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. Schnabel1, C. Lawley1, A. Pirani1, F. Brew1,
              C. Soans2, H. Jorjani6, G. Evans7, B. Simpson3, I. Fojadelli1, F. Strozzi1, R. D. Schnabel2, C. Lawley3, A. Pirani1, F. Brew1,
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10:45 AM 262 Genetic Variation in Resistance to Pancreas Disease in Atlantic Salmon.  
S. Gonen1, A. Norris2, P. Arnexen2, S. C. Bishop1 and R. D. Houston1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Marine Harvest, Sandvikenboder 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. Cabrejos1, J. Gilbey2, L. Bernatchez2, A. Norris2, C. Soto2, J. Eisenhart2, B. Simpson2, R. Neira2, J. P. Lhorente2, P. Schnable10,11, S. Newman1, A. Mileham12 and N. Deeb2, 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, 12Genus plc, DeForest, WI

J. J. Tosh1,2, R. V. Ventura1,2, K. P. Ang1, J. A. K. Elliot1, M. P. Kent1, S. Lien1, E. G. Boulding1 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. Tinche2, J. B. Taggart1, J. E. Bron1, A. Downing1, M. J. Stear2, K. Garbi1 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.  
R. Guymard1, Y. Guiguen1, M. Bernard1, A. Charlet1, N. Dechamp1, C. Hervet1, C. Chantry-Darmon1, F. Krieg1 and E. Quillert1, 1Institut National de la Recherche Agronomique, Jouy-en-Josas, France, 2Institut National de la Recherche Agronomique, Rennes, France, 3LABOGENA, Jouy-en-Josas, France

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. Duroc2, 1INRA, UMR 1313 GABI, Jouy-en-Josas, France, 2INRA, UMR 1313 GABI, Jouy-en-Josas, France

10:45 AM 002 Factors Affecting Rankings 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. Miller1, 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 Werf3 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. Østergaard, J. Ettema, L. Hjortø, J. Pedersen and M. K. Sørensen, Aarhus University, Tjele, Denmark, SimHerd Inc., Tjele, Denmark, Knowledge Centre for Agriculture, Aarhus, Denmark


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. Cheng, 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. Preeyanon, H. H. Cheng and C. T. Brown, Michigan State University, East Lansing, USDA, 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 Pinto, A. M. Molin, R. Gilbert, C. Honaker, P. B. Siegel, G. Andersson, L. Andersson and D. J. de Koning, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, Virginia Polytechnic Institute and State University, Blacksburg, Department 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. Boettcher, I. Hoffmann, R. Baumung, 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-Boichard, INRA, AgroParisTech, Jouy-en-Josas, France

Conservation of Animal Genetic Resources (AnGR): the Next Decade.
S. R. Paiva, C. M. Pimentel and H. D. Blackburn, Embrapa - Labex - Secretariat International Affairs, Brasilia, Brazil, Universidade de Brasilia, Brasilia, Brazil, USDA-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. Garrick, J. C. M. Dekkers, B. L. Golden and R. L. Fernando, Iowa State University, Ames, Calpoly, San Luis Obispo, CA
Genomic Heritability: What Is It?  
G. de los Campos1*, D. A. Sorensen2 and D. Gianola3, 1University of Alabama at Birmingham, Birmingham, AL, 2Aarhus University, Tjele, Denmark, 3University of Wisconsin, Madison

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

Genetic Improvement of Meat Production in Reindeer.  
K. Muuttoranta1*, O. Holand2, K. H. Roed3, M. Nieminen4 and A. Mäki-Tanila5, 1MTT Agrifood Research Finland, Jokioinen, Finland, 2Norwegian University of Life Sciences, Ås, Norway, 3Norwegian University of Life Sciences, Oslo, Norway, 4Finnish Game and Fisheries Research Institute, Inari, Finland, 5MTT 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


Genome Wide Association Analysis of Lung Lesions in Cattle using Sample Pooling.  

Definition and Utilization of Among Hosts Heritable Variation in Reproduction Ratio R0 for Infectious Diseases.  
M. Anche8, M. C. M. de Jong9 and P. Bijma10, Animal Breeding and Genomics Centre, Quantitative Veterinary Epidemiology Group, Wageningen University, Wageningen, Netherlands, 10Quantitative Veterinary Epidemiology
Dynamic and Genetic Signatures of Resistance and Tolerance of Pigs to PRRS.
G. Lough1,2, I. Kyriazakis3, S. Fornì1 and A. Doeschl-Wilson4,1, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Newcastle University, Newcastle upon Tyne, United Kingdom, 3Genus Plc, Hendersonville, TN

Mediation Analysis of Milk Losses Associated With Clinical Mastitis.
J. Detilleux1, J. P. Kastelic2 and H. Barkema1, University of Liege, Liege, Belgium, Agriculture & Agri-Food Canada, Calgary, AB, Canada, 1University of Calgary, Calgary, AL, Canada

Simultaneous Inference of Genetic Parameters Underlying Susceptibility and Infectivity of Livestock from Epidemiological Data.
O. Anacleto1,2, D. Lipschutz-Powell1, L. A. García-Cortés2, J. A. Woolliams1 and A. Doeschl-Wilson1, The 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

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

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. Saintilan2, B. Picard1, D. Maupetit1 and G. Renand3,1Universidad de Córdoba, Cordoba, Spain, 2INRA, UMR1313 GABI, Jouy-en-Josas, France, 3UNCEA, Jouy-en-Josas, France, 4INRA, Theix, France, 5INRA, Bourges, France, 6INRA, Jouy en Josas, France

Genotypic and Genetic Analysis of Meat Eating Quality Traits in Irish Cattle.
F. Kearney1,2, A. P. Moloney1, R. Prendiville1, P. Allen1, B. Meredith2 and S. Conroy3, Irish Cattle Breeding Federation, Cork, Ireland, 2TEAGASC, Dunsany, Meath, Ireland, 3Teagasc, Grange, Co. Meath, Ireland, 4Teagasc, Ashtown, Dublin 15, Ireland, 5Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland

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, J. A. Aguilar1 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

Angus at High Altitude: Genetic Relationships and Initial Genome-Wide Association Analyses of Pulmonary Arterial Pressure.
R. R. Cockrum1,2, X. Zeng2, N. F. Berge3, J. M. Neary4, F. B. Garry1, T. N. Holt5, H. D. Blackburn4, S. P. Thomas5, S. E. Speidel1, D. J. Garrick6, R. M. Enns2 and M. G. Thomas3, 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

A Haplotype Diagnostic for Polled in Australian Beef Cattle.
E. K. Piper, The University of Queensland, School of Veterinary Science, Gatton, Australia
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. Bennewitz* 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. Bates3, C. W. Ernst3, D. Nonneman4, G. A. Rohrer5, D. A. King5, S. D. Shackelford6, T. L. Wheeler1, R. J. C. Canter† and J. P. Steibel1, 1Department of Animal Science, University of Buenos Aires, Buenos Aires, Argentina, 2USDA/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. Iraqui2, 1Hebrew University of Jerusalem, Jerusalem, Israel, 2Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel

M. G. Usai1, 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, T. Sechi1, M. G. Usai1, S. Miari1, M. Casula1, G. Mulas1, R. Giannico1, B. Lazzari1, A. Stella2,3 and A. Carta1, 1Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy, 2Fundazione Parco Tecnologico Padano, Lodigiani, Italy, 3IBBA CNR, Lodigiani, Italy

2:45 PM 189 Footprints of Parallel Selection Revealed by Direct Sequencing in Egg Laying Chicken.
S. Qanbari1, M. Seidel1, T. M. Strom2, R. Preisinger1 and H. Simianer2, 1Georg-August University, Göttingen, Germany, 2Helmholtz Zentrum München, München, Germany, 3Lohmann Tierzucht GmbH, Cuxhaven, Germany

