eenennaam, H. L. Neibergs, J. S. Neibergs and J. E. Womack, Colorado State University, Department of Animal Sciences, Fort Collins, New Mexico State University, Clovis, NM, New Mexico State University, Las Cruces, NM, University of California, Davis, Washington State University, Pullman, Texas A&M University, College Station

10:45 AM  226  Attracting and Retaining Minorities in the Biomedical Sciences Including Genomics: A Community-Based Approach.

E. Smith, D. Bevan, F. A. McNabb and K. DePauw, Virginia Tech, Blacksburg

11:00 AM  227  DNA Subway – An Educational Bioinformatics Platform for Gene and Genome Analysis: DNA Barcoding, and RNA-Seq.

J. Williams, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

11:15 AM  228  How to Teach Animal Breeding and Genetics to Undergraduate Students: Presentation of a ‘Thinking Process.

L. van der Waaij, D. Lont and H. A. Mulder, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

11:30 AM  229  Capitalisation of Experiences in Implementing Genetic Improvement Programs in India – Role of Training and Education.

A. Sudhakar, M. K. Kunju, G. Suresh and G. Kishore, National Dairy Development Board, Anand, India, Vellore-Tiruvannamalai District Co-operative Milk Producers' Union, Vellore, India

12:00 PM  231  Breeding Program as a Tool for Education and Training of Young.

R. N. B. Lobo, Embrapa Goats and Sheep, Sobral, Brazil

Statistical and Genomic Tools for Mapping QTL and Genes (Dairy and Beef)

Chair: Michael E. Goddard, Department of Environment and Primary Industries

Bayshore Grand Ballroom E-F

10:30 AM  193  A Bayesian Analysis to Exploit Imputed Sequence Variants for QTL Discovery.

I. M. MacLeod, University of Melbourne, Melbourne, Australia
10:45 AM 194 **Genetic Architecture of Milk, Fat, Protein, Mastitis and Fertility Studied using NGS Data in Holstein Cattle.**
G. Sahana¹, L. Janss, B. Guldbrandtsen and M. S. Lund, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

11:00 AM 195 **Mapping QTL in Australian Dairy Cattle using Genomic Selection Methodologies.**
K. E. Kemper², University of Melbourne, Melbourne, Australia

11:15 AM 196 **Application of a Three-Haplotype LDLA Model to the French Holstein Population.**
D. Jonas³, INRA, UMR1313 GABI, Jouy-en-Josas, France

11:30 AM 197 **Extremely Non-Uniform: Patterns of Runs of Homozygosity in Bovine Populations.**
J. Sölkner¹, M. Ferencakovic², Z. Karimi³, A. M. Pérez O’Brien⁴, G. Mézáros⁵, S. Eaglen⁶, S. A. Boison⁷ and I. Curić⁸, ¹University of Natural Resources and Life Sciences, Vienna, Austria, ²University of Zagreb, Zagreb, Croatia

11:45 AM 198 **Haplotype Tests for Diagnosis of QTL and Genes.**
J. M. Henshall¹, E. K. Piper² and B. Tier³, ¹Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Armidale, Australia, ²The University of Queensland, School of Veterinary Science, Gatton, Australia, ³Animal Genetics and Breeding Unit, Armidale, Australia

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**Symposium: Genetics of Trait Complexes - Reproduction**

Chair: Jennie E. Pryce, Department of Environment and Primary Industries

Bayshore Grand Ballroom B-C

10:30 AM 154 **World Trends in Dairy Cow Fertility.**
J. E. Pryce¹, R. Woolaston¹, D. P. Berry², E. Wall³, M. Winters³, R. Butler² and M. Shaffer², ¹Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, ²Arlie Solutions, Pullmanvale, Queensland, Australia, ³Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ⁴SRUC, Edinburgh, United Kingdom, ⁵DairyCo, Kentworth, Warwickshire, United Kingdom, ⁶Holstein Australia, Melbourne, Victoria, Australia, ⁷Dairy Australia, Melbourne, Victoria, Australia

11:00 AM 155 **Improving Dairy Cow Fertility using Milk-Based Indicator Traits.**
C. Bastin¹, J. Vandenplas¹ and N. Gengler¹, ¹University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium, ²National Fund for Scientific Research, Brussels, Belgium

11:30 AM 156 **Using Genomics to Improve Reproduction Traits in Sheep.**
H. D. Daetwyler¹,²,³, S. Bolormaa¹,³, K. E. Kemper³, D. Brown³, A. A. Swan¹,², J. H. van der Werf⁴ and B. J. Hayes¹,²,³, ¹Department of Environment and Primary Industries, Bundoora, Australia, ²La Trobe University, Bundoora, Australia, ³CRC for Sheep Industry Innovation, Armidale, Australia, ⁴University of Melbourne, Melbourne, Australia, ⁵Animal Genetics and Breeding Unit, Armidale, Australia, ⁶University of New England, Armidale, Australia

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**Symposium: Improving Difficult Traits in Beef Cattle**

Chair: Roberto Carvalheiro, Sao Paulo State University (UNESP)

Stanley Park Ballroom

10:30 AM 249 **Genomic Prediction of Beef Tenderness in Canadian Beef Cattle.**
S. P. Miller¹,²,³, D. Lu¹, G. VanderVoor¹ and I. B. Mandell¹, ¹AgResearch, Invermay, Mosgiel, New Zealand, ²Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³University of Alberta, Edmonton, AB, Canada, ⁴University of Guelph, Guelph, ON, Canada

11:00 AM 250 **Genetic Markers in Transcription Factors of Differentially Expressed Genes Associated with Post-partum Anoestrus Predict Pregnancy Outcome in an Independent Population of Beef Cattle.**
M. R. Fortes¹,², L. R. Porto-Neto¹, K. L. DeAtley¹, A. Reverter-Gomez², M. G. Thomas², S. S. Moore², S. A. Lehnert² and W. M. Snelling², ¹The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, ²CSIRO Food Futures Flagship, Brisbane, Australia, ³Califomia State University, Chico, Chico, CA, ⁴Colorado State University, Department of Animal Sciences, Fort Collins, ⁵USDA, ARS, US MARC, Clay Center, NE
11:30 AM 251 Reducing the Incidence of Early Embryonic Mortality in Beef Cattle.
R. D. Schnabel¹, J. F. Taylor¹, D. S. Brown, M. F. Smith¹, M. Rolf², M. D. MacNeil², B. P. Kinghorn³ and D. J. Patterson, ¹University of Missouri, Columbia, ²Oklahoma State University, Stillwater, OK, ³Kansas State University, Manhattan, ⁴University of New England, Armidale, Australia

Symposium: Poultry Genomic Architecture and Genomic Selection
Chair: William M. Muir, Purdue University
Bayshore Grand Ballroom D

10:30 AM 323 Allele-Specific Expression, a New Genomics Tool for Development of Value-Added SNP Chips and to Fine Map QTL.
W. M. Muir¹, S. Perumbakkam³, A. Black-Pyrokes³, J. R. Dunn³ and H. H. Cheng³, ¹Purdue University, West Lafayette, IN, ²Michigan State University, East Lansing, ³USDA, ARS, ADOL, East Lansing, MI

11:00 AM 324 Single Step Methods with a View towards Poultry Breeding.
A. Legarra¹, I. Misztal² and I. Aguilar³, ¹INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, ²University of Georgia, Athens, ³INIA, Las Brujas, Uruguay

11:30 AM 325 GWAS using ssGBLUP.
I. Misztal, University of Georgia, Athens

Whole Genome Scans for Disease Resistance
Chair: John W. Keele, USDA, ARS, U.S. Meat Animal Research Center
Bayshore Grand Ballroom A

10:30 AM 100 Regional Heritability Mapping of Production Traits in Epidemic Porcine Reproductive and Respiratory Syndrome.
C. M. Orret¹, N. Deebe², R. Pong-Wong², O. Matika¹, C. R. G. Lewis¹, D. G. McLaren³, A. L. Archibald⁴ and S. C. Bishop, ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²Genus, plc, Hendersonville, TN, ³PIC Europe, Nantwich, United Kingdom, ⁴Genus PLC, De Forest, WI

10:45 AM 101 A Genome-Wide Association Study for the Incidence of Persistent Bovine Viral Diarrhea Virus Infection in Cattle.
E. Casas¹, B. E. Hessman², J. W. Keele² and J. F. Ridpath³, ¹USDA, ARS, National Animal Disease Center, Ames, IA, ²Haskell County Animal Hospital, Haskell, KS, ³USDA-ARS, Clay Center, NE, ⁴National Animal Disease Center, USDA-ARS, Ames, IA

11:00 AM 102 A Meta-Analysis for Bovine Tuberculosis Resistance in Dairy Cattle.
S. Tsairidou¹, J. Woolliams³, A. Allen³, R. Skuce³, S. H. McBride³, R. Pong-Wong¹, O. Matika¹, E. Finlay¹, D. P. Berry¹, D. Bradley³, S. McDowell³, E. Glass³ and S. C. Bishop, ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ³Agri-Food and Biosciences Institute, Belfast, United Kingdom, ²School of Biological Sciences, Queen’s University of Belfast, Belfast, United Kingdom, ⁴Department of Genetics, Trinity College Dublin, Dublin, Ireland, ⁵Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

11:15 AM 103 Whole-Genome Scan And Validation Of Regions Previously Associated With Prrs Antibody Response And Growth Rate using Gilts Under Health Challenge In Commercial Settings.
N. V. L. Serão¹, R. A. Kemp¹, B. E.MOTE¹, J. C. S. Harding², P. Willson¹, S. C. Bishop³, G. S. Plastow⁴ and J. C. M. Dekkers¹, ¹Iowa State University, Ames, ²Genesus Inc, Lethbridge, AB, Canada, ³Fast Genetics Inc., Saskatoon, SK, Canada, ⁴University of Saskatchewan, Saskatoon, SK, Canada, ⁵The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ⁶University of Alberta, Edmonton, AB, Canada

11:30 AM 104 A Comprehensive Genetic Study of Resistance to Nematodes in Sheep using the Ovine SNP Chip.
V. Riggio¹, O. Matika¹, R. Pong-Wong¹, C. R. Moreno², A. Carta¹ and S. C. Bishop, ³The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, ³Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy
R. Rachel1, I. Palhière1, C. R. Moreno2, G. Foucras2, C. Maroteau1, A. Tircazes1, G. Salle2, G. Balocch1 and G. Tossier-Klopp2, INRA UMR 1388 GenPhySE, Castanet-Tolosan, France, INRA UMR1388 GenPhySE, Castanet-Tolosan, France, Université François Rabelais de Tours, Tours, France

Breeding in Aquaculture Species: Non-Salmonids
Chair: Roberto Neira, University of Chile, Aquainnovo
Cypress Room

1:30 PM 270 A Genome-Wide Association Study for Resistance to Viral Nervous Necrosis in Atlantic Cod using a 12K Single Nucleotide Polymorphism Array.
R. Banger1, M. Baranski2 and S. Lien3, Norwegian Institute of Food, Fisheries and Aquaculture Research, Tromsø, Norway, Centre for Integrative Genetics, Norwegian University of Life Sciences, Ås, Norway

1:45 PM 271 Genetic Variability of Selected Populations of Yellow Perch over Six Generations of Commercial-Scale Marker-Aided Cohort Selection for Growth.
H. Wang1, Ohio State University, Columbus, OH

2:00 PM 272 Estimation of Body Weight of European Sea Bass (Dicentrarchus labrax) and Nile Tilapia (Oreochromis niloticus) Larvae by Image Analysis.
H. de Verdal1,2,3, M. Vandeputte1,4, E. Pepey1, M. O. Vidal3, C. Ouedraogo2, M. Canonne2, H. D'Cotta2, J. F. Baroiller2, E. Baras2 and B. Chatain1, WorldFish, Penang, Malaysia, CIRAD, Montpellier, France, INRA, Jouy en Josas, France, IFREMER, Palavas les Flots, France, IRD, Montpellier, France

2:15 PM 273 Genetic Parameters for Within-family Variance of Harvest Weight in Nile Tilapia (Oreochromis niloticus).
J. Marjanovic1,2,3, H. A. Mulder1, H. L. Khaw4,5 and P. Bijma6, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

2:30 PM 274 Evolution of Genetic Variability for Growth-Out Survival Rate in a Selected Population of Pacific White Shrimp Penaeus (Litopenaeus) vannamei.
N. Cala1, H. H. Montalda2, G. R. Campos-Montes3,4 and H. Castilla-Juárez2, Universidad Nacional Autónoma de México, DF, Mexico, Universidad Autónoma Metropolitana, DF, Mexico, Maricultura del Pacífico, Mazatlán, Mexico

2:45 PM 275 RAD Sequencing Reveals Genome-Wide Heterozygote Deficiency in Pair Crosses of the Chilean Mussel Mytilus spp.
C. Penaloza1,2, S. C. Bishop2, J. Toro2 and R. D. Houston1, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, Austral University, Valdivia, Chile

Genomic Prediction across Populations
Chair: Esa A. Mäntysaari, MTT Agrifood Research Finland
Bayshore Grand Ballroom A

1:30 PM 073 Holstein-Friesian Relationships and the Impact on the Accuracy of an Across-Breed Evaluation.
A. Brown1, G. Banos1, M. P. Coffey2, J. A. Woolliams3 and R. Mrode1, Scotland's Rural College, Edinburgh, United Kingdom, SRUC, Edinburgh, United Kingdom, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

1:45 PM 074 Effect of Genetic Architecture on Accuracy of Multi Breed Genomic Prediction.
Y. C. J. Wientjes1,2, M. P. L. Calus3, M. E. Goddard4,5 and B. J. Hayes1,6, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Department of Environment and Primary Industries, Bundoora, Australia, University of Melbourne, Parkville, Australia, Dairy Futures Cooperative Research Centre, Bundoora, Australia, La Trobe University, Bundoora, Australia
Across-Breeds Ancestral Relationships and Metafounders for Genomic Evaluation. A. Legarra¹, O. F. Christensen², Z. G. Vitezica³, J. A. Aguilar⁴ and J. M. Misztal⁵. ¹INRA, Toulouse, France, ²Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ³Unité Mixte ENSAT- INRA, Toulouse, France, ⁴INIA, Las Brujas, Uruguay, ⁵University of Georgia, Athens

Accuracy of Genomic Breeding Values Predicted Within and Across Breeds in Pig Populations. A. M. Hidalgo¹,², J. W. M. Bastiaansen¹, M. S. Lopes³, B. Harlizius³, M. A. Groenen¹ and D. J. D. Koning². ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, ³TOPIGS Research Center IPG, Beuningen, Netherlands

Genomic Selection in Admixed Populations. R. Rekaya, The University of Georgia, Athens

Influence of Foreign Genotypes on Genomic Breeding Values of National Candidates in Brown Swiss. L. Plieschke¹ and C. Edel². ¹Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Poing, Germany, ²Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Grub, Germany

Selection Theory - Non-Additive Effects
Chair: Jack C. M. Dekkers, Iowa State University
Bayshore Grand Ballroom D

Opportunities for Improvement of Phenotypic Variability: Influence of Direct vs Epistatic Effects. X. Shen¹ and W. G. Hill². ¹Division of Computational Genetics, Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden, ²Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom

Estimation of Genetic Variance Components Including Mutation and Epistasis using Bayesian Approach in a Selection Experiment on Body Weight in Mice. N. Widyas, J. Jensen and V. H. Nielsen, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Genetic Variance in Environmental Variance Leads to Non-Linear Relationships between Traits with Application to Birth Weight and Survival in Piglets. H. A. Mulder¹, W. G. Hill² and E. F. Knol³. ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom, ³TOPIGS Research Center IPG, Beuningen, Netherlands

Design of Reference Populations for Genomic Selection in Crossbreeding Programs. I. van Grevenhof¹ and J. van der Werf². ¹Wageningen University, Wageningen, Netherlands, ²School of Environmental & Rural Science, University of New England, Armidale, Australia

The Standard Error of the Estimated Purebred-Crossbred Genetic Correlation. P. Bijma¹ and J. W. M. Bastiaansen². ¹Wageningen University, Wageningen, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Use of Genome Editing in Animal Breeding Programs. J. Jenko¹, G. Gorjanc², G. Mészáros³, B. C. A. Whitelaw¹, J. A. Woolliams¹, M. A. Cleveland² and J. M. Hickey¹. ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²Genus, Plc, Hendersonville, TN

Symposium: Adaptation and Selection in Harsh Environments
Chair: Paul Boettcher, FAO
Bayshore Grand Ballroom B-C
Symposium: Utilizing Whole Genome Sequence Information in Swine Breeding
Chair: Graham S. Plastow, University of Alberta

Stanley Park Ballroom

1:30 PM 375 Novel Tools Provide New Opportunities for Genetic Improvement of Swine.
M. F. Rothschild*, E. S. Kim* and G. S. Plastow*, Iowa State University, Ames; University of Alberta, Edmonton, AB, Canada

2:00 PM 376 Utilizing Whole Genome Sequence Information in Swine Breeding: Where Next for Application?
R. A. Kemp*, Genesus Inc, Lethbridge, AB, Canada
Sequencing Millions of Animals for Genomic Selection 2.0.
J. M. Hickey1, G. Goriarc1, M. A. Cleveland2, A. Krani3, J. Jenko4, G. Mészáros1, J. A. Woolliams1 and M. Perez-Enciso5, 1The Roslin Institute and R(D)S VS, University of Edinburgh, Midlothian, United Kingdom, 2Genus, Plc, Hendersonville, TN, 3Aviagen Ltd, Edinburgh, United Kingdom, 4Universitat Autònom de Barcelona, Bellaterra, Spain

Genetics of Trait Complexes - Feed Intake and Efficiency (Swine & Poultry)
Chair: Paul F. Arthur, NSW Department of Primary Industries
Bayshore Grand Ballroom D

The Genetic and Phenotypic Relationship Between Feed Efficiency and Pendulous Crop in the Turkey (Meleagris gallopavo).
O. W. Willems6, N. J. H. Buddiger2, B. J. Wood2 and S. P. Miller3, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Hybrid Turkeys, Kitchener, ON, Canada

Association of SNPs with Components of Residual Feed Intake Parameters in a Meat-Type Chicken Population.
S. E. Aggrey1, F. Gonzalez-Ceron2 and R. Rekaya3, 1NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, 2NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, 3Department of Animal and Dairy Science, University of Georgia, Athens

QTL Detection for Excretion Traits in Broilers.
S. Mignon-Graustec1, B. Carre1, J. Gabriel1, N. Rideau1, C. Chantry-Darmon2, M. Y. Boscher1, D. Bastianelli1, N. Sellier1, M. Chapault-Dhui3, E. Le Bihan-Duval1 and A. Narcy3, 1INRA, Nouzilly, France, 2Labogena, Jouy-en-Josas, France, 3CIRAD, Montpellier, France, 4INRA UR83, Nouzilly, France

Does Selection for RFI Affect the Sensitivity to Environmental Variation in Pigs?.
H. Gilbert1, 2, J. David1, Y. Billon1 and S. Hermesch2, 1INRA UMR1388, F-31326 Castanet-Tolosan, France, 2AGBU - University of New England, Armidale, NSW, Australia, 3INRA UE1372, F-17700 Surgères, France

Genomic Prediction and Genomic Variance Partitioning of Daily and Residual Feed Intake in Pigs using Bayesian Power Lasso Models.
D. N. Do1, L. Janss1, A. B. Strathe2, J. Jensen1 and H. N. Kadarmideen1, 1Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Danish Agriculture & Food Council, Pig Research Centre, Copenhagen, Denmark

Longitudinal Analysis of Residual Feed Intake in Mink using Random Regression with Heterogeneous Residual Variance.
M. Shirali1, V. H. Nielsen1, S. H. Moller1 and J. Jensen1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Department of Animal Science Epidemiology and management, Aarhus University, Tjele, Denmark

Poultry Breeding (2)
Chair: William M. Muir, Purdue University
Cypress Room

Prediction Accuracy of Pedigree and Genomic Estimated Breeding Values over Generations in Layer Chickens.
Z. Q. Weng1, A. Wole1, R. L. Fernando1, J. C. M. Dekkers1, J. Arango1, J. E. Fulton1, P. Settar1, N. P. O'Sullivan1 and D. J. Garrick1, 1Iowa State University, Ames, 2Hy-Line International, Dallas Center, IA

Association between Metabolites in Egg Yolk and Hatchability Traits in Laying Hens.
A. R. Sharifi1, Y. Zhang1, S. Weigend1, A. Weigend1, R. Preisinger3, M. Schmutz1, L. Roemisch-Margl1, R. Jonczyk1, M. C. Gülersönne2, H. P. Piepho3, W. A. Malik2, F. Sittenstock4 and H. Simianer3, 1Georg-August-University, Göttingen, Germany, 2Institute of Farm Animal Genetics of the Friedrich-Loeffler-Institute, Neustadt-Mariensee, Germany, 3Lohmann Tierzucht GmbH, Cuxhaven, Germany, 4Technical University Munich, Munich, Germany, 5Hohenheim University, Hohenheim, Germany, 6University of Applied Sciences, Osnabrück, Germany
4:30 PM  328  New Insights on the Influence of Leptin Receptor Gene in Bone Traits in Broilers.
A. M. G. Ibelli, J. O. Peixoto, J. A. P. Marchesi, L. L. Coutinho and M. C. Ledur, EMBRAPA Swine and Poultry, Concórdia, Brazil, Universidade do Contestado, Concórdia, Brazil, Universidade de São Paulo/Esalq, Piracicaba, Brazil

4:45 PM  329  Detection of QTL Influencing Egg Quality Traits in Layers Receiving Various Diets.

5:00 PM  330  Detecting Signatures of Selection in Lines of Broiler Chickens.
J. J. Stainton, C. Haley, B. Charlesworth, A. Kranis, K. Watson and P. Wiener, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, United Kingdom, Aviagen Ltd, Edinburgh, United Kingdom

5:15 PM  331  Detection Of Pleiotropic QTL Related To Protein Expression And Foie Gras Quality Traits.
Y. François, C. Molette, A. Vignal, S. Davail and C. Marie-Etancelin, JUT des Pays de l’Adour, UMR CNRS 5254 IPREM-EEM, Mont De Marsan, France, INRA UMR 1388 GenPhySe, Castanet-Tolosan, France, INRA UMR1388 GenPhySe, Castanet-Tolosan, France

Swine Genomics and Difficult Traits
Chair: Max F. Rothschild, Iowa State University
Bayshore Grand Ball Room B-C

4:00 PM  369  Genome-Wide Association Analyses For Boar Taint Components in Different Pietrain Sired Crosses.
C. Grosse-Brinkhaus, L. C. Storck, C. Neuhoff, L. Frieden, K. Schellander, C. Looft and E. Tholen, Institute of animal science, University of Bonn, Bonn, Germany

4:15 PM  370  Genome-Wide Association Study For Growth And Feed Intake in Duroc boars Utilizing Random Regression Models.
J. T. Howard, F. Tiezzi, S. Jiao, K. A. Gray and C. Maltecca, North Carolina State University, Raleigh, Smithfield Premium Genetics, Rose Hill, NC

4:30 PM  371  From Phenotype to QTN and Back: Identification and Characterization of a Genetic Variant of the Porcine Glucocorticoid Receptor With a Major Effect on HPA Axis Activity.
E. Murani, H. Reyer, A. Görres, A. Tuchscherer, E. Kanitz, S. Fonsuksil and K. Wimmers, Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, Genetics and Biometry, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, Behavioural Physiology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany

4:45 PM  372  Genetic Associations of Farrowing Length in Two Maternal Lines of Pigs.
R. Zanella, A. M. G. Ibelli, J. O. Peixoto, M. E. Cantão, M. V. G. da Silva, P. F. Giachetto, M. Freitas, J. Lopes and M. C. Ledur, EMBRAPA Swine and Poultry, Concórdia, Brazil, Embrapa Dairy Cattle, Juiz de Fora, Brazil, Embrapa Agricultural Informatics, Campinas, Brazil, BRF S/A, Curitiba, Brazil

5:00 PM  373  Genome-Wide Association Study for Conformation Traits and Osteochondrosis in Pigs.
E. Grindflek, H. Hamland and T. Aasmundstad, Norsvin, Hamar, Norway

5:15 PM  374  Studies of the Genetic Background of a Teat Defect in Pigs Born in Germany and Sweden.
E. Jonas, H. Chalkias, C. Neuhoff, G. Lindgren and D. J. D. Koning, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, Institute of Animal Sciences, University of Bonn, Bonn, Germany
Symposium: Challenges in Industry Application of Genomic Prediction
Chair: Dorian J. Garrick, Iowa State University
Stanley Park Ballroom

4:00 PM 079 Challenges in Industry Application of Genomic Prediction - Experiences from Dairy Cattle.
E. A. Mäntysaari1, MIT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

4:30 PM 080 Applications of Genomic Selection in Poultry.

5:00 PM 081 Genomic Predictions in Aquaculture: Reliabilities in an Admixed Atlantic Salmon Population.
J. Ødegård1, T. Moen1, N. Santi2, S. A. Korsvoll2, S. Kjøglum3 and T. H. E. Meuwissen2, AquaGen AS, Trondheim, Norway, Norwegian University of Life Sciences, Ås, Norway

Symposium: Integrating the Discovery and Usage of Functional Mutations into Dairy Genomic Selection Programs for Complex Traits
Chair: Hermann Swalve, Martin Luther University Halle-Wittenberg
Bayshore Grand Ballroom E-F

4:00 PM 302 Use of High Density Marker Data – The Role of Individual Functional Mutations.
H. Swalve1, Martin Luther University Halle-Wittenberg, Wittenberg, Germany

4:30 PM 303 Genomic Feature Models.
P. Sørensen1, S. M. Edwards2 and P. Jensen1, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

5:00 PM 304 The Hunt for a Functional Mutation Affecting Conformation and Calving Traits on Chromosome 18 in Holstein Cattle.
J. B. Cole1,2, J. L. Hutchison1, D. J. Null1, P. M. VanRaden2, G. E. Liu1, S. G. Schroeder1, T. P. L. Smith4, T. S. Sonstegard3, C. P. VanTassell2 and D. Bickhart1, Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USDA, ARS, BFGL, Beltsville, MD, Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD, USDA-ARS-APPL, Beltsville, MD

Symposium: Methods and Tools - Bioinformatics (1)
Chair: Paul Stothard, University of Alberta
Bayshore Grand Ballroom A

4:00 PM 163 Bioinformatics Tools and Lessons from the Canadian Cattle Genome Project.
P. Stothard1, X. Liao2, A. S. Arantes3, M. De Paw4, C. Coros2, G. S. Plastow5, S. S. Moore2,3 and S. P. Miller1,4, University of Alberta, Edmonton, AB, Canada, Delta Genomics Centre, Edmonton, AB, Canada, The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, AgResearch, Invermay, Mosgiel, New Zealand

4:30 PM 164 Using the Whole Read: Structural Variant Detection using NGS Data.
D. Bickhart1, J. B. Cole2, J. L. Hutchison3, L. Xu4 and G. E. Liu4, USDA-ARS-APPL, Beltsville, MD, Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, University of Maryland, College Park, Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD
Ruminant Comparative Genomics: A Tool for Tracing Rumen Evolution.