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, F. Barillet1, G. Baloche1, J. M. Astruc2, D. Buisson1, F. Shumbusho1,2, V. Clément1, G. Lagriffoul1, I. Palhière1, R. Rupp1, C. Carillier2, C. Robert-Granié2 and A. Legarra3, 1INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, 2Institut de l’Elevage, Castanet-Tolosan, France

2:00 PM 333 Genomic Selection in New Zealand Dual Purpose Sheep.
K. G. Dodds1, B. Auvray2, M. A. Lee2, S. A. N. Newman2 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. Kelly2, B. J. Hayes2, N. Moghaddar2 and J. van der Werf3, 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, Bandooora, 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
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. Yao2, P. C. Hoffman3, L. E. Armentano2, D. M. Spurlock4, R. J. Tempelman2 and M. J. VandeHaar5,
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. Pryce2, D. P. Berry3 and R. F. Veerkamp4, 1Animal 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. Spurlock5, R. J. Tempelman2, K. A. Weigel1, L. E. Armentano1, G. R. Wiggins4, R. F. Veerkamp2, Y. de Haas8, M. P. Coffey6, E. E. Connor7, M. D. Hanigan5, C. R. Staples6 and M. J. VandeHaar5, 1Iowa State University, Ames, 2Michigan State University, East Lansing, 3University of Wisconsin, Madison, 4Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, 5Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 6Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 7SRUC, Edinburgh, United Kingdom, 8USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, 9Virginia Polytechnic Institute and State University, Blacksburg, 10Dept. 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. Lippi4, P. Martin1, N. Iannuccelli1, Y. Billon4, L. Canario1 and L. Liaubet4, 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. Westrø2, S. Cirera3, M. Fredholm1, L. Franke3 and H. N. Kadarmideen1, 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. Iannuccelli1, Y. Lippi4, P. Martin1, Y. Billon4, M. San Cristobal6 and L. Liaubet4, 1INRA UMR1388, F-31266 Castanet-Tolosan, France, 2INRA, Castanet-Tolosan, France, 3INRA, Castanet-Tolosan, 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.  
Georg-August University, Göttingen, Germany; Uppsala University, Uppsala, Sweden;  
Institute of Farm Animal Genetics of the Friedrich-Loeffler-Institute, Neustadt-Mariensee, Germany;  
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, B. D. Valente, J. P. Steibel, R. O. Bates, C. W. Ernst, H. Khatibi and G. J. M. Rosa,  
University of Wisconsin, Madison; 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, J. Ertl, R. Emmerling, C. Edel, K. U. Götz and J. Bennewitz,  
Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany;  
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, T. Strabel and M. P. L. Calus,  
Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poznan, Poland;  
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, H. Bruce, R. Kemp, P. Charugu, C. Zhang, A. Huisman and Z. Wang,  
University of Alberta, Edmonton, AB, Canada; Genesis Genetics Inc., Oakville, MB, Canada;  
Hypor Inc, Regina, SK, Canada; Hendrix Genetics, Boxmeer, Netherlands

4:45 PM 059 Prediction of Heterosis in White Leghorn Crossbreds using Paternal 60K SNP Genotypes.  
E. N. Amuzu-Aweh, H. Bovenhuis, D. J. de Koning and P. Bijma,  
Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands;  
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, U. S. Nielsen, G. R. Wiggans, G. P. Aamand, B. Guldbrandtsen and M. S. Lund,  
Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark;  
Knowledge Center for Agriculture, Aarhus, Denmark; Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD;  
Nordic Cattle Genetic Evaluation, Aarhus, Denmark

5:15 PM 061 Maximizing Crossbred Performance through Purebred Genomic Selection.  
H. Esfandyarpour, A. C. Sørensen and P. Bijma,  
Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark;  
Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands;  
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 and J. van der Werf,  
School of Environmental & Rural Science, University of New England, Armidale, Australia;  
Sheep-CRC, Armidale, Australia; University of New England, Armidale, Australia

5:45 PM 063 Genomic Prediction using QTL Derived from Whole Genome Sequence Data.  
R. F. Brøndum, 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. McEwan, 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-Viala4, P. Guibert5, P. Panis6, A. Legarra7 and F. Barillet8, 1INRA, Toulouse, France, 2Institut de l'Elevage, Castanet-Tolosan, France, 3Ovitest, 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. Carillier1*, 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. Elsen1 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 Genome Wide Association for Heat Stress Tolerance/Susceptibility in Florida Dairy Goats.
A. Zidi1, H. Abo-Shady1, A. Molina1, A. Menéndez-Buxadera1, M. Sánchez-Rodríguez1, C. J. Díaz1, M. J. Carabaño2 and J. M. Serradilla3, 1Universidad de Córdoba, Córdoba, Spain, 2INIA, Madrid, Spain

5:30 PM 341 Expression of the Ovine Hippocampal Glucocorticoid Receptor (GR) and Mineralcorticoid 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. Gorkhali1, 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. Wood\textsuperscript{1,2}, and O. W. Willems\textsuperscript{3}, \textsuperscript{1}Hybrid Turkeys, Kitchener, ON, Canada, \textsuperscript{2}Centre 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\textsuperscript{*}, 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. Khansafid\textsuperscript{1,2,3}, J. E. Pryce\textsuperscript{4}, S. Bolormad\textsuperscript{4}, S. P. Miller\textsuperscript{4}, Z. Wang\textsuperscript{4}, C. Li\textsuperscript{4} and M. E. Goddard\textsuperscript{4}, \textsuperscript{1}The University of Melbourne, Melbourne, Australia, \textsuperscript{2}Department of Environment and Primary Industries, Melbourne, Australia, \textsuperscript{3}Dairy Futures Cooperative Research Centre (CRC), Melbourne, Australia, \textsuperscript{4}Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, \textsuperscript{5}CRC for Sheep Industry Innovation, Armidale, Australia, \textsuperscript{6}Centre for Genetic Improvement of Livestock - University of Guelph, Guelph, ON, Canada, \textsuperscript{7}University of Alberta, Edmonton, AB, Canada, \textsuperscript{8}The 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\textsuperscript{*}, Jiangxi Agricultural University, Nanchang, China

4:30 PM 356 SNP Effects Depend on Genetic and Environmental Context.
J. W. M. Bastiaansen\textsuperscript{1}, H. Bovenhuis\textsuperscript{1}, M. S. Lopes\textsuperscript{1,2}, F. F. Silva\textsuperscript{3}, H. J. Megens\textsuperscript{1} and M. P. L. Calus\textsuperscript{1}, \textsuperscript{1}Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, \textsuperscript{2}TOPIGS Research Center IPG, Beuningen, Netherlands, \textsuperscript{3}Universidade Federal de Viçosa, Viçosa, Brazil, \textsuperscript{4}Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

5:00 PM 357 Beyond Genomic Selection.
B. P. Kinghorn\textsuperscript{*}, 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. Estelle\textsuperscript{*}, N. Mach\textsuperscript{1}, Y. Ramayo-Calda\textsuperscript{2}, F. Levenez\textsuperscript{2}, G. Lemonnier\textsuperscript{1}, C. Denis\textsuperscript{1}, J. Dor\textsuperscript{7}, C. Larzu\textsuperscript{2}, P. Lepage\textsuperscript{2} and C. Rogel-Gaillard\textsuperscript{2}, \textsuperscript{1}INRA, UMR1313 GABI, Jouy-en-Josas, France, \textsuperscript{2}INRA, UMR1319 MICALIS, Jouy-en-Josas, France

5:45 PM 359 Genome Wide Perspective of Genetic Variation in Pig Metabolism and Production Traits.
L. Fontanesi\textsuperscript{1}, S. Bovo\textsuperscript{1}, G. Mazzoni\textsuperscript{1}, A. B. Samorè\textsuperscript{2}, G. Schiavo\textsuperscript{1}, E. Scotti\textsuperscript{1}, F. Fanelli\textsuperscript{2}, F. Bertolini\textsuperscript{2}, M. Gallo\textsuperscript{1}, L. Buttazzoni\textsuperscript{1}, G. Galimberti\textsuperscript{3}, D. G. Calò\textsuperscript{4}, M. Mezzullo\textsuperscript{5}, P. L. Martelli\textsuperscript{5}, R. Casadio\textsuperscript{5}, U. Pagotto\textsuperscript{5}, V. Russo\textsuperscript{5} and S. Dall’Olio\textsuperscript{5}, \textsuperscript{1}Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, \textsuperscript{2}Department of Surgical and Medical Sciences, Endocrinology Unit, University of Bologna, Bologna, Italy, \textsuperscript{3}ANAS, Roma, Italy, \textsuperscript{4}Consiglio per la Ricerca e la Sperimentazione in Agricoltura - Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Roma, Italy, \textsuperscript{5}Department of Statistical Sciences “Paolo Fortunati”, University of Bologna, Bologna, Italy, \textsuperscript{6}Biocomputing 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. Simianer\textsuperscript{1}, Y. Ma\textsuperscript{2} and S. Qanbari\textsuperscript{2}, \textsuperscript{1}Georg-August University, Göttingen, Germany, \textsuperscript{2}China Agricultural University, Beijing, China, \textsuperscript{3}Georg-August University, Göttingen, Germany
4:30 PM 203 New Methods for Capturing Unidentified Genetic Variation underlying Infectious Disease in Livestock Populations.
A. Doeschl-Wilson\textsuperscript{1,4}, D. Lipschutz-Powell\textsuperscript{1}, O. Anacleto\textsuperscript{1}, L. A. García-Cortés\textsuperscript{2}, G. Lough\textsuperscript{1}, A. Lengeling\textsuperscript{1}, S. Bergmann\textsuperscript{3} and J. A. Woolliams\textsuperscript{1,4}, \textsuperscript{1}The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{2}SGIT - INIA, Ministerio de Ciencia e Innovación, Madrid, Spain, \textsuperscript{3}Helmholtz Centre for Infection Research, Braunschweig, Germany

5:00 PM 204 My P Value is Lower than Your P Value! Beyond GWAS in Livestock Genomics.
J. Szyda\textsuperscript{1,2}, M. Fraszczak\textsuperscript{3}, R. Giannico\textsuperscript{4}, S. Kaminski\textsuperscript{5}, M. Mielczarek\textsuperscript{1}, G. Minozzi\textsuperscript{6}, E. L. Nicolazzi\textsuperscript{4}, T. Suchocki\textsuperscript{3}, K. Wojdak-Maksymiec\textsuperscript{4} and A. Zarnecki\textsuperscript{2}, \textsuperscript{1}Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, \textsuperscript{2}National Research Institute of Animal Production, Cracow-Balice, Poland, \textsuperscript{3}Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, \textsuperscript{4}Fondazione Parco Tecnologico Padano, Lodi, Italy, \textsuperscript{5}University of Warmia and Mazury, Olsztyn, Poland, \textsuperscript{6}Parco Tecnologico Padano, Lodi, Italy, \textsuperscript{7}West Pomeranian University of Technology, Szczecin, Poland

5:30 PM 205 Heritability of Complex Human Diseases in the UK Biobank.
M. Muñoz\textsuperscript{1}, R. Pong-Wong\textsuperscript{2}, C. Haley\textsuperscript{3} and A. Tenesa\textsuperscript{4}, \textsuperscript{1}The Roslin Institute and R(D)SVS, University of Edinburgh, Roslin, United Kingdom, \textsuperscript{2}The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{3}MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, \textsuperscript{4}The 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. Butler1, M. O’Donovan1, B. McCarthy1, E. Pryce1 and D. P. Berry1, 2, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 1Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Biosciences 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 Linde2 and Y. de Haas3, 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, 2, M. H. A. Santana1, G. A. Oliveira Jr1, F. M. Rezende1, H. Fukumatsu1, P. A. Alexandre1, A. S. M. Cesar1, M. E. Carvalho1, L. L. Coutinho1, J. P. Eler1, E. C. Mattos1, F. Baldi1 and D. J. Garrick1, 1NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, 2Federal University of Uberlandia, Patos de Minas, Brazil, 1LZT/ESALQ/University of Sao Paulo, Piracicaba, Brazil, 1Universidade de Sao Paulo/Esalq, Piracicaba, Brazil, 1Universidade Estadual Paulista “Julio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 1Iowa 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. Keeler2, L. A. Kuehn3, H. C. Freely4, A. K. Lindholm-Perry4 and R. M. Lewis5, 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
Identification and Comparison of MicroRNAs from Mammary Glands from Two Porcine Breeds using Solexa Deep-Sequencing technology.

J. Peng*, College of Animal Sciences, Zhejiang University, Hangzhou, China

Polymorphism and Mobilization of Transposons in Bos taurus.

B. Guldbrandtsen*, G. Sahana and M. S. Lund, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Consequences of Splitting Sequencing Effort over Multiple Breeds on Imputation Accuracy.

A. C. Bouwman* and R. F. Veerkamp, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands

Genomic Predictions using Whole Genome Sequence Data and Multi-breed Reference Populations.

O. O. M. Iheshiulor1, J. A. Woolliams2, X. Yu1, R. Wellmann3 and T. H. E. Meuwissen4, 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

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

Linear and Nonlinear Models: Prediction

Chair: Marco C.A.M. Bink, Wageningen University

Bayshore Grand Ballroom A

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

Genomic Prediction of Health Traits in Humans: Demonstrating the Value of Marker Selection.

M. L. Bermingham1, R. Pong-Wong2, A. Spiliopoulou1, C. Hayward1, J. Rudan1, H. Campbell3, A. F. Wright1, J. F. Wilson3, F. V. Agakov3, P. Navarro1 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, 4Pharmatics Limited, Edinburgh, United Kingdom


A. Ehret1, D. Hochstuhl1 and G. Thaller1, 1Institute of Animal Breeding and Husbandry, University Kiel, Kiel, Germany, 2Institute for Theoretical Physics and Astrophysics, University Kiel, Kiel, Germany

Improved Accuracy of Genomic Prediction for Traits with Rare QTL by Fitting Haplotypes.

X. Sun*, R. L. Fernando, D. J. Garrick and J. C. M. Dekkers, Iowa State University, Ames

Correcting For Unequal Sampling in Principal Component Analysis of Genetic Data.

W. O. Burgos-Paz1, S. E. Ramos-Onsins1, M. Perez-Enciso1 and L. Ferretti1, 1Centre for Research in Agricultural Genomics, Bellaterra, Spain, 2Universitat Autònoma de Barcelona, Bellaterra, Spain, 3UMR 7138, UPMC and CIRB, College de France, Paris, France

Evaluation of Antedependence Model Performance and Genomic Prediction for Growth in Danish Pigs.

L. Wang*, 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

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<th>Time</th>
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<tr>
<td>10:30 AM</td>
<td><strong>Genomic Signatures of Selection in the Modern Horse.</strong>&lt;br&gt;J. R. Mickelson, J. L. Petersen, S. J. Valberg and M. E. McCue, University of Minnesota, Saint Paul</td>
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<tr>
<td>11:00 AM</td>
<td><strong>Cat Domestication &amp; Breed Development.</strong>&lt;br&gt;L. A. Lyons*, Department of Veterinary Medicine &amp; Surgery, College of Veterinary Medicine, University of Missouri - Columbia, Columbia, MO</td>
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<td>11:30 AM</td>
<td><strong>Genetic Interactions Among Three Pigmentation Loci in Domestic Dogs.</strong>&lt;br&gt;S. M. Schmutz and D. L. Dreger, University of Saskatchewan, Saskatoon, SK, Canada</td>
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## Symposium: Genetics of Trait Complexes - Lactation
**Chair:** Juan F. Medrano, University of California