D. M. Larkin and M. Farre, Royal Veterinary College, London, United Kingdom
Friday, August 22, 2014

Plenary Speaker - Friday
Chairs: E. John Pollak, USDA, ARS, U.S. Meat Animal Research Center and Filippo Miglior, Canadian Dairy Network and University of Guelph
Bayshore Grand Ballroom

8:30 AM  Plenary 5  Population Genetics in the Personal Genome Era.
C. D. Bustamante*, Department of Genetics, Stanford University, Stanford, CA

Breeding of Companion Animals
Chair: Sheila M. Schmutz, University of Saskatchewan
Cypress Room

10:30 AM  279  Indications for Presence of a Major Gene for Thyroid Cancer in German Longhaired Pointers.
L. van der Waaij1, R. Crooijmans2, R. Keesler2 and J. de Vos1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Veterinary Faculty, Utrecht University, Utrecht, Netherlands, 3Veterinary Oncology Referral Centre ‘De Ottenhorst’, Terneuzen, Netherlands

10:45 AM  280  Good Possibilities to Select Against Fearfulness in Rough Collie.
P. Arvelius*, H. Eken Asp, W. F. Fikse, E. Strandberg and K. Nilsson, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

11:00 AM  281  Building Effective Systems to Manage Inbreeding in Pedigree Dog Breeds.
T. W. Lewis1, S. C. Blott2, D. M. Howard3 and J. A. Woollams4, 1Animal Health Trust, Suffolk, United Kingdom, 2University of Nottingham, Leicestershire, United Kingdom, 3The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

11:15 AM  282  Is Heterozygote at the “Gait Keeper” Gene an Advantage for the Trotteur Français?
A. Ricard*, INRA, UMR 1313, Jouy-en-Josas, France; IFCE, Recherche et Innovation, Exmes, France

11:30 AM  283  The Role of Maternal Lineages in Horse Breeding: Effects on Conformation and Performance Traits.
N. Krattenmacher1, J. Tetens2, S. Hedt3, E. Stamer4 and G. Thaller5, 1Institute of Animal Breeding and Husbandry, Kiel University, Kiel, Germany, 2TiDa GmbH, Westensee/Brux, Germany, 3Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany

11:45 AM  284  Influence Of Specialisation On Connectedness And Genetic Parameters In Dutch Warmblood Riding Horses.
G. Rovere1,2, P. Madsen1, E. Norberg1, J. A. M. van Arendonk2 and B. J. Ducro3, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Genomic Selection in Beef Cattle
Chair: Roberto Carvalheiro, Sao Paulo State University (UNESP)
Bayshore Grand Ballroom D

10:30 AM  252  Genomic Breeding values from Across Breed Prediction in Practice: Accuracy of Beef-CRC Genomic Breeding Values in Australian Angus and Australian Brahman beef cattle.
V. Boerner1, D. Johnston2 and B. Tier2, 1Animal Genetics and Breeding Unit, University of New England, Armidale, Australia, 2Animal Genetics and Breeding Unit, Armidale, Australia

10:45 AM  253  Dynamic Genomic Selection in Crossbreed Beef Cattle Populations.
R. V. Ventura1,2, S. G. Larter1, F. S. Schenkel1, S. P. Miller2 and P. G. Sullivan3, 1Beef Improvement Opportunities, Guelph, ON, Canada, 2Centre for Genetic Improvement of Livestock - University of Guelph, Guelph, ON, Canada, 3Centre For Genetic Improvement of Livestock - University of Guelph, Guelph, ON, Canada
11:00 AM 254 Preliminary Identification and Characterization of Copy Number Variations in the Genome of South African Nguni Cattle.
M. Wang1,2, J. Rees1, K. Dzama1 and F. C. Muchadeyi1, 1Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa, 2University of Stellenbosch, Stellenbosch, South Africa

11:15 AM 255 Genome-Wide Analysis of Genetic Diversity in Autochthonous Spanish Populations of Beef Cattle.
A. González-Rodríguez1, M. A. Torro1, L. Varona2, M. J. Carabaño2, J. J. Cañas Álvarez3, J. Altarriba1, T. B. R. Da Silva4, J. A. Baró1, A. Molina1 and C. J. Díaz4, 1Universidad de Zaragoza, Zaragoza, Spain, 2ETS Ingenieros Agrónomos, Madrid, Spain, 3INIA, Madrid, Spain, 4Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 5UNESP-Jaboticabal, Brazil, Jaboticabal, Brazil, 6INIA, Spain, Madrid, Spain, 7Universidad de Valladolid, Palencia, Spain, 8Universidad de Córdoba, Córdoba, Spain

11:30 AM 256 Selection Signatures in Autochthonous Spanish Cattle Breeds using Site Frequency Spectrum Statistics.
S. Munilla1,2, A. González-Rodríguez2, E. F. Muresan3, J. J. Cañas Álvarez3, J. Altarriba2, C. J. Díaz3, A. Molina3, P. Martínez Camblo8 and L. Varona2, 1Universidad de Buenos Aires, Buenos Aires, Argentina, 2Universidad de Zaragoza, Zaragoza, Spain, 3Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 4INIA, Madrid, Spain, 5Universidad de Córdoba, Córdoba, Spain, 6Universidad de Oviedo, Oviedo, Spain

11:45 AM 257 Fat Cows - Selection Signatures in Korean Hanwoo and Australian Wagyu Cattle.
E. M. Strucken1, E. K. Piper2, H. K. Lee2, K. D. Song3, J. Gibson4, S. W. Lee5 and C. Gondro6, 1University of New England, Armidale, Australia, 2National Institute of Animal Sciences, Jeju, Korea, 3Hankyong National University, Anseong, South Korea, 4Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea, 5School of Environmental & Rural Science, University of New England, Armidale, Australia

Industry Application of Genomic Prediction
Chair: Dorian J. Garrick, Iowa State University
Bayshore Grand Ballroom B-C

10:30 AM 082 Genomic Relationships give Improved Prediction Ability for a Selection of Traits in Norsvin Landrace and Duroc.
Nordab1,2, E. Gjerlaug-Enger1, T. Aasmundstad1 and E. Grindflek1, 1Norsvin, Hamar, Norway, 2Geno SA, Hamar, Norway

M. Koivula1, I. Strandén2, G. P. Aamand3 and E. A. Mäntysaari1, 1MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 2NAV Nordic Cattle Genetic Evaluation, Aarhus, Denmark

11:00 AM 084 The Effect of Training Population Size and Chip Density on Accuracy and Bias of Genomic Predictions in Broiler Chickens.
J. J. Ilska1, A. Kranis2 and J. A. Woolliams1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom, 2Aviagen Ltd, Edinburgh, United Kingdom, 3The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

11:15 AM 085 Selective Breeding Against Infectious Diseases In Atlantic Cod With Whole Genome Sequence Data.
X. Yu1, T. H. E. Meuwissen1, M. Baranski2 and A. K. Soneson1, 1Norwegian University of Life Sciences, Ås, Norway, 2Norwegian Institute of Food, Fisheries and Aquaculture Research, Tromsø, Norway, 3NOFIMA, Ås, Norway

11:30 AM 086 Genomic Predictions of Economically Important Traits in Nelore Cattle of Brazil.
P. R. Boddhireddy1, K. C. Prayaga1, P. S. Barros1, R. B. Lôbo1 and S. K. DeNise1, 2Zoetis Inc., Kalamazoo, MI, 2Zoetis Inc., Parkville, Australia, 3Zoetis Inc., Sao Paulo, Brazil, 4Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil

M. Stoop, H. Eding1, M. van Pelt, L. de Haer and G. de Jong, CRV, Arnhem, Netherlands
Symposium: Advances in Selection Theory
Chair: Ricardo Pong-Wong, The Roslin Institute and University of Edinburgh
Stanley Park Ballroom

10:30 AM 018 Predicting Gain the Sustainable Way and its Relevance to Genomic Selection.  
J. A. Woolliams, K. G. Nirea and T. H. E. Meuwissen, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, Norwegian University of Life Sciences, Ås, Norway, Department of Animal and Aquacultural Sciences, University of Life Sciences, Ås, Norway

11:00 AM 019 Contribution of Gene-Gene Interaction to Genetic Variation and its Utilisation by Selection.  
A. Mäki-Tanila and W. G. Hill, MTT Agrifood Research Finland, Jokioinen, Finland, University of Edinburgh, Edinburgh, United Kingdom

T. H. E. Meuwissen, A. K. Sonesson and J. Ødegård, Norwegian University of Life Sciences, Ås, Norway, NOFIMA, Ås, Norway, AquaGen AS, Trondheim, Norway

Symposium: Developing Effective Dairy Genomic Selection Programs for Traits or Breeds that Lack Massive Reference Populations
Chair: Christian Maltecca, North Carolina State University
Bayshore Grand Ballroom E-F

C. Maltecca, North Carolina State University, Raleigh

11:00 AM 312 Assembling a Reference Population – from Genetic Architecture to New Phenotypes.  
K. Schoepke, Martin-Luther-University Halle-Wittenberg, Halle, Germany

11:30 AM 313 How to Improve Genomic Predictions in Small Populations.  
M. S. Lund, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Symposium: Developments in Sheep Genetics
Chair: John C McEwan, AgResearch
Bayshore Grand Ballroom A

10:30 AM 351 Genomic Selection in Sheep Breeding Programs.  
J. van der Werf, School of Environmental & Rural Science, University of New England, Armidale, Australia

11:00 AM 352 Association of TMEM154 Missense Mutations with Lentiviral Infection and Virus Subtypes in Sheep.  
M. P. Heaton, K. A. Leymaster and M. L. Clawson, USDA, Meat Animal Research Center, Clay Center, NE

11:30 AM 353 Association between Raw SNP Data and Growth and Meat Yield Traits in Sheep.  
G. Jenkins, J. C. McEwan, M. A. Black, M. E. Goddard, B. Auveray and K. G. Dodds, AbacusBio Limited, Dunedin, New Zealand, AgResearch, Invermay, New Zealand, University of Otago, Dunedin, New Zealand, Department of Primary Industries, Melbourne, Australia, University of Melbourne, Melbourne, Australia, AgResearch, Mosgiel, New Zealand

11:45 AM 354 Inferring Ancestral Demography of Domestic and Wild Sheep using Whole-Genome Sequence.  
S. Bolormaa, J. Kijas, D. Colman, H. D. Daetwyler and I. M. MacLeod, Department of Environment and Primary Industries, Bundoora, Australia, CRC for Sheep Industry Innovation, Armidale, Australia, CSIRO Animal, Food and Health Sciences, Brisbane, Australia, University of Alberta, Edmonton, AB, Canada, La Trobe University, Bundoora, Australia, University of Melbourne, Melbourne, Australia
Bioinformatics: Analysis and Discovery
Chair: James M. Reecy, Iowa State University
Cypress Room

1:30 PM 166 Fine Scale Population Structure of Global Cattle Breeds using Dense Haplotype Data.
M. Neuditschko, M. S. Khaitar and H. W. Raadsma, Agroscope - Swiss National Stud Farm, Avenches, Switzerland, Reprogen Animal Bioscience Group, Faculty of Veterinary Science, University of Sydney, Camden, Australia

1:45 PM 167 Runs of Homozygosity and Distribution of Functional Variants in Cattle Genome.
Q. Zhang, B. Guldbrandtsen, M. Bosse, M. S. Lund and G. Sahand, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

2:00 PM 168 Systems Genetics Analysis of Obesity in a Porcine Model using WISH Network Method.
L. J. Kogelman, S. D. Pant, J. Karjalainen, L. Franke, M. Fredholm and H. N. Kadarmideen, Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, Department of Genetics, University Medical Center Groningen, Groningen, Netherlands

2:15 PM 169 Separating Signal from Noise Estimating SNP-effects and Decomposing Genetic Variation to the Level of QTLs in Pure Breed Duroc Pigs.
P. M. Sarup, J. Jensen, S. M. Edwards, T. Ostersen, P. Sørensen and M. A. Henryon, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Pig Research Centre, Copenhagen, Denmark

2:30 PM 170 Regulatory and Coding Genome Regions are Enriched for Trait Associated Variants in Dairy Cattle.
L. Koufariotis, Y. P. P. Chen, S. Bolormaa and B. J. Hayes, La Trobe University, Melbourne, Australia, Department of Environment and Primary Industries, Melbourne, Australia, Dairy Futures Co-operative Research Centre, Melbourne, Australia, Faculty of Science, Technology and Engineering, La Trobe University, Melbourne, CA, Australia, CRC for Sheep Industry Innovation, Armidale, Australia, The Department of Environment and Primary Industries, Bundoora, Australia

2:45 PM 171 A Tale Of Two Birds: SNP Discovery and Genomic Architecture of Highly Inbred Leghorn and Fayoumi Chicken Breeds using Whole Genome Resequencing.
D. S. Fleming, J. E. Koltes, E. Fritz-Waters, J. M. Reecy and S. J. Lamont, Iowa State University, Ames, Iowa State University, Ames

Improving Nutrient Utilization and Reducing the Environmental Impact of Dairy Operations through Genetic or Genomic Selection
Chair: Kent A. Weigel, University of Wisconsin
Bayshore Grand Ballroom E-F

1:30 PM 305 Genetic Parameters for Methane Emissions of Dairy Cows Predicted Based on Milk Fatty Acids.
M. H. P. W. Visker, S. van Engelen, J. Dijkstra, J. A. M. van Arendonk and H. Bovenhuis, TI Food and Nutrition, Wageningen, Netherlands, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Animal Nutrition Group, Wageningen University, Wageningen, Netherlands

1:45 PM 306 Genome Wide Association Studies for Milk Fatty Acids as a Basis for Methane Prediction.
S. van Engelen, H. Bovenhuis, J. Dijkstra, J. A. M. van Arendonk and M. H. P. W. Visker, TI Food and Nutrition, Wageningen, Netherlands, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Animal Nutrition Group, Wageningen University, Wageningen, Netherlands

2:00 PM 307 Strategies for Use of Reproductive Technologies in Genomic Dairy Cattle Breeding Programs.
J. R. Thomasen and A. C. Sorensen, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Viking Genetics, Assentoft, Denmark
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<tr>
<td>2:15 PM</td>
<td>308 Inbreeding and Crossbreeding Parameters for Production and Fertility Traits in Holstein, Montbéliarde and Normande Cows.</td>
<td>C. Dezetter*, Groupe ESA, Angers, France; ONIRIS, Nantes, France; Coopex Montbéliarde, Roulans, France</td>
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<td>2:30 PM</td>
<td>309 Genomic Predictions of Fertility Related Disorders in Norwegian Red using 30 Years of Data.</td>
<td>K. Haugaard1, B. Heringstad1,2 and M. Svendsen1,1Norwegian University of Life Sciences, Ås, Norway; 2Geno, Ås, Norway</td>
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<td>2:45 PM</td>
<td>310 Milk Flow Traits of Friesian, Jersey and Friesian-Jersey Crossbred Cows Under Grazing Conditions in New Zealand.</td>
<td>N. Lopez-Villalobos1, J. P. Edwards2 and J. G. Jago1,1Massey University, Palmerston North, New Zealand; 2DairyNZ, Hamilton, New Zealand</td>
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**Linear and Nonlinear Models: Inference**  
Chair: Daniel Gianola, University of Wisconsin  
Bayshore Grand Ballroom D

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<tr>
<td>1:30 PM</td>
<td>216 Selective Shrinkage of Genomic Effects using Synthetic Dependencies in Neighboring Chromosome Regions.</td>
<td>D. Wittenburg and N. Reinsch, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany</td>
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<td>1:45 PM</td>
<td>217 Improving REML Estimates of Genetic Parameters through Penalties on Correlation Matrices.</td>
<td>K. Meyer*, Animal Genetics and Breeding Unit, University of New England, Armidale, Australia</td>
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<td>2:00 PM</td>
<td>218 Inferring the Ancestral Dynamics of Population Size from Genome Wide Molecular Data: An ABC Approach.</td>
<td>S. Boitard1,2 and S. Sochacki1,1GABI (INRA / AgroParisTech), Jouy-en Josas, France; 2UMR 7205 ISYEB (MNHN / CNRS / EPHE / UPMC), Paris, France</td>
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<td>2:30 PM</td>
<td>220 Using SNP Markers to Estimate Additive, Dominance and Imprinting Genetic Variance.</td>
<td>M. S. Lopes1,2, J. W. M. Bastiaansen1, L. Janss1, H. Bovenhuis1 and E. F. Knol2,1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands; 2TOPIGS Research Center IPG, Beuningen, Netherlands; 3Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark</td>
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<td>2:45 PM</td>
<td>221 Estimation of Single Locus Effects on Susceptibility, Infectivity and Recovery Rates in an Epidemic using Temporal Data.</td>
<td>C. M. Pooley1, S. C. Bishop1 and G. Marion2,1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom; 2Biomathematics and Statistics Scotland, Edinburgh, United Kingdom</td>
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**Swine Breeding (2)**  
Chair: Brian P. Kinghorn, University of New England  
Bayshore Grand Ballroom A

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<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Authors</th>
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<tr>
<td>1:30 PM</td>
<td>378 Genetic Parameter for Litter Quality Traits.</td>
<td>H. R. Brandt1, Institute of Animal breeding and Genetics, Giessen, Germany</td>
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<td>1:45 PM</td>
<td>379 Genetic Analysis of Birth Weight Uniformity in Pigs: Comparison of Methods.</td>
<td>E. Sell-Kubiak1, P. Bijma1, E. F. Knol1 and H. A. Mulder1,1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands; 2TOPIGS Research Center IPG, Beuningen, Netherlands</td>
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<td>2:00 PM</td>
<td>380 Social Genetic Effects for Litter Size of Sows Housed in Groups During Gestation.</td>
<td>K. L. Bunter*, Animal Genetics and Breeding Unit, UNE, Armidale, Australia</td>
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Most of the Long-Term Genetic Gains from Optimum- Contribution Selection can be Realised with Restrictions Imposed.
M. Henryon1,2, T. Ostersen3, B. Ask4, A. C. Sørensen4 and P. Berg5, 1Danish Agriculture and Food Council, Pig Research Center, Copenhagen, Denmark, Copenhagen, Denmark, 2School of Animal Biology, University of Western Australia, Crawley, Australia., Crawley, Australia, 3Pig Research Centre, Copenhagen, Denmark, 4Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 5Nordic Genetic Resource Centre, Ås, Norway

Effect of a Low Energy, High Fiber Diet Challenge on Yorkshire Pigs Selected for Residual Feed Intake.
E. D. Mauch1, J. M. Young2, J. F. Patience1, N. K. Gabler1 and J. C. M. Dekkers2, 1Iowa State University, Ames, 2North Dakota State University, Fargo

X. Guo1, O. F. Christensen2, T. Ostersen2, D. A. Sørensen3, Y. Wang4, M. S. Lund4 and G. Su1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Pig Research Centre, Copenhagen, Denmark, 3College of Animal Science and Technology, China Agricultural University, Beijing, China

Symposium: Genetics of Trait Complexes - Disease Resistance
Chair: Larry A. Kuehn, USDA, ARS, U.S. Meat Animal Research Center
Stanley Park Ballroom

Is There a Genetic Solution to Bovine Respiratory Disease Complex?

Disease Genetics: Successes, Challenges and Lessons Learnt.
S. C. Bishop*, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Genetic Resistance to Parasites in Small Ruminants: from Knowledge to Implementation in the Tropics.
N. Mandonnet*, M. Mahieu, G. Alexandre, M. Gunia and J. C. Bambou, INRA-UR0143, Unité de Recherches Zootechniques, INRA Antilles-Guyane, Petit-Bourg, France

Symposium: Genomic Selection in Beef Cattle
Chair: David Johnston, University of New England
Bayshore Grand Ballroom B-C

Genomic Selection in Nelore Cattle in Brazil.
R. Carvalheiro*, Sao Paulo State University (UNESP), Jaboticabal, Brazil

Genome Wide Imputation in Canadian Beef Cattle.
F. S. Schenkel*, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Genomics for Pedigree and Cross-bred Beef Cattle Populations; Some Experiences from Ireland.
A. Cromie1, F. Kearney1, R. Evans2 and D. P. Berry1, 1Irish Cattle Breeding Federation, Cork, Ireland, 2Irish Cattle Breeding Federation, Co Cork, Ireland, 3Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

Symposium: Genetics of Trait Complexes - Lactation
Chair: Juan F. Medrano, University of California
Bayshore Grand Ballroom A

Milking Efficiency – A Milkability Trait for Automatically Milked Cows.
P. Lovendahl*, J. Lassen1 and M. G. Chagunda1, 1Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Center of Quantitative Genetics and Genomics,
4:15 PM 141 Genome Wide Association Analyses Identify New Loci for Milking Speed and Temperament in North American Holsteins.
M. K. Abo-Ismail1,2, S. P. Miller3,4,5, M. Sargolzaei1,6, D. A. Grossi1, S. Nayeri1, S. S. Moore2, G. S. Plastow4, P. Stoehard6 and F. S. Schenkel1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Animal and Poultry Science, Damahonour University, Damahonour, Egypt, 3AgResearch, Invermay, Mosgiel, New Zealand, 4University of Alberta, Edmonton, AB, Canada, 5University of Queenslands, Centre for Animal Science, 6Embrapa, Brasilia, Brazil, 7The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St. Lucia, Australia

4:30 PM 142 Beta-Lactoglobulin Content of Bovine Milk is Affected by Multiple Mutations on BTA11.
H. Boovenhuis1 and N. Bédère2, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Wageningen University, Wageningen, Netherlands, 3Wageningen University, Wageningen, Netherlands

4:45 PM 143 Identification of QTL and Candidate Mutations Affecting Major Milk Proteins in Three French Dairy Cattle Breeds.
M. P. Sanchez1, A. Govignon-Gion1, M. Ferrand2, M. Gelé2, D. Pourcher1, M. N. Rossignol1, S. Fritz2, M. Boussaha1, A. Capitan1, D. Rocha1, G. Miranda1, P. Martin1, M. Brochard2 and D. Boichard1, INRA, UMR1313 GABI, Jouy-en-Josas, France, 2Idéle, Paris, France, 3ECEL, Roullans, France

5:00 PM 144 Genomic Regions Affecting Cheese Making Properties Identified in Danish Holsteins.
V. R. Gregersen1, H. P. Bertelsen1, N. A. Poulsen2, L. B. Larsen1, F. Gustavsson1, M. Glantz1, M. Paulsson1, A. J. Buitenhuis1 and C. Bendixen1, Aarhus University, Molecular Biology and Genetics, Tjele, Denmark, 2Lund University, Food Technology, Engineering and Nutrition, Lund, Sweden, 3Aarhus University, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Tjele, Denmark, 4Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

5:15 PM 145 Genetics of Milk Coagulation Properties Predicted by Milk Mid-Infrared Spectroscopy Analysis of Irish Dairy Cows.
G. Visentin1,2, A. A. Mc Dermott1, S. McParland1, D. P. Berry1 and M. De Marchi2, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Legnaro, Italy, 3Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

Management of Animal Genetic Resources
Chair: Paul Boettcher, FAO
Cypress Room

4:00 PM 047 The Use of Whole Genome Sequence Data to Estimate Genetic Relationships Including Rare Alleles Information.
S. E. Eynard1,2, J. J. Windig1,4, G. Leroy2,3, E. Verrier2,3, S. J. Hiemstra1,4, R. van Binsbergen1,5 and M. P. L. Calus1, 1Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 2AgroParisTech, Paris, France, 3INRA UMR 1313 GABI, Jouy en Josas, France, 4Centre for Genetic Resources the Netherlands, Wageningen UR, Wageningen, Netherlands, 5Biometris, Wageningen UR, Wageningen, Netherlands

4:15 PM 048 A Dedicated SNP Panel for Evaluating Genetic Diversity in a Composite Cattle Breed.
H. D. Blackburn1, S. R. Paiva1, B. P. Sollero1, P. Biegelemyer2, A. R. Caetano3 and F. F. Cardoso4, USDA-ARS-National Animal Germplasm Program, Fort Collins, CO, 2EMBRAPA, Brasilia, Brazil, 3Embrapa Southern Region Animal Husbandry, Bagé, Bagé, Brazil, 4Federal University of Pelotas, Pelotas, Brazil, 5Embrapa Genetic Resources and Biotecnology, Brasilia, Brazil, 6Embrapa Southern Region Animal Husbandry, Bagé, Brazil

4:30 PM 049 Optimizing Genetic Management within Populations with a Simulation Tool.
J. J. Windig1,2, S. J. Hiemstra1,2 and K. Oldenbroek2, 1Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 2Centre for Genetic Resources the Netherlands, Wageningen UR, Wageningen, Netherlands, 3Animal Breeding & Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

5:00 PM 051 Assessing the Effects on Litter Size of Age of Inbreeding in an Ancient Line of Large White Pigs.
L. Silió*, J. Rodriguez and M. C. Rodríguez, INIA, Madrid, Spain

5:15 PM 052 An Observatory of the Genetic Variability of Ruminants and Equids Breeds.

Selection Theory - Managing Genetic Variance
Chair: Jack C. M. Dekkers, Iowa State University
Bayshore Grand Ballroom D

4:00 PM 021 Selection on Recombination Rate to Increase Genetic Gain.
G. Mészáros*, G. Gorjanc, J. Jenko, J. A. Woolliams and J. M. Hickey, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

4:15 PM 022 Optimum Contribution Selection Combined with Weighting Rare Favourable Alleles Increases Long-Term Genetic Gain.
H. Liu*, A. C. Sørensen and P. Berg, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

4:30 PM 023 An Iterative Algorithm for Optimum Contribution Selection in Large Scale Breeding Programs.
B. S. Dagnachew* and T. H. E. Meuwissen*, 1Norwegian University of Life Sciences, Aas, Norway, 2Norwegian University of Life Sciences, Ås, Norway

4:45 PM 024 The Structural Impact of Implementing Optimal Contribution Selection in a Commercial Pig Breeding Population.
D. M. Howard*, R. Pong-Wong, P. W. Knap, V. D. Kremer* and J. A. Woolliams*, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Genus-PIC, Schleswig, Germany

5:00 PM 025 Increased Genetic Gains in Sheep Breeding Programs from using Female Reproductive Technologies Combined with Genomic Selection.
T. Granleese*1,2, S. Clark* and J. van der Werf*, 1University of New England, Armidale, Australia, 2Sheep Cooperative Research Council, Armidale, Australia

5:15 PM 026 Diminishing Marginal Returns From Genomic Selection As More Selection Candidates Are Phenotyped.
T. O. Okeno*, M. Henryon and A. C. Sørensen*, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, 2School of Animal Biology, University of Western Australia, Crawley, Australia, 3Danish Agriculture and Food Council, Pig Research Center, Copenhagen, Denmark, 4Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Symposium: Genetics of Trait Complexes: Growth and Development
Chair: Michael D. MacNeil, Delta G
Bayshore Grand Ballroom B-C

4:00 PM 134 Metabolomics: A Pathway for Improved Understanding of Genetic Modulation of Mammalian Growth and Tissue Deposition.
F. Widmann, R. Weikard and C. Kühn*, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany
4:30 PM 135 Convergence of Genetic and Environmental Factors on Epigenome to Regulate Animal Growth and Development.
M. Du* and M. J. Zhu, Washington State University, Pullman

5:00 PM 136 Epigenetics and Phenotypic Variability: Some Interesting Insights from Birds.
L. Frésard1, M. Morisson1, J. M. Brun1, A. Collin1, B. Pain1, F. Minvielle1 and F. Pitel,*1 1UMR 1388 INRA / INPT ENSAT / INPT ENV, GenPhySE, Castanet-Tolosan, France, 1INRA, UR83, Recherches Avicoles, Nouzilly, France, 1INSERM, U846, INRA, USC1361, Institut Cellule Souche et Cerveau, Bron, France, *1UMR 1313 INRA/AgroParisTech, GABI, Jouy en Josas, France

Symposium: Methods and Tools - Bioinformatics (2)
Chair: James M. Reecy, Iowa State University
Bayshore Grand Ballroom E-F

4:00 PM 172 Cyberinfrastructure for Life Sciences - iAnimal Resources for Genomics and Other Data Driven Biology.
J. M. Reecy*, Iowa State University, Ames

4:30 PM 173 Pedigree-Based Haplotype Reconstruction, Identification of Cross-Overs and Detection of Map and Genotyping Errors using PHASEBOOK.
T. Druet* and M. Georges, University of Liège, Liège, Belgium

5:00 PM 174 From Data to Knowledge: Translating Functional Genomics Data into Information for Livestock Production.
F. McCarthy1, C. R. Gresham1, J. E. Koltes1, M. T. Arick1, E. Lyons1, M. W. Vaughn1, E. T. Dawson1, N. Hopkins1 and S. C. Burgess1, 1University of Arizona, Tucson, 1Mississippi State University, Starkville, 1Iowa State University, Ames, 1Texas Advance Computing Center, University of Texas, Austin, 1Texas Advanced Computing Center, Austin, TX

Symposium: Statistical Tools for Mapping QTL and Genes
Chair: Michael E. Goddard, Department of Environment and Primary Industries
Stanley Park Ballroom

4:00 PM 199 A Research Plan for the Identification of QTL.
M. E. Goddard*, Department of Primary Industries, Melbourne, Australia

4:30 PM 200 Application of Large-Scale Sequence Datasets for the Discovery of Genomic Variations of Economic Importance in Dairy Cattle.

5:00 PM 201 Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach.
R. L. Fernando1, D. J. Garrick2, A. Toosi1 and J. C. M. Dekkers1, 1Iowa State University, Ames, 2Massey University, Palmerston North, New Zealand
Poster Presentations

The posters will be presented as ePosters at the 2014 WCGALP meeting. Large computer screens will be setup in the poster area and will display the electronic version of the posters. The posters will be available for viewing all day on the day of their listing starting at 7:30 AM. The presenting authors will be available for questions during the time indicated for that session.

Monday, August 18, 2014

Posters: Beef Cattle Breeding (Group 1)

Chair: Stephen P. Miller, AgResearch, David Johnston, University of New England and Roberto Carvalheiro, Sao Paulo State University (UNESP)

Presentation Time: 9:30 AM – 10:00 AM

709 Genomic-Polygenic Evaluation of Multibreed Angus-Brahman Cattle for Postweaning Ultrasound and Weight Traits with Actual and Imputed Illumina50k SNP Genotypes.
M. A. Elzo1, M. G. Thomas2, D. D. Johnson3, C. A. Martinez1, G. C. Lamb4, D. O. Rae1, J. D. Wasdin1 and J. D. Driver1,
1Department of Animal Sciences, University of Florida, Gainesville, 2Colorado State University, Department of Animal Sciences, Fort Collins, 3University of Florida, Gainesville, 4University of Florida, Marianna

S. Eaglen1, J. Soelkner1, B. fuerst-Waltl6 and C. Fuerst1, 1University of Natural Resources and Life Sciences, Vienna, Austria, 6Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

711 Imputation Accuracy using Flmpute and BEAGLE Software in Brazilian Synthetic Cattle Breed.
T. C. S. Chud1, R. V. Ventura2,4, J. S. Schenkel1, R. Carvalheiro5, M. E. Buzanskas1, I. Urbinati1, L. C. Almeida Regitano7, C. R. Marcondes1 and D. P. Munari1, 1Univ Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil, 2University of Guelph, Guelph, ON, Canada, 4Beef Improvement Opportunities, Guelph, ON, Canada, 5Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 6ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria, 7Embrapa Southern Region Animal Husbandry, Bage, Brazil

712 Selection Signatures in Canchim Beef Cattle.
I. Urbinati1, M. E. Buzanskas1, T. C. S. Chud1, F. B. Mokry4, L. C. Almeida Regitano7, R. H. Higa6 and D. P. Munari1, 1Univ Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil, 6Univ Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 7Embrapa Southern Region Animal Husbandry, Bage, Brazil

713 Accuracy of Genomic Prediction for Tick Resistance in Braford and Hereford Cattle.
F. F. Cardoso1,2, B. P. Sollero1, H. B. Comin1, C. G. Gomes1, V. M. Roso1, R. H. Higa6 and A. R. Caetano1, 1Obihiro University of Agriculture and Veterinary medicine, 2INIA, Las Brujas, Uruguay

714 Breed Additive and Heterosis Effects on Feedlot and Carcass Traits in Beef Cattle.
A. Theunissen2, M. M. Scholtz2,3, M. D. MacNeil1,4 and F. W. C. Nesar1, 1Vaalharts Research Station, Northern Cape, Jan Kempdorp, South Africa, 2University of the Free State, Bloemfontein, South Africa, 3ARC-Animal Production Institute, Irene, South Africa, 4Kansas State University, Manhattan

715 Genetic Trend of Stillbirths in Japanese Black Cattle.
S. Maeda1, K. Kuchida1, M. Hosono2, M. Sato2 and K. Inoue3, 1Obihiro University of Agriculture and Veterinary medicine,
Crossbreeding to Increase Beef Production: Breed-specific Effects on Sensory Properties.
A. Theunissen, Northern Cape Department of Agriculture, Land Reform and Rural Development, Jan Kempdorp, South Africa

Accuracy of Genomic Prediction using Two Admixed Crossbred Populations.
A. Vallee1,2, J. A. M. van Arendonk3 and H. Bovenhuis4, 1Genes Diffusion, Douai, France, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Genetic Parameters for Body Conformation Scores and Carcass Traits Measured by Real-Time Ultrasound in Nellore Cattle.
J. L. B. M. Grosso1, G. A. Oliveira Junior, I. R. Menezes, E. C. Mattos, J. B. S. Ferraz and J. P. Eler, NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil

Microarray Analysis Indicates that Vitamin A Alters Expression Profiles of Bovine Intramuscular Preadipocytes during Adipogenesis.
D. Taniguchi1,2, A. Hasegawa2, I. Matsuno2 and Y. Mizoguchi2, 1Meiji University, kawasaki, Japan, 2Meiji University, Kawasaki, Japan

Effect of Acetic Acid and Glucose on Fatty Acid Synthesis Related Gene Expression Profiles During Bovine Intramuscular Adipogenesis.
I. Matsuno1, Meiji University, Kawasaki, Japan

Evaluation of Cytoplasmic Genetic Effects for Production and Reproduction Traits in Afrikaner Cattle.
F. W. C. Neser1, J. B. van Wyk1 and M. M. Scholtz1,2, 1University of the Free State, Bloemfontein, South Africa, 2ARC-Animal Production Institute, Irene, South Africa

M. Méndez1, Institute of Animal Science, San José de las Lajas, Cuba

Effects of Quantitative Trait Loci on Iron Content of Bovine Longissimus Dorsi Muscle.
P. C. Tiziotot1, J. F. Taylor2, J. E. Decker2, C. F. Grombont3, M. A. Mudada4, R. D. Schnabel5, L. L. Coutinho5, G. B. Mourao6, R. T. Nassau7, F. A. Donatoni Bressani7, P. Tholon7, T. S. Sonstegard7, M. M. D. Alencar7, R. R. Tullio7, J. M. Reecy8, A. R. Nogueirat and L. C. Almeida Regitano9, 1Federal University of São Carlos, São Carlos, Brazil, 2University of Missouri, Columbia, 3Instituto Federal de Educaçao, Ciência e Tecnologia da Bahia (IFBA), Valença, Brazil, 4Embrapa Pecuária Sudeste, São Carlos, Brazil, 5Universidade de São Paulo/Esalq, Piracicaba, Brazil, 6Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, 7USDA, ARS, BFGL, Beltsville, MD, 8Iowa State University, Ames

Estimation Of Genetic Parameters Of Type Traits For Namibian Brahman Beef Cattle.
M. D. Fair1, F. W. C. Neser and J. B. van Wyk, University of the Free State, Bloemfontein, South Africa

Posters: Prediction using Molecular Information (Group 1)
Chair: Dorian J. Garrick, Iowa State University, Roel F. Veerkamp, Wageningen University, and Esa A. Mäntysaari, MTT Agrifood Research Finland

Presentation Time: 9:30 AM – 10:00 AM

Genome-Wide Association Study for Loin Marbling Score in Duroc Pigs.
A. Neustaeter1, D. A. Gross3, M. Jafarikia2, M. Sargolzaei and F. S. Schenkel2, 1University of Guelph, Guelph, ON, Canada, 2Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 3 Canadian Centre for Swine Improvement, Ottawa, ON, Canada, 4 The Semex Alliance, Guelph, ON, Canada

Genomic Evaluation using 50K and Imputed HD Genotypes in Guzera (Bos indicus) Breed.
S. A. Boisson1,2, J. D. J. A. Santos3, J. F. Garcia4, J. Soelkner5, M. G. C. D. Peixoto5, J. E. Decker6, M. V. G. B. da Silva7, 1University of Natural Resources and Life Sciences, Vienna, Austria, 2UNESP Univ Estadual Paulista, Jaboticabal, Brazil, 3University of Guelph, Guelph, ON, Canada, 4The Semex Alliance, Guelph, ON, Canada, 5ARC Animal Breeding and Genomics, University of Sydney, Sydney, Australia, 6University of Natural Resources and Life Sciences, Vienna, Austria, 7Departamento de Genética Animal, Embrapa, Piracicaba, Brazil
B. Greyling, B. van Vuuren, P. van Hooft and A. A. Mauwashe, Agricultural Research Council, Centurion, South Africa.