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<td>10:30 AM</td>
<td><strong>RNA Sequencing for the Analysis of Complex Traits in Milk: Detection of Bacteria.</strong>&lt;br&gt;J. F. Medrano¹, A. Canovas and A. Islas-Trejo², University of California, Davis, University of California, Davis, CA</td>
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<td>11:00 AM</td>
<td><strong>Functional Variation in the Prolactin Receptor of Pigs.</strong>&lt;br&gt;R. C. Hovey¹, A. Schennink, M. K. VanKlompenberg, R. Manjarin and J. F. Trott, University of California, Davis, CA</td>
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<td>11:30 AM</td>
<td><strong>Rare Genetic Variants and the Regulation of Bovine Milk Composition.</strong>&lt;br&gt;S. Davis and M. Littlejohn, Livestock Improvement Corporation, Hamilton, New Zealand</td>
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## Symposium: Genomic Tools for Mapping QTL and Genes
**Chair:** Michel Georges, University of Liège

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<td>10:30 AM</td>
<td><strong>NGS-based Reverse Genetic Screen Reveals Loss-of-Function Variants Compromising Fertility in Cattle.</strong>&lt;br&gt;M. Georges³¹, C. Charlier², W. Li², C. Harland², M. Littlejohn², F. Creagh³, M. D. Keehan², T. Drue³, W. Coppoet² and R. Spelman², University of Liège, Liège, Belgium, University of Liège, Liège, Belgium, Livestock Improvement Corporation, Hamilton, New Zealand, LIC, Hamilton, New Zealand</td>
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<td>11:00 AM</td>
<td><strong>Exploiting Whole Genome Sequence Data for the Identification of Causal Trait Variants in Cattle.</strong>&lt;br&gt;H. Pausch¹, C. Warns², C. Edel², R. Emmerling², K. U. Götz² and R. Fries¹, Chair of Animal Breeding, Technische Universität München, Freising, Germany, Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Grub, Germany</td>
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<td>11:30 AM</td>
<td><strong>Cis and Trans-Acting eQTL Mapping from RNAseq Data in Swine Populations.</strong>&lt;br&gt;J. P. Steibel¹, Michigan State University, East Lansing</td>
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## Developments in Beef Cattle Genetics
**Chair:** David Johnston, University of New England

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<td>1:30 PM</td>
<td><strong>The Genetics of Brahman Cow Weight in Northern Australia and its Relationship with Female Reproductive Performance.</strong>&lt;br&gt;M. L. Wolcott¹, Animal Genetics and Breeding Unit, Armidale, Australia</td>
</tr>
</tbody>
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Genetic Parameter Estimates for Calving Difficulty and Birth Weight in a Multi-breed Population.
C. M. Ahlberg1, L. A. Kuehn1, R. M. Thallman2, S. D. Kachman3 and M. L. Spangler1, 1University of Nebraska, Lincoln, 2USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 3University 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. Lee1, J. K. Naberg 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. Lassen1, P. C. Garnsworthy2, M. G. Changada3, E. Negussie4, P. Lovendahl5 and Y. de Haas6, 1Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, 2The University of Nottingham, Loughborough, United Kingdom, 3Scottish Rural University College (SRUC), Edinburgh, United Kingdom, 4MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 5Animal 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. Negussie1, P. Mäntysaari2, E. A. Mäntysaari1 and M. H. Lidauer1, 1MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 2MTT Agrifood Research Finland, Animal Production Research, Jokioinen, Finland

Genetic Variation for Methane Traits in Beef Cattle.
P. F. Arthur1, R. M. Herd2, S. S. Bird2, K. A. Donoghue3 and R. S. Hegarty4, 1NSW Department of Primary Industries, Narellan, NSW, Australia, 2NSW Department of Primary Industries, Armidale, Australia, 3NSW Department of Primary Industries, Trangie, Australia, 4University of New England, Armidale, Australia

Rumen Differences between Sheep Identified as Being Low or High Methane Emitters.
W. E. Bain1, L. Bezuidenhout1, N. B. Jopson2, C. S. Pinares-Patino3 and J. C. McEwan4, 1AgResearch Invermay, Dunedin, New Zealand, 2Abacusbio, Dunedin, New Zealand, 3AgResearch, Palmerston North, New Zealand, 4AgResearch, Invermay, New Zealand

Consequences of Selection for Environmental Impact Traits in Dairy Cows.
P. B. Kandel1, S. Vanderick1, M. L. Vanrobaey1, A. Vanlierde2, F. Dehareng2, E. Froidmont2, H. Soyeurt1 and N. Gengler1, 1University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium, 2Walloon Agricultural Research Center, Gembloux, Belgium

Symposium: Breeding in Aquaculture Species
Chair: William S. Davidson, Simon Fraser University
Cypress Room
1:30 PM  267  Genomics in Selective Breeding of Atlantic Salmon.
T. Moen¹ and J. Ødegård², ¹AquaGen AS, Trondheim, Norway, ²AquaGen, Aas, Norway

2:00 PM  268  The Development and Characterization of a 57K SNP Chip for Rainbow Trout.
Y. Palti¹, G. Gao¹, T. Moen¹, S. Liu¹, M. P. Kent¹, S. Lien¹, M. R. Miller¹ and C. E. Rexroad¹, ¹NCCWA-ARS-USDA, Kearneysville, WV, ²Aquagen, Aas, Norway, ³Centre of Integrative Genetics, Aas, Norway, ⁴UC Davis, Davis, CA, ⁵NCCWA-ARS-USDA, Kearneysville, WV

2:30 PM  269  Evolution of Coho Salmon (Oncorhynchus kisutch) Breeding Programs.
R. Neira¹, University of Chile, Aquainnovo, Santiago, Chile

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

1:30 PM  064  (A)cross-Breed Genomic Prediction.
M. P. L. Calus¹, H. Huang¹, Y. C. J. Wientjes², J. ten Napel³, J. W. M. Bastiaansen³, M. D. Price³, R. F. Veerkamp³, A. Vereijken¹ and J. J. Windig¹, ¹Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ³Animal Breeding and Genetics Centre, Wageningen UR Livestock Research, Lelystad, Netherlands, ⁴Hendrix Genetics, Boxmeer, Netherlands

2:00 PM  065  Across Breed Genomic Predictions in Beef Cattle.
M. Saatchi¹ and D. J. Garrick², ¹Iowa State University, Ames, ²Massey University, Palmerston North, New Zealand

2:30 PM  066  Across-Breed Genomic Prediction in Dairy Cattle.
B. L. Harris¹, LIC, Hamilton, New Zealand

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

1:30 PM  360  Genome-Wide Analysis of the Differential Response to Experimental Challenges with Porcine Circovirus 2b.
T. Engle¹, E. Jobman¹, T. Moural¹, A. Knikne¹, S. Barnes¹, E. Davis¹, J. Qiu¹, J. Bundy¹, J. Tant¹, T. Johnson¹, M. F. Rothschild¹, J. Galeota¹, R. K. Johnson¹, G. Plastow¹, S. D. Kachman¹ and D. C. Ciobanu³, ¹University of Nebraska, Lincoln, ²Iowa State University, Ames, ³University of Nebraska, Lincoln, ⁴University of Alberta, Edmonton, AB, Canada

2:00 PM  361  Strategies for using Genomics to Improve Swine Resistance to PRRS.
L. R. Schaeffer¹, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

2:30 PM  362  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. Li¹, 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

1:30 PM  094  A Genome-Wide Association Study of Immune Response in Holstein Bulls.
K. A. Thompson-Crispi¹, M. Sargolzaei¹, F. Miglior², F. S. Schenkel² and B. Mallard¹, ¹Dept Pathobiology, University of Guelph, Guelph, ON, Canada, ²Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³The Semex Alliance, Guelph, ON, Canada, ⁴Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ⁵Canadian Dairy Network, Guelph, ON, Canada
Longitudinal Analysis of Somatic Cell Count for Joint Genetic Evaluation of Mastitis and Recovery Liability.
B. G. Welderufael, D. J. D. Koning, L. Janss, J. Franzen, and W. F. Fikse, 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, Department of Statistics, Stockholm University, Stockholm, Sweden