Improving Predictive Ability of Selected Subsets of Single Nucleotide Polymorphisms in a Moderately Sized Dairy Cattle Population.

Is the use of Formulas a Reliable way to Predict the Accuracy of Genomic Selection?
S. Brard, A. Ricard, INRA, UMR 1388, Castanet-Tolosan, France.

Association between GDF9, FecB and Prolactin Gene Polymorphisms and Prolificacy of Awassi Sheep.
K. I. Jawasreh, A. Al-Qaisi and F. T. Awawdeh, Jordan University of Science and Technology, Irbid, Jordan.

The Role of Obesity Genes for Milk Fat Yield in Holstein Dairy Cattle.

Accuracy of Genomic Prediction in French Charolais Cattle Population using High-density Chip.


Estimation of Linkage Disequilibrium and Effective Population Size using Whole Genome Single Nucleotide Polymorphisms in Korean Native Pig and Landrace.
J. E. Park, J. H. Lee, J. H. Son and D. Lee, Seoul National University, Seoul, South Korea.

Estimating Variance Components for Growth, Feed Efficiency and Carcass Merit Traits in Angus Steers using Additive and Dominance Genomic Relationship Matrices.
L. Chen, University of Alberta, Edmonton, AB, Canada.

T. Knärr, I. Strandén, M. Koivula, G. P. Aamand and E. A. Mäntysaari, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland.

Imputation of Genotypes in Danish Two-Way Crossbreed Pigs using Low Density Panels.
T. Xiang, O. F. Christensen, A. Legarra and T. Ostersen, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark.

Genomic Breeding Values for Ungenotyped Individuals.
B. Tier, Animal Genetics and Breeding Unit, Armidale, Australia.

Ancestral Haplotypes, Quantal Genomics and Healthy Beef.
Bias of Genetic Trend of Genomic Predictions Based on both Real and Simulated Dairy Cattle Data.
P. Ma1, M. S. Lind2, U. S. Nielsen3, G. P. Aamand5, A. C. Sørensen4 and G. Su1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjøle, Denmark, 2Knowledge Center for Agriculture, Aarhus, Denmark, 3NAV Nordic Cow Genetic Evaluation, Aarhus, Denmark

Posters: Beef Cattle Breeding (Group 2)
Chair: Stephen P. Miller, AgResearch, David Johnston, University of New England and Roberto Carvalheiro, Sao Paulo State University (UNESP)
Presentation Time: 10:00 AM – 10:30 AM

Genetic Relationship amongst Reproductive Traits in Nellore Cattle.
A. R. Guarini1, H. H. R. Neves2, F. S. Schenkel3, R. Carvalheiro4, P. Tholon5, J. A. Oliveira6 and S. A. Queiroz7, 1Universidade Estadual Paulista, Jaboticabal, Brazil, 2GenSys Associated Consultants, Porto Alegre, Brazil, 3Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 4Embrapa Pecuária Sudeste, São Carlos, Brazil

Non-Hierarchical Cluster Analysis with the Breeding Values for Reproductive and Productive Traits in Beef Cattle.
C. C. P. Paz1,2,3, H. L. Moreira4, R. P. Savegnago4, M. E. Buzanska5, R. B. Lób6 and D. P. Munari7, 1SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Setúbal, SP, Brazil, 2Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 3Universidade Estadual Paulista Júlio de Mesquita, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Ciências Exatas, Jaboticabal-SP, Brazil, 4Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil

Accuracy of Genotype Imputation with Different Low Density Panels in Braford and Hereford Cattle.
M. L. Piccoli1,2,3, J. Bracconi Neto1, F. F. Cardoso4, M. Sargolzaei3,5 and F. S. Schenkel3, 1Universidade Federal do Rio Grande do Sul - Departamento de Zootecnia, Porto Alegre, Brazil, 2GenSys Consultores Associados S/S, Porto Alegre, Brazil, 3Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 4Embrapa Southern Region Animal Husbandry, Bage, Brazil, 5The Semex Alliance, Guelph, ON, Canada

Haplotype Diversity of Ten US Beef Cattle Breeds Captured by Different Definitions of Haplotypes Based on BovineSNP50K Chip.
H. Su1, R. L. Fernando and D. J. Garrick, Iowa State University, Ames

Determining the Number of Animals Required to Accurately Determine Breed Composition using Genomic Data.
S. Connolly1, E. K. Piper2, J. M. Seddon2, M. R. Fortes3 and M. j. Kelly4, 1The University of Queensland, School of Agriculture & Food Science, Gatton, Australia, 2The University of Queensland, School of Veterinary Science, Gatton, Australia, 3Interbull center, Uppsala, Sweden, 4INRA GABI, Jouy en Josas, France, 5INRA UMR 1313 GABI, Jouy-en-Josas, France

Relationships among Genome DNA Methylation Patterns in each Upstream CG Region on the 22 of Genes Controlled by Epigenetic System and Economic Traits in Japanese Black Cattle.
Y. Suda1, Miyagi University, Sendai, Japan

Across-Country Genetic Parameters in Beef Cattle for Interbull Weaning Weight Genetic Evaluation.
T. Pabiou1, M. Nilforooshan2, D. Laloe1, E. Hjerpe2 and E. Venot2, 1Irish Cattle Breeding Federation, Cork, Ireland, 2Interbull center, Uppsala, Sweden, 3INRA GABI, Jouy en Josas, France, 4INRA UMR 1313 GABI, Jouy-en-Josas, France

Beef Performance Evaluations in a Multi-Layered and Mainly Crossbred Population.
R. Evans1, F. Kearney1, J. McCarthy2, A. Cromie3 and T. Pabiou4, 1Irish Cattle Breeding Federation, Co.Cork, Ireland, 2Irish Cattle Breeding Federation, Cork, Ireland
Genetic Parameters of Body Condition Score and Reproductive Traits of Nellore Cows.
S. A. Queiroz1, F. M. Paterno1, A. F. D. A. Fernandes1, H. H. R. Neves1, J. A. Oliveira1 and R. Carvalheiro3, 4 Universidade Estadual Paulista, Jaboticabal, Brazil, 2GenSys Associated Consultants, Porto Alegre, Brazil, 3Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

Economic Values for a Production System with Nellore Beef Cattle in the Central Region of Brazil.
H. L. Moreira1, M. A. Prata1, A. E. Vercesi Filho2, M. L. P. Lima1, R. B. Lôbo3 and C. C. P. Paz4, 5 Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 6 Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CEN/USP, Piracicaba-SP, Brazil, 7 SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Analysis of Copy Number Variation Regions in a Nellore Population Evaluated for Feed Efficiency.
G. A. Oliveira Junior1, F. S. B. Rey2, M. V. G. B. da Silva3, M. H. A. Santana1, P. A. Alexandre1, J. P. Eler1 and J. B. S. Ferraz1, 2 NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 3 Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 4 Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CEN/USP, Piracicaba-SP, Brazil, 5 SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Genetic and Phenotypic Correlation between Gestation Period and Growth Traits Pre and Post Weaning.
H. L. Moreira4, E. B. Canova5, A. E. Vercesi Filho3, M. L. P. Lima1 and C. C. P. Paz4, 5 Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 6 Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CEN/USP, Piracicaba-SP, Brazil, 7 SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Estimation of Genetic Parameters for Age at Last Calving as a Measure of Cow Survival in a Population of Nellore Beef Cattle in Brazil.
S. B. Ramos1, S. L. Caetano2, R. B. Lôbo1, L. A. F. Bezerra1, A. Bonjácio3 and D. P. Munari4, 5 Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 6 Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CEN/USP, Piracicaba-SP, Brazil, 7 SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Genetic Architecture Of Birth And Weaning Traits In Charolais Beef Cattle.
R. Saintilan1, 2, M. N. Fouilloux2, A. Capitan3, B. Servin4, T. Tribout5, E. Venot5 and F. Phocas6, 7 UNCEIA, Jouy-en-Josas, France, 8 INRA UMR 1313 GABI, Jouy-en-Josas, France, 9 Institut de l’Elevage - Idele, Jouy-en-Josas, France, 10 INRA, UMR1313 GABI, Jouy-en-Josas, France, 11 UNCEIA, Paris, France, 12 INRA UMR 1388 GenPhySE, Castanet-Tolosan, France

Genetic Parameters of Body Condition Score and Growth Traits of Nellore Cows.
A. F. D. A. Fernandes1, 2, H. H. R. Neves2, N. Hurtado-Lugo2, R. Carvalheiro4, J. A. Oliveira1 and S. A. Queiroz1, 2 Universidade Estadual Paulista, Jaboticabal, Brazil, 2 GenSys Associated Consultants, Porto Alegre, Brazil, 3 State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 4 Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

Genetic Diversity and Relationships among Spanish Beef Breeds Assessed by a Bovine High-Density Chip.
J. J. Cañas-Alvarez1, A. González-Rodríguez1, S. Munilla2, L. Varona2, C. J. Díaz2, J. A. Baró3, C. Moreno3, A. Molina3 and J. Piedrafita1, 1 Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 2 Universidad de Zaragoza, Zaragoza, Spain, 3 INIA, Madrid, Spain, 4 Universidad de Valladolid, Palencia, Spain, 5 Universidad de Córdoba, Córdoba, Spain

Posters: Prediction using Molecular Information (Group 2)
Chair: Dorian J. Garrick, Iowa State University, Roel F. Veerkamp, Wageningen University, and Esa A. Mäntysaari, MTT Agrifood Research Finland

Presentation Time: 10:00 AM – 10:30 AM

Predictive Performance Yielded by Approximate Genomic Matrices.
E. Manfredi1, C. Carrel2 and M. A. Toro4, 5 INRA, Toulouse, France, 6 IMT Université Paul Sabatier, Toulouse, France, 7 Animal Production Department, Universidad Politecnica de Madrid, Madrid, Spain

Comparison of Accuracies of Genomic Prediction in French Limousin Cattle Population according to the Number of Markers and to Pedigree Relationship between Training and Validation Populations.
M. Barbat1, T. Tribout2, R. Saintilan1, E. Venot1, M. N. Fouilloux4 and F. Phocas3, 4 UNCEIA, Jouy-en-Josas, France, 5 INRA
Estimating Rate of Inbreeding and Effective Population Size using Genomic Data in Norwegian Red Cattle.
B. Hillestad, J. A. Woolliams, T. H. E. Meuwissen, D. I. Våge and G. Klemdal, Norwegian University of Life Sciences, Ås, Norway, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Quality Control of Genomic Heritability Estimates of Gene Content.
N. S. Forneris, A. Legarra, Z. G. Vitezica, S. Tsuruta, I. Aguilar, R. J. C. Cantel and I. Misztal, Department of Animal Science, University of Buenos Aires, Buenos Aires, Argentina, INRA, Castanet-Tolosan, France, University of Georgia, Athens, INIA, Las Brujas, Uruguay, CONICET, Buenos Aires, Argentina

M. Nishio and M. Satoh, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan

Compression Efficiency Relationship Matrix: Developing New Methods to Determine Genomic Relationships for Improved Breeding.
N. J. Hudson, J. Kijas, L. R. Porto-Neto and A. Reverter-Gomez, CSIRO, Brisbane, Australia, CSIRO Animal, Food and Health Sciences, Brisbane, Australia, CSIRO Food Futures Flagship, Brisbane, Australia, Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Brisbane, Australia

Genomic Evaluation of Both Purebred and Crossbred Performances.
O. F. Christensen, B. Nielsen, P. Madsen and G. Su, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Pig Research Centre, Copenhagen, Denmark

Genome-Wide Association using High Density Genotypes for Calving Difficulty in Dairy and Beef Cattle.

Impact of Relationships between Test and Reference Animals and between Reference Animals on Reliability of Genomic Prediction.
X. Wu, M. S. Lund, D. Sun, Q. Zhang and G. Su, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, College of Animal Science and Technology, China Agricultural University, Beijing, China, China Agricultural University, Beijing, China

Towards Genomic Selection in Danish Warmblood Horses: Expected Impacts and Selective Genotyping Strategy.
T. Mark, L. Jönsson, M. Holm and K. Christiansen, University of Copenhagen, Frederiksberg C, Denmark, Danish Warmblood Association, Maarslet, Denmark, Knowledge Centre for Agriculture, Aarhus, Denmark

Polymorphism Of Three Milk Protein Genes in Mexican Jersey Cattle.
J. L. Zepeda-Batista, B. Alarcon-Zuniga, A. Ruiz-Flores, R. Nunez-Dominguez and R. Ramirez-Valverde, UNIVERSIDAD AUTONOMA CHAPINGO, TEXCOCO, Mexico, Universidad Autónoma Chapingo, Chapingo, Mexico, Universidad Autónoma Chapingo, Chapingo, Mexico

Impact of Adding Foreign Genomic Information on the Mexican Holstein Imputation Process.
F. J. Ruiz-Lopez, A. García-Ruiz, G. R. Wiggans, C. P. VanTassell and H. H. Montaldo, Natl. Cent. for Research on Physiology and Animal Breeding INIFAP, Queretaro, Mexico, National Autonomous University of Mexico (UNAM), Mexico, DF, Mexico, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD, Universidad Nacional Autónoma de México, DF, Mexico

Genome Regions Associated to Milk Production Traits and Somatic Cell Score in the Mexican Holstein Population.
A. García-Ruiz, F. J. Ruiz-Lopez, C. P. VanTassell and H. H. Montaldo, National Autonomous University of Mexico (UNAM), Mexico, DF, Mexico, Natl. Cent. for Research on Physiology and Animal Breeding INIFAP, Queretaro, Mexico, Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD, Universidad Nacional Autónoma de México, DF, Mexico
Metabolism of CLA Isomers, e9,t11- & t10,c12 in Adipocyte Cultures and their Effect on Delta-6 Desaturase Expression.
W. J. Meadus1, Agriculture & Agri-Food Canada, Lacombe, AB, Canada

Association of SNPs and Haplotypes in Adiponectin and Adiponectin Receptors with Pig Meat Quality Traits.
M. F. Palint1, M. Jafarkia1,2, C. Gariépy1, F. Fortin1, L. Maigne5, S. Wyss2 and B. Sullivan2, 1Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, 2Canadian Centre for Swine Improvement, Ottawa, ON, Canada, 3Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 4Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada, 5Centre de développement du porc du Québec, Québec, QC, Canada

The Effect of Inbreeding on the Prediction of Genomic Values.
R. P. Savegnago1, Univ. Estadual Paulista – FCAV/UNESP, Jaboticabal, Brazil

Posters: Beef Cattle Breeding (Group 3)
Chair: Stephen P. Miller, AgResearch, David Johnston, University of New England and Roberto Carvalheiro, Sao Paulo State University (UNESP)
Presentation Time: 3:00 PM – 3:30 PM

Genetic Differences in Beef Terminal Traits and Index is Reflected in Phenotypic Performance Difference in Commercial Beef Herds.
S. M. Connolly1, A. Cromie2 and D. P. Berry1, 1Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Irish Cattle Breeding Federation, Cork, Ireland

Metalloproteomics Study of Bovine Longissimus dorsi Muscle Tissue in Selected Animals of the Nellore Breed (Bos indicus).
L. A. L. Chardulo1, W. A. Baldassini2, L. G. Albuquerque3, H. N. Oliveira4, J. A. Silva5 and P. M. Padilha6, 1FMVZ - Sao Paulo State University, Botucatu, Brazil, 2ESALQ - Sao Paulo University, Piracicaba, Brazil, 3State University of Sao Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 4Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 5Universidade Estadual Paulista, Botucatu, Brazil, 6IBB - Sao Paulo State University, Botucatu, Brazil

Analysis of Copy Number Variants in Spanish Autochthonous Beef Cattle Breeds.
T. B. R. Da Silva1, A. Gonzalez-Rodriguez1, C. Aviles1, E. F. Mounesan1, J. J. Canas-Alvarez1, L. Varona1, M. J. Carabaño1, P. Martinez-Cambor1 and C. J. Diaz1, 1INIA, Spain, Madrid, Spain, 2UNESP-Jaboticabal, Brazil, 3Universidad de Zaragoza, Zaragoza, Spain, 4Universidad de Cordoba, Cordoba, Spain, 5Universitat Autonoma de Barcelona, Bellaterra (Barcelona), Spain, 6INIA, Madrid, Spain, 7Universidad de Oviedo, Oviedo, Spain

Phenotypic and Genetic Traits with Growth Traits in Nellore Cattle.
R. L. Tonussi1, A. F. B. Magalhaes1, R. Espigolan1, D. G. M. Gordo1, W. B. Andrade1, G. C. Venturini1, 1FMVZ, Jaboticabal, Brazil, 2Universidade Estadual Paulista, Jaboticabal, Brazil, 3Sao Paulo State University (UNESP), Botucatu, Brazil, 4State University of Sao Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Analysis of Age at First Calving Dealing with Censored Data.
D. Anastacio Garcia1, R. Carvalheiro1, G. J. M. Rosa1, B. D. Valente3 and L. G. Albuquerque4, 1Sao Paulo State University (UNESP), Jaboticabal, Brazil, 2Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 3University of Wisconsin, Madison, 4State University of Sao Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Genetic Analysis of Feet and Legs in Nellore Cattle.
G. Vargas1, H. H. R. Neves1, V. Cardoso1, D. P. Munari1 and R. Carvalheiro1, 1Sao Paulo State University, Jaboticabal, Brazil, 2GenSys Associated Consultants, Porto Alegre, Brazil, 3Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 4Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

Accuracy of Genomic Breeding Values for Meat Quality Traits in Nellore Cattle.
A. F. Braga Magalhaes1, State University of Sao Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Sao Paulo, Brazil, Jaboticabal, Brazil, Jaboticabal, Brazil
Assessment of Genetic Variability using Pedigree Analysis of the Brahman Breed in Brazil.
L. Cavani1, R. Medeiros de Oliveira Silva1,2, R. K. Ono3, M. Marques Farah1, L. O. Dutia mate Carreto4 and R. da Fonseca4, 1São Paulo State University “Júlio de Mesquita Filho”, Dracena, Brazil, 2São Paulo State University “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 3São Paulo State University “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 4National Livestock Breeding Center, Shinjyo, Yamagata, Japan

K. Inoue1,2,3, B. D. Valente2, N. Shoji1, T. Honda2, K. Oyama3 and G. J. M. Rosa4, 1National Livestock Breeding Center, Nishinshirakawa-gun, Fukushima, Japan, 2Kobe University, Kasai, Hyogo, Japan, 3University of Wisconsin, Madison, 4Yamagata General Agricultural Research Center, Shinjo, Yamagata, Japan

Genomic Inbreeding Coefficients in a Sample of Canadian Beef Cattle Breeds.
D. Lu1, J. Crowley1, C. Li2, C. Coros3, M. DePauw1, G. S. Plastow4, S. S. Moore5, S. P. Miller5 and P. Stothard4, 1University of Alberta, Edmonton, AB, Canada, 2Agriculture and Agri-Food Canada, Edmonton, AB, Canada, 3Delta Genomics Centre, Edmonton, AB, Canada, 4The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 5Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Genetic Associations between True Fertility Index and Growth and Reproductive Traits in Beef Cattle.
Esa A. Mäntysaari, MTT Agrifood Research Finland, 1The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 2Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Monoallelic Expression of NNAT Gene in Nellore Steers Skeletal Muscle.
M. M. Souza1, A. Zerlotini2, P. C. Tschiotto3, P. S. N. Oliveira4, A. L. Somavilla4, F. B. Mokry1, A. S. M. Cesar1, W. J. S. Diniz1, M. A. Madada6, S. C. M. Nicura4, L. L. Coutinho2 and L. C. A. Regitano2, 1Federal University of São Carlos, São Carlos, Brazil, 2Embrapa Agricultural Informatics, Campinas, Brazil, 3Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 4Universidade Federal de São Carlos, São Carlos, Brazil, 5University of Sao Paulo, Piracicaba, Brazil, 6Embrapa Pecuária Sudeste, São Carlos, Brazil, 7Embrapa Southeast Livestock, São Carlos, Brazil, 8Universidade de São Paulo/Esalq, Piracicaba, Brazil

Estimation of Linkage Disequilibrium, Persistence of Phase and Effective Population Size of Brazilian Hereford and Brahford Breeds.
P. Biegelmeier1, M. M. Oliveira2,3, L. L. Cardoso2,3, C. G. Gomes2, R. H. Higa2, N. L. Dionello2, A. R. Caetano3, J. P. Steibel4 and F. F. Cardoso5, 1Federal University of Pelotas, Pelotas, Brazil, 2Embrapa Southern Region Animal Husbandry, Baie, Brazil, 3Coordination for the Improvement of Higher Level Personnel (CAPES/PNPD), Brasilia, Brazil, 4Embrapa Informática Agropecuária, Campinas, Brazil, 5Embrapa Genetic Resources and Biotecnology, Brasilia, Brazil, 6Michigan State University, East Lansing

Heritability Estimates of Calving Date in Nellore Cattle.
J. A. Silva1, W. B. Andrade1, A. M. Maiorano1, R. A. Curi1, L. A. L. Chardulo1, L. G. Albuquerque4, G. Moraes1 and L. F. Souza1, 1Universidade Estadual Paulista, Botucatu, Brazil, 2Universidade Estadual Paulista, Jaboticabal, Brazil, 3State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 4Qualitas Agronegócios, Goiania, Brazil

Adequacy of Different Pseudo-Phenotypes for Model Training and Validation of Genomic Predictions in Beef Cattle.
H. H. R. Neves1, R. Carvalheiro2 and S. A. Queiroz2, 1GenSys Associated Consultants, Porto Alegre, Brazil, 2Universidade Estadual Paulista “Júlio de Mesquita Filho”, 3UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 4Universidade Estadual Paulista, Jaboticabal, Brazil

Evaluation of the Protein Change in the Meat of Nellore Beef Cattle with Contrasting Shear Force.
M. E. Carvalho1, G. Gasparin2, J. P. Eler3, J. C. D. C. Balieiro4, L. C. A. Regitano5, J. B. S. Ferraz1 and L. L. Coutinho6, 1NAP-GMABT - Dep. of Veterinary Medicine, University of Sao Paulo - FZEA, Pirassununga, Brazil, 2Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, 3NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 4University of Sao Paulo-USP/FMVZ, Pirassununga, Brazil, 5Embrapa Pecuária Sudeste, São Carlos, Brazil, 6Universidade de São Paulo/Esalq, Piracicaba, Brazil

Posters: Prediction using Molecular Information (Group 3)
Chair: Dorian J. Garrick, Iowa State University, Roel F. Veerkamp, Wageningen University, and Esa A. Mäntysaari, MTT Agrifood Research Finland
Presentation Time: 3:00 PM – 3:30 PM
Inbreeding by Pedigree and Genomic Markers in Selection Lines of Pigs.
Y. Zhang,1,2 J. M. Young,3 C. Wang,3 X. Sun,3 A. Wolfe and J. C. M. Dekkers1, 1Iowa State University, Ames, 2China Agricultural University, Beijing, China

Approximation of Reliability of Direct Genomic Breeding Values.
M. Sargolzaei,1,2, L. R. Schaeffer3, J. P. Chesnais4, G. Kistemaker5, G. R. Wiggans6 and F. S. Schenkel5, 1The Semex Alliance, Guelph, ON, Canada, 2Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 3Canadian Dairy Network, Guelph, ON, Canada, 4Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD

A Novel use of High Density SNP Assays to Optimize Choice of Different Crossbred Dairy Cattle Genotypes in Small-Holder Systems in East Africa.
J. M. Ojango1,2, A. G. Marete1, F. D. N. Mujibi1, J. Rao1, J. Poole2, E. O. Rege2, S. Weerasinghe1, C. Gondro1, J. Gibson1 and O. Mwai1, 1International Livestock Research Institute, Nairobi, Kenya, 2PICO- Eastern Africa, Nairobi, Kenya, 3University of New England, Armidale, Australia

Single Nucleotide Polymorphism in Dairy Cattle Populations of West Siberia.
V. L. Petukhov*1, Novosibirsk State Agrarian University, Novosibirsk, Russia

Do Rare Variants Contribute to the Genomic Prediction Accuracy?
T. Sachocki1, J. Szyda2 and A. Zarnecki3, 1Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, 2National Research Institute of Animal Production, Cracow-Balice, Poland, 3National Research Institute of Animal Production, Cracow, Poland

Comparative Study of 13 Candidate Genes Applying Multi-reference Normalization to Detect the Expression of Different Fineness in Skin Tissues of Wool Sheep.
Y. Tian1, X. Huang1, J. Di2, K. Tian3, W. Wu1, X. Xu1, Y. Zhang2 and H. Tuafa2, 1College of Animal Science, Xinjiang Agricultural University, Urumqi, China, 2Xinjiang Academy of Animal Science, Urumqi, China

Across Breed QTL Detection And Genomic Prediction In French And Danish Dairy Cattle Breeds.
I. van den Berg1,2,3, B. Guldbrandtsen1, C. Hoze2,4, R. F. Brondum1, D. Boichard1 and M. S. Lund1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjøle, Denmark, 2INRA, UMR1313 GABI, Jouy-en-Josas, France, 3AgroParisTech, UMR1313 GABI, Paris, France, 4UNCEIA, Paris, France

Development of Low Density Genotype Panels for Dairy and Beef Cattle.
M. M. Judge1, F. Kearney2, M. C. McClure3 and D. P. Berry4, 1Teagasc, Moorepark, Co. Cork, Ireland, 2Irish Cattle Breeding Federation, Cork, Ireland, 3Irish Cattle Breeding Federation, Bandon, Ireland, 4Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

Accuracy of Genomic Prediction in Simulated Pig Populations.
J. Son1, H. Kang1, J. Kim1, J. E. Park2,3 and D. Lee4, 1Hankyung National University, Anseong, South Korea, 2Seoul National University, Seoul, South Korea

Efficiency of Including Cows in Genomic Prediction Versus Multivariate Models for Fertility Traits in Dairy Cattle in the United Kingdom.
R. Mrode4 and M. P. Coffey4, 1Scotland’s Rural College, Edinburgh, United Kingdom, 2SRUC, Edinburgh, United Kingdom

A. Baur1,2, S. Fritz1, J. Promp1,2, O. Boulot1, D. Boichard1, V. Ducrocq1 and P. Croiseau1, 1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2UNCEIA, Paris, France, 3IDALE, Jouy en Josas, France, 4BGS, Paris, France

Combining SNPs in Latent Variables to Improve Genomic Prediction.
H. C. Heuven1, University of Utrecht, Utrecht, Netherlands

Potential Application of Genomics to Reduce Boar Taint Levels in Three Canadian Swine Breeds.
J. Squires1, M. Jafarikia2, F. S. Schenkel1, S. Wyss2, F. Fortin1, R. de Wolde1, W. Van Berkel4 and B. Sullivan5, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Centre for Swine Improvement,
Bovine Spastic Paresis: A Genome-Wide Study in Fleckvieh.
H. Schwarzenbacher,1,2 and H. Pausch,1 Zuchtdata EDV-Dienstleistungen GmbH, Vienna, Austria, 1Chair of Animal Breeding, Technische Universität München, Freising, Germany

H. E. Theron,1,2, R. R. van der Westhuizen,2 E. van Marle-Koster1 and J. van der Westhuizen,1,2, 1SA Stud Book, Bloemfontein, South Africa, 2University of Pretoria, Pretoria, South Africa

A General Approach for Calculation of Genomic Relationship Matrices for Epistatic Effects.
L. Varona,1, Z. G. Vitezica,2 S. Munilla1 and A. Legarra,1 1Universidad de Zaragoza, Zaragoza, Spain, 2Unite Mixte ENSAT-INRA, Toulouse, France, 3INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France

Posters: Beef Cattle Breeding (Group 4)
Chair: Stephen P. Miller, AgResearch, David Johnston, AUniversity of New England and Roberto Carvalheiro, Sao Paulo State University (UNESP)

Presentation Time: 3:30 PM – 4:00 PM

Genome Wide Association Study between Copy Number Variation Regions with Marbling Score in Nelore cattle.
F. Baldi,1, F. Feitosa,1, A. S. C. Pereira,1, G. C. Venturini,1, R. L. Tonussi,1, R. Espigolan,1, D. G. M. Gordo,1, G. M. de Camargo,1, L. A. L. Chardulo,1 and L. G. Albuquerque,1 1Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 2State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, Jaboticabal, Brazil, 3State University of São Paulo, Jaboticabal, Brazil, 4Sao Paulo State University (UNESP), Jaboticabal, Brazil, 5State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 6Sao Paulo State University (UNESP), Botucatu, Brazil

Alternatives Triple Crosses for Intensified Production Systems Beef Cattle in Brazil.
F. J. Gomes,1, R. A. A. Torres Júnior,1, G. R. D. O. Menezes,2, J. V. F. Battistelli,1, T. F. Rocha,1, M. R. Reggiore1 and M. E. Buzanskas,1 1Universidade Estadual Paulista Júlio de Mesquita, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Ciências Exatas, Jaboticabal, Brazil, 2Embrapa Gado de Corte, Campo Grande, Brazil, 3Geneplus – Embrapa Gado de Corte, Campo Grande, Brazil, 4Universidade Federal do Mato Grosso do Sul, Campo Grande, Brazil, 5Universidade Estadual Paulista Júlio de Mesquita, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Ciências Exatas, Jaboticabal-SP, Brazil

Estimates of Genetic Parameters for Weights between 60 and 600 Days of Age for Brahman Cattle using Random Regression Models.
T. Bertipaagli,1, L. O. Duitama Carreño,1, R. R. Aspilcueta Borquis,2, A. A. Boligon1, R. da Fonseca1, M. M. Farah1, G. C. Venturini1 and F. Baldi2, 1São Paulo State University “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 2State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 3Federal University of Pelotas, Pelotas, Brazil, 4São Paulo State University “Júlio de Mesquita Filho”, Dracena, Brazil, 5Department of Animal Science, São Paulo State Univ. (UNESP), Jaboticabal, São Paulo, Brazil, Jaboticabal, Brazil, 6Sao Paulo State University (UNESP), Jaboticabal, Brazil, 7Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

Genetic Parameters for Cow Weight in Pasture Fed Hereford Cattle.
O. Ravagnolo, Instituto Nacional de Investigación Agropecuaria, Canelones, Uruguay

Accuracy of Genomic Selection for Growth Traits in Nelore Cattle.
A. P. Nascimento Terakado, Universidad Estadual de Sao Paulo, Jaboticabal, Brazil

Racial Composition of Composite Bovine for Mating with Different Female Genetic Groups.
R. S. Bueno,1, G. B. Mourao,1 E. C. Mattos,1 J. C. D. C. Balieiro1, J. P. Eler2 and J. B. S. Ferraz,1 1University of Sao Paulo/FZEA, Pirassununga, Brazil, 2Department of Animal Science, University of Sao Paulo/ESALQ, Piracicaba, Brazil, 3NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 4University of Sao Paulo- USP/FMVZ, Pirassununga, Brazil
Genetic Analysis of Growth Traits in Polled Nellore Cattle from Tropical Region.
M. M. S. Mamede1, R. D. Sainz2, C. Uilhôa Magnabosco1, M. Correa da Silva1, R. B. Lôbo3, F. Nakagawa4 and F. B. Lopes5,
1Federal University of Goiás, Goiânia, Brazil, 2University of California, Davis, 3Embrapa Cerrados, Brasília, Brazil, 4Federal University of Goiás, Goiânia, Brazil, 5ANCP-Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, ©OB Brand, Pontes e Lacerda, Brazil