Genetics of Tolerance and Resistance to Nematode Infection in Sheep.
H. Rashid, H. A. Mulder, J. A. M. van Arendonk, M. C. M. de Jong, and M. J. Stear, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Quantitative Veterinary Epidemiology Group, Wageningen University, Wageningen, Netherlands, Veterinary 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, J. M. Higgins, and D. P. Berry, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, Trinity College Dublin, Dublin 2, Ireland, University College Dublin, Dublin, Ireland, University of Agriculture, Wageningen, Netherlands, INRA, UMR1313 GABI, Jouy-en-Josas, France, AgroParisTech, UMR1313 GABI, Paris, France, Department of Molecular Biology and Genetics, Aarhus University, Foulum, Denmark, INRA UMR1313 GABI, Jouy-en-Josas, France, INRA, UE1206 EASM, Suresnes, France, Cobb-Vantress Inc., Siloam Springs, AR, INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, INRA, Castanet-Tolosan, France, Agrocampus Ouest, UMR1348 PEGASE, Rennes, France, INRA, UMR1348 PEGASE, Saint-Gilles, France

Plasma Components as Traits for Resistance to Coccidiosis in Chicken.
E. Hanic, B. Bedhom, H. Jun, R. Hawken, M. S. Abrahamson, J. M. Elsen, B. Servin, M. H. Pinard-van der Laan, and O. Demeure, INRA, UMR1313 GABI, Jouy-en-Josas, France, AgroParisTech, UMR1313 GABI, Paris, France, Department of Molecular Biology and Genetics, Aarhus University, Foulum, Denmark, INRA UMR1313 GABI, Jouy-en-Josas, France, INRA, UE1206 EASM, Suresnes, France, Cobb-Vantress Inc., Siloam Springs, AR, INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, INRA, Castanet-Tolosan, France, Agrocampus Ouest, UMR1348 PEGASE, Rennes, France, INRA, 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. Kadri, G. Sahana, C. Chartier, I. T. Terhi, B. Gulbrandsen, L. Karim, U. S. Nielsen, F. Paniz, G. P. Aamand, N. Schulman, M. Georges, J. Vilkkil, M. S. Lund, and T. Druet, University of Liege, Liege, Belgium, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, Knowledge Center for Agriculture, Aarhus, Denmark, Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Nordic Cattle Genetic Evaluation, Aarhus, Denmark

A Gene Network Inferred from Genome-wide Association: Prioritization of QTLs Associated with Tropical Cattle Reproduction.
L. R. Porto-Neto, M. R. Fortes, M. J. Kelly, S. A. Lehnert, and A. Reverter-Gomez, CSIRO Food Futures Flagship, Brisbane, Australia, The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, The 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.

Effect of Selection for Residual Variance of Litter Size on Components of Litter Size in Rabbits.
M. J. Argente, M. D. L. L. Garcia, and A. Blasco, Universidad Miguel Hernández de Elche, Orihuela, Spain, Universidad 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. Proulx1,3, O. W. Willems1 and B. J. Wood2,1, Centre for the Genetic Improvement of Livestock, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, 1Hybrid 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, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Department 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. Miglior2,3, J. Jamrozik2, 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

Intergrating 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. Thaller4 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, P. M. VanRaden2, J. B. Cole3 and J. O’Connell4, National 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. (vit), Verden, Germany

5:45 PM  295 Genetic Analysis of Longevity in Dutch Dairy Cattle using Random Regression.
M. L. van Pelt1,2* and R. F. Veerkamp1, 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*, AbacasBio 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 Hollandier1,2, N. Moghaddas3, K. R. Kelman2, G. E. Gardner3,5 and J. van der Werf1, 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, 4Murdock 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. Dominik1, J. E. Newton1, B. J. Hayes1 and J. van der Werf1, 1CSIRO Animal Food and Health Sciences, Armidale, Australia, 2Animal Genetics and Breeding Unit, UNE, Armidale, Australia, 3The Department of Environment and Primary Industries, Bundook, 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. Kijas1, 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. Pena1, D. Foulquié2, Y. Bourdillon1 and D. François4, 1INRA, UMR1388 GenPhySE, Toulouse, France, 2INRA UE03321, La Fage, France, 3INRA UE0322, La Sapinière, Bourges, France, 4INRA UMR1388 GenPhySE, 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
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. Moore*1, T. Pritchard, S. Wilkinson, R. Mrode, F. Pearson, 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. Dillon1, J. O. Sanders1, A. D. Herring1 and D. G. Riley1, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 1Department of Animal Science, Pennsylvania State University, University Park, 1Texas A&M University, College Station

5:00 PM 246 Genetic Improvement of Reproduction in Beef Cattle.
D. Johnston*, 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. Jamrozik*, 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. Pabio2, E. Hjerpe3, M. Niflorooshan1, A. Launay3 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. Gianola*1, G. Morota1 and J. Crossa2, 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  296  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  297  Are Evaluations on Young Genotyped Dairy Bulls Benefiting from the Past Generations?

D. Lourenco¹, I. Misztal², S. Tsuruta³, I. Aguilar² and T. J. Lawlor³, ¹University of Georgia, Athens, ²INIA, Las Brujas, Uruguay, ³Holstein Association USA Inc., Brattleboro, VT, 4ARO, The Volcani Center, Bet Dagan, Israel

11:00 AM  298  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. Hayes³, ¹Bioscience 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  299  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. Calus², 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  300  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  301  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  317  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
J. Recoillay¹, C. Leterrier², L. Calandrau³, A. Bertin⁴, F. Petet⁵, D. Gourichon⁶, A. Vignafr¹, C. Beaumont⁷, E. Le Bihan-Duval² and C. Arnould³, ¹INRA, UR83 Recherches Avicoles, Nouzilly, France, ²INRA, UMR85 Physiologie de la Reproduction et des Comportements, Nouzilly, France, ³UMR 1388 INRA / INPT ENSAT / INPT ENV, GenPhySE, Castanet-Tolosan, France, ⁴UE1295 Pôle d’Expérimentation Avicole de Tours, Nouzilly, France, ⁵INRA UMR1388 GenPhySe, Castanet-Tolosan, France

Genetic Parameters for Feather Pecking and Aggressive Behavior in Laying Hens using Poisson and Linear Models.
V. Grams¹, W. Bessei², H. P. Piepho³ and J. Bennwitz⁴, ¹Institute of Animal Husbandry and Breeding, University Hohenheim, Hohenheim, Germany, ²Institute of Crop Science, University of Hohenheim, Hohenheim, Germany, ³Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

A Genome Wide Association Analysis Confirms a Complex, Polygenic Determinism of Resistance to Salmonella Carrier-State in Chicken.
F. Calenge¹, A. Vignafr¹, B. Bed’Hom¹, P. Kaiser¹, P. Menanteau¹, P. Velge¹ and C. Beaumont¹, ¹INRA UMR1313 GABI, Jouy-en-Josas, France, ²INRA UMR1388 GenPhySe, Castanet-Tolosan, France, ³The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ⁴INRA UMR1282 ISP, Nouzilly, France, ⁵INRA UR083 URA, Nouzilly, France

Identification of SNP Markers for Resistance to Salmonella and IBDV in Indigenous Ethiopian Chickens.
A. Psifdi¹, G. Banoš², O. Matika¹, T. Desse¹, R. Christley¹, P. Wigley¹, J. Bettridge¹, O. Hanotte², T. Desta² and P. Kaiser¹, ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²Scotland’s Rural College, Edinburgh, United Kingdom, ³International Livestock Research Institute, Addis Ababa, Ethiopia, ⁴Institute of Infection & Global Health, University of Liverpool, Liverpool, United Kingdom, ⁵School of life Sciences, University of Nottingham, Nottingham, United Kingdom