Genetic Correlations Estimate between Meat Tenderness, Growth and Carcass Traits in a Population of Polled Nellore Cattle in Brazil.
L. Mendes de Castro1, C. Uilhôa Magnabosco2, R. D. Sainz1,4, C. Ubirajara Faria3, R. B. Lôbo4, F. Nakagawa7 and F. B. Lopes2,
1Federal University of Goiás, Goiânia, Brazil, 2Embrapa Cerrados, Brasília, Brazil, 3University of California, Davis, 4Embrapa-Brazilian Agricultural Research Corporation, Brasília, Brazil, 5Federal University of Uberlândia, Uberlândia, Brazil, 6ANCP-Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, 7OB Brand, Pontes e Lacerda, Brazil

Genomic analysis of Canadian Simmental Population.
N. Zare1, G. VanderVoort1, M. Sargolzaei2, D. Lu and S. P. Miller1, 1University of Guelph, Guelph, ON, Canada, 2The Semex Alliance, Guelph, ON, Canada, 3University of Alberta, Edmonton, AB, Canada, 4Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Effect of Genetics Level of Beef Cow Milk Production on Longevity in Diverse Environments.
M. M. Culbertson1, S. E. Speidel1, M. G. Thomas1, L. Keenan2 and R. M. Enns1, 1Colorado State University, Department of Animal Sciences, Fort Collins, 2Red Angus Association of America, Denton, TX

Single Nucleotide Polymorphisms in the DRD2 and XKR4 Genes may be Beneficial to Missouri Beef Cattle Grazing Endophyte-Infected Tall Fescue.
K. M. Ely1, A. M. Saxton1, R. L. Kallenbach2, R. Lock2 and C. J. Kojima1, 1University of Tennessee, Knoxville, 2University of Missouri, Columbia

Meat Tenderness could be Associated with Fatty Acids Metabolism in Nellore Cattle.
T. M. Gonçalves1, Escola Superior de Agricultura Luiz de Queiroz, ESALQ-USP, Piracicaba, Brazil

Genetic Correlation between Live Body Measurements and Loin Production in Hanwoo Steers.
Y. H. Choy1, NIAS, Chonan, South Korea

Relationship between Beef Heifer Residual Feed Intake and Productivity as Cows.
C. D. Callum1, University of Manitoba, Winnipeg, MB, Canada

Genotype-Environment Interaction for Growth and Reproductive Traits in Nellore Cattle, using Reaction Norms.
H. L. J. Chiaia1, M. V. A. Lemos, C. Aboujaoude, R. Carvalheiro, L. G. de Albuquerque, H. N. Oliveira and F. Baldi, Universidade Estadual Paulista “Júlio de Mesquita Filho”, UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

Posters: Prediction using Molecular Information (Group 4)
Chair: Dorian J. Garrick, Iowa State University, Roel F. Veerkamp, Wageningen University, and Esa A. Mäntysaari, MTT Agrifood Research Finland

Presentation Time: 3:30 PM – 4:00 PM

Prioritizing Cows for Genotyping in Genomic Selection.
T. Luan1, X. Yu and T. H. E. Meuwissen, Norwegian University of Life Sciences, Ås, Norway

Evaluation of the Use of a Meta-Population for Genomic Selection in Spanish Beef Cattle Breeds.
E. F. Mouresan1, S. Munilla2, C. J. Díaz2, A. González-Rodríguez3, J. Piedrafita1, C. Aviles1, J. A. Baró4, C. Moreno1 and L. Varona1, 1Universidad de Zaragoza, Zaragoza, Spain, 2Universidad de Buenos Aires, Buenos Aires, Argentina, 3INIA, Madrid, Spain, 4Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 5Universidad de Córdoba, Córdoba, Spain, 6Universidad de Valladolid, Palencia, Spain
Linkage Disequilibrium and Persistence of Phase in Five Spanish Local Beef Cattle Breeds.
J. J. Cañas-Alvarez, E. F. Mournes, L. Varona, C. J. Díaz, C. A. Vilez, J. A. Baro, J. A. Altarriba, J. Casellas and J. Piedrafito, Universitat Autònoma de Barcelona, Bellatera (Barcelona), Spain, 2Universidad de Zaragoza, Zaragoza, Spain, 3INIA, Madrid, Spain, 4Universidad de Córdoba, Córdoba, Spain, 5Universidad de Valladolid, Palencia, Spain

Generalization of Henderson's T-inverse to Include Genomic Data.
A. A. Maitwase, ARC-Animal Production Institute, Irene, South Africa; University of the Free State, Bloemfontein, South Africa

Genome-Assisted Multiple-Trait Analysis of Carcass Traits in Nellore Cattle.
G. A. Fernandes Júnior, G. J. M. Rosa, R. B. Costa, R. Carvalheiro, L. A. L. Chardulo, D. G. M. Gordo, F. Baldi, H. N. Oliveira, H. Tonnati, L. G. Albuquerque and R. M. O. Silva, Sao Paulo State University (UNESP), Jaboticabal, Brazil, 2University of Wisconsin, Madison, 3Universidade Estadual Paulista, Botucatu, Brazil, 4Universidade Estadual Paulista “Júlio de Mesquita Filho”. UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 5State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Evaluating the Effects of QTN for Milk Fat Yield and their Impact on Accuracy and Bias of Genomic Prediction in New Zealand Holstein-Friesian Cows.
M. K. Hayr, M. Saatchi, R. Sherlock, D. Johnson and D. J. Garrick, Iowa State University, Ames, 2LIC, Hamilton, New Zealand

Genomics Tools for Improving Health and Production Performance of Canadian Pigs.
M. Jafarikia, and B. Sullivan, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Centre for Swine Improvement, Ottawa, ON, Canada

Comparison of Breeding Values from Single-Step and Bivariate Blending Methods.
M. Taskinen, E. A. Mäntysaari, G. P. Aamand and I. Strandén, MT Agrifood Research Finland, Jokioinen, Finland, 2Nordic Cattle Genetic Evaluation, Aarhus, Denmark, 3MT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

Implementation of Genomic Selection in Norsvin Genetic Program; Genetic Gain in Production and Maternal Traits in Norsvin Landrace.
I. Andersen-Ranberg and E. Grindflek, Norsvin, Aas, Norway, 2Norsvin, Hamar, Norway

Use of Genomic Recursions and Algorithm for Proven and Young Animals for Single-Step Genomic BLUP Analyses with a Large Number of Genotypes.
B. D. Fragomeni, J. Misztal, D. Lourenco, S. Tsuruta, Y. Masuda and T. J. Lawlor, University of Georgia, Athens, 2Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, 3Holstein Association USA Inc., Brattleboro, VT

Use of Field Data in Genomic Reference Populations for Pig Breeding.
M. Lillemann, T. H. E. Meuwissen and A. K. Sonesson, Nofima As, Ås, Norway, 2Norwegian University of Life Sciences, Ås, Norway, 3NOMA, Ås, Norway

Different Strategies for Genomic Prediction of Average Daily Weight Gain in Feedlot in Nellore Finishing Steers.
A. L. Somavilla, L. C. A. Regitano, F. B. Mokry, M. A. Mudadi, R. R. Tullio, M. L. Nascimento, L. L. Coutinho and D. P. Munari, Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, Brazil, 2Embrapa Pecuária Sudeste, São Carlos, Brazil, 3Universidade Federal de São Carlos, São Carlos, Brazil, 4Universidade de São Paulo/Esalq, Piracicaba, Brazil

Association Of A Bovine Chromosome 19 Region, 51 Mb, With The Variation Of Oleic Acid In Hanwoo.
J. Kim, Yeungnam University, Gyeongsan, South Korea

Accuracy of Molecular Breeding Values for Production and Efficiency Traits of Canadian Crossbred Beef Cattle using a Cross-Validation Approach.
E. C. Akanno, G. Plastov, C. Li, S. P. Miller and J. A. Basarab, University of Alberta, Edmonton, AB, Canada, 2Agriculture and Agri-Food Canada, Edmonton, AB, Canada, 3Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 4Alberta Agriculture and Rural Development, Lacombe, AB, Canada

Flexibility of Bayesian LASSO under Different Genetic Structure.
L. O. Duitama, UNESP, Jaboticabal, Brazil
SNP Analysis of the Growth Hormone Gene in Indigenous Philippine Cattle, Ilocos Genetic Group by PCR-RFLP.
A. J. Salces, P. J. C. Icalia, M. S. Mendioro and C. C. Sevilla, University of the Philippines Los Baños, Calamba, Philippines, Mariano Marcos State University, Batac, Philippines.

Tuesday, August 19, 2014

Posters: Dairy Cattle Breeding (Group 1)
Chair: Kent A. Weigel, University of Wisconsin, Hermann Swalve, Martin Luther University Halle-Wittenberg, and Christian Maltecca, North Carolina State University

Performance of Different Genetic Group of Cows Under Bangladesh Condition.
M. A. S. Khan, M. S. R. Siddiqi and M. E. Uddin, Bangladesh Agricultural University, Mymensingh, Mymensingh, Bangladesh.

Estimation of Genetic Parameters and Trends for Milk Production in a Libyan Holstein Population under Arid Mediterranean Subtropical Conditions.
S. A. Hermas and M. A. Elzo, University of Tripoli, Tripoli, Libya, Department of Animal Sciences, University of Florida, Gainesville.

Genome-Wide Association Study For Milk And Protein Yields In Portuguese Holstein Cattle.
J. G. V. Carvalheira, ICBAS – University of Porto, Porto, Portugal; Research Center in Biodiversity and Genetic Resources (CIBIO) - INBio, Porto, Portugal.

Genome-Wide Association Study For Milk-Fat Yield In Portuguese Holstein Cattle.
M. M. I. Salem, Dep. of Animal Production, Fac. of Agriculture, Alexandria University, Alexandria, Egypt; Research Center in Biodiversity and Genetic Resources (CIBIO) - INBio, Porto, Portugal.

Including Cow Information in Genomic Prediction of Holstein Dairy Cattle in the US.
T. A. Cooper, G. R. Wiggins and P. M. VanRaden, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD; USDA-ARS-AIPL, Beltsville, MD.

Estimates of Genetic Parameters for Economic Traits in Dairy Buffalo.
C. D. C. Barros, D. P. de Oliveira, N. A. Hurtado Lugo, R. R. Aspilcueta Borquis and H. Tonhati, Universidade Estadual Paulista “Júlio de Mesquita Filho” (FCAV-UNESP), Jaboticabal, Brazil, Departamento de Zootecnia, Faculdade de Ciências Agrárias e Veterinárias (FCAV), Universidade Estadual Paulista “Júlio de Mesquita Filho” (UNESP), Jaboticabal, Brazil, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil.

Genome Wide Association Study on Cow Mortality in Three US Regions.
S. Tsuruta, I. Misztal, I. Aguilar and T. J. Lawlor, University of Georgia, Athens, INIA, Las Brujas, Uruguay, Holstein Association USA Inc., Brattleboro, VT.

Genetic Analysis of Reproductive Traits, Milk Yield, and Persistency during the First 3 Lactations of Holstein cows.
T. Yamazaki, K. Hagiya, H. Takeda, S. Yamaguchi, T. Osawa and Y. Nagamine, NARO Hokkaido Agricultural Research Center, Sapporo, Hokkaido, Japan, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, Livestock Improvement Association of Japan, Tokyo, Japan, National Livestock Breeding Center, Fukushima, Japan, Nihon University, Fujisawa, Japan.

Comparison between Sire and Animal Model to Estimate Genetic (Co)variances for Milk Yield Traits.
H. G. El-Awady, E. A. Badr, A. S. Khattab and S. Z. Ouda, Kafer El Sheikh, Egypt, Animal Production Department, Kafer El Sheikh, Egypt, Animal Production Research Institute, Cairo, Egypt, Tanta University, Faculty of Agriculture, Animal Production Department, Tanta, Egypt, Mansoura University, Faculty of Agriculture, Animal Production Department, Mansoura, Egypt.

Genetic Parameters of Test Day Records in Brazilian Holstein Cattle using an Autoregressive Multiple Lactation Animal Model.
C. N. Costa, G. G. Santos, J. A. Cobuci, G. Thompson and J. G. V. Carvalheira, Embrapa Dairy Cattle, Juiz de Fora.
T. Kawahara*1, Y. Gotoh1, M. Sugimoto2, T. Baba1, S. Yamaguchi1, M. Suzuki4, and Y. Sugimoto5,
1Holstein Cattle Association of Japan, Hokkaido Branch, Sapporo, Hokkaido, Japan,
2National Livestock Breeding Center, Odakura, Nishigo, Fukushima, Japan,
3Hokkaido Dairy Milk Recording and Testing Association, Sapporo, Hokkaido, Japan,
4Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan,
5Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Fukushima, Japan

Industry Application of Genomic Predictions in The Netherlands.
M. Stoop*1, E. Mullaart1, and G. de Jong2,
1CRV BV, Arnhem, Netherlands,
2CRV, Arnhem, Netherlands

Genetic Parameters for Somatic Cell Count and Clinical Mastitis in the First Lactation of Iranian Holstein Cattle.
S. Zakizadeh*1 and M. Jafari2,
1Institute Of Scientific-Applied Higher Education of Jihad-e-Agriculture, Mashhad, Iran,
2Animal breeding center of North-east, Mashhad, Iran

D. Laborde1, J. E. Dutour2, N. Lopez-Villalobos3, P. Chilibroste4, and A. Meikle5,
1Productor, Trinidad, Uruguay,
2Consultor privado, Paysandu, Uruguay,
3Massey University, Palmerston North, New Zealand,
4Universidad de la Republica, Montevideo, Uruguay,
5Facultad de Veterinaria, Universidad de la Republica, Montevideo, Uruguay

Genetic Relationships between Herd Life and Type Traits of Holstein Cattle in Japan using Random Regression Test-day Models.
O. Sasaki*1, M. Aihara2, A. Nishiura1, H. Takeda1, and M. Satoh1,
1NARO Institute of Livestock and Grassland Science, Tsukuba, Japan,
2Livestock Improvement Association of Japan, Inc., Tokyo, Japan

Posters: Sheep and Goats Breeding (Group 1)
Chair: Julius H.J. van der Werf CRC for Sheep Industry Innovation and John C McEwan, AgResearch
Presentation Time: 9:30 AM – 10:00 AM

Characterization of Indigenous Fat-Tailed Sheeps in Iran: Diversity in Blood Proteins.
H. Mohammadif, University of Tabriz, Tabriz, Iran

M. N. Bemji*, E. O. Awotunde, O. Olowofeso and A. O. Adebambo, Federal University of Agriculture, Abeokuta, Nigeria

Genetic Structure and Phylogeny of Three Goat Populations in the Middle East.
R. S. Aljumaah1, M. A. Alshaikh2 and R. M. Al-Atiyat1,
1King Saud University, Riyadh, Saudi Arabia,
2King Saud university, Riyadh, Saudi Arabia

J. M. Elsen1, F. Shumbusho2, J. Raoul1, J. M. Astruc1, J. Palhière1, S. Lemarié2 and A. Fugeray-Scarbel3,
1INRA, Castanet Tolosan, France,
2INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France,
3idele, Castanet tolosan, France

Genetic Distances and Phylogenetic Trees of Different Awassi Sheep Populations Based on DNA Sequencing.
R. M. Al-Atiyat1, King Saud University, Riyadh, Saudi Arabia

CSN1S1 Variants are Highly Associated with Milk Performance Traits in Lacaune Sheep.
G. Erhardt1, Department of Animal Breeding and Genetics, Giessen, Germany
B. Fuers-Walit1 and C. Fuersz1, University of Natural Resources and Life Sciences (BOKU), Vienna, Austria, 2ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria

Signatures of Selection for Age at First Lambing in Brazilian Local Adapted Sheep.
A. M. B. O. Lobo1, S. R. Paiva2 and R. N. B. Lobo1, 1Embrapa Goats and Sheep, Sobral, Brazil, 2Embrapa Secretariat of International Affairs, Brasilia, Brazil, 1Federal University of Ceará, Fortaleza, Brazil

Genetic Analysis of Daily Maximum Milking Speed by a Random Walk Model in Dairy Cows.
B. Karacoen1, L. Janss2 and H. N. Kadarmideen1, 1Section of Biometry and Genetics, Department of Animal Science, Akdeniz University of Natural Resources and Life Sciences (BOKU), Vienna, Austria, 2ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria

Genome-Wide Association Identifies Genomic Regions Associated with Entropion in Domestic Sheep.
M. R. Mousel1, S. N. White2, J. O. Reynolds1 and D. P. Knowles2, 1USDA, ARS, Animal Disease Research Unit, Pullman, WA, 2Washington State University, Pullman

Diallel Cross between Texel and Corriedale: Lamb Growth and Survival.
G. Ciappesoni1, G. Banchero2 and A. Vazquez3, 1INIA, Rincón del Colorado, Uruguay, 2INIA, Colon, Uruguay

S. Andonov1, G. Klemetsdal2 and T. Adnoy1, 1Faculty of Agricultural Sciences and Food, Skopje, Macedonia, 2Norwegian University of Life Sciences, Ås, Norway, 3Norwegian University of Life Sciences, As, Norway

Impact Of The Hypermuscularity GDF8 Gene On Sheep Maternal Abilities Traits.
D. Francois1, D. Carpenter1, Y. Bourdillon1, D. Grasset2, F. Tortereau2 and J. Raouf1, 1INRA, Toulouse, France, 2INRA, Toulouse, France, 3INRA UE0322, La Sapinière, Bourges, France, 4GID Lacaune, Lauras, France, 5Idele, Castanet tolousan, France

Characterization of Linkage Disequilibrium and Consistency of Gametic Phase in Canadian Goats.
L. F. Brito1, M. Jafarikia2, D. A. Grossi2, L. Maignel3, M. Sargolzaei1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Centre for Swine Improvement, Ottawa, ON, Canada, 3The Semex Alliance, Guelph, ON, Canada

Genetic Analysis of Wool Shedding Scores of Ewes from a Composite Flock using a Threshold Model and Bayesian Methodologies.
N. Vargas Jurado1, K. A. Leymaster2, L. A. Kuehn2 and R. M. Lewis2, 1Virginia Polytechnic Institute and State University, Blacksburg, 2USDA, Meat Animal Research Center, Clay Center, NE, 3USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 4University of Nebraska, Lincoln

Does The Genetics Of Lamb Survival Differ Between Single And Twin Born Merino Lambs?
S. Hatcher1, K. D. Atkins2 and S. Mortimer3, 1NSW DPI, Orange, Australia, 2Shoal Bay, Australia, 3NSW DPI, Trangie, Australia

Posters: Dairy Cattle Breeding (Group 2)
Chair: Kent A. Weigel, University of Wisconsin, Hermann Swalve, Martin Luther University Halle-Wittenberg, and Christian Maltecca, North Carolina State University

Presentation Time: 10:00 AM – 10:30 AM

Effects of Housing type × Feeding System on Milk Yield of Holstein Cows.
K. Hagiya1, S. Yamaguch1, K. Hayasaka1, T. Yamazaki1, T. Osawa1, H. Abe2, S. Nakagawa2, T. Kawahara1 and M. Suzuki3, 1NARO Hokkaido Agricultural Research Center, Sapporo, Hokkaido, Japan, 2Hokkaido Dairy Milk Recording and Testing Association, Sapporo, Hokkaido, Japan, 3National Livestock Breeding Center, Fukushima, Japan, 4Holstein Cattle Association of Japan, Hokkaido Branch, Sapporo, Hokkaido, Japan, 5Ohihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan

Genetic Analysis of Daily Maximum Milking Speed by a Random Walk Model in Dairy Cows.
B. Karacoen1, L. Janss2 and H. N. Kadarmideen3, 1Section of Biometry and Genetics, Department of Animal Science, Akdeniz University

Posters: Dairy Cattle Breeding (Group 2)
Comparison of Natural Antibodies Measured in Milk and Blood Samples of Dutch Dairy Cattle.
B. de Klerk1, B. J. Dicro2, H. C. Heuven1, I. den Uyl1, J. A. M. van Arendonk1, K. K. Parmentier1 and J. J. van der Poel1,
1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2University of Utrecht, Utrecht, Netherlands,
3Animal health Services, Deventer, Netherlands, 4Adaptation Physiology Group, Wageningen University, Wageningen, Netherlands

Genetic Parameter Estimates and Cluster Analysis of Breeding Values for Milk Production in Guzerá Cattle.
L. El Faro1, D. A. C. Cruz2, M. G. Campolina Diniz Peixoto3, R. P. Savegnago4, C. H. C. Machado5 and F. A. T. Brunelli6,
1SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil, 2Instituto de Zootecnia, Sertãozinho, Brazil,
3Embrapa Dairy Cattle, Juiz de Fora, Brazil, 4UNESP, Jaboticabal, Brazil, 5ABCZ, Uberaba, Brazil

S. T. Rodriguez-Ramírez1, J. Fernández1, M. A. Toró2, D. Hernández2 and B. Villanueva1, 1INIA, Madrid, Spain, 2ETS Ingenieros Agrónomos, Madrid, Spain, 3CONAFE, Madrid, Spain

Estimates of Genetic Parameters for Test Day and 305-day Milk Yield in First Lactation of Mambí de Cuba Cows.
A. Hernández1, Institute of Animal Science, Mayabeque, Cuba

Genetic Variation of Cheese Yield-Related Traits Predicted using Fourier-Transform Infrared Spectroscopy of Samples Collected during Milk Recording on Holstein, Brown Swiss and Simmental Cows.
A. Cecchinato1, University of Padova, Legnaro PD, Italy

Genetic Evaluation of Milk Traits under Whole-Season Once-a-Day Milking.
K. Stachowicz1, G. Jenkins1, P. Amer2 and C. V. Pfly2, 1AbacusBio Limited, Dunedin, New Zealand, 2DairyNZ, Hamilton, New Zealand

A. Nishiura1, O. Sasaki1, M. Aihara2, H. Takeda1 and M. Sato1, 1NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, 2Livestock Improvement Association of Japan, Inc., Tokyo, Japan

Claw Lesions and Risk Factors in Spanish Dairy Cows.
M. Pérez-Caballero1 and N. Charfeddine1, 1University Complutense of Madrid, Madrid, Spain, 2CONAFE, Madrid, Spain

New Simulation Method to Create Data Sets With a Desired Genetic Trend.
A. M. Tyrisevä1, M. H. Lidae1, G. P. Aamand2 and E. A. Mäntysaari2, 1AbacusBio Limited, Dunedin, New Zealand, 2DairyNZ, Hamilton, New Zealand

Genetic Parameters for Rank of Dairy Gir Cattle in Agricultural Shows using Thurstonian Procedures.
M. P. M. Gama1, F. R. Araújo Neto2, H. N. de Oliveira1, A. R. Fernandes1, A. E. Vercesi Filho3, L. El Faro3 and C. C. P. Paz4, 5,
1Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil,
2Instituto Federal de Goiás, Rio Verde-GO, Brazil, 3Sao Paulo State University (UNESP), Jaboticabal, Brazil,
4Associação Brasileira de Criadores de Gir Leiteiro, Uberaba-MG, Brazil, 5SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Descriptive Analysis of Copy Number Variation Regions in a Population of Dairy Gyr Cattle.
M. V. G. B. da Silva1, G. A. Oliveira Junior1, F. S. B. Rey1, P. F. Giachetto3, M. A. Machado4, R. D. S. Verneque5 and J. B. S. Ferrez1,
1Embrapa Dairy Cattle, Juiz de Fora, Brazil, 2NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil,
3Sao Paulo State University (UNESP), Jaboticabal, Brazil, 4Embrapa Agricultural Informatics, Campinas, Brazil

Application for Herd Total Production Forecast based on the Solutions from the National Test Day Evaluations.
T. Pitkänen1, E. A. Mäntysaari and M. H. Lidae1, MITT Agrifood Research Finland, Jokioinen, Finland
Genetic Associations between Behavior Traits Recorded by Automatic Milking Systems and Temperament of Swedish Holsteins.
E. Rinell, Norwegian University of Life Sciences, Ås, Norway

Posters: Sheep and Goats Breeding (Group 2)
Chair: Julius H.J. van der Werf CRC for Sheep Industry Innovation and John C McEwan, AgResearch
Presentation Time: 10:00 AM – 10:30 AM

Preliminary Refined Localization of QTL for Fleece Traits in Five Goat Chromosomes using SNP Markers in a Backcross Population.
H. Taddeo*, EEA Bariloche-INTA, San Carlos de Bariloche, Argentina

Genetic Improvement Of Sheep In Ireland.
T. Pabion†, T. Byrne#, E. Wall† and N. McHugh†, †Irish Cattle Breeding Federation, Bandon, Ireland, ‡AbacusBio ltd, Dunedin, New Zealand, §SheepIreland, Bandon, Ireland, Teagasc Moorepark, Fermoy, Ireland

W. Olivier*, Grootefontein ADI, Middelburg, South Africa

ASIP and MC1R Mutations Causing Black Coat Colour in Five Swedish Sheep Breeds.
C. M. Rochus†, S. Mikko†, A. Näsholm† and A. M. Johansson†, †Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, AgroParisTech, Paris, France, GenPhySE, INRA, Castanet-Tolosan, France

Relationships of Faecal Worm Egg Count with Body Weight and Male Fertility In South African Merinos.
P. A. M. Matebesi-Ranthimo*, S. W. Cloete*, J. B. van Wyk# and J. J. Olivier†, †National University of Lesotho, Maseru, Lesotho, ‡University of the Free State, Bloemfontein, South Africa, †Directorate Animal Sciences, Elsenburg, South Africa, ¶University of Stellenbosch, Elsenburg, South Africa

Null Genetic Differentiation among Flocks Contributing to the Ripollesa Sheep Herdboob.
J. Casellas*, M. Fina†, R. Bach† and J. Piedrafita*, †Universitat Autònoma de Barcelona, Bellaterra, Spain, ‡ANCRI, Monells, Spain, ¶Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain

Breech Strike Indicator Traits for Merino Sheep in Non-Seasonal Rainfall Environments.
T. L. Bird-Gardiner*, J. L. Brown†, J. L. Smith*, S. Mortimer* and G. Refshauge*, †Cooperative Research Centre for Sheep Industry Innovation, Armidale, Australia, ‡University of New England, Armidale, Australia, §NSW Department of Primary Industries, Trangie, Australia, ‡Animal Genetics and Breeding Unit, UNE, Armidale, Australia, ¶CSIRO Animal, Food and Health Sciences, Armidale, Australia, ¶NSW DPI, Trangie, Australia, ¶NSW Department of Primary Industries, Cowra, Australia

Genetic Parameters and QTL Detection for Milking Speed in Dairy Alpine and Saanen Goats.
I. Palhière*, H. Larroque†, C. Virginie‡, G. Tossler-Klopp and R. Rachel*, †INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, ¶Institut de l'Elevage, Castanet-Tolosan, France, ¶INRA, UMR1388 GenPhySE, Castanet-Tolosan, France

Genetic Parameters and Trends for Hogget Live Weight, Wrinkle Score and Scrotal Traits in Merino Lines Divergently Selected for the Ability of Ewes to rear Multiples.
J. B. van Wyk†, S. W. Cloete* and J. J. Olivier†, †University of the Free State, Bloemfontein, South Africa, †Directorate Animal Sciences, Elsenburg, South Africa

Effects of Buck and Doe Size on the Growth Performance and Survival of their Progeny.
D. R. Kugonza*, M. F. Rothschild† and K. J. Stalder†, †Department of Agricultural Production, College of Agricultural and Environmental Sciences (CAES), Makerere University, Kampala, Uganda, ‡Iowa State University, Ames, ‡Department of Animal Science, College of Agriculture and Life Sciences, Iowa State University, Ames

Relative Economic Value for Merino Sheep in South Africa.
A. Van Graan*, Agricultural Research Council, Middelburg, South Africa
896 Genetics of Sheep Health Traits.
N. McHugh¹, S. Potton², E. Wall³ and T. Pabion⁴, ¹Teagasc Moorepark, Fermoy, Ireland, ²Sheep Ireland, Co. Cork, Ireland, ³SheepIreland, Bandon, Ireland, ⁴Irish Cattle Breeding Federation, Cork, Ireland

897 Genetic Association between Body Measurements and Weight in Santa Inês Sheep.
E. J. Oliveira¹,², I. El Faro³, A. P. Freitas⁴, F. F. Simili⁵, A. E. Vercesi Filho⁶, M. L. P. Lima⁶, R. L. D. Costa⁶ and C. C. P. Paz¹², ¹Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, ²SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

D. Buissin¹², G. Lagriffoul¹², G. Baloche¹, X. Aguerre¹, P. Boulenc², F. Fidelle³, G. Fregeat³, B. Giral-Viola³, P. Guibert³, P. Panis³, C. Soulas³, J. M. Astruc⁴ and F. Barillet⁴, ¹INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, ²OS Upra Lacaune, Rodez, France, ³CDEO, Ordiau, France, ⁴Idele, Toulouse, France, ⁵Ovitest, Rodez, France, ⁶Confédération Générale de Roquefort, Millau, France

M. Tolone¹, J. M. Yáñez², A. M. Satera³, L. M. Scatassa³ and B. Portolano¹, ¹Università degli Studi di Palermo, Palermo, Italy, ²University of Chile, Santiago, Chile, ³IZS della Sicilia “A. Mirri”, Palermo, Italy

900 Genetic Effects of αs1-casein Locus on Estimated Cheese Yields in Italian Alpine and Saanen Goats.
S. Frattini¹, University of Milan - Department of Veterinary Science and Public Health, Milan, Italy

Posters: Dairy Cattle Breeding (Group 3)
Chair: Kent A. Weigel, University of Wisconsin, Hermann Swalve, Martin Luther University Halle-Wittenberg, and Christian Maltecca, North Carolina State University

Presentation Time: 3:00 PM – 3:30 PM

829 Genetic Evaluations of Milkability in Norwegian Red Based on Data from Automatic Milking Systems.
B. Heringstad¹² and H. K. Bagsten¹, ¹Geno, Ås, Norway, ²Norwegian University of Life Sciences, Ås, Norway

830 Genome-Wide Association Study for 13 Udder Traits from Linear Type Classification in Cattle.
C. Flury¹, Bern University of Applied Sciences, School of Agricultural, Forest and Food Sciences, Zollikofen, Switzerland

831 Improving the Accuracy of Mid-Infrared Prediction Models by Selecting the Most Informative Wavelengths through Uninformative Variable Elimination.
M. De Marchi¹, P. Gottardo, M. Cassandro and M. Penasa, Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Legnaro, Italy

832 Trend Validation Procedures Applied by Interbull – A Historical Overview.
V. Palucci¹ and J. W. Dürr, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

833 Genetic Analysis of Milk Fat Globule and Casein Micelle Size in Canadian Holsteins.
A. Fleming¹, A. Koeck¹, F. Miglior², M. Corredig³, J. Chen², B. Mallard², A. Ali² and F. S. Schenkel¹, ¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³Dept Food Science, University of Guelph, Guelph, ON, Canada

834 Genetic Characterization of Two Populations of Murrah Buffaloes From Brazil and Cuba.
S. B. P. Barbosa¹, Universidade Federal Rural de Pernambuco, Recife, Brazil

835 Multivariate Outlier Detection in Genetic Evaluation in Nordic Jersey Cattle.
H. Gao¹, P. Madsen¹, J. Pöös³, J. Pedersen³, M. H. Lidauer¹ and J. Jensen¹, ¹Center for Quantitative Genetics and Genomics,
Heterosis and Breed Effects for Milk Production, Udder Health and Fertility in Danish Herds applying Systematic Crossbreeding.
E. Norberg1, L. H. Sørensen2, K. Bykov1 and M. Kargo1,4, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Knowledge Centre for Agriculture, Aarhus, Denmark, 4Knowledge Center for Agriculture, Aarhus, Denmark

Assessing Admixture by Quantifying Breed Composition to Gain Historical Perspective on Dairy Cattle in Canada.
S. G. Larmer1, Center For Genetic Improvement of Livestock - University of Guelph, Guelph, ON, Canada