Genomic Evaluation for Egg Weight in Crossbred Layers Receiving Various Diets.
H. Chapuis¹, F. Hérault², A. Varenne³, H. Rome³, C. Alleno³, P. Dehais³, A. Vignafr², T. Burlo³ and P. Le Roy², ¹SYSAAF, Nouzilly, France, ²Agrocampus Ouest UMR1348 PEGASE, Rennes, France, ³INRA UMR1348 PEGASE, Saint-Gilles, France, ⁴Novogen, Le Fœil, France, ⁵Zootests, Ploufragan, France, ⁶INRA UMR1388 GenPhySe, Castanet-Tolosan, France

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

Genomic Prediction using a Weighted Relationship Matrix to Account for Trait Architecture in US Holstein Cattle.
F. Tietze¹ and C. Maltecca, North Carolina State University, Raleigh

Hierarchical Quantitative Genetic Model using Genomic Information.
G. Gorjanc¹, J. A. Woolliams and J. M. Hickey, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Comparison of Some Equivalent Equations to Solve Single-Step GBLUP.
I. Strandén¹ and E. A. Mäntysaari¹, ¹MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, ²MTT Agrifood Research Finland, Jokioinen, Finland

Semi-Supervised Learning Combining Phenotyped and Non-Phenotyped Individuals for Enhancing Prediction in Residual Feed Intake.
C. Yao¹, X. Zhu¹ and K. A. Weigel¹, ¹University of Wisconsin, Madison, ²Department of Computer Science University of Wisconsin, Madison

A Single Step SNP Model Applied to Test-Day Data of Dairy Cows.
Z. Liu¹, vit Germany, Verden, Germany
**Haplotyp Base Geno Enabled Prediction of Traits Across Nordic Red Cattle Breeds.**

*B. Castro Dias Carabano*, Aarhus University, Tjelle, Denmark

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**Swine Breeding (1)**

Chair: Brian P. Kinghorn, University of New England

Bayshore Grand Ballroom D

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**Consequences of Selection for Indirect Genetic Effect for Growth in Pigs on Behavior and Production.**

I. Camerlink, N. Duivesteijn, W. W. Ursinus, J. E. Bolhuis and P. Bijma, 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

**Genetic Analysis of Skin Lesion Traits in Pigs and their Relationship with Growth Traits.**

S. Desire, S. P. Turner, C. R. G. Lewis, R. B. D'Eath, A. Doeschl-Wilson and R. Roehe, SRUC, Edinburgh, United Kingdom, PIC Europe, Nantwich, United Kingdom, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

**Genetic Relationships between Measures of Sexual Development, Boar Taint, Health and Aggressiveness in Pigs.**

S. Parois, A. Prunier, M. J. Mercar, N. Muller, E. Merlet and C. Larzelere, INRA, Saint-Gilles, France, IFIP, Le Rheu, France, INRA, Le Rheu, France, INRA, UMR1313 GABI, Jouy-en-Josas, France

**Genetic Control of Skatole Intake and Taste Sensation.**

B. Castro Dias Cuyabano, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

**Maternal Genetic Effects for Lifetime Growth Should be Considered More in Pig Breeding.**

S. Hermesch, C. R. Parke, M. M. Bauer and H. Gilbert, Aarhus University, Tjelle, Denmark, University of Queensland, Gatton QLD, Australia, INRA UMR1388, F-31326 Castanet-Tolosan, France

**Nurse Capacity in Crossbred Sows and Genetic Correlation to Purebred Fertility.**

B. Nielsen, I. Velander, T. Ostersen, M. A. Henryson and O. F. Christensen, Pig Research Centre, Copenhagen, Denmark, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjelle, Denmark

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**Symposium: Education and Training**

Chair: Ronald M. Lewis, University of Nebraska

Bayshore Grand Ballroom A

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**Filling the Knowledge Gap: Integrating Quantitative Genetics and Genomics in Graduate Education and Outreach.**


**Interdisciplinarity, Internationalization, Interculturality: Three Challenges of Training in Animal Breeding and Genetics in Europe.**

E. Verrier and H. Thomas, INRA UMR 1313 GABI, Jouy en Josas, France, AgroParisTech, Paris, France

**Training and Human Capacity Development in Australasia, S. and S.E. Asia and Sub-Saharan Africa.**

J. Gibson, E. O. Rege and M. G. Chaganda, University of New England, Armidale, Australia, PICO- Eastern Africa, Nairobi, Kenya, Scottish 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. Canmack, 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. Pickering, NSW Department of Primary Industries, Armidale, NSW, Australia, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, Alberta Agriculture and Rural Development, Lacombe, AB, Canada, Department of Animal Science, University of Wyoming, Laramie, WY, Department of Environment and Primary Industries, Bundoora, Australia, University of New England, Armidale, NSW, Australia, Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, AgResearch, Invermay, New Zealand, AgResearch, Palmerston North, New Zealand, University of Western Australia, Perth, WA, Australia, AgResearch, 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.
S. J. Rowe, J. C. McEwan, S. M. Hickey, R. A. Anderson, D. Hyndman, E. A. Young, H. Baird, K. G. Dodds, C. S. Pinares-Patino and N. K. Pickering, AgResearch, Mosgiel, New Zealand, AgResearch, Hamilton, New Zealand, AgResearch, Palmerston North, New Zealand
**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.  
P. Visscher*, Queensland Brain Institute, University of Queensland Diamantina Institute, Brisbane, Australia

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**Education and Training**

Chair: Ronald M. Lewis, University of Nebraska  
Cypress Room

10:30 AM Research Trainee Participation is a Bonus to Teaching Aims in the Bovine Respiratory Disease Complex Coordinated Agricultural Project.  
M. G. Thomas1*, N. F. Berge1, R. M. Enns1, R. Hagevoort2, T. T. Ross1, A. L. Van Eenennaam3, H. L. Neibergs3, J. S. Neibergs3 and J. E. Womack1, 1Colorado State University, Department of Animal Sciences, Fort Collins, 2New Mexico State University, Clovis, NM, 3New Mexico State University, Las Cruces, NM, 1University of California, Davis, 1Washington State University, Pullman, 1Texas A&M University, College Station

10:45 AM 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 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

11:30 AM 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

11:45 AM Capitalisation of Experiences in Implementing Genetic Improvement Programs in India – Role of Training and Education.  
A. Sudhakar1*, M. Kunju1, G. Suresh2 and G. Kishore1, 1National Dairy Development Board, Anand, India, 2Vellore-Tiruvannamalai District Co-operative Milk Producers' Union, Vellore, India

12:00 PM Breeding Program as a Tool for Education and Training of Young.  
R. N. B. Lobo*, Embrapa Goats and Sheep, Sobral, Brazil

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**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 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. Kemper5, University of Melbourne, Melbourne, Australia

D. Jonas1, 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. Karim1, A. M. Pérez O’Brien1, G. Mészáros1, S. Eaglen1, S. A. Boison1 and I. Curić2,  
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, 4Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Armidale, Australia, 5The University of Queensland, School of Veterinary Science, Gatton, Australia, 6Animal Genetics and Breeding Unit, Armidale, Australia

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. Woolaston2, D. P. Berry3, E. Wall4, M. Winters5, R. Butler6 and M. Shaffer7, 8Biosciences Research Division, Department of Environment and Primary Industries, Victoria, Australia, 9Arlie Solutions, Pullmanvale, Queensland, Australia, 10Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 11SRUC, Edinburgh, United Kingdom, 12DairyCo, Kentworth, Warwickshire, United Kingdom, 13Holstein Australia, Melbourne, Victoria, Australia, 14Dairy Australia, Melbourne, Victoria, Australia

11:00 AM 155 Improving Dairy Cow Fertility using Milk-Based Indicator Traits.  
C. Bastin1, J. Vandenplas1,2 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. Bolormaa4,5, K. E. Kemper6, D. Brown6, A. A. Swain1,2, J. H. van der Werf6,8 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

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. Lu4, G. VanderVoorde5 and I. B. Mandell4, 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, L. R. Porto-Neto2, K. L. DeAtley3, A. Reverter-Gomez4, M. G. Thomas1, S. S. Moore1, S. A. Lehnert1 and W. M. Snelling1, 1The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 2CSIRO Food Futures Flagship, Brisbane, Australia, 3California State University, Chico, Chico, CA, 4Colorado State University, Department of Animal Sciences, Fort Collins, 5USDA, ARS, US MARC, Clay Center, NE
Reducing the Incidence of Early Embryonic Mortality in Beef Cattle.
R. D. Schnabel\textsuperscript{1}, J. F. Taylor\textsuperscript{1}, D. S. Brown\textsuperscript{1}, M. F. Smith\textsuperscript{1}, M. Rolf\textsuperscript{1}, M. D. MacNeill\textsuperscript{1}, B. P. Kinghorn\textsuperscript{2} and D. J. Patterson\textsuperscript{1}, University of Missouri, Columbia,\textsuperscript{2} Oklahoma State University, Stillwater, OK, \textsuperscript{3} Kansas State University, Manhattan, \textsuperscript{4} University of New England, Armidale, Australia

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

Allele-Specific Expression, a New Genomics Tool for Development of Value-Added SNP Chips and to Fine Map QTL.
W. M. Muir\textsuperscript{2}\textsuperscript{,} S. Perumbakkam\textsuperscript{1}, A. Black-Pyrkosz\textsuperscript{2}, J. R. Dunn\textsuperscript{2} and H. H. Cheng\textsuperscript{2}, Purdue University, West Lafayette, IN, \textsuperscript{3} Michigan State University, East Lansing, \textsuperscript{4} USDA, ARS, ADOL, East Lansing, MI

Single Step Methods with a View towards Poultry Breeding.
A. Legarra\textsuperscript{1}, I. Misztal\textsuperscript{2} and J. Aguilar\textsuperscript{3}, INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, \textsuperscript{4} University of Georgia, Athens, \textsuperscript{5} INIA, Las Brujas, Uruguay

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

Regional Heritability Mapping of Production Traits in Epidemic Porcine Reproductive and Respiratory Syndrome.
C. M. Orret\textsuperscript{1}, N. Dee\textsuperscript{2}, R. Pong-Wong\textsuperscript{1}, O. Matika\textsuperscript{1}, C. R. G. Lewis\textsuperscript{1}, D. G. McLaren\textsuperscript{2}, A. L. Archibald\textsuperscript{3} and S. C. Bishop\textsuperscript{1}, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{4} Genus, plc, Hendersonville, TN, \textsuperscript{5} PIC Europe, Nantwich, United Kingdom, \textsuperscript{6} Genus PLC, De Forest, WI

A Genome-Wide Association Study for the Incidence of Persistent Bovine Viral Diarrhea Virus Infection in Cattle.
E. Casas\textsuperscript{1}, B. E. Hessman\textsuperscript{1}, J. W. Keele\textsuperscript{1} and J. F. Ridpath\textsuperscript{1}, USDA, ARS, National Animal Disease Center, Ames, IA, \textsuperscript{2} Haskell County Animal Hospital, Haskell, KS, \textsuperscript{3} USDA-ARS, Clay Center, NE, \textsuperscript{4} National Animal Disease Center, USDA-ARS, Ames, IA

A Meta-Analysis for Bovine Tuberculosis Resistance in Dairy Cattle.
S. Tsairidou\textsuperscript{1}, J. Woolliams\textsuperscript{2}, A. Allen\textsuperscript{2}, R. Skuce\textsuperscript{2}\textsuperscript{,} S. H. McBride\textsuperscript{2}, R. Pong-Wong\textsuperscript{2}, O. Matika\textsuperscript{2}, E. Finlay\textsuperscript{2}, D. P. Berry\textsuperscript{2}, D. Bradley\textsuperscript{2}, S. McDowell\textsuperscript{2}, E. Glass\textsuperscript{2} and S. C. Bishop\textsuperscript{2}, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{3} Agri-Food and Biosciences Institute, Belfast, United Kingdom, \textsuperscript{4} School of Biological Sciences, Queen’s University of Belfast, Belfast, United Kingdom, \textsuperscript{5} Department of Genetics, Trinity College Dublin, Dublin, Ireland, \textsuperscript{6} Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

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. Serão\textsuperscript{1}, R. A. Kemp\textsuperscript{1}, B. E. Moto\textsuperscript{1}, J. C. S. Harding\textsuperscript{1}, P. Willson\textsuperscript{2}, S. C. Bishop\textsuperscript{3}, G. S. Plastow\textsuperscript{2} and J. C. M. Dekkers\textsuperscript{1}, Iowa State University, Ames, \textsuperscript{4} Genesus Inc, Lethbridge, AB, Canada, \textsuperscript{5} Fast Genetics Inc., Saskatoon, SK, Canada, \textsuperscript{6} University of Saskatchewan, Saskatoon, SK, Canada, \textsuperscript{7} The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{8} University of Alberta, Edmonton, AB, Canada

A Comprehensive Genetic Study of Resistance to Nematodes in Sheep using the Ovine SNP Chip.
V. Riggio\textsuperscript{1}, O. Matika\textsuperscript{1}, R. Pong-Wong\textsuperscript{1}, C. R. Moreno\textsuperscript{2}, A. Carta\textsuperscript{2} and S. C. Bishop\textsuperscript{1}, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, \textsuperscript{2} INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, \textsuperscript{3} Research Unit: Genetics and Biotechnology, AGRIS Sardinia, Sassari, Italy
Breeding in Aquaculture Species: Non-Salmonids
Chair: Roberto Neira, University of Chile, Aquainnovo
Cypress Room

R. Rachel1, I. Palhière1, C. R. Moreno2, G. Foucras1, C. Maroteau3, A. Tircazes2, G. Salles2, G. Balocchi1 and G. Tosser-Klopp3, INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, 2INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 3ENVT-INRA, Castanet-tolosan, France, 4Université François Rabelais de Tours, Tours, France

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. Bangera1, M. Baranski1 and S. Lien2, 1Norwegian Institute of Food, Fisheries and Aquaculture Research, Tromsø, Norway, 2Centre 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, M. Vandeputte3,4, E. Pepey1, M. O. Vidal1, C. Ouédraogo1, M. Canonne2, H. D’Cotta2, J. F. Barrié2, E. Baras2 and B. Chatain2, 1WorldFish, Penang, Malaysia, 2CIRAD, Montpellier, France, 3INRA, Jouy en Josas, France, 4IFREMER, Palavas les Flots, France

2:15 PM 273 Genetic Parameters for Within-family Variance of Harvest Weight in Nile Tilapia (Oreochromis niloticus).
J. Marjanovic1,2, H. A. Mulder1, H. L. Khaw3,4 and P. Bijma1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 3The WorldFish Center, Penang, Malaysia

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. Montaldo1, G. R. Campos-Montes2,3 and H. Castillo-Juárez2, 1Universidad Nacional Autónoma de México, DF, Mexico, 2Universidad Autónoma Metropolitana, DF, Mexico, 3Maricultura 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, S. C. Bishop1, J. Toro2 and R. D. Houston1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Austral 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. Mrode4, 1Scotland’s Rural College, Edinburgh, United Kingdom, 2SRUC, Edinburgh, United Kingdom, 3The 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. Calus1, M. E. Goddard1,2 and B. J. Hayes1,5,6, 1Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 3The Department of Environment and Primary Industries, Bundoora, Australia, 4University of Melbourne, Parkville, Australia, 5Dairy Futures Cooperative Research Centre, Bundoora, Australia, 6La Trobe University, Bundoora, Australia
Across-Breeds Ancestral Relationships and Metafounders for Genomic Evaluation.
A. Legarra, O. F. Christensen, Z. G. Vitezica, J. Aguilar, and I. Misztal
INRA, Toulouse, France, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, Unité Mixte ENSAT-INRA, Toulouse, France, INIA, Las Brujas, Uruguay, University of Georgia, Athens