Fertility and Production of 3-Breed and Third Generation Holstein-Sired Crossbreds Compared to Pure Holstein Cows in a Seasonal Pasture Production System.
B. J. Heins1, A. R. Hazel2 and L. B. Hansen3, 1University of Minnesota West Central Research and Outreach Center, Morris, MN, 2University of Minnesota, Saint Paul

Novel Function Describing Dairy Cow Lactation of Holstein Breed.
T. M. Gonçalves1, Federal University of Lavras, Lavras, Brazil

Correlation Between PTA for Milk and Beef Traits of Guzerá Animals from Dual-Purpose Herds in Brazil.
M. G. C. D. Peixoto1, R. A. Camada2, F. A. T. Bruneli3, G. G. Santos4, H. T. Ventura5 and P. S. Lopes6, 1Embrapa Dairy Cattle, Juiz de Fora, Brazil, 2Universidade Eduardo Mondlane, Vilanculos, Mozambique, 3Associação Brasileira de Criadores de Zebu, Uberaba, Brazil, 4Universidade Federal de Viçosa, Viçosa, Brazil

Phenotypic and Genetic Trends for Growth and Milk Traits of Guzera Breed in Dual Purpose Herds.
B. J. Heins1, A. R. Hazel2 and L. B. Hansen3, 1University of Minnesota West Central Research and Outreach Center, Morris, MN, 2University of Minnesota, Saint Paul

Genomic Estimates of Inbreeding and Coancestry in Austrian Brown Swiss Cattle.
F. Gómez-Romano1, J. Soelkner2, B. Villanueva3, G. Mészáros4, A. de Carda5, A. M. Pérez O’Brien6 and J. Fernández7, 1INIA, Madrid, Spain, 2University of Natural Resources and Life Sciences, Vienna, Austria, 3Museum National d’Histoire Naturelle, Paris, France

Phenotypic and Genetic Analysis Of Milk Fatty Acids in UK Holstein-Friesians.
S. Smith1, M. P. Coffey and E. Wall, SRUC, Edinburgh, United Kingdom

Posters: Sheep and Goats Breeding (Group 3)
Chair: Julius H.J. van der Werf CRC for Sheep Industry Innovation and John C McEwan, AgResearch
Presentation Time: 3:00 PM – 3:30 PM

H. J. Husson1, T. S. Sonstegard2, J. Silverstein3, J. Woodward-Greene4, C. Masiga5, F. C. Muchadeyi6, J. Rees7, B. Sayre8, A. R. Elbelawy9, 10M. F. Rothschild11, D. F. Mujib12, O. Mwai13, S. Kemp14, L. Colli15, P. Ajmone-Marsan16, P. Crepaldi17, J. Soelkner18, C. P. Van Tassell19 and S. Abegaz20, 1Cornell University, Ithaca, NY, 2USDA, ARS, BFGL, Beltsville, MD, 3USDA-ARS, Beltsville, MD, 4ASERECA, Entebbe, Uganda, 5Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa, 6Virginia State University, Petersburg, VA, 7Animal Production Research Institute, Cairo, Egypt, 8Iowa State University, Ames, 9International Livestock Research Institute, Nairobi, Kenya, 10Università Cattolica del Sacro Cuore, Piacenza, Italy, 11Università Cattolica del Sacro Cuore, Piacenza, Italy, 12Università di Milano, Milano, Italy, 13University of Natural Resources and Life Sciences, Vienna, Austria, 14Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD
902 Lamming Ease is Heritable but not Correlated to Litter Size in Danish Meat Sheep Breeds.  
A. C. Sørensen¹, P. Valasek², J. Pedersen¹ and E. Norberg³, ¹Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ²Czech University of Agriculture, Prague, Czech Republic, ³Knowledge Centre for Agriculture, Aarhus, Denmark

903 Characterization of a New Allele Encoding α₁ₐ-casein in the Lacaune Dairy Sheep: Possible Phylogenetic Relationship among CSN1S2 Alleles.  
Z. H. Fang¹,², G. Miranda¹,² and P. Martin¹,², INRA, UMR1313 GABI, Jouy-en-Josas, France, ²Agroparistech, UMR 1313, GABI, Jouy-en-Josas, France, ¹Wageningen University, Animal Breeding and Genomics Centre, Jouy-en-Josas, Netherlands

904 Using Phantom Groups to Increase the Accuracy of Breeding Values of Dohne Merinos Upgraded from a Commercial Base to the Pedigreed Population.  
W. M. Jordaan¹, S. W. Cloete², B. J. Olivier²,³ and K. Dzama⁴, ¹University of Stellenbosch, Stellenbosch, WV, South Africa, ²Department of Animal Sciences, Elsenburg, South Africa, ³Institute for Animal Production, Elsenburg, South Africa, ⁴University of Stellenbosch, Stellenbosch, South Africa

905 Targeted Association Mapping in Merinoland Crossbred Lambs.  
K. Schiller¹,², P. Straizė³, P. Preuss³ and J. Bennewitz³, ¹Institute for Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany, ²Institute of Animal Husbandry and Breeding, University Hohenheim, Hohenheim, Germany, ³Institute for Animal Husbandry and Breeding, University of Hohenheim, 70599 Stuttgart, Germany

906 Genomic Analysis of the Spring Leg Defect in the Canadian Dorset Sheep Breed.  
J. Cameron¹, M. Jafarikia²,³, L. Maignel⁴ and R. Morel⁴, ¹Centre d'expertise en production ovine du Québec, La Pocatière, QC, Canada, ²Canadian Centre for Swine Improvement, Ottawa, ON, Canada, ³Canadian Centre for Swine Improvement, Ottawa, ON, Canada, ⁴Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

907 Genetic Analysis of Adult Body Weight and Condition Scores in Merino Sheep.  
D. J. Brown¹ and A. A. Swan, Animal Genetics and Breeding Unit, UNE, Armidale, Australia

908 Breed Variation in Wool Quality, Growth and Plasma Metabolites of Prime Lambs Fed Degummed Canola.  
A. E. Malau-Adul¹,²,³, P. D. McEvoy¹, D. Parsons¹ and P. A. Lane¹, ¹University of Tasmania, Hobart, Tasmania, Australia, ²James Cook University, Townsville, Australia, ³University of Tasmania, Hobart, Australia

909 Screening for Footrot Resistant Gene Markers and White Blood Cell Types in Katahdin and Katahdin Crossbred Sheep.  
T. Wuliji¹, W. R. Lamberson¹, S. Azarpajouh¹, J. G. Hickford¹, B. C. Shanks¹ and J. D. Caldwell¹, ¹Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO, ²University of Missouri, Columbia, ³Lincoln University, Lincoln, New Zealand

910 Genetic Parameters of Objectionable Fibres, Skin Spots and Halo-hair in Corriedale Sheep.  
A. Sanchez¹, J. I. Urioste¹, F. Peñagaricano², K. Neimaur¹, J. Sienra¹ and R. Kremer¹, ¹Universidad de la República, Montevideo, Uruguay, ²University of Wisconsin, Madison

911 Situation Analysis for the Performance Recording of Australian Meat Goats.  
M. N. Aldridge¹, D. J. Brown², T. Hooke³ and W. S. Pitchford³, ¹School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia, ²Animal Genetics and Breeding Unit, UNE, Armidale, Australia, ³Meat and Livestock Australia Limited, Armidale, Australia

912 Effects of Selection Accuracy, Risk and Young Ewe Fertility on Breeding Program Design.  
J. E. Newton¹,²,³, D. J. Brown¹, A. A. Swan¹, S. Dominik² and J. van der Werf³, Animal Genetics and Breeding Unit, UNE, Armidale, Australia, ²CSIRO Animal Food and Health Sciences, Armidale, Australia, ³University of New England, Armidale, Australia

913 The Relationship of OPP Infection to TMEM154 Genotype in a Midwestern Sheep Flock.  
T. W. Murphy¹, D. L. Thomas¹, T. A. Taylor¹, M. J. Maroney² and K. M. Nelson², ¹University of Wisconsin-Madison, Department of Animal Sciences, Madison, WI, ²University of Wisconsin-Madison, Research Animal Resources Center, Madison, WI
Effects of Boer Crossbreeding and Base Kiko and Spanish Influences on Meat Goat Doe Performance in the Southeastern United States.
R. Browning, Jr.,1, A. S. Nguluma1, L. Wang1, J. L. Groves1 and M. L. Leite-Browning2,1Tennessee State University, Nashville, TN, 2Alabama A&M University, Huntsville

Transcriptome Comparison between the Pubertal and Adult Testis in Goats.
Z. Liu1,2, J. Li3, H. Xiao1, W. Liu1, X. Yue1 and Y. Ma1,1Inner Mongolia Agriculture University, Hohhot, China, 2Inner Mongolia Agriculture University, Hohhot, China, 3The Pennsylvania State University, University Park

Posters: Statistical and Genomic Tools for Mapping QTL and Genes (Group 1)
Chair: Michael E. Goddard, Department of Environment and Primary Industries
Presentation Time: 3:00 PM – 3:30 PM

Comparison of Linkage Disequilibrium Uncovered by Moderate and High Density Arrays in Brown Swiss Dairy Cattle and in White Leghorn Layer Chickens.
E. Lipkin1, M. A. Doleza, A. Bagnato1, J. E. Fulton2, N. P. O’Sullivan1, E. Santus2, D. Burt3 and M. Soller1,1Hebrew University of Jerusalem, Jerusalem, Israel, 2Università degli Studi di Milano, Milano, Italy, 3Hy-Line International, Dallas Center, IA, 4ANARB, Italian Brown Cattle Breeders' Association, Basolengo (VR), Italy, 5The Roslin Institute and Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom

Posters: Dairy Cattle Breeding (Group 4)
Chair: Kent A. Weigel, University of Wisconsin, Hermann Swalve, Martin Luther University Halle-Wittenberg, and Christian Maltecca, North Carolina State University
Presentation Time: 3:30 PM – 4:00 PM

Combi-Cross – The Use of New Technologies for Improving Dairy Crossbreeding Programs.
M. Kargo1,2, J. Ettema1, L. H. Sørensen1, M. Fjordside1 and L. Hjortø6,1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Knowledge Center for Agriculture, Aarhus, Denmark, 3SimHerd Inc., Tjele, Denmark, 4Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 5VikingDenmark, Viborg, Denmark, 6Knowledge Centre for Agriculture, Aarhus, Denmark

Use of DNA Markers in Parentage Testing in Mexican Jersey Cattle.
R. Cuevas-Pat, R. Niñez-Dominguez1, E. Valadez-Moctezuma, R. Ramirez-Valverde and A. Raiz-Flores, Universidad Autónoma Chapingo, Chapingo, Mexico

The Impact of Daughter Misidentification on the Genetic Evaluation of Dairy Sires.
A. M. Winkelman1, Livestock Improvement Corporation, Hamilton, New Zealand

Genetic Parameters of Milk Yield at Different Somatic Cell Count Levels using Multiple-Trait Random Regression in Holsteins.
K. Kheirabadi1, S. O. Peters1, I. G. Imumor1,2 and M. Ghaderi-Zefrehel1,1University of Yasouj, Yasouj, Iran, 2Berry College, Mount Berry, GA, 3Cornell University, Ithaca, NY

Genomic Predictions of Feed Utilization and Associations with Milk Yield, Body Weight and Activity Levels in an Independent Population of Holsteins.
C. D. Dechow1 and I. W. Haagen, Pennsylvania State University, University Park

An Approach to Genomic Analysis of Longitudinal Data using Random Regression.
D. J. A. Santos1, S. A. Boisson2, A. T. H. Utsanomiy2, M. G. C. Peixoto1, H. Tonhat1, J. Sölkner2 and M. V. G. B. da Silva1,1State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 2University of Natural Resources and Life Sciences, Vienna, Austria, 3UNESP Univ Estadual Paulista, Jaboticabal, Brazil, 4Embrapa Dairy Cattle, Juiz de Fora, Brazil
**Posters: Methods and Tools - Genome Sequencing**

**Chair:** Ben J. Hayes, Department of Environment and Primary Industries

**Presentation Time:** 3:30 PM – 4:00 PM

659  **Genome Data from a 16th Century Pig Illuminates Modern Breed Relationships.**  
* M. Perez-Enciso, Universitat Autònoma de Barcelona, Bellaterra, Spain

660  **High Imputation Accuracy in Layer Chicken from Sequence Data on a Few Key Ancestors.**  
* M. Heidaritabar, M. P. L. Calus, A. Vereijken, M. A. Groenen and J. W. M. Bastiaansen, Wageningen University, Wageningen, Netherlands, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, Hendrix Genetics, Boxmeer, Netherlands, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

661  **Imputation of Sequence Level Genotypes in the Franches-Montagnes Horse Breed.**  
* M. Frischknecht, M. Neuditschko, V. Jagannathan, C. Droegemuller, J. Tetens, T. Leeb and S. Rieder, Agroscope - Swiss National Stud Farm, Avenches, Switzerland, Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, Swiss Competence Center of Animal Breeding and Genetics, Bern, Switzerland, Graduate School for Cellular and Molecular biology, University of Bern, Bern, Switzerland, Institute of Animal Breeding and Husbandry, Christian-Albrechts-Universität zu Kiel, Kiel, Germany, Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany

662  **Post Alignment Reads Quantification of the Pig Transcriptome Sequencing.**  
* K. Zakowski, K. Ropka-Molik, K. Piorkowska and A. Gurgul, National Research Institute of Animal Production, Balice, Poland

664  **Genomic Prediction with 12.5 Million SNPs for 5503 Holstein Friesian Bulls.**  

665  **Characterization of Genetic Variation in Icelandic Cattle.**  
* L. E. Holm, A. Das, J. Momeni, F. Panitz, C. Bendixen and E. Eythorsdottir, Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Faculty of Land and Animal resources, Agricultural University of Iceland, Reykjavik, Iceland

666  **Identification and Annotation of Genetic Variants (SNP/Indel) in Danish Jutland Cattle.**  
* A. Das, F. Panitz and L. E. Holm, Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

667  **Accuracy of Whole-Genome Sequence Genotype Imputation in Cattle Breeds.**  
* H. Li, M. Sargolzaei and F. S. Schenkel, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, The Semex Alliance, Guelph, ON, Canada

668  **Comparison of Variant Calling Methods for Whole Genome Sequencing Data in Dairy Cattle.**  
* C. F. Baes, M. A. Dolezal, E. Fritz-Waters, J. E. Koltes, B. Bapst, C. Flury, H. Signer-Hasler, C. Stricker, R. L. Fernando, F. Schmitz-Hsu, D. J. Garrick and B. Gredler, Bern University of Applied Sciences, School of Agriculture, Forest and Food Sciences, Zollikofen, Switzerland, Qualitas AG, Zug, Switzerland, University of Veterinary Medicine Vienna, Vienna, Austria, Università degli Studi di Milano, Milano, Italy, Iowa State University, Ames, Bern University of Applied Sciences, School of Agricultural, Forest and Food Sciences, Zollikofen, Switzerland, Bern University of Applied Sciences, School of Agriculture, Forest and Food Sciences, Zoll, Switzerland, agn-genetics, Davos, Switzerland, swissgenetics, Zollikofen, Switzerland

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**Posters: Statistical and Genomic Tools for Mapping QTL and Genes (Group 2)**

**Chair:** Michael E. Goddard, Department of Environment and Primary Industries and Michel Georges, University of Liège

**Presentation Time:** 3:30 PM – 4:00 PM
Local Score Based Method Applied On Pool-Sequenced Behavior-Divergent Lines Precisely Detected Selection Signatures Related To Autism In Quail.
M. I. Fariello Rico1,2,3, S. Bottard4,5, S. Mercier6,7, D. Robelin8, T. Faraut9, C. Arnould9, E. Lebihan10, J. Recoco11, G. Salin12, P. Dehais13,14, F. Petel15, C. Letterrier16 and M. San Cristobal17,18, 1Institut Pasteur Montevideo, Montevideo, Uruguay, 2IMERL, Facultad de Ingeniería, Universidad de la Republica, Montevideo, Uruguay, 3INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 4GABI (INRA / Agroparistech), Jouy-en-Josas, France, 5UMR 7205 ISYEB (MNHN / CNRS / EPHE / UPMC), Paris, France, 6Université Toulouse Le Mirail, Toulouse, France, 7Institut de Mathématiques de Toulouse, Toulouse, France, 8INRA, UMR85 Physiologie de la Reproduction et des Comportements, Nouzilly, France, 9INRA, UR83 Recherches Avicoles, Nouzilly, France, 10INRA, GeF, Castanet-Tolosan, Castanet-Tolosan, France, 11INRA Toulouse, SIGENAE, France, Castanet-Tolosan, France, 12INRA UMR1388 GenPhySE, Castanet-Tolosan, France, 13UMR 1388 INRA / INPT ENSAT / INPT ENVT, GenPhySE, Castanet-Tolosan, France, 14INSA Toulouse, GMH, Toulouse, France

A New Method to estimate Recombination Rate Based on SNP Allelic Dosage Data.
T. Yang, Z. Wang, Z. Hu and G. S. Plastow, University of Alberta, Edmonton, AB, Canada

The Impact of Linkage Disequilibrium on Estimable Genetic Effects at Markers in the Presence of Dominance.
C. Heuer1 and G. Thaller2, 1Institute of Animal Breeding and Husbandry, Kiel University, Kiel, Germany, 2Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany

Gene Based Association Approach Identify Genes Across Stress Traits in Fruit Flies.
P. Jensen1,2, S. M. Edwards1, P. M. Sarup1 and P. Sørensen1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Section of Genetics, Ecology and Evolution, Department of Bioscience, Aarhus University, Aarhus, Denmark

Counting for Population Structure and Haplotype Diversity in Whole Genome Scans for Selection Signatures.
B. Servin1, S. Bottard4, C. Chevalier, M. I. Fariello, F. Phocas5 and M. San Cristobal6, 1InRA, Castanet-Tolosan, France, 2Museum National d'Histoire Naturelle, Paris, France, 3INRA, Jouy-en-Josas, France, 4Universidad de la Republica, Montevideo, Uruguay, 5INRA, UMR1313 GABI, Jouy-en-Josas, France, 6INRA, UMR1388 GenPhySE, Castanet-Tolosan, France

Applying Runs of Homozygosity to the Detection of Associations between Genotype and Phenotype in Farm Animals.
F. Biscarini1, S. Biffani2, E. L. Nicolazzi3, N. Morandi4 and A. Stella4, 1Fondazione Parco Tecnologico Padano, Lodi, Italy, 2IBBA-CNRCNR, Lodi, Italy, 3Parco Tecnologico Padano (PTP), Lodi, Italy

Haplo-Block Structure of Southern African Village Chicken Populations.
K. S. Khanyile1,2, E. F. Dzomba3 and F. C. Muchadeyi3, 1University of KwaZulu-Natal, Pietermaritzburg, South Africa, 2ARC-OVI Biotechnology Platform, Pretoria, South Africa, 3Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa

Using Haplotype Mapping to Uncover the Missing Heritability: A Simulation Study.
M. Shirali1, R. Pong-Wong2, S. Knott3, C. Hayward4, V. Vitart1, I. Rudan5, H. Campbell6, N. Hastie7, A. F. Wright1, P. Navarro1 and C. Haley1,2, 1MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 3Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, United Kingdom, 4Centre for Population Health Sciences, University of Edinburgh, Edinburgh, United Kingdom, 5Croatian Centre for Global Health, Faculty of Medicine, University of Split, Split, Croatia

Association between Copy Number Variation Regions and Meat Tenderness in Nelore Cattle.
M. P. Berton1, M. V. A. Lemos2, C. Aboujaoude3, G. M. de Camargo4, L. A. L. Chardona5, L. G. Albuquerque6 and F. Baldi7, 1State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, Jaboticabal, Brazil, 2Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 3State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 4State University of São Paulo, Botucatu, São Paulo, Brazil, 5State University of São Paulo, Botucatu, São Paulo, Brazil

Bayes U: A Genomic Prediction Method Based on the Horseshoe Prior.
R. Pong-Wong* and J. A. Woolliams, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

POSTGSF90: Computational Tools for the Implementation of Single-Step Genomic Selection and Genome-Wide Association with Unenotyped Individuals in BLUPF90 Programs.
Wednesday, August 20, 2014

Posters: Breeding Objectives, Economics of Selection Schemes, and Advances in Selection Theory

(Group 1)

Chair: Jack C. M. Dekkers, Iowa State University

Presentation Time: 9:30 AM – 10:00 AM

384  Evaluation of Brazilian Dairy Goat Breeding Programs.
R. N. B. Lobo  1, 2, L. H. dos Santos  2, O. Faci  3, and A. M. B. O. Lobo  1, 4, Embrapa Goats and Sheep, Sobral, Brazil,  2Federal University of Ceará, Fortaleza, Brazil,  3Federal University of Maranhão, Imperatriz, Brazil

R. I. Cue  1, K. Wade  1, A. Sewalem  2, H. A. Delgado  1, D. M. Lefebvre  3, E. Bouchard  3, D. Haine  3, and J. Dubuc  3,  1McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada,  2University of British Columbia, Vancouver, BC, Canada,  3McGill University, Ste-Anne de Bellevue, QC, Canada,  4University of Saskatchewan, Saskatoon, SK, Canada,  5University of British Columbia, Vancouver, BC, Canada,  6University of Montreal, Saint-Hyacinthe, QC, Canada,  7University of Saskatchewan, Saskatoon, SK, Canada

386  Approximate Multivariate Genetic Evaluation of Functional Longevity and Type Traits in Austrian Fleckvieh Cattle.
C. Pfeiffer  1, B. Fuerst-Waltl  1, V. Durocq  4, and C. Fuerst  1,  1University of Natural Resources and Life Sciences, Vienna, Austria,  2University of Natural Resources and Life Sciences (BOKU), Vienna, Austria,  3INRA, UMR1313 GABI, Jouy-en-Josas, France,  4ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria

387  Genetic Parameters for Milk Production Traits and Breeding Goals for Gir Dairy Cattle in Brazil.
M. A. Prata  1, 4, H. Luis Moreira  1, R. D. Silva Verneque  3, A. Eugênio Vercesi Filho  1, M. G. Campolina Diniz Peixoto  2, L. El Faro  4, and V. Lúcia Cardoso  1,  1Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto-Departamento de Genética,  2Fundação de Amparo à Pesquisa do Estado de São Paulo, Faculdade de Medicina de Ribeirão Preto, São Paulo, Brazil,  3Universidade Estadual Paulista “Júlio de Mesquita Filho”, Sao Paulo, Brazil,  4State University of Maranhão, Imperatriz, Brazil
E. Sodjinou¹, A. Henningsen², D. O. Koudande*¹, G. Biaou³ and G. A. Mensah¹, ¹Institut National des Recherches Agricoles du Bénin, Cotonou, Benin, ²Department of Food and Resource Economics, University of Copenhagen, Copenhagen, Denmark, ³Faculté des Sciences Agronomiques, Université d’Abomey-Calavi, Abomey-Calavi, Benin

A Comparison of Restricted Selection Procedures Based on Restricted Best Linear Unbiased Prediction of Breeding Values.
M. Satoh* and M. Nishio, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan

Preliminary Results of an Investigation on Innovative Breeding Objectives to Improve Efficiency in Extensive Cow-Calf Production Systems in the Bonsmara Breed.
M. C. Mokolobate¹,², M. M. Scholtz¹,², F. W. C. Nesar, F. J. Jordaan¹,² and S. D. Mulugeta¹, ¹ARC-Animal Production Institute, Irene, South Africa, ²University of the Free State, Bloemfontein, South Africa, ³North West University, Mahikeng, South Africa

Did Genetic Change Improve Production Efficiency in Three Landrace Breeds of South Africa?.
F. J. Jordaan¹,², M. M. Scholtz¹,², F. W. C. Nesar¹, N. A. Malwase¹ and Z. King¹, ¹University of the Free State, Bloemfontein, South Africa, ²ARC-Animal Production Institute, Irene, South Africa

J. Mbuthia¹,², T. Rewe³, T. Okeno³ and A. Kahi³, ¹Egerton University, Njoro, Kenya, ²Pwani University, Kilifi, Kenya, ³Aarhus University, Tjele, Denmark

M. J. Kelly¹ and J. M. Thompson², ¹The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia, ²The University of New England, Armidale, Australia

Selection Strategies Utilizing Genetic Resources to Adapt Livestock to Climate Change.
B. A. Åby* and T. H. E. Meuwissen, Norwegian Institute of Livestock and Grassland Science, Tsukuba, Japan

Optimization of a Meat Index for Austrian Land Sheep.
L. Grill, A. Willam¹, R. Baumung and B. Fuerst-Waltl, University of Natural Resources and Life Sciences (BOKU), Vienna, Austria

Genetic Gain and Economic Weights of Selection Strategies Including Boar Semen Traits in a Cross-Breeding System.
D. Gonzalez-Peña Fundora¹,², R. V. Knox³, M. D. MacNeil² and S. L. Rodriguez Zas³, ¹University of Illinois, Urbana, ²University of the Free State, Bloemfontein, South Africa

AccuAssign, Software for Accurate Maximum-Likelihood Parentage Assignment.
D. Boichard¹,², L. Barbotte and L. Genestour¹, ¹INRA, UMR1313 GABI, Jouy-en-Josas, France, ²Labogena-DNA, Jouy en Josas, France

Posters: Genetics of Trait Complexes - Lactation
Chair: Juan F. Medrano, University of California
Presentation Time: 9:30 AM – 10:00 AM

Using Random Regression Models to Optimize Selection for Yield, Persistency and Calving Interval in Philippine Dairy Buffaloes.
E. B. Flores¹,² and J. van der Werf³, ¹School of Environmental and Rural Science University of New England, Armidale, Australia, ²Philippine Carabao Center, Muñoz Nueva Ecija, Philippines, ³University of New England, Armidale, Australia
610 Initial RNA-Seq Analysis on the Milk Transcriptional Profiling of Two Sheep Breeds.
A. Suarez-Vega1, B. Gutiérrez-Gil2, C. Esteban3 and J. J. Arranz4, 1Universidad de León, Leon, Spain, 2Universidad de León, León, Spain, 3Supercomputing Center of Castile and León, León, Spain

611 Principal Components for Reproductive and Productive Traits in Buffaloes from Brazil.
D. Portela de Oliveira1,2, C. D. C. Barros1, F. Ribeiro Araujo Neto1, D. Lourenco1, N. A. Hurtado Lugo1 and H. Tonhathi1, 1Universidade Estadual Paulista “Júlio de Mesquita Filho” (UNESP), Jaboticabal, Brazil, 2CAPES Foundation, Ministry of Education of Brazil, Brasília – DF 70.040-020, Brasília, Brazil

612 Fine-Mapping of a Candidate Region Associated with Milk-Fat Composition on Bos Taurus Autosome 17.
S. I. Duchemin1,2, M. H. P. W. Visser1, J. A. M. van Arendonk1 and H. Bovenhuis1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

613 Comparison of Genetic Parameters Estimation of Fatty Acids from Gas Chromatography and FT-IR in Holsteins.
N. A. Poulsen1, C. E. Eskildsen2, T. Skov2, L. B. Larsen1 and A. J. Buitenhuis1, 1Aarhus University, Food Science, Tjelle, Denmark, 2University of Copenhagen, Food Science, Copenhagen, Denmark, 3Aarhus University, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Tjele, Denmark

614 Estimation of Genetic Parameters for the Protein Profile in Danish Holstein Milk.
A. J. Buitenhuis1, N. A. Poulsen1 and L. B. Larsen2, 1Aarhus University, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Tjele, Denmark, 2Aarhus University, Food Science, Tjele, Denmark

615 QTL Detection for Milk Fatty Acids in French Dairy Cattle.
A. Govignon-Gion1, S. Fritz2, H. Larroque2, M. Brochard2, C. Chantry6, F. Lahalle7,8 and D. Boichard4, 1INRA, UMR 1313 GABI, Jouy-en-Josas, France, 2INRA, UMR1313 GABI, Jouy-en-Josas, France, 3UNCEIA, Paris, France, 4INRA, UMR 1388 GenPhysE, Castanet-Tolosan, France, 5Idéele, Paris, France, 6LABOGENA, Jouy-en-Josas, France, 7Institut de l’Elevage, Paris, France, 8CNIEL, Paris, France

616 Genetic Parameters of Average Milk Flow Recorded Electronically from Milking Parlours and Automatic Milking Systems in Estonian Holstein Dairy Cows.
D. Pretto1, A. Tänavots1,2, H. Kiiman1,2, E. Pärna1,2, H. Viinalass1,2 and T. Kaart1,2, 1Institute of Veterinary Medicine and Animal Sciences, Estonian University of Life Sciences, Tartu, Estonia, 2Bio-Competence Centre of Healthy Dairy Products (BioCC) LLC, Tartu, Estonia

617 QTL Detection for Fat Yield on BTA14 using Linkage Disequilibrium Based Methods.
M. J. Berihe1, H. A. Carignano1, N. Lopez-Villalobos2, M. Poli1 and D. L. Roldan1, 1Instituto de Genética CICVyA-INTA, Buenos Aires, Argentina, 2Massey University, Palmerston North, New Zealand

618 Mid-infrared Spectroscopy to Predict Important Milk Quality Traits in Irish Cows.
A. A. Mc Dermott1,2, G. Visentin1,2, M. De Marchi2, O. A. Kenny3, M. Fenlon1 and S. McParland4, 1Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Legnaro, Italy, 3Food Science Research Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 4Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

619 Using SNP to Enhance Fatty Acids Composition in Goat Milk.
S. Chessa1, P. Cremonesi, R. Moretti, F. Turri and B. Castiglioni, Institute of Agricultural Biology & Biotechnology - CNR, Lodi, Italy

620 Genetic Relationship between Lactation Curve Traits in Dairy Cattle.
C. B. Wasike1, K. J. Peters2 and A. K. Kahi1, 1Department of Animal Science, Maseno University, Maseno, Kenya, 2Sheep and Goat Association of Berlin- Brandenburg, Berlin, Germany

621 Genome-Wide Association Study for Milk Total Unsaturated Fatty Acids in Brazilian Holstein Cows.
J. Petrini1, L. H. S. Iung1, M. A. P. Rodriguez1, F. Pétrille1, L. D. Cassol1, P. F. Machado1, L. L. Coutinho2 and G. B. Mourao1,
Random Regression Model Analysis for Total Milk Solids in First Lactation Dairy Cattle.
A. Zampari¹, F. S. Cavalcante², P. F. Machado², L. E. Bastos², A. B. Fraga¹ and G. B. Mourão¹, ¹Federal University of Alagoas, Maceio, Brazil, ²University of São Paulo, Piracicaba, Brazil

MicroRNAs are involved in Bovine Mammary Gland Response to Dietary Supplementation with Safflower Oil.
R. Li³,², F. Beaudoin¹, X. Zhao¹, C. Lei¹ and E. M. Ibeagha-Awemu¹, ¹Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, ²Northwest A&F University, Xi’an, China, ³McGill University, St Ann De Bell, PQ, Canada

Genome-Wide Association for Somatic Cell Score in Holstein Cows Raised in Tropical Conditions.
L. H. S. Jung¹, J. Ramírez-Díaz¹, S. F. N. Pertile¹, J. Petrin¹, M. Salvian¹, M. A. P. Rodriguez¹, R. R. Lima², P. F. Machado³, L. L. Coutinho⁴ and G. B. Mourao⁴, ¹Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, ²Federal University of Lavras, Lavras, Brazil, ³University of São Paulo, Piracicaba, Brazil, ⁴Universidade de São Paulo/Esalq, Piracicaba, Brazil

Posters: Breeding Objectives, Economics of Selection Schemes, and Advances in Selection Theory (Group 2)
Chair: Jack C. M. Dekkers, Iowa State University
Presentation Time: 10:00 AM – 10:30 AM

Prediction of Industry Production of Milk Components, Yields of Dairy Products and Lactose Deficit under the Current Breeding Objective of New Zealand Dairy Cattle.
N. W. Sneddon¹, ², N. Lopez-Villalobos¹, R. E. Hickson¹, L. Shallow¹, D. J. Garrick¹ and U. Geary², ¹Massey University, Palmerston North, New Zealand, ²Teagasc, Fermoy Co. Cork, Ireland, ³Iowa State University, Ames

R. B. Onzima¹, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands; Kachwerkano Zonal Agricultural Research & Development Institute - NARO-Uganda, Kabale, Uganda

Analysis of Breeding Strategies against Genetic Disorders in Austrian Fleckvieh Cattle.
C. Egger-Danner¹, H. Schwarzenbacher¹, C. Fuerst¹ and A. Willam², ¹ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria, ²University of Natural Resources and Life Sciences, Vienna, Austria

Genetic Parameters and Genetic Trends For Growth Litter Traits in the Tai Zumu line.
M. Banville¹,², L. Canario³, M. Sourdoux³, D. Bahon³, J. Riquer³ and L. Flatres-Grall¹, ¹GENE+, Erin, France, ²INRA UMR1388, F-31326 Castanet-Tolosan, France

Heterogeneity of Variance for Lactation Persistency and Milk Yield at 305 Days of Gir Cows in Different Environments.
G. G. Santos¹, C. E. Enriquez-Valencia¹, D. C. Scales³, D. J. A. Santos¹, M. G. Campolina Diniz Peixoto¹ and A. Eugénio Vercesi Filho¹, ¹Embrapa Dairy Cattle, Juiz de Fora, Brazil, ²State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, ³UNESP Univ Estadual Paulista, Jaboticabal, Brazil, ¹Instituto de Zootecnia, Sertãozinho, Brazil

Economic Values of Milk Production and Milk Coagulation Properties in Italian Holstein-Friesian Dairy Cattle.
M. Cassandro¹, D. Pretto¹, M. De Marchi¹, M. Penasa¹ and N. Lopez-Villalobos¹, ¹Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Legnaro, Italy, ²Estonian University of Life Sciences, Tartu, Estonia, ³Massey University, Palmerston North, New Zealand

Economic Values for Milk Production and Composition Traits in the South and Southeast Regions of Brazil.
V. L. Cardoso¹, M. L. Pereira Lima¹, A. E. Vercesi Filho¹, R. L. R. Carneiro¹, R. C. Sesana¹ and L. El Faro¹, ¹Apta Regional - PRDTA Centro Leste SAA/SP, Ribeirão Preto-SP, Brazil, ²Instituto de Zootecnia APTA SAA/SP, Sertãozinho-SP, Brazil, ³SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil, ⁴CRV-Lagoa, Sertaozinho-SP, Brazil
An Estimate of the Economic Gain from Selection to Reduce BRDC Incidence in Dairy Calves.

J. S. Neibergs¹, H. L. Neibergs¹, J. F. Taylor¹, C. M. Seabury¹, T. W. Lehenbauer¹, A. L. Van Eenennaam² and J. E. Womack³,
¹Washington State University, Pullman, ²University of Missouri, Columbia, ³Texas A&M University, College Station, ¹University of California, Davis, Davis, CA, ¹University of California, Davis

Development of Selection Indexes for a Beef Cattle Production System from Available EPDs.

M. I. Pravia¹,², O. Ravagnolo³ and J. Urioste²,
¹Instituto Nacional de Investigación Agropecuaria, Montevideo, Uruguay, ²Facultad de Agronomía. Universidad de la República, Montevideo, Uruguay, ³Instituto Nacional de Investigación Agropecuaria, Canelones, Uruguay

Expected Genetic Gain from Newly Developed Selection Indices for South African Holstein Cattle.

C. B. Banga¹ and A. A. Maiwashe²,
¹Agricultural Research Council, Irene, South Africa, ²ARC-Animal Production Institute, Irene, South Africa

Use of Mate Selection Software to Manage Lethal Recessive Conditions in Livestock Populations.

A. L. Van Eenennaam¹ and B. P. Kinghorn²,
¹University of California, Davis, ²University of New England, Armidale, Australia

The Effect of using Genomic Breeding Values to Manage the Loss in Response to Selection Caused by Genotype by Environment Interactions.

S. Clark³, D. Brown³ and J. van der Werf³,
³University of New England, Armidale, Australia, ³Animal Genetics and Breeding Unit, Armidale, Australia

Optimising Current Generation Gains to Supplement Genetic Gain in Commercial Sheep Flocks.

J. S. Richards¹, B. P. Kinghorn¹ and K. D. Atkins³,
¹University of New England, Australian Cooperative Research Centre for Sheep Industry Innovation, NSW Department of Primary Industries, Orange, Australia, ³University of New England, Armidale, Australia, ³Shoal Bay, Australia

Posters: Breeding of Companion Animals
Chair: Sheila M. Schmutz, University of Saskatchewan
Presentation Time: 10:00 AM – 10:30 AM

Heterotic Components of Carcass and Meat Quality Traits for Crossing Gabali with V-Line Rabbits.

M. H. Khalil¹, Department of Animal Production. Faculty of Agriculture, Benha University, Moshtohor, 13736, Qalubia, Egypt, Moshtohor, Egypt

Genetic Correlations between Young Horse and Dressage Competition Results in Danish Warmblood Horses.

L. Jönsson¹,², K. Christiansen³, M. Holm³ and T. Mark¹,
¹Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, ²Danish Warmblood Association, Maarslet, Denmark, ³Knowledge Centre for Agriculture, Skejby, Denmark

Genome-Wide Association Study Leads to a DNA Assay for Dwarfism in the Friesian Horse Population.

A. Schurink¹,², I. Hellinga¹, P. A. J. Leegwater¹, W. Back¹,², J. W. M. Bastiaansen¹ and B. J. Ducro¹,
¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Koninklijke Vereniging “Het Friesch Paarden-Stamboek”, Drachten, Netherlands, ³Department of Clinical Sciences of Companion Animals, Faculty of Veterinary Medicine, Utrecht University, Utrecht, Netherlands, ⁴Department of Equine Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, Netherlands, ⁵Department of Surgery and Anaesthesiology of Domestic Animals, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium

Genetic Analysis Of Hunting Traits In Norwegian Elkhounds.

M. Wetten¹ and T. Aasmundstad²,
¹Geninova, Hamar, Norway, ²Norsvin, Hamar, Norway

QTL Mapping for Canine Hip Dysplasia in UK Labrador Retriever.

E. Sanchez-Molano¹, J. A. Woolliams¹, R. Pong-Wong¹, D. N. Clements¹, S. C. Blott² and P. Wiener³,
¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²University of Nottingham, Leicestershire, United Kingdom
Genetics of Aggression, Fear and Sociability in Everyday Life of Swedish Dogs.
H. Eken Asp, P. Arvelius, W. F. Fikse, K. Nitsson and E. Strandberg, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

A Mutation in the SLC45A2 Gene is Associated with Albinism in a Lhasa Apso Dog.
H. R. Wijesena and S. M. Schmutz, Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada

Genetic Diversity and Measures to Reduce Inbreeding in Friesian Horses.

Model Assessment for Ranking Traits of Criollo Horses Participating in Endurance Trials.
R. López-Correa, F. Peñagaricano, G. Rovere and J. I. Urioste, Universidad de la República, Montevideo, Uruguay, University of Wisconsin, Madison, Wageningen University, Wageningen, Netherlands

Posters: Methods and Tools - Bioinformatics
Chair: Paul Stothard, University of Alberta and James M. Reecy, Iowa State University

Presentation Time: 10:00 AM – 10:30 AM

Evaluation of the BEAGLE Haplotype Reconstruction Algorithm.
M. H. Ferdosi, J. van der Werf, B. Tier and C. Gondro, School of Environmental and Rural Science, University of New England, Armidale, Australia, University of New England, Armidale, Australia, Animal Genetics and Breeding Unit, Armidale, Australia, School of Environmental & Rural Science, University of New England, Armidale, Australia

Sequence Analyses of Bovine PAG-1 Gene.
M. O. Ozoje, S. O. Durosaro, P. E. Esada and S. O. Peters, Federal University of Agriculture, PMB 2240, Abeokuta, Nigeria, New Mexico State University, Mount Berry, GA

Inferring a Core Transcriptional Regulatory Network in Cows.
S. Strunz, T. Kacprowski, N. Melzer, J. Friedrich and A. de la Fuente, Leibniz-Institute for Farm Animal Biology, Dummerstorf, Germany, University Medicine Greifswald, Greifswald, Germany, University of Rostock, Rostock, Germany

Copy Number Variation in Brown Swiss Dairy Cattle.
M. A. Dolezal, A. Bagnato, F. Schiavini, E. Santus, L. E. Holm, C. Bendixen and F. Paniz, Università degli Studi di Milano, Milano, Italy, University of Veterinary Medicine Vienna, Vienna, Austria, ANARB, Italian Brown Cattle Breeders' Association, Bussolengo (VR), Italy, Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Accelerating the Shift to SNP-Based Parentage Verification through Microsatellite Imputation in Ireland.
M. C. McClure, Irish Cattle Breeding Federation, Bandon, Ireland

Biotrack Software: Making Genetics a Part of the Whole Farm Picture.
M. R. McMorris, Beef Improvement Opportunities, Guelph, ON, Canada

In-Silico Analysis of Missense Mutation of Bovine RYR1 Protein.
J. D. Leal Gutierrez, Universidad Nacional de Colombia, Bogotá, Colombia

Approximation of the Structural Forms of the Variances and Covariances between Molecular and Phenotypic Breeding Values.
S. D. Kachman, University of Nebraska, Lincoln

Thursday, August 21, 2014
Posters: Genetics of Trait Complexes - Disease Resistance (Group 1)
Chair: Larry A. Kuehn, USDA, ARS, U.S. Meat Animal Research Center
Presentation Time: 9:30 AM – 10:00 AM

C. R. Moreno1, P. Jacquier2, F. Bouvier3, J. Corret4,5, A. Blanchard-Letorté5,6, F. Guégnard6, D. Francois1, Y. Bourdillon1, C. Grisè2,3, F. Prevo1, A. Averadère2, J. Demars5, J. Sarry5, A. Stella6, F. Wolozycki6, K. Canale-Tabet7, J. Cabarelli8, G. Tisser-Klopp1 and G. Salle1,6, 1INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 2ENVIT-INRA IHPAP, Toulouse, France, 3UMT Santé des petits ruminants, Toulouse, France, 4INRA de Bourges la Sapinière, Bourges, France, 5INRA ISP, Tours, France, 6Université François Rabelais de Tours, Tours, France, 7INRA GenPhySE UMR1388, Toulouse, France, 8Fondazione Parco Tecnologico Padano, Lodi, Italy

517 Cytokine Gene Expression in Holstein-Friesian and Jersey Calves Infected with Mycobacterium Avium Subsp. Paratuberculosis.
N. A. Karrow1, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada

518 Genome-Wide Association Mapping of Response to Infection by the Aleutian Mink Disease Virus.
A. H. Farié1, K. Gardner, L. F. Butler, P. P. Rupasinghe and S. Myles, Dalhousie University Faculty of Agriculture, Truro, NS, Canada

519 Genetic Analysis of Receiving Weight, Ultrasound Back Fat, Ultrasound Rib Eye Area, Ultrasound Percent Intramuscular Fat and Bovine Respiratory Disease in Feedlot Cattle.
S. E. Speidel1, R. R. Cockram2, J. Salak-Johnson1, C. Chase1, M. G. Thomas1, R. K. Peel1 and R. M. Enns1, 1Colorado State University, Department of Animal Sciences, Fort Collins, 2Virginia Polytechnic Institute and State University, Blacksburg, 3University of Illinois, Urbana, 4South Dakota State University, Brookings, 5Colorado State University, Fort Collins

520 Association Study of Single Nucleotide Polymorphisms in STATA5A with Mastitis Susceptibility in Chinese Holstein Cattle.
T. Usman1, Y. Wang1, Y. Yu1, C. Liu1, X. Wang1 and Y. Zhang1, 1China Agriculture University, Beijing, China, 2College of Animal Science and Technology, China Agricultural University, Beijing, China

521 Genetic Parameters and Genomic Markers Associated with Mastitis Resistance in Dairy Sheep.
A. Psifidi1,2, G. Bramis1, G. Arsenos2 and G. Banos1,2,3, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece, 3Scotland’s Rural College, Edinburgh, United Kingdom

522 The Association Between Sire Estimated Breeding Value for Antibody-Mediated Immune Response (AMIR) and Offspring AMIR Phenotype.
M. E. Emam1, M. A. Paibomesai1, K. A. Thompson-Crispi1, F. S. Schenkel1, F. Miglior2, M. Sargozaei3 and B. Mallard1, 1University of Guelph, Guelph, ON, Canada, 2Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 3Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 4The Semex Alliance, Guelph, ON, Canada

523 Search of Genomic Regions Influencing Faecal Egg Count, as an Indicator of Resistance to Gastrointestinal Nematode Infections, Based on the Analysis of the OvineSNP50 BeadChip.
M. Atlija1, J. J. Arranz2, M. Martinez-Valladares1 and B. Gutierrez-Gil3, 1Universidad de León, León, Spain, 2Instituto de Ganadería de Montaña, CSIC-ULE, León, Spain

524 Genome-Wide Association Analyses for Mastitis in Canadian Holsteins.
D. A. Grossi1, M. K. Abo-Ismail2, A. Koeck1, S. P. Miller1,4,5, P. Stothard1, G. S. Plastow4, F. Miglior1,6, S. S. Moore7, M. Sargozaei3,8 and F. S. Schenkel2, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Animal and Poultry Science, Damanhour University, Damanhour, Egypt, 3AgResearch, Invermay, Mosgiel, New Zealand, 4University of Alberta, Edmonton, AB, Canada, 5University of Queensland, Centre for Animal Science, QAAFI, St. Lucia, Australia, 6Canadian Dairy Network, Guelph, ON, Canada, 7The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 8The Semex Alliance, Guelph, ON, Canada
Goodness of Fit Comparisons among Five Bayesian Models in Genome-Wide Association of Tick Resistance in Brazilian Hereford and Brahford Beef Cattle.
B. P. Sollero1,2, C. G. Gomes3, V. M. Roso1, R. H. Higa1, M. J. Yokoo1, L. L. Cardoso4, A. R. Caetano2 and F. F. Cardoso4,
1Embrapa Southern Region Animal Husbandry, Bagé, Bagé, Brazil, 2Coordination for the Improvement of Higher Level Personnel (CAPES/PNPD), Brasilia, Brazil, 3Embrapa Southern Region Animal Husbandry, Bagé, Bagé, Brazil, 4Gensys Consultores Associados, Porto Alegre, Brazil, 5Embrapa Informática Agropecuária, Campinas, Brazil, 6Embrapa Southern Region Animal Husbandry, Bagé, Bagé, Brazil, 7Embrapa Genetic Resources and Biotecnology, Brasilia, Brazil

Genetic Sensitivity to Pathogenesis: Response to E. maxima Challenge in High and Low Antibody Selection Lines of Chickens.
R. M. Lewis1,2, P. B. Siegel3 and I. Kyriazakis4, 1University of Nebraska, Lincoln, 2Virginia Tech, Blacksburg, VA, 3Virginia Polytechnic Institute and State University, Blacksburg, 4Newcastle University, Newcastle upon Tyne, United Kingdom

Identification and Characterization of Candidate DNA Markers Associated with Primary Antibody Response to Sheep Red Blood Cells in Chicken.
T. Geng1, E. Smith2 and J. Xu2, 1Yangzhou University, Jiangsu, China, 2Virginia Tech, Blacksburg

No Association Between β-Defensin 103B (DEFB103B) Single Nucleotide Polymorphisms (SNPs) or Haplotypes and Staphylococcus aureus Mastitis in Holstein Cattle.
A. Mirabzadeh-Ardakani1,2, P. J. Griebel3 and S. M. Schmuck1, 1Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, 2Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, SK, Canada

Variation of Lactoferrin and Total Immunoglobulin G Concentrations in Colostrum from Canadian Holstein Dairy Cattle Classified as High, Average or Low Immune Responders.
K. Fleming1, K. A. Thompson-Crispi2, D. C. Hodgins3, F. Miglior3,2 and B. Mallard2,1, 1Dept Pathobiology, University of Guelph, Guelph, ON, Canada, 2Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 3Canadian Dairy Network, Guelph, ON, Canada

SSC4 WUR Genotype and Vaccination Effect on Nursery Pigs Co-infected with PRRSV and PCV2b.
M. S. Herrmann1,2, M. C. Niederwerder2, N. V. L. Serão1, M. A. Kerrigan1, R. R. R. Rowland3, J. K. Lumney4 and J. M. Dekkers1, 1Iowa State University, Ames, 2Kansas State University, Manhattan, 3USDA, ARS, BARC, APDL, 4Beltsville, MD

Analysis Of Biological Pathways Associated With Immune-capacity Traits In Pig.
T. Okamura1,2, Y. Takahagi1, T. Matsumoto1, H. Uenishi1, K. Suzuki2 and M. Satoh3, 1NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, 2Tohoku University, Aoba-ku, Sendai City, Japan, 3Nippon Meat Packers, Inc. R&D Center, Tsukuba, Japan, 4National Institute of Agrobiological Sciences, Tsukuba, Japan

Posters: Genetics of Trait Complexes - Feed Intake and Efficiency (Group 1)
Chair: Donagh P. Berry, Teagasc, Moorepark

Presentation Time: 9:30 AM – 10:00 AM

Feed Restriction and Subsequent Re-Alimentation Affect the Expression of Oxidative Phosphorylation Genes in Skeletal Muscle of Holstein Friesian Bulls.
K. Keogh1,2, D. A. Kenny1, A. K. Kelly1, P. Cormican1 and S. M. Waters2, 1School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, 2Teagasc Grange, Meehan, Ireland

Systems Genetics Investigations for Feed Intake, Feed Efficiency and Performance in Nellore (Bos indicus) Cattle.
M. H. A. Santana1, H. N. Kadarmideen1, S. D. Pant1, P. A. Alexandre1, G. A. Oliveira Junior1, R. C. Gomes1, Y. T. Utsunomiya1, H. H. Neves1, J. F. Garcia1, H. Fukumatsu1 and J. B. Sermano Ferraz2, 1NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 2Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 1University of Sao Paulo, Pirassununga, Brazil, 2CNPGC/EMBRAPA, Campo Grande, Brazil, 3UNESP Univ Estadual Paulista, Jaboticabal, Brazil, 4Faculdade de Ciências Agrárias e Veternínarias – UNESP, Jaboticabal, Brazil, 3UNESP Univ Estadual Paulista, Araçatuba, Brazil, 1University of Sao Paulo, Pirassununga, Brazil

Genetic Parameters and Accuracy of Recording Dry Matter Intake in First Parity Holstein-Friesian Cows.
C. I. V. Manzanilla Pech1,2,3, R. F. Veerkamp1,2, M. P. L. Calus1, J. E. Pryce4 and Y. de Haas5, 1Animal Breeding and Genomics...
Positional Candidate Genes for Residual Intake and Gain in Nellore Beef Cattle.
P. S. N. Oliveira1, A. A. S. Cesar2, M. L. Do Nascimento1, M. M. Souza1, R. R. Tullio1, D. P. Lanna1, G. B. Mourão5, J. M. Reecy6, D. J. Garrick3, M. A. Mudadi2, L. L. Coutinho1 and L. C. Almeida Regitano1, 1Federal University of São Carlos, São Carlos, Brazil, 2IZT/ESALQ/University of Sao Paulo, Piracicaba, Brazil, 3Universidade de São Paulo/Esalq, Piracicaba, Brazil, 4Embrapa Pecuária Sudeste, São Carlos, Brazil, 5University of São Paulo, Piracicaba, Brazil, 6Iowa State University, Ames, 7Embrapa Southeast Livestock, Sao Carlos, Brazil

Identification of Genomic Regions Associated with Lactation Performance in Yorkshire Sows.
D. M. Thekkoot1, R. A. Kemp2, M. F. Rothschild3, G. S. Plastow4 and J. C. M. Dekkers5, 1Iowa State University, Ames, 2Genesus Inc, Lethbridge, AB, Canada, 3University of Alberta, Edmonton, AB, Canada

Lifecyle Biological Efficiency of Mice Selected for Heat Loss.
A. Bhatnagar6 and M. K. Nielsen7, 1University of Nebraska, Lincoln, 2University of Nebraska, Lincoln

Efficiency of Weight and Retail Product Gain of Brahman, Boran, Belgian Blue, Piedmontese, and Hereford or Angus Sired Crossbred Steers to Alternative Endpoints.
L. V. Cundiff1, USDA-ARS, U.S. MARC, Clay Center, NE

Feed Intake Variation in Crossbred Lambs Supplemented with Spirulina.
B. W. Holman2 and A. E. Malau-Aduli2, 1NSW Dept of Primary Industries, COWRA, Australia, 2University of Tasmania, Hobart, Tasmania, Australia

P. A. Alexandre1, M. H. A. Santana, J. P. Eler, H. Fukumusu, G. A. Oliveira Jr. and J. B. S. Ferraz, NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil

Selection for Postweaning Weight and Residual Feed Intake in Nellore Cattle.
M. E. Z. Mercadante1, T. M. Ceacero, M. Morelli, J. N. S. G. Cyrillo, F. M. Monteiro and R. H. Branco, Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil

Genetic Modelling of Feed Intake in Rabbits.
I. David1, H. Garreau and J. Raesche, INRA UMR1388, F-31326 Castanet-Tolosan, France

Mapping of Quantitative Trait Loci Affecting Feed Efficiency in Laying Common Ducks.
C. Marie-Etancelin1, B. Basso1, K. Feve1, F. Vignoles1, P. Morganz1 and A. Vignali1, 1INRA UMR 1388 GenPhysE, Castanet-Tolosan, France, 2INRA UMR1388, F-31326 Castanet-Tolosan, France, 3INRA UE 89 UEFPG, Benquet, France

Estimation and Validation of Indirect Genetic Effects for Average Daily Gain in Two Purebread Sire Lines.
N. Duijvesteijn1, E. F. Knol1 and P. Bijma1, 1TOPIGS Research Center IPG B.V., Beuningen, Netherlands, 2TOPIGS Research Center IPG, Beuningen, Netherlands, 3Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Estimation of Genetic Parameters for Growth and Feed Efficiency Traits in Two Commercial Lines.
H. Garreau1, INRA, Castanet-Tolosan, France

Variability of Organic Matter Digestibility within Lactation and across Cows based on NIRS Scans from Fecal Samples.
T. Mehto2, M. Rinne1, L. Nyholm2, A. Sairanen1, T. Pirkkänen1, E. A. Mäntysaari2 and M. H. Lindauer1, 1MTT Agrifood Research Finland, Jokioinen, Finland, 2Valio Ltd., Helsinki, Finland, 3MTT Agrifood Research Finland, Maaninka, Finland

Genetic Basis of Digestibility in Nursery Pigs under PRRSV Infection.
L. C. Hardie1, N. V. L. Serão1, R. K. R. Rowland2, J. F. Patience1, J. C. M. Dekkers1 and N. K. Gabler1, 1Iowa State University, Ames, 2Kansas State University, Manhattan
Posters: Genetics of Trait Complexes - Disease Resistance (Group 2)
Chair: Larry A. Kuehn, USDA, ARS, U. S. Meat Animal Research Center
Presentation Time: 10:00 AM – 10:30 AM

532 Predicting MHC Haplotypes from High-Density SNP Genotypes in Pigs.
J. Dunkelberger, S. Ho, H. Hess, N. V. L. Serão, J. K. Lunney and J. C. M. Dekkers, Iowa State University, Ames, Gift of Life Michigan, Ann Arbor, MI, USDA, ARS, BARC, APDL, Beltsville, MD

533 The Homology Modeling Study of the Bovine ì-calpain Inhibitor-Binding Domains.
H. H. Choi, Animal Genome & Bioinformatics Division, National Institute of Animal Science, Suwon, South Korea

534 Genetic and Non-Genetic Indirect Effects for Bite Mark Traits in Group Housed Mink.
S. W. Alemu, P. Berg, L. Janss, S. H. Moller, J. C. M. Dekkers, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Animal Breeding and Genomics Center, Wageningen University, Wageningen, Netherlands, Nordic Genetic Resource Centre, As, Norway, Department of Animal Science Epidemiology and management, Aarhus University, Tjele, Denmark, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

535 Genetic Relationship of Eye Infection and Grading Traits in Finnish Blue Fox.
R. Kempe and I. Strandén, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

536 Genetic Analysis of Elevated Mastitis Risk Based on Mastitis Indicator Data.
L. P. Sørensen, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

537 Divergent Transcriptome Signature in Blood of Cows Exposed to Vaccination Pre- or Postpartum.
R. Weikard, W. Demasius, F. Hadlich and C. Kühn, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany

538 Using Transcriptome-Wide Analysis of Constitutive Hepatic Gene Expression to Identify Genetic Defects in Porcine Innate Immunity.
H. N. Snyman, J. D. Hammermueller, K. J. Jagel, J. Squires, A. M. Hayes and B. N. Lillie, Department of Pathobiology, University of Guelph, Guelph, ON, Canada, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada

539 Genetic Parameters of Immune Traits in Dairy Cattle.
S. J. Denholm, T. N. McNeilly, G. Banos, M. P. Coffey, G. C. Russell, A. Bagnall, M. C. Mitchell and E. Wall, Scotland's Rural College, Edinburgh, United Kingdom, Moredun Research Institute, Edinburgh, United Kingdom, SRUC, Edinburgh, United Kingdom

540 Epigenetic Differences in IFN and IL-4 Promoter Regions of Dairy Cows Identified With Type 1 and 2 Immune Response Bias.
M. A. Paibomesai and B. Mallard, University of Guelph, Guelph, ON, Canada, Dept Pathobiology, University of Guelph, Guelph, ON, Canada, Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

541 Construction of a Reporter Mycobacterium avium subsp. paratuberculosis (Map) Strain and Infection of Monocyte-Derived Macrophages from Cows Homozygous for SNP -298 A> G in the Macrophage Migration Inhibitory Factor (MIF) Gene.
Q. You, University of Guelph, Guelph, ON, Canada

542 Genetics of Susceptibility to Bovine Viral Diarrhea, Infectious Bovine Respiratory Disease, and Liver Fluke in Cattle.
Genetic Parameters and Effects for a Major QTL of Piglets Experimentally Infected with a Second Porcine Reproductive and Respiratory Syndrome Virus.
A. Hess1, N. Boddicker1, R. R. Rowland1, J. K. Lunnemy2, G. S. Plastow3 and J. C. M. Dekkers4,1Iowa State University, Ames, 2Genoves, Oakville, MB, Canada, 3Kansas State University, Manhattan, 4USDA, ARS, BARC, APDL, Beltsville, MD, 5University of Alberta, Edmonton, AB, Canada

Identification and Mapping of a Bovine MHC Classical Class I Locus Missing from the Reference Assembly.
E. D. Downey1,2, R. D. Schnabel1, J. F. Taylor’ and L. C. Skow1,1Texas A&M University, College Station, 2University of Missouri, Columbia

Transcriptomic Analysis of Lung from Pigs Exhibiting Differential Susceptibility to Influenza.
J. M. Wilkinson1, G. Foxcroft2, G. Plastow1 and J. C. S. Harding1,1University of Alberta, Edmonton, AB, Canada, 2University of Saskatchewan, Saskatoon, SK, Canada

Genetic Parameters of Tick-Infestation on Lambs of the Norwegian White Sheep Breed.
L. Grøva1, Bioforsk, Tingvoll, Norway

Estimation of (Co)variance Components for Body Weight and Survival in the Presence of a White Spot Syndrome Virus (WSSV) Natural Outbreak in the Pacific White Shrimp Penaeus (Litopenaeus) vannamei.
A. Caballero-Zamora1, H. H. Montaldo1, G. R. Campos-Montes1,2, E. Cienfuegos-Rivas1, A. Martínez-Ortega2 and H. Castillo-Juárez1,1Universidad Autónoma Metropolitana, DF, Mexico, 2Universidad Nacional Autónoma de México, DF, Mexico, 3Maricultura del Pacífico, Mazatlán, Mexico, 4Universidad Autónoma de Tamaulipas, Ciudad Victoria, Tamaulipas, Mexico, 5Maricultura del Pacífico S.A. de C.V., México, Mexico

Genetic Parameters and Effects for a Major QTL of Piglets Experimentally Infected with a Second Porcine Reproductive and Respiratory Syndrome Virus.
A. Hess1, N. Boddicker1, R. R. Rowland1, J. K. Lunnemy2, G. S. Plastow3 and J. C. M. Dekkers4,1Iowa State University, Ames, 2Genoves, Oakville, MB, Canada, 3Kansas State University, Manhattan, 4USDA, ARS, BARC, APDL, Beltsville, MD, 5University of Alberta, Edmonton, AB, Canada

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E. D. Downey1,2, R. D. Schnabel1, J. F. Taylor’ and L. C. Skow1,1Texas A&M University, College Station, 2University of Missouri, Columbia

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J. M. Wilkinson1, G. Foxcroft2, G. Plastow1 and J. C. S. Harding1,1University of Alberta, Edmonton, AB, Canada, 2University of Saskatchewan, Saskatoon, SK, Canada

Genetic Parameters of Tick-Infestation on Lambs of the Norwegian White Sheep Breed.
L. Grøva1, Bioforsk, Tingvoll, Norway

Estimation of (Co)variance Components for Body Weight and Survival in the Presence of a White Spot Syndrome Virus (WSSV) Natural Outbreak in the Pacific White Shrimp Penaeus (Litopenaeus) vannamei.
A. Caballero-Zamora1, H. H. Montaldo1, G. R. Campos-Montes1,2, E. Cienfuegos-Rivas1, A. Martínez-Ortega2 and H. Castillo-Juárez1,1Universidad Autónoma Metropolitana, DF, Mexico, 2Universidad Nacional Autónoma de México, DF, Mexico, 3Maricultura del Pacífico, Mazatlán, Mexico, 4Universidad Autónoma de Tamaulipas, Ciudad Victoria, Tamaulipas, Mexico, 5Maricultura del Pacífico S.A. de C.V., México, Mexico

Posters: Genetics of Trait Complexes - Feed Intake and Efficiency (Group 2)
Chair: Donagh P. Berry, Teagasc, Moorepark
Presentation Time: 10:00 AM – 10:30 AM

Estimation of Additive Genetic and Maternal Genetic Effects in Mice Selected for High and Low Oxygen Consumption.
K. Suzuki1, Tohoku University, Aoba-ku, Sendai City, Japan

Genetic Structure of Quantitative Traits for Effective Feeding during the Growing to Finishing Phases in Landrace Pigs.
M. Taniguchi1, A. Arakawa1, K. Hirose2, S. Nakado1, T. Matsamoto1, A. Ishida1, T. Ito1, K. Fukawa2 and S. Mikawa1,1National Institute of Agrobiological Sciences, Tsukuba, Japan, 2Zen-Noh Central Research Institute for Feed and Livestock, Kamishihoro, Japan, 3Zen-Noh Livestock Co. Ltd, Shizukuishi, Japan, 4NARO Institute of Livestock and Grassland Science, Tsukuba, Japan

Preliminary Investigation into Genetic Parameters for Feedlot Traits of Angus Cattle in South Africa.
J. Hendriks1, Agricultural Research Council, Pretoria, South Africa; University of the Free State, Bloemfontein, South Africa

Whole Genome Characterization and Associations Studies in Two Divergent Pig Lines Selected on Residual Feed Intake.
J. Riquet1, Y. Labrunet, K. Feve1, Y. Billon2 and H. Gilbert1,1INRA UMR1388, F-31326 Castanet-Tolosan, France, 2INRA UE1372, F-17700 Surgères, France

Prediction of Body Weight of Primiparous Dairy Cows Throughout Lactation.
M. L. Vanrobays1, J. Vandenhols1,2, H. Hammami1 and N. Gengler1,1University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium, 2National Fund for Scientific Research, Brussels, Belgium

Variation among Dairy Cows in Rumen Liquid Fermentation Characteristics.
J. Lassen1, P. Lovendahl2, L. Kristensen3, Z. Zhu4, O. Højberg5, M. Poulsen6 and S. J. Noel7,1Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, 2Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 4Department of Animal Science, Aarhus University, Tjele, Denmark, 5Dept. Animal Science, Aarhus University, Tjele, Denmark, 6Dept. Animal Science, aarhus University, Tjele, Denmark
The Value of Group Records in Predicting Breeding Values for Individual Feed Intake in Pigs.
J. P. Sanchez, M. Piles, M. Tulsaw, J. Reixa, and R. Quadranni, IRTA, Caldes de Montbui, Spain, 1IRTA, Monells, Spain, 2Selección Batallé, Riudarenes, Spain

Genetic Parameters for Dry Matter Intake at Different Lactation Stages among Primiparous Holstein, Jersey and Red Cows.
B. Lj, Swedish University of Agricultural Sciences, Uppsala, Sweden

Genetic Variation in Efficiency to Deposit Lean Meat and Fat in Norwegian Landrace Pigs.
K. H. Martinsen, T. Ødegård, D. Olsen, and T. H. E. Meuwissen, Norwegian University of Life Sciences, Ås, Norway, AquaGen, Ås, Norway, Norsvin, Ås, Norway

Residual Feed Intake in Beef Cattle; Genes, Metabolites and Beyond.
B. K. Karisa, J. M. Thomson, and G. S. Plastow, University of Alberta, Edmonton, AB, Canada, Montana State University, Bozeman, MT

Genomic Selection for Feed Intake and Weight Gain Assuming Different Prior Distributions in Nellore Beef Cattle.
F. M. Rezende, M. H. A. Santana, G. A. Oliveira Junior, F. Baldi, A. S. M. Cesar, E. C. Mattos, B. S. Ferraz, and N. Ibáñez-Escriche, Federal University of Uberlandia, Patos de Minas, Brazil, NAP-GMABT/FZEAG/University of Sao Paulo, Pirassununga, Brazil, Universidade Estadual Paulista "Júlio de Mesquita Filho" - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, University of Sao Paulo, Piracicaba, Brazil, IRTA - Cataluña, Lleida, Spain

Rumen Microbial Taxa and By-products Associated with Feed Efficiency in Sheep.
K. M. Cammack, M. Ellison, G. C. Conant, W. R. Lamberson, and K. J. Austin, Department of Animal Science, University of Wyoming, Laramie, WY, University of Wyoming, Laramie, WY, University of Missouri, Columbia

Genetics of Alternative Definitions of Feed Efficiency in Grazing Lactating Dairy Cows.

Functional Cluster Analysis of Genome Wide Associations for Energy Balance for Cows in Experimental Herds in Four European Countries.
A. Tolkamp, E. Wall, E. Strandberg, and R. F. Veerkamp, Scotland’s Rural College (SRUC), Edinburgh, United Kingdom, SRUC, Edinburgh, United Kingdom, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Increased Fat EBVs Reduce Need for Supplemental Feeding.
W. S. Pitchford and S. F. Walkom, School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy SA 5351, Australia

Establishing the Relationship Between Feed Efficiency and Maternal Traits in New Zealand Sheep.
P. L. Johnson, AgResearch, Mosgiel, New Zealand

Posters: Genetics of Trait Complexes - Disease Resistance (Group 3)
Chair: Larry A. Kuehn, USDA, ARS, U. S. Meat Animal Research Center
Presentation Time: 3:00 PM – 3:30 PM

L. C. Wagter-Lesperance, D. C. Hodgens, M. Emam, M. A. Paihomesai, and B. Mallard, University of Guelph, Guelph, ON, Canada, Dept Pathobiology, University of Guelph, Guelph, ON, Canada, Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada
Major Histocompatibility Complex Plays a Role in Survival Kinetics of Chicken infected by Marek’s Disease Virus.
M. H. Pinard-van der Laan, B. Bed‘Hom, N. Bruneau, O. Chazara and B. Besbes, INRA, UMR1313 GABI, Jouy-en-Josas, France, INRA UMR1313 GABI, Jouy-en-Josas, France, Department of Pathology, University of Cambridge, Cambridge, United Kingdom, FAO, Roma, Italy

Predicting Susceptibility to Johne’s Disease in New Zealand Dairy Cattle.
R. G. Sherlock, Livestock Improvement Corporation, Hamilton, New Zealand

Genetic Parameters for Natural Antibodies in a Chicken Layer Line.
T. V. Berghof, J. J. van der Poel, J. A. Arts, van Engelen, H. K. Parmentier and H. Bovenhuis, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Adaptation Physiology Group, Wageningen University, Wageningen, Netherlands

Genomic Centre, Wageningen University, Wageningen, Netherlands, T. V. Berghof, J. J. van der Poel, J. A. Arts, van Engelen, H. K. Parmentier and H. Bovenhuis, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Adaptation Physiology Group, Wageningen University, Wageningen, Netherlands

Posters: Genetics of Trait Complexes - Reproduction (Group 1)
Chair: Jennie E. Pryce, Department of Environment and Primary Industries
Presentation Time: 3:00 PM – 3:30 PM

Polymorphisms in TOX and NCOA2 Genes and their Associations with Reproductive Traits in Cattle.
G. M. de Camargo, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboricabal, Brazil

Genetic Parameters of Atypical Progesterone Profiles in Holstein-Friesian Cows using Data from Four European Experimental Research Herds.
S. Nyman, K. Johansson, D. J. D. Koning, D. P. Berry, R. F. Veerkamp, E. Wall and B. Berglund, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, Västra Sverige, Uppsala, Sweden, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, SRUC, Edinburgh, United Kingdom

Bayesian Estimates of Genetic Parameters for Reproductive Traits in Nellore Cows Raised on Pasture in the Tropics.
F. B. Lopez, C. U. Magnabosco, M. M. S. Mamede, L. C. Moreira, F. M. Souza, M. G. Narcizo, R. B. Lóbo, G. J. M. Rosa and R. D. Sainz, Embrapa Cerrados, Brasília, Brazil, Federal University of Goiás, Goiânia, Brazil, Embrapa, Santo Antônio de Goiás, Brazil, Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, University of Wisconsin, Madison

Assessment of Genetic and Non-Genetic Factors Related to Survival Probabilities of Farmed White-Tailed Deer Neonates.
M. Parra-Bracamonte, Centro De Biotecnologia Genomica - Instituto Politecnico Nacional, Reynosa, Mexico

Estrus Traits Derived from Activity Measurements are Heritable and Closely Related to Conventional Estrus Traits.
A. Ismael, M. Kargo, A. Fogh, E. Strandberg and P. Lovendahl, Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Knowledge Center for Agriculture, Aarhus, Denmark

Genome-Wide Scan for Reproductive Traits of Beef Heifers using High Density SNP Panels.
A. Michenet, F. Phocas, R. Saintilan and E. Venot, MIDATEST, Soual, France, INRA, UMR1313 GABI, Jouy-en-Josas, France, INRA UMR 1313 GABI, Jouy-en-Josas, France, University Complutense of Madrid, Madrid, Spain

Effect of Selection for Residual Variance of Litter Size on Hematology Parameters as Immunology Indicators in Rabbits.
M. J. Argente, M. D. L. L. García and A. Blasco, Universidad Miguel Hernández de Elche, Orihuela, Spain, Universidad Politecnica De Valencia, Valencia, Spain

Genetic Control of the Environmental Variance for Birth Weight in a Divergent Selection Experiment in Mice.
N. Formoso-Rafferty, J. P. Gutiérrez García, O. Lizarraza, M. Pérez-Cabal and I. Cervantes, University Complutense of Madrid, Madrid, Spain

Additive Genetic, Non-additive Genetic and Permanent Environmental Effects for Female Reproductive Performance in Seasonal Calving Dairy Cows.
Genetic Control of Ovulation Rate in Maine-Anjou Cattle.
A. Vinet1, J. L. Touze2, J. Sapa1, L. Bodin3, S. Fabre1 and F. Phocas1
1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2INRA, UMR0085 PRC, Nouzilly, France, 3INRA, UMR1388 GenPhySE, Castanet-Tolosan, France

Impact of Long Term Selection on Reproductive Efficiency in Linebred Rambouillet.
J. D. Swartz, C. J. Yeoman, J. G. Berardinelli and J. M. Thomson*
Montana State University, Bozeman, MT

Genome-Wide Association of Age at First Calving in Nelore Cattle using Phenotypes from Genotyped and Ungenotyped Animals.
T. P. de Melo1, R. Carvalheiro2, L. Takada1, F. S. B. Rey1, H. N. de Oliveira1, M. M. Dias1 and L. G. Albuquerque3
1Sao Paulo State University (UNESP), Jaboticabal, Brazil, 2Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 3State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Posters: Swine Breeding (Group 1)
Chair: Graham S. Plastow, University of Alberta
Presentation Time: 3:00 PM – 3:30 PM

Assessment of Genetic Variation among Domestic and Wild Pigs (Sus scrofa) across its Range: An Improved Phylogeography to Understand the Pig Domestication.
A. Kumar1 and S. K. Gupta2
1Wildlife Institute of India, Dehradun, India, Dehradun, India, 2Wildlife Institute of India, Dehradun, India, Dehra Dun, India

Osteochondrosis in Duroc Pigs Scored by Computed Tomography; Heritabilities based on Genomic and Pedigree Relationship Matrices.
T. Aasmundstad1,2, E. Grindflek1, Nordbø1, J. Kongsro1 and O. Vangen2
1Norsvin, Hamar, Norway, 2Norwegian University of Life Sciences, Ås, Norway

Gene Copy Number Detection of AADAT and ZNF622 across Diverse Pig Breeds.
H. Wang*, China Agricultural University, Beijing, China

Genetic Parameter Estimates for Reproductive, Growth and Longevity Traits in Alentejano Pigs Raised Extensively.
L. T. Gama1, F. David2 and H. Paixim3
1FMV - University of Lisbon, Lisbon, Portugal, 2ACEPA, Évora, Portugal

Validation of Repeatability Models in Genetic Evaluation of Reproductive Traits in Pigs.
S. Andonov1, V. Vukovic1, A. Uzunov1 and A. Mijakova Murdzeva2
1Faculty of Agricultural Sciences and Food, Skopje, Macedonia, 2Agria Grup, Veles, Macedonia

Identification of Signatures of Selection for Intramuscular Fat in Two Duroc Populations.
E. S. Kim1, R. Ros-Freixedes2, R. N. Pena2, T. J. Baas1, J. Estany1 and M. F. Rothschild4
1Iowa State University, Ames, 2Universitat de Lleida, Lleida, Spain

Analysis of Single Nucleotide Polymorphisms (SNPs) in Stearoyl-CoA Desaturase (SCD) Gene Promoter Region of Six Pig Breeds.
A. Hasegawa1, D. Taniguchi2, I. Matsuno1 and Y. Mizoguchi1
1Meiji University, Kawasaki, Japan, 2Meiji University, kawasaki, Japan

Genome-Wide Association Studies on Piglet Splay leg Syndrome.
1Huazhong Agricultural University, Wuhan, China, 2University of Alberta, Edmonton, AB, Canada, 3Wuhan Tianzhong Stock Corporation, Wuhan, China
Genome-Wide Association Studies (GWAS) Identify a QTL Close to PRKAG3 Affecting Meat pH and Colour in Crossbred Commercial Pig Lines.
C. Zhang¹, Z. Wang¹, H. Bruce², R. A. Kemp³, P. Charagu⁴, Y. Miar⁵ and G. S. Plastow⁶, ¹University of Alberta, Edmonton, AB, Canada, ²Genesis Inc, Lethbridge, AB, Canada, ³Hypor Inc, Regina, SK, Canada

Strategies to Implement Genomic Selection in Pig Breeding using Very Low Marker Density.
P. Stratzi¹, R. Wellmann² and J. Bennewitz², ¹Institute of Animal Husbandry and Breeding, University Hohenheim, Hohenheim, Germany, ²Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

Reliability of Genomic Selection of Reproduction Traits in Finnish Yorkshire Pig Breed.
P. Uimari¹, M. L. Sevon², and T. Serenius², ¹University of Helsinki, Helsinki, Finland, ²MTT Agrifood Research Finland, Jokioinen, Finland, ³Figen Ltd, Seinäjoki, Finland

Crossbreeding Effects and Genetic Parameters on Piglet Survival from Three Iberian Strains.
N. Ibáñez-Escriche¹, L. Varona², E. Magallón¹ and J. L. Noguera¹, ¹IRTA, Lleida, Spain, ²Universidad de Zaragoza, Zaragoza, Spain, ³Inga Food, Zaragoza, Spain

Genetic and Epigenetic Analysis of FUT1 (fucosyltransferase 1) Transgenic Cloned Yorkshire Piglets.
Y. Yu¹ and Y. Dong², ¹College of Animal Science and Technology, China Agricultural University, Beijing, China, ²China Agricultural University, Beijing, China

Genome-Wide Association Study for Intramuscular Fat Content and Composition in Duroc Pigs.
R. Ros-Fréixedes¹, S. Gol³, R. N. Pena¹, M. Tor¹, J. C. M. Dekkers² and J. Estany², ¹Universitat de Lleida, Lleida, Spain, ²Iowa State University, Ames

Genetic Correlations of Intramuscular Fat and Oleic Acid Content among Muscles and with Subcutaneous Fat in Duroc Pigs.
R. Ros-Fréixedes¹, E. Henríquez¹, J. Reixach², M. Tor¹ and J. Estany², ¹Universitat de Lleida, Lleida, Spain, ²Selección Batallé, Riudarenes, Spain

Posters: Genetics of Trait Complexes - Reproduction (Group 2)
Chair: Jennie E. Pryce, Department of Environment and Primary Industries
Presentation Time: 3:30 PM – 4:00 PM

Genetic Correlations among Detailed Reproductive Traits, Traditional Reproductive Traits and Milk Production in Irish Dairy Cows.
T. R. Carthy¹, D. P. Berry², R. Evans¹ and D. P. Ryan⁴, ¹Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland, ²Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ³Irish Cattle Breeding Federation, Co.Cork, Ireland, ⁴Reprodoc Ltd, Fermoy, Cork, Ireland

Effects of the FeCL Major Gene on Mean and Variance of Litter Size in the Lacanue Meat Sheep Population.
L. Bodin¹, P. M. Martin¹ and J. Raoul², ¹INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, ²Idéle, Castanet tolosan, France

Single Nucleotide Polymorphisms in Candidate Genes Related to Daughter Pregnancy Rate in Holstein Cows.
M. S. Ortega¹, A. C. Denicol¹, D. J. Null⁴, J. B. Cole² and P. J. Hansen³, ¹Department of Animal Sciences, University of Florida, Gainesville, ²Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD

The Fertility of South African Holstein and Jersey Heifers.
C. J. Muller², Directorate Animal Sciences, Elsenburg, South Africa

Follicular Dynamics and Uterine Environment Associations with Production and Performance Traits in Irish Dairy Cows.
A. Fitzgerald¹, D. P. Berry² and D. P. Ryan¹, ¹Teagasc, Fermoy, Ireland, ²Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ³Reprodoc Ltd, Fermoy, Cork, Ireland
642  
**Prediction of Genomic Breeding Values for Reproductive Traits in Nellore Heifers.**  
R. B. Costa¹, J. D. P. S. Diaz², N. Iraño³, L. Takada¹, R. Carvalheiro¹, F. Baldi¹, H. N. Oliveira¹, H. Tonhati¹ and L. G. Albuquerque¹.  
¹São Paulo State University (UNESP), Jaboticabal, Brazil, ²Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, ³State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

643  
**Genome-Wide Association Study of First Service Conception Rate in Brangus Heifers using Probit, Robit and Logit Models.**  
S. O. Peters¹, K. Kizilkaya², D. J. Garrick³, R. L. Fernando⁴, J. M. Reecy⁵, I. G. Imumonir⁶ and M. G. Thomas⁷, ¹Berry College, Mount Berry, GA, ²Adnan Menderes University, Aydın, Turkey, ³Iowa State University, Ames, ⁴Cornell University, Ithaca, NY, ⁵Colorado State University, Department of Animal Sciences, Fort Collins

644  
**Testes Size as Predictor for Semen Production of Boars and Relation to Female Reproductive Traits.**  
F. Ytournel⁸, E. Brunet⁹, P. Derks⁹ and A. Huisman⁹, ¹Hypor, Boxmeer, Netherlands, ²France Gènes, Saint Gérand, France, ³Hendrix Genetics, Boxmeer, Netherlands

645  
**Genome-Wide Association Study on Long-Yearling Scrotal Circumference in Canchim Cattle.**  
M. E. Buzanska¹, D. A. Grossi², R. V. Ventura³, T. C. S. Chud³, I. Urbina³, S. Meirelles³, F. B. Mokry³, F. S. Schenkel³, L. C. A. Regitano³, M. M. D. Alencar³ and D. P. Munari³. ¹Universidade Estadual Paulista Júlio de Mesquita, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Ciências Exatas, Jaboticabal-SP, Brazil, ²Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³Univ Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil

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**Genetic Parameters of Days Open and Protein Yield Across Lactations for the Uruguayan Holstein Population.**  
N. Frioni, Facultad de Agronomía, Uruguay, Montevideo, Uruguay

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**Genome Wide Scan for Age at First Calving in Gyr Dairy Cattle.**  
A. T. H. Utsunomiya¹, S. A. Boison³, D. J. A. dos Santos³, Y. T. Utsunomiya¹, M. A. Machado³, R. S. Verneque¹, J. Sölkner², J. F. Garcia¹, R. da Fonseca⁸ and M. V. G. B. da Silva⁸, ¹UNESP Univ Estadual Paulista, Jaboticabal, Brazil, ²University of Natural Resources and Life Sciences, Vienna, Austria, ³State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, ⁴Embrapa Dairy Cattle, Juiz de Fora, Brazil, ⁵UNESP Univ Estadual Paulista, Araçatuba, Brazil, ⁶São Paulo State University “Júlio de Mesquita Filho”, Dracena, Brazil

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**Genome Wide Association Study for Calving Interval in Gyr Dairy Cattle.**  
M. A. Machado¹, A. T. H. Utsunomiya¹, S. A. Boison³, D. J. A. dos Santos³, Y. T. Utsunomiya², R. da Fonseca³, J. Sölkner², J. F. Garcia¹, R. S. Verneque¹ and M. V. G. B. da Silva³, ¹Embrapa Dairy Cattle, Juiz de Fora, Brazil, ²UNESP Univ Estadual Paulista, Jaboticabal, Brazil, ³University of Natural Resources and Life Sciences, Vienna, Austria, ⁴State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, ⁵São Paulo State University “Júlio de Mesquita Filho”, Dracena, Brazil, ⁶UNESP Univ Estadual Paulista, Araçatuba, Brazil

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**Mapping of a Major Gene for Bovine Ovulation Rate.**  
B. W. Kirkpatrick¹ and C. A. Morris², ¹University of Wisconsin, Madison, ²AgResearch, Ruakura, New Zealand

650  
**Use of High Density SNP Genotypes to Determine the Breed Composition of Cross Bred Dairy Cattle in Smallholder Farms: Assessment of Reproductive and Health Performance.**  
F. D. N. Mujibi¹, J. M. Ojango¹, J. Rao¹, A. Kihara¹, A. G. Marete¹, J. Baltenweck¹, J. Poole¹, E. O. Rege¹, C. Gondro¹, S. Weerasinghe¹, J. Gibson¹, A. M. Okeyo¹ and T. Karanja¹. ¹International Livestock Research Institute, Nairobi, Kenya, ²International Livestock Research Institute (ILRI), Nairobi, Kenya, ³PICO- Eastern Africa, Nairobi, Kenya, ⁴University of New England, Armidale, Australia, ⁵Aga Khan Foundation, Geneva, Switzerland

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**Posters: Swine Breeding (Group 2)**  
Chair: Graham S. Plastow, University of Alberta

Presentation Time: 3:30 PM – 4:00 PM
Genetic Parameters for Individual Birth Weight, Weaning Weight and Final Weight of Crossbred Pigs from Piétrain Boars.
M. Dafrasne*, University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium; Fonds pour la formation à la Recherche dans l'Industrie et dans l'Agriculture, Brussels, Belgium

Does Direct Genetic Selection for Production Traits Degrade Maternal Ability in Landrace Pigs?
B. Dube*, A. Davids and K. Dzama, University of Stellenbosch, Stellenbosch, South Africa

Candidate Genes Network for Number of Teats in Pigs.
S. E. Guimaraes¹, L. L. Verardo², F. F. Silva¹, M. J. Kelly¹, M. S. Lopes¹, J. W. M. Bastiaansen¹, P. S. Lopes¹ and E. F. Knol¹,
¹Universidade Federal de Viçosa, Viçosa, Brazil, ²UNIVERSIDADE FEDERAL DE VICOSA, vicosa, Brazil, ³The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia, ⁴Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ⁵TOPIGS Research Center IPG BV, Beuningen, Netherlands

Tracking Footprints of an Experiment of Selection in Iberian Pigs.
M. C. Rodríguez*, Y. Núñez, A. Fernandez, A. Fernandez, C. Barragan and L. Silió, INIA, Madrid, Spain

Genomic Selection in Pig Breeding for Improved Meat Quality.
E. Gjerløv-Enger*, Nordfø and E. Grindflek, Norsvin, Hamar, Norway

A Genome-Wide Scan Reveals Novel Loci Associated with Liability to Scrotal and Inguinal Hernia in Large White Pigs.
C. Sevillano¹, M. S. Lopes², J. W. M. Bastiaansen² and B. Harlizius³, ¹TOPIGS Research Center IPG BV, Beuningen, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ³TOPIGS Research Center IPG BV, Beuningen, Netherlands

Effectiveness of genomic prediction of boar taint components in different Pietrain sired breeding populations.
C. Grosse-Brinkhaus, C. Neuhoff, K. Schellander, C. Loof and E. Tholen*, Institute of animal science, University of Bonn, Bonn, Germany

Estimation of Ancient and Recent Effective Population Size from Linkage Disequilibrium in a Closed Herd of Iberian Pigs.
M. Saura¹, J. A. Woolliams², A. Tenesa³ and B. Villanueva¹, ¹INIA, Madrid, Spain, ²The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ³The Roslin Institute and R(D)SVS & The MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine, University of Edinburgh, Midlothian, United Kingdom

Genome-Wide Association Analysis with Correlated Traits in Duroc Pigs: Growth, Feed Intake and Ultrasound Backfat Thickness.
S. Jiao¹, C. Maltecca¹, K. A. Gray², Y. Huang¹ and J. P. Cassady¹, ¹North Carolina State University, Raleigh, ²Smithfield Premium Genetics, Rose Hill, NC, ³South Dakota State University, Brookings

Long-Term Selection for Litter Size Results in Significant Shifts in Allelic Frequency in Regions Involved in Reproductive Processes.
M. D. Trenhalle¹, J. L. Petersen², K. L. Luco³, S. D. Kachman¹, R. K. Johnson¹ and D. C. Ciobanu³, ¹University of Nebraska, Lincoln, ²University of Minnesota, Saint Paul

Identification of Genomic Regions Associated with Swine Growth.
N. J. Boddicker¹, P. Mwansa² and R. A. Kemp³, ¹Genesus Inc, Oakville, MB, Canada, ²Genesus Inc, Lethbridge, AB, Canada

Genetic Association between Leg Conformation in Young Pigs and Longevity of Yorkshire Sows.
H. T. Le¹, K. Nilsson¹, E. Norberg¹ and N. Lundheim¹, ¹Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, ²Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, ³Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

K. Ishii² and M. Satoh, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan
Changes in Connectedness among Herds and Birth Years of Duroc Pigs in Korea.

Friday, August 22, 2014

Posters: Adaptation and Selection in Harsh Environments (Group 1)
Chair: Alessandra Stella, Fondazione Parco Tecnologico Padano

Presentation Time: 9:30 AM – 10:00 AM

411 Estimation of Breeding Values by Different Animal Models for Selection of Sires in Crossbred Cattle.
C. V. Singh*, G.B. Pant University of Agriculture & Technology, Pantnagar, India

412 Estimation Of Slaughter Parameters For Ethiopian Arsi Cattle At Adama City Abattoir.
A. Gebeeyehu*, Adami Tulu Agricultural Research Center, Batu (Ziway), Ethiopia

413 Genetic Analyses of Conformation Traits and their Relationships with Reproductive Traits in Holstein Cows.
M. Rabbani khourasgani, S. Ansari Mahyari* and M. A. Edriss, Department of Animal Science, College of Agriculture, Isfahan University of Technology, Isfahan, Iran

414 Genotype X Environment Interaction for Milk Yield in Buffaloes.
N. A. Hurtado-Lugo*, F. Araujo Neto, F. Borba, C. E. Enriquez-Valencia, V. Roldan and H. Tonhati, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

415 MITF Gene Locus is Associated with Coat Color Variation of Ethiopian Cattle Populations Adapted to Different Altitude Environments.
K. S. Kim* and Z. Edea, Chungbuk National University, Cheongju, South Korea

416 Direct and Maternal Additive Effects and Heterosis in Prolificacy Weaning Traits in Rabbits.
Y. García*, Instituto de Animal Science, San José, Cuba

417 Direct and Maternal Additive Effects and Heterosis in Productivity Traits at Weaning in Rabbits.
R. E. Ponce de León*, Instituto de Animal Science, San José de las Lajas, Cuba

418 Selection for Economic Feed Conversion Efficiency of Dairy Cattle under Co-operative Dairy Conditions in the North of Argentina.
R. Gagliardi* and N. Lopez-Villalobos*, 1Cooperativa Tambera Nueva Alpina Ltda., Colonia Alpina, Argentina, 2Massey University, Palmerston North, New Zealand

419 The Complex and Gender Differentiated Objectives of Livestock Keeping for Somali Pastoralists.

420 Iberian Pig Selection in Two Different Open-Air Production Systems: GxE Interactions for Premium Cuts Percentage and Intramuscular Fat Content.
J. M. García-Casco*, M. C. Rodríguez and L. Silió*, 1INIA, Zafra, Spain, 2INIA, Madrid, Spain

A. Hamrouni*, M. Djemali* and S. Bendhiaf*, 1Institut National Agronomique de Tunisie, Rude de kornich Chot El Salem Gabès, Tunisie, 2Carthage University-INAT-TUNISIA, Laboratoire des Ressources Animales et Alimentaires, 1082 Cité Mahrajène, Tunisie, Tunisie, 3Institut National de Recherche Agronomique de Tunis, Tunis, Tunisia

422 Influences of Environmental Describer for Detect Genotype by Environmental Interaction in Cuban Zebu Population.
Y. Rodríguez*, Institute of Animal Science, San José de las Lajas, Cuba

423 Sexually Dimorphic Environmental Sensitivity In Beef Cattle Studied By Principal Component Analyses In A Developmental Reaction Norm Model.
N. T. Pegolo\(^1\), R. B. Lôbo\(^2\) and H. N. de Oliveira\(^3\), \(^1\)Federal Institute of Education, Science and Technology of São Paulo, Avaré, Brazil, \(^2\)Ribeirão Preto Medical School, USP, Ribeirão Preto, Brazil, \(^3\)Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil

424 Genetic Diversity And Adaptability Exist Among Backyard Poultry Populations In Sri Lanka.
P. Silva\(^1\), N. Abeykone\(^1\), M. Samaraweera\(^2\), H. Jianlin\(^3\), M. N. M. Ibrahim\(^3\) and O. Mwai\(^4\), \(^1\)Department of Animal Science, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka, \(^2\)Faculty of Animal Science and Export Agriculture, Uva Wellassa University, Badulla, Sri Lanka, \(^3\)International Livestock Research Institute, Nairobi, Kenya

425 Efficiency of Random Regression Model over Conventional Univariate Animal Model for Estimation of Breeding Values for First Lactation 305-Day Milk Yields in Mehsana Buffaloes.
S. Saha\(^1\), A. Sudhakar\(^1\), M. N. Prajapati\(^2\), N. Nayee\(^1\) and K. R. Trivedi\(^1\), \(^1\)National Dairy Development Board, Anand, India, \(^2\)Mehsana District Co-operative milk producers’ union, Mehsana, India

426 Genome-Wide Association Studies for Growth Traits in Colombian Creole Cattle using a Single-Step Genomic Best Linear Unbiased Prediction (gBLUP).
R. Martinez\(^5\), CORPOICA, Bogotá, Colombia

Posters: Poultry Breeding (Group 1)
Chair: Hans H Cheng, USDA, ARS, ADOL and William M. Muir, Purdue University
Presentation Time: 9:30 AM – 10:00 AM

850 Two Major QTL in Chromosome 4 of Laying Hens with the Effects on Egg Traits. M.G. Smaragdov, O.Yu. Barkova and K. V. Plemyashov National Research Institute for Animal Genetics and Breeding, St. Petersburg, Russia.
M. Smaragdov\(^5\), National Research Institute of Animal Genetics and Breeding, St. Petersburg, Russia

851 The Effect of Inbreeding on Linkage Disequilibrium.
G. B. Nascimento\(^1\), R. P. Savegnago\(^1\), R. V. Ventura\(^2\), M. C. Ledur\(^4\) and D. P. Munari\(^5\), \(^1\)Univ. Estadual Paulista – FCAV/UNESP, Jaboticabal, Brazil, \(^2\)University of Guelph, Guelph, ON, Canada, \(^3\)Beef Improvement Opportunities, Guelph, ON, Canada, \(^4\)Embrapa Suínos e Aves, Concórdia, Brazil, \(^5\)Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil

852 Impact of Egg Weight Selection on Body Weight of Japanese Quail.
A. E. Eldlebshany\(^1\), Alexandria University, Alexandria, Egypt

853 Improving Analysis of Direct and Indirect Genetic Effects on Survival Data in Laying Hens.
T. Brinker\(^1\), E. D. Ellen\(^1\), J. Visscher\(^2\) and P. Bijma\(^1\), \(^1\)Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, \(^2\)Institut de Sélection Animale B.V., Hendrix Genetics, Boxmeer, Netherlands

854 Genetic Parameters for Production Traits of Rhode Island Red and White Plymouth Rock Breeds Selected under Tropical Condition in Thailand.
S. Tongsiri\(^1\), Animal Genetics and Breeding Unit, University of New England, UNE., Armidale, Australia

855 Neural Networks to Predict Breeding Values of Egg Production using Phenotypic Information.
V. A. R. Cruz\(^1\), R. P. Savegnago\(^2\), G. S. Schmidt\(^3\), M. C. Ledur\(^4\) and D. P. Munari\(^5\), \(^1\)São Paulo State University, Jaboticabal, Brazil, \(^2\)Univ. Estadual Paulista – FCAV/UNESP, Jaboticabal, Brazil, \(^3\)Embrapa Swine and Poultry, Concórdia, Brazil, \(^4\)Embrapa Suínos e Aves, Concórdia, Brazil, \(^5\)Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil

856 Bivariate Analysis of Individual Survival Data and Pooled Early Egg Production Data on Crossbred Laying Hens.
K. Peeters\(^1\), J. Visscher\(^2\) and P. Bijma\(^1\), \(^1\)Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, \(^2\)Institut de Sélection Animale B.V., Hendrix Genetics, Boxmeer, Netherlands

857 SNP Discovery in a QTL Region Associated With Breast Muscle Deposition on Chicken Chromosome 2.
C. Boschiero\(^1\), Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil
**Fine Mapping of QTL for Carcass and Meat Quality Traits in a Chicken Slow-Growing Line.**
S. Allais 1,2, C. Hennequet-Antier 1, C. Berry 1, M. Chabault-Dhuit 1, F. D’Abbadié 1, E. Le Bihan-Duval 1 and O. Demeure 1,2, INRA, UMR1348 PEGASE, Saint-Gilles, France, 1Agrocampus Ouest, UMR1348 PEGASE, Rennes, France, 2Université Européenne de Bretagne, RENNES, France, 3INRA UR3, Nouzilly, France, 3SASSO, Sabres, France

**Genetic Analysis of Meat-Type Quali Growth Under Different Nutritional Environments.**
L. Pinheiro da Silva 1, J. Correa Ribeiro 2, A. Camporez Crispim 2, G. Costa Caetano 2, R. Reis Mota 2, F. F. Silva 2 and R. Almeida Torres 2, 1Universidade Federal do Ceará, Fortaleza, Brazil, 2Universidade Federal de Viçosa, Viçosa, Brazil

**Genetic Parameters for Early Reproduction Traits in Ostriches.**
S. W. Cloete 1 and Z. D. Brand 2, 1Directorate Animal Sciences, Elsaenburg, South Africa, 2Directorate Animal Sciences, Oudtshoorn, South Africa

**Sex-specific Association of a SNP in the ADIPOR2 Gene with Carcass Traits in a Paternal Broiler Line.**
L. T. Fernandes 1, T. F. Godoy 2, V. H. Silva 2, J. R. Pandolfi 2, M. E. Cantão 1, J. O. Peixoto 1, L. L. Coutinho 1 and M. C. Ledur 1, EMBRAPA Swine and Poultry, Concórdia, Brazil, 1University of Sao Paulo, Piracicaba, Brazil, 1Universidade de Sao Paulo/Esalq, Piracicaba, Brazil

**RUNX2 Plays an Essential Role in the Manifestation of Femoral Head Necrosis in Broilers.**
E. Paludo 1, A. M. G. Ibelfi 1, J. O. Peixoto 1, F. C. Tavernari 1, R. Zanella 1, J. R. Pandolfi 2, L. L. Coutinho 2, C. A. Lima-Rosa 1 and M. C. Ledur 1, EMBRAPA Swine and Poultry, Concórdia, Brazil, 1Universidade de Sao Paulo/Esalq, Piracicaba, Brazil, 1Santa Catarina State University, Lages, Brazil

**Variations Of The Melanocortin 1 Receptor Gene Associated With Partridge Phenotypes In Wenchang Chickens.**
X. Zhang, South China Agroiculutural University, Guangzhou, China

**Genetic Evaluation of Body Weight and Tibia Resistance in Broilers.**
J. O. Peixoto 1, V. L. Kawski 1, A. M. G. Ibelfi 1, R. Zanella 1, H. Mazzuco 1, C. G. Souza 1, D. P. Munari 1, F. R. F. Jaenisch 1 and M. C. Ledur 1, EMBRAPA Swine and Poultry, Concórdia, Brazil, 1Universidade Estadual Paulista "Júlio de Mesquita Filho", Concórdia, Brazil, 1Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil

**Discovery Of SNPs Potentially Associated with Fatness in a QTL Region on Chicken Chromosome 3.**
G. C. M. Moreira 1, T. F. Godoy 1, C. Boschiero 1, A. Gheyas 1, G. Gasparin 1, M. Paduan 1, S. C. S. Andrade 1, H. Montenegro 1, D. Burr 1, M. C. Ledur 1 and L. L. Coutinho 1, 1Department of Animal Science, University of Sao Paulo/ESALQ, Piracicaba, Brazil, 2The Roslin Institute and Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom, 3Department of Genetics, University of Sao Paulo (ESALQ), Piracicaba, Brazil, 4EMBRAPA Swine and Poultry, Concórdia, Brazil, 5Universidade de Sao Paulo/Esalq, Piracicaba, Brazil

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**Posters: Adaptation and Selection in Harsh Environments (Group 2)**
**Chair**: Alessandra Stella, Fondazione Parco Tecnologico Padano

**Presentation Time**: 10:00 AM – 10:30 AM

**QTL for Body Composition Traits During Heat Stress Revealed in an Advanced Intercross Line of Chickens.**
A. G. Bjorkquist, Iowa State University, Ames

**Genetic Correlation and Genome Wide Association Study of Pulmonary Arterial Pressure and Post Weaning Growth Traits in Angus Heifers from a High Altitude Breeding Program.**
X. Zeng 1, R. Cockrum 2, N. F. Berge 1, J. M. Neary 1, F. B. Garry 1, T. N. Holt 1, H. D. Blackburn 1, S. E. Speidel 1, D. J. Garrick 2, R. M. Enns 1 and M. G. Thomas 1, 1Colorado State University, Department of Animal Sciences, Fort Collins, 2Virginia Polytechnic Institute and State University, Blacksburg, 3Colorado State University, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO, 4USDA-ARS-National Animal Germplasm Program, Fort Collins, CO, 5Iowa State University, Ames

**Relationship of Endocrine Pathway SNP and Molecular Breeding Value with Milk Production in Heat Stressed Holstein Cows.**
A. J. Hernandez 1, P. Luna 2, G. Rincon 1, J. F. Medrano 1, R. M. Enns 1 and M. G. Thomas 1, 1Colorado State University, Fort Collins, 2Instituto Tecnologico de Sonora, Ciudad Obregon, Mexico, 3Zoetis Inc., Kalamazoo, MI, 4University of California, Davis, 5Colorado State University, Department of Animal Sciences, Fort Collins
Genetic Relationships between Pulmonary Arterial Pressure and Performance Traits in Colorado State University Beef Improvement Center Angus herd.
N. F. Berge, S. E. Speidel, X. Zeng, M. M. Calbertson, M. G. Thomas and R. M. Enns, Colorado State University, Department of Animal Sciences, Fort Collins

Participatory Definition of Trait Preferences for Designing Village Breeding Schemes for Goats in Harsh Environments of Ethiopia.


Posters: Breeding in Aquaculture Species (Group 1)
Chair: William S. Davidson, Simon Fraser University, Thomas Moen, AquaGen AS, and Roberto Neira, University of Chile, Aquainnovo

Experimental Designs for Genetic Parameters and Response to Selection of Social Interaction Traits in Aquaculture.
P. Sae-Lim and P. Bijma, Nofima, Ås, Norway, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Indirect Genetic Effects for Harvest Weight in Nile Tilapia (Oreochromis niloticus).
H. L. Khaw, R. W. Ponsoni, H. Y. Yee, M. A. Aziz and P. Bijma, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, The WorldFish Center, Penang, Malaysia, WorldFish, Penang, Malaysia

Sexual Maturation of 1 and 2 Year Old Farmed Atlantic Cod – Prevalence and Heritability Estimates.
T. M. K. Drangsholt, H. M. Nielsen, R. Bangera and V. Puvanendran, Nofima, Tromsø, Norway, Nofima, Ås, Norway, Norwegian Institute of Food, Fisheries and Aquaculture Research, Tromsø, Norway

Genetic Analysis of Resistance to Acute or Chronic Temperature Stress using Isogenic Lines of Rainbow Trout (Oncorhyncus mykiss).
M. Dupont-Nivet, M. Crusol, D. Rigaudaud and E. Quiller, INRA, UMR 1313 GABi, Jouy en Josas, France, INRA, UE 907 IERP, Jouy en Josas, France

Effect of Family Structure and Size on Genomic Selection Accuracy in Aquaculture Breeding.
K. G. Nirea, A. K. Sonesson, M. Lillehammer and T. H. E. Meuwissen, Norwegian University of Life Sciences, Ås, Norway, NOFIMA, Ås, Norway, NOFIMA As, Ås, Norway

Correcting for Early Within-Family Pre-Selection in Genetic Evaluation - A Simulation on Rainbow Trout Growth.
M. Janhunen, A. Kause, H. Vehviläinen, H. Koskinen and A. Nousiainen, MTT Agrifood Research Finland, Jokioinen, Finland, Finnish Game and Fisheries Research Institute, Tervo, Finland

MicroRNA Profiling of Atlantic Salmon Challenged with Infectious Pancreatic Necrosis Virus: Comparison between Resistant and Susceptible Fish.
N. R. Lowe, M. Bekker, S. C. Bishop, J. E. Bron, J. B. Taggart and R. D. Houston, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, Institute of Aquaculture, School of Natural Sciences, University of Stirling, Stirling, United Kingdom
The Efficacy of Walk-Back Selection and Optimized Parent Selection in the Presence of Unequal Family Distributions.

Improving Uniformity of Growth by Mating and Selection Strategies in Rainbow Trout.
A. Kause, M. Janhunen, H. Vehviläinen, H. Koskinen and A. Nousiainen, MTT Agrifood Research Finland, Jokioinen, Finland.

Genotype by Diet Interactions on Growth and Processing Traits in Rainbow Trout (O. mykiss), Sea Bass (D. labrax), Sea Bream (S. aurata) and Meagre (A. regius) Fed Diets Highly Substituted in both Fish Meal and Fish Oil by Vegetal Ingredients.
A. Bestin, SYSAAF, Rennes, France.

Genome-Wide Association Study (GWAS) for Growth Rate and Sexual Maturation in Atlantic Salmon (Salmo salar).
A. P. Gutierrez, J. M. Yañez, S. Fukui, B. Swift and W. S. Davidson, Simon Fraser University, Burnaby, BC, Canada.

A Co-association Network Analysis of the Genetic Determination of Pig Growth and Shape.
A. M. Puig Oliveras, Centre de Recerca en Agrigenòmica, Barcelona, Spain.

Using Next-Generation Sequencing To Identify Candidate Genes For QTLs Affecting Body Weight And Fat Weight In the Mouse.
A. Ishikawa, Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan.

A Genome-Wide Association Study for Morphometric Traits in Quarter Horse.
R. A. Curi, Universidade Estadual Paulista, Botucatu, Brazil.

Heritability Estimates of Conjugated Linoleic Acid Isomers in Brisket Adipose Tissue of Canadian Crossbred Beef Steers.
C. Li, Agriculture and Agri-Food Canada, Edmonton, AB, Canada.

Growth Curves Changes in Nellore Males Selected for Postweaning Weight.

Identification of Selection Footprints in a Brown Hanwoo (Korean cattle) Population for Production Traits.
D. Lim, Animal Genomics & Bioinformatics Division, NIAS, RDA, Suwon, South Korea.

Induction of Differentiation by AAV2-Mediated Follistatin Overexpression in Ovine Primary Myoblasts.
M. Nazari and L. Zhang, Animal science, Beijing, China.

Regional Heritability Mapping of Age-Dependent Loci Affecting Growth Traits in Scottish Blackface Lambs.
G. Hadjipavlou, V. Riggio, R. Pong-Wong, O. Matika and S. C. Bishop, Agricultural Research Institute, Lefkosia, Cyprus.

Investigation of Candidate Regions Associated With Fat Deposition in Thin and Fat Tail Sheep Breeds.
M. H. Moradi, Arak University, Arak, Iran.

Genetic Parameter Estimation of Body Size and Birth Weight in Chinese Holstein Cows.
Agricultural University, Beijing, China; Beijing Sanyuan Lvhe Dairy Cattle Center, Beijing Sanyuan Breeding Technology Co., Ltd., Beijing, China

Posters: Poultry Breeding (Group 2)
Chair: Hans H Cheng, USDA, ARS, ADOL and William M. Muir, Purdue University
Presentation Time: 10:00 AM – 10:30 AM

Parameter Estimates of Average Daily Feed Consumption and Association with CCKAR Genotypes in White and Brown Egg-Type Laying Hens.
K. Rowland1, A. Wolc2, J. Arango2, P. Settar2, J. E. Fulton2, N. P. O’Sullivan2 and J. C. M. Dekkers1, 1Iowa State University, Ames, 2Hy-Line International, Dallas Center, IA

Using Multiple Regression, Bayesian Networks and Artificial Neural Networks for Prediction of Total Egg Production in European Quails.
V. P. Felipe1, M. A. Silva2, B. D. Valente1 and G. J. M. Rosa1, 1University of Wisconsin, Madison, 2Federal University of Vales do Jequitinhonha and Mucuri, Diamantina, Brazil

Quantitative Morphological Traits as a Measure of Genetic Diversity in Two Indigenous Chicken Ecotypes in Ethiopia.
E. Aklilu1, G. Gebreyesus1, K. Kebede1 and T. Dessie1, 1International Livestock Research Institute, Addis Ababa, Ethiopia, 2Haramaya University, Haramaya, Ethiopia, 3International Livestock Research Institute, Addis Abeba, Ethiopia

Posters: Management of Animal Genetic Resources (Group 1)
Chair: Michèle Tixier-Boichard, INRA
Presentation Time: 3:00 PM – 3:30 PM

Animal Genetic Resources in Slovakia.
P. Chrenek1, Slovak University of Agriculture, Nitra, Slovakia

Genetic Diversity of the Afrikaner Cattle Breed.
L. Pienaar1, University of the Free State, Bloemfontein, South Africa; Agricultural Research Council - Animal Production Institute, Pretoria, South Africa

Using Adaptive Simulated Annealing For Optimal Selection With Several Constraints.
H. Chapuis1, SYSAAF, Nouzilly, France

Understanding the Structure of the Brazilian Red Sindhi Population using Genomic Information.
J. C. C. Panetto1, R. M. H. Leite2, G. G. Santos3, F. A. T. Bruneli4, R. B. Teixeira3, L. G. D. Castro4, D. R. L. Reis5, M. A. Machado1, M. G. Campolina Diniz Peixoto1 and R. D. Silva Verneque1, 1Embrapa Dairy Cattle, Juiz de Fora, Brazil, 2Paraiba Agricultural State Research Company, Joao Pessoa, Brazil, 3Minas Gerais Federal Institute, Bambui, Brazil, 4President Antonio Carlos University, Juiz de Fora, Brazil

European Gene Bank Network for Animal Genetic Resources (EUGENA).
S. J. Hiemstra1, E. Martyniuk2, Z. Duchev3 and F. Begemann et al.4, 1Centre for Genetic Resources the Netherlands, Wageningen UR, Wageningen, Netherlands, 2Warsaw University of Life Sciences/National Research Institute of Animal Production, Warsaw, Poland, 3Executive Agency for Selection and Reproduction in Animal Breeding, Sofia, Bulgaria, 4European Regional Focal Point (Secretariat), BLE, Bonn, Germany, Bonn, Germany

Determination of Non-Market Values to Inform Conservation Strategies for the Threatened Alistana-Sanabresa Cattle Breed.
D. Martin-Collado1, C. Díaz2, A. G. Drucker3, M. J. Carabaño2 and K. Zander4, 1AbacusBio Ltd., Dunedin, New Zealand, 2INIA, Madrid, Spain, 3Biouversity International, Rome, Italy, 4The Northern Institute, Darwin, Australia, Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Australia

K-casein Genotypic and Allelic Frequencies in the Tropical Milking Criollo Cattle.
C. M. Becerril-Pérez1, Colegio de Postgraduados, Montecillo, Texcoco, Mexico
Facing the Estimation of Effective Population Size Based on Molecular Markers: Comparison of Estimators.
B. Jiménez-Mena1,2, E. Verrier1,2 and F. Hospital1,2, 1INRA UMR 1313 GABI, Jouy en Josas, France, 2AgroParistech, Paris, France, 3Bioinformatics Research Center, Aarhus University, Aarhus, Denmark

New Parentage Testing SNP Panel for Commercial Breeds will be a Useful Tool for Conservation of Creole Sheep.
F. Macedo1, E. A. Navajas2, I. Aguilar1, N. Grasso2, F. Pieruccioni2 and G. Ciappessonii, 1Universidad de la República, Montevideo, Uruguay, 2INIA, Rincón del Colorado, Uruguay, 3INIA, Las Brujas, Uruguay

Merging Molecular Data for Evaluating Cross Country Genetic Diversity of Pigs.
A. S. Mariante1, EMBRAPA Genetic Resources And Biotechnology, Brasilia, Brazil

Major Histocompatibility Complex Genetic Diversity Of Kenyan Indigenous Chicken Populations Based On Microsatellite Markers.
K. Ngeno1, Wageningen University, Wageningen, Netherlands; Egerton University, Egerton, Kenya

The Use of Genomic Coancestry Matrices in the Optimization of Contributions for Maintaining Diversity at Specific Regions of the Genome.
F. Gómez-Romano1, B. Villanueva1, J. Fernández2, J. A. Woolliams2 and R. Pang-Wong2, 1INIA, Madrid, Spain, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Persistence Of Linkage Disequilibrium Phase Amongst Five South African Beef Cattle Populations.
S. O. Makina1, E. van Marle-Koster1, F. C. Muchadeyi1 and N. A. Maiwashe1, 1Agricultural Research Council, Pretoria, South Africa, 2University of Pretoria, Pretoria, South Africa, 3Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa, 4University of the Free State, Bloemfontein, South Africa

Genetic Diversity in the Ramo Grande Cattle Breed Assessed by Pedigree Information and Microsatellite Markers.
A. L. Payão1, C. Ginjá and L. T. Game1, 1Direcció Regional da Agricultura e Desenvolvimento Rural, Angra do Heroísmo, Açores, Portugal, 2Centro de Biologia Ambiental, Faculdade de Ciências - Universidade de Lisboa, Lisboa, Portugal, 3FMV - University of Lisbon, Lisbon, Portugal

D. M. Motiang1 and E. C. Webb2, 1Agricultural Research Council, Pretoria, South Africa, 2Department of Animal and Wildlife Sciences, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa

Population Genetic Structure of Sri Lankan Backyard Chicken Flocks: Implication for Conservation and Genetic Improvement Programs.
M. Samaranweera1, P. Silva2, N. Abeykone2, M. N. M. Ibrahimm, A. M. Okeyo3 and J. Han1, 1Faculty of Animal Science and Export Agriculture, Uva Wellaussa University, Badulla, Sri Lanka, 2Department of Animal Science, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka, 3International Livestock Research Institute, Nairobi, Kenya

Posters: Statistical Methods - Linear and Nonlinear Models (Group 1)
Chair: Marco C.A.M. Bink, Wageningen University

Presentation Time: 3:00 PM – 3:30 PM

Simultaneous Estimation of Spatial and Genetic Effects using Hierarchical Generalized Linear Models.
L. Rönnegård2, M. Fellek2, M. Alam3 and X. Shen1, 1Dalarna University, Falun, Sweden, 2SLU, Uppsala, Sweden, 3Division of Computational Genetics, Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden

Properties of Mendelian Residuals when Regressing Breeding Values using a Genomic Covariance Matrix.
R. J. C. Cantet1 and Z. G. Vitezica2, 1Department of Animal Science, University of Buenos Aires, Buenos Aires, Argentina, 2Unite Mixte ENSAT- INRA, Toulouse, France

Can a Model with Genetic Groups for Mendelian Sampling Deviations Correct for Pre-Selection bias?
F. Fiske2, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden
Aggregation of Methods for Genetic Prediction.
C. Carre\textsuperscript{1,2}, L. Tusell\textsuperscript{2}, S. Form\textsuperscript{1}, F. Gamboa\textsuperscript{1}, D. Gianola\textsuperscript{1} and E. Manfredi\textsuperscript{2}, \textsuperscript{1}IMT Université Paul Sabatier, Toulouse, France, \textsuperscript{2}INRA, Toulouse, France, \textsuperscript{3}Genus Plc, Hendersonville, TN, \textsuperscript{4}University of Wisconsin, Madison

Bayesian Analysis of Heterogeneous Residual Variance in Canine Behaviour.
S. M. van den Berg\textsuperscript{1}, I. Schwabe\textsuperscript{2}, F. Fikse\textsuperscript{3}, H. C. Heuven\textsuperscript{1} and C. A. Glas\textsuperscript{1}, \textsuperscript{1}University of Twente, Enschede, Netherlands, \textsuperscript{2}University of Twente, Enschede, Netherlands, \textsuperscript{3}Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, \textsuperscript{4}University of Utrecht, Utrecht, Netherlands

Influence of Family Structure on Variance Decomposition.
S. M. Edwards\textsuperscript{1}, P. M. Sarup\textsuperscript{1} and P. Sørensen\textsuperscript{2}, \textsuperscript{1}Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, \textsuperscript{2}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

A Bayesian Modeling Framework to Integrate Genetics and Epidemiology in Field Disease Data.
M. Nath\textsuperscript{1}, C. M. Pooley\textsuperscript{2}, S. C. Bishop\textsuperscript{2} and G. Marion\textsuperscript{1}, \textsuperscript{1}Biomathematics and Statistics Scotland, Edinburgh, United Kingdom, \textsuperscript{2}The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Variational Bayesian Method to Estimate Variance Components.
A. Arakawa\textsuperscript{1}, M. Taniguchi\textsuperscript{2}, T. Hayashi\textsuperscript{1} and S. Mikawa\textsuperscript{1}, \textsuperscript{1}National Institute of Agrobiological Sciences, Tsukuba, Japan, \textsuperscript{2}NARO Institute of Agricultural Research Center, Tsukuba, Japan

Parallel Computing to Speed up Whole-Genome Analyses using Independent Metropolis-Hastings Sampling.
H. Cheng\textsuperscript{1}, R. L. Fernando and D. J. Garrick, Iowa State University, Ames

Results of Genome Wide Association Studies Improve the Accuracy of Genomic Selection.
Z. Zhang\textsuperscript{1}, J. He\textsuperscript{1}, H. Zhang\textsuperscript{1}, P. Gao\textsuperscript{1}, M. Erbe\textsuperscript{2}, H. Simianer\textsuperscript{2} and J. Li\textsuperscript{3}, \textsuperscript{1}South China Agricultural University, Guangzhou, China, \textsuperscript{2}Georg-August University, Göttingen, Germany

Parallel Computing to Speed up Whole-Genome Analyses using Independent Metropolis-Hastings Sampling.
H. Cheng\textsuperscript{1}, R. L. Fernando and D. J. Garrick, Iowa State University, Ames

Estimation of Genetic Parameters and Breeding Values in Honey Bees.
E. W. Brascamp\textsuperscript{1}, R. F. Veerkamp and P. Bijma, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Genetic Variance Components when Fluctuating Imprinting Patterns are Present.
I. Blank\textsuperscript{1} and N. Reinsch, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany

Approximation of Standard Errors of Estimates as a By-Product for MC EM REML Analysis.
K. Matilainen\textsuperscript{1}, J. Strandén and E. A. Mäntysaari, MIT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

DMU - A Package for Analyzing Multivariate Mixed Models in Quantitative Genetics and Genomics.
P. Madsen\textsuperscript{1}, J. Jensen, R. Labouriau, O. F. Christensen and G. Sahana, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

A New Nonparametric Approach to Delineating Spatial Population Genomic Variation.
Z. Hu\textsuperscript{1} and R. C. Yang\textsuperscript{1,2}, \textsuperscript{1}University of Alberta, Edmonton, AB, Canada, \textsuperscript{2}Alberta Agriculture and Rural Development, Edmonton, AB, Canada

Genetic Analysis of Micro-environmental Plasticity in Drosophila melanogaster.
F. Morgante\textsuperscript{1}, D. A. Sorensen\textsuperscript{2}, P. Sorensen\textsuperscript{2}, C. Maltecca\textsuperscript{1} and T. F. Mackay\textsuperscript{1}, \textsuperscript{1}Department of Biological Sciences, North Carolina State University, Raleigh, \textsuperscript{2}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, \textsuperscript{3}North Carolina State University, Raleigh

Posters: Breeding in Aquaculture Species (Group 2)
Chair: William S. Davidson, Simon Fraser University, Thomas Moen, AquaGen AS, and Roberto Neira, University of Chile, AquaInnovo
Effects of Inbreeding on Body Weight at Harvest Size and Grow-Out Survival Rate in a Selected Population of Pacific White Shrimp Penaeus (Litopenaeus) vannamei.
L. De los Ríos-Pérez1, G. R. Campos-Montes2, A. Martínez-Ortega1, H. Castillo-Juárez2 and H. H. Montaldo4, 1Universidad Nacional Autónoma de México, México, Mexico, 2Universidad Autónoma Metropolitana, DF, Mexico, 3Maricultura del Pacífico S.A. de C.V., México, Mexico, 4Universidad Nacional Autónoma de México, DF, Mexico

Compensation of Loss in Genetic Gain Due to Genotype by Environment Interaction by Increasing the Size of the Breeding Nucleus in an Aquaculture Population.
B. Gjerde, H. M. Nielsen2 and P. Sue-Lim, Nofima, Ås, Norway

Genetic Bases of Resistance versus Susceptibility to Flavobacterium psychrophilum in Rainbow Trout.
E. Quillet1, N. Dechamp2, C. Hervel3, F. Krieg4, C. Chantry-Darmon5, M. Bousaada1, A. Bérand6, V. Laurens89, T. Rochat10, E. Duchaud88, P. Boudinot11, J. F. Bernardel12 and C. Michel11, 1INRA, UMR 1313 GABI, Jouy en Josas, France, 2INRA, UMR 1313 GABI, Jouy-en-Josas, France, 3INRA, UMR 1313 GABI, Jouy-en-Josas, France, 4LABOGENA, Jouy-en-Josas, France, 5INRA, UMR1313 GABI, Jouy-en-Josas, France, 6INRA, US 1279 EPGV (Etude du Polymorphisme des Génomes Végétaux), Evry, France, 7CEA/Institut de Génomique/Centre National de Génotypage, Evry, France, 8INSEM UMR 866, Dijon, France, 9Université de Bourgogne, Institut Fédératif de Recherche Santé STIC, Dijon, France, 10INRA, UR 892 VIM, Jouy-en-Josas, France, 11INRA, UR 892 VIM, Jouy en Josas, France

O. O. T. Aşgibi and S. S. O. Shofela, Federal University of Agriculture, Abeokuta, Nigeria

Genetic Analysis of Shape in Trout using Image Analysis.
H. Komen1, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Accuracy of Genomic Selection for BCWD Resistance in Rainbow Trout.

Integrating Quantitative Genetics and Practical Aspects in a Fish Breeding Network in Denmark.
K. Meier11, A. C. Sørensen2, E. Norberg2 and B. Thomsen4, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Danish Aquaculture Organization, Silkeborg, Denmark

Posters: Genetics of Trait Complexes: Growth and Development (Group 2)
Chair: Michael D. MacNeil, Kansas State University

Presentation Time: 3:30 PM – 4:00 PM

Genome-Wide Linkage Disequilibrium Linkage Analysis (LDLA) of Body Fat Traits in an F2 Porcine Model for Human Obesity.
S. D. Pant1, P. K. Mortensen1, S. C. Salicio1, L. J. Kogelman1, M. J. Jacobsen1, C. S. Braun1, C. B. Jørgensen1, T. H. E. Meuwissen1, H. N. Kadarmadeen2 and M. Fredholm3, 1Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 2Department of Animal and Aquacultural Sciences, Federal University of Agriculture, Abeokuta, Nigeria

RNA Sequencing Analysis Identifies Retinoic Acid Pathway Genes as Differentially Expressed in Animals with Extreme Intramuscular Fat GEBVs in Nellore Steers.
A. S. M. Cesar1, L. C. A. Regitano2, J. E. Koltes3, E. Fritz-Waters4, G. Gasparin4, G. B. Mourao5, D. P. D. Lanna6, J. M. Reecy6 and L. L. Coutinho7, 1University of Sao Paulo, Piracicaba, Brazil, 2Embrapa Pecuária Sudeste, São Carlos, Brazil, 3Iowa State University, Ames, 4University of São Paulo/ESALQ, Piracicaba, Brazil, 5Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, 6University of Sao Paulo / ESALQ, Piracicaba, Brazil, 7Universidade de São Paulo/Esalq, Piracicaba, Brazil
Estimation of Direct and Maternal Genetic Effect on Weaning Weight and Average Daily Gain to Wean in Japanese Black Cattle.
A. Supriyanto,
The State University of Papua, Manokwari, Indonesia

Response to Selection for Intramuscular Content and Correlated Responses in Carcass and Meat Traits in Rabbits.
M. Martínez-Alvaró,
Universitat Politècnica de València, Valencia, Spain

Genome-Wide Association Study on Body Weight Reveals Major Loci on OAR6 in Australian Merino Sheep.
H. A. Al-Mamun1, S. Clark1, P. Kwan1 and C. Gondro2,1University of New England, Armidale, Australia,2School of Environmental & Rural Science, University of New England, Armidale, Australia

Genome-Wide Association for Growth Curve Parameters in Brahman Cattle.
A. Camporez Crispim1, M. J. Kelly2, F. F. Silva2, M. R. Fortes2, S. E. Guimaraes2, P. S. Lopes1 and S. S. Moore3,1Universidade Federal de Viçosa, Viçosa, Brazil,2Embrapa Southeast Livestock, São Carlos, Brazil,3Teagasc Moorepark, Fermoy, Ireland

MyoD1 Expression Levels Affect Meat Tenderness in Nellore Beef Cattle.
P. C. Tizuto1, G. Gasparini1, L. L. Coutinho1, G. B. Mourao1, M. A. Mudaud1, M. M. Souza1, W. Malagó Jr1, F. A. Donatoni Bressani1, R. R. Tullio1, R. T. Nasso1 and L. C. A. Regitano1,2,1Federal University of São Carlos, São Carlos, Brazil,2University of São Paulo/ESALQ, Piracicaba, Brazil

Estimation of Genetic Parameters For Body Weight From Birth To 10 Years Old In Nellore Females.
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A Novel SNP Polymorphism in the Ovine Leptin Gene Related to Back Fat Depth.
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Genome Wide Association for Growth Curve Parameters in Brahman Cattle.
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Genetic Analysis of Growth in Performance Tested Young Bulls accounting for Indirect Genetic Effects.
C. Sartori1, Department of Agronomy Food Natural resources Animals and Environment, University of Padua, Legnaro (PD), Italy

Identification of Epistatic Interactions Among Fatty Acid Traits, in Angus Sired Beef Cattle.
L. M. Kramer1, Iowa State University - Department of Animal Science, Ames

Genome-wide Association Study For Carcass Traits in Simmental Cattle Based on High-density SNP Chip.
J. Li1, X. Qi and J. Zhang, Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China, Beijing, China

Posters: Management of Animal Genetic Resources (Group 2)
Chair: Michèle Tixier-Boichard, INRA
Lactation Curve Modeling for Murrah and Surti Buffalo Breeds in Sri Lanka.
C. M. Dematawewa∗, University of Peradeniya, Peradeniya, Sri Lanka

Assessment of Generation Interval and Inbreeding in a Peruvian Alpaca Population.
J. Vilela∗1 and V. Montenegro2, 1Universidad Nacional Agraria La Molina, Lima, Peru, 2D-Agro Perú Consultant, Lima, Peru

Posters: Statistical Methods - Linear and Nonlinear Models (Group 2)
Chair: Marco C.A.M. Bink, Biometris, Wageningen UR

Genomic Prediction Within Family Combining Linkage Disequilibrium and Cosegregation Information.
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Y. Masuda∗1,2, I. Aguilar3, S. Tsuruta4 and I. Misztal5, 1University of Georgia, Athens, 2Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, 3INIA, Las Brujas, Uruguay

Exploring Extensions and Properties of Expectation-Maximization Methods for Whole Genome Prediction.
C. Chen∗, H. Wang, W. Yang and R. J. Tempelman, Michigan State University, East Lansing

Using Factor Analysis Modeling Multiple Traits in Genetic Improvement of Nelore Beef Cattle.
M. J. Yokoo∗1, G. de los Campos2, G. J. M. Rosa3, F. F. Cardoso4, B. P. Sollero5, L. L. Cardoso6, R. B. Lôbo7 and L. G. Albuquerque8, 1Embrapa Southern Region Animal Husbandry, Bagé, Brazil, 2University of Alabama at Birmingham, Birmingham, AL, 3University of Wisconsin, Madison, 4Embrapa Southern Region Animal Husbandry, Bagé, Bagé, Brazil, 5Coordination for the Improvement of Higher Level Personnel (CAPES/PNPD), Brasília, Brazil, 6ANCP-Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, 7State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Joint Prediction of Multiple Quantitative Traits using a Bayesian Multivariate Antedependence Model.
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Efficient Approximations of the Inverse of a Part of the Additive Relationship Matrix.
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