Accuracy of Genomic Breeding Values Predicted Within and Across Breeds in Pig Populations.
A. M. Hidalgo, J. W. M. Bastiaansen, M. S. Lopes, B. Harlizius, M. A. Groenen, and D. J. D. Koning
Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, TOPIGS 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. Plieschke and C. Edel
Bavarian State Research Center for Agriculture, Institute of Animal Breeding, Poing, Germany, Bavarian 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. Shen and W. G. Hill
Division of Computational Genetics, Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden, Institute 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. Mulder, W. G. Hill, and E. F. Knol
Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom, TOPIGS Research Center IPG, Beuningen, Netherlands

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

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

Use of Genome Editing in Animal Breeding Programs.
J. Jenko, G. Gorjanc, G. Mézátos, B. C. A. Whitelaw, J. A. Woolliams, M. A. Cleveland, and J. M. Hickey
The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, Genus, Plc, Hendersonville, TN

Symposium: Adaptation and Selection in Harsh Environments
Chair: Paul Boettcher, FAO
Bayshore Grand Ballroom B-C
1:30 PM 044 Relationships between Adaptive and Productive Traits in Cattle, Goats and Sheep in Tropical Environments.
H. M. Burrow\textsuperscript{1,2} and J. M. Henshall\textsuperscript{1}, \textsuperscript{1}University of New England, Armidale, N.S.W., Australia, \textsuperscript{2}Food Futures Flagship, CSIRO Animal, Food and Health Sciences, Armidale, Australia

2:00 PM 045 Insights into the Interaction of Goat Breeds and their Environment.
A. Stella\textsuperscript{1}, Fondazione Parco Tecnologico Padano, Lodi, Italy

2:30 PM 046 Genomics of Heat Stress in Chickens.
S. J. Lamont\textsuperscript{1}, Iowa State University, Ames

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

Bayshore Grand Ballroom E-F

1:30 PM 181 Genomic Prediction and Genome Wide Association in Humans with Whole Genome Sequence Data.
A. Price\textsuperscript{1}, Harvard School of Public Health, Boston, MA

2:00 PM 182 Rapid Discovery of Mutations Responsible for Sporadic Dominant Genetic Defects in Livestock using Genome Sequence Data: Enhancing the Value of Farm Animals as Model Species.
A. Capitan\textsuperscript{1,2,13}, P. Michol\textsuperscript{1,2}, F. Guillaume\textsuperscript{1}, C. Grohs\textsuperscript{1}, A. Djari\textsuperscript{1,2}, S. Fritz\textsuperscript{1,2,13}, S. Barbe\textsuperscript{1,2}, P. Orc\textsuperscript{1,2}, E. Bourneuf\textsuperscript{1,2}, D. Rocha\textsuperscript{1}, D. Esquerrel\textsuperscript{1,2,13}, Y. Gallard\textsuperscript{1}, C. Klopp\textsuperscript{1,2} and D. Boichard\textsuperscript{1,2,13}, INRA, UMR1313 GABI, Jouy-en-Josas, France, \textsuperscript{2}INRA, UMR755 Biométrie et Intelligence Artificielle, Castanet-Tolosan, France, \textsuperscript{13}INRA, UMR826, Domaine expérimental du Pin-au-Haras, Exmes, France, \textsuperscript{14}VetAgro Sup, Unité Clinique Rurale, L'Arbresle, France, \textsuperscript{15}DST/IRCM/SREIT/LREG, CEA, Jouy-en-Josas, France, \textsuperscript{16}Université de Toulouse INPT ENVT, UMR1388 Génétique, Physiologie et Systèmes d’Elevage, Castanet-Tolosan, France, \textsuperscript{17}INRA, UMR1388 Génétique, Physiologie et Systèmes d’Elevage, GetPlaGe Genomic Facility, Castanet-Tolosan, France, \textsuperscript{18}Université de Toulouse INPT ENSAT, UMR1388 Génétique, Physiologie et Systèmes d’Elevage, Castanet-Tolosan, France

2:30 PM 183 Genomic Prediction from Whole Genome Sequence in Livestock: The 1000 Bull Genomes Project.
B. J. Hayes\textsuperscript{1,2,3,14}, I. M. MacLeod\textsuperscript{1,2}, H. D. Daetwyler\textsuperscript{1,2}, B. J. Phil\textsuperscript{1,2}, A. J. Chamberlain\textsuperscript{1,2}, C. Vander Jagt\textsuperscript{1,2}, A. Capitan\textsuperscript{1,2}, H. Pausch\textsuperscript{1,2}, P. Stothard\textsuperscript{1,2}, X. Liao\textsuperscript{1,2}, C. Schroten\textsuperscript{1,2}, E. Mullaart\textsuperscript{1,2}, R. Fries\textsuperscript{1,2}, B. Guldbrandtsen\textsuperscript{1,2}, M. S. Lund\textsuperscript{1,2}, D. Boichard\textsuperscript{1,2}, R. F. Veerkamp\textsuperscript{1,2}, C. P. VanTassell\textsuperscript{1,2}, B. Gredler\textsuperscript{1,2}, T. Druet\textsuperscript{1,2}, A. Bagnato\textsuperscript{1,2,13}, J. Vilkki\textsuperscript{1,2}, D. J. de Koning\textsuperscript{1,2}, E. Santus\textsuperscript{1,2,13} and M. E. Goddard\textsuperscript{1,2}, 1Department of Environment and Primary Industries, Bundoora, Australia, 2Dairy Futures Cooperative Research Centre, Bundoora, Australia, 3La Trobe University, Bundoora, Australia, 4University of Melbourne, Melbourne, Australia, 5CRC for Sheep Industry Innovation, Armidale, Australia, 6The Department of Environment and Primary Industries, Bundoora, Australia, 7UNCEA, Paris, France, 8Chair of Animal Breeding, Technische Universität Muenchen, Freising, Germany, 9University of Alberta, Edmonton, AB, Canada, 10CRV, Arnhem, Netherlands, 11CRV BV, Arnhem, Netherlands, 12Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 13INRA, UMR1313 GABI, Jouy-en-Josas, France, 14Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 15Animal Genetics Laboratory ARS-USAID, Beltsville, MD, 16Qualitas AG, Zug, Switzerland, 17University of Liège, Liège, Belgium, 18Università degli Studi di Milano, Milano, Italy, 19MTRA Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 20Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 21ANARB, Italian Brown Cattle Breeders’ Association, Bussolengo (VR), Italy, 22Department of Primary Industries, Melbourne, Australia

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\textsuperscript{1,2}, E. S. Kim\textsuperscript{1} and G. S. Plastow\textsuperscript{1}, \textsuperscript{1}Iowa State University, Ames, \textsuperscript{2}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\textsuperscript{1}, Genesus Inc, Lethbridge, AB, Canada
Sequencing Millions of Animals for Genomic Selection 2.0.
J. M. Hickey1*, G. Gorjanic1, M. A. Cleveland2, A. Krain2, J. Jenko1, G. Mézéros1, J. A. Woolliams1 and M. Perez-Enciso6, 1The Roslin Institute and R(D)S VS, University of Edinburgh, Midlothian, United Kingdom, 2Genus, Plc, Hendersonville, TN, 3Aviagen Ltd, Edinburgh, United Kingdom, 4Universitat Autònoma 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. Willems1*, N. J. H. Budigker2, 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 between Metabolites in Egg Yolk and Hatchability Traits in Layers.
D. J. Garrick1, Z. Q. Weng2, 1University of New England, Armidale, NSW, Australia, 2Institute for Clinical Veterinary and Animal Sciences, University of Sydney, Coffs Harbour, NSW, Australia

Genetic Power Lasso Models in the Analysis of Residual Feed Intake in Hybrid Turkeys, Kitchener, ON, Canada
M. Chabault1, M. Y. Boscher2, D. Bastianelli1, N. Sellier1, M. Chabault-Dhui1, E. Le Bihan-Duval1 and A. Narcy2, 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*, J. David4, 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. Strathe1, 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. Moller2 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. Wolfe1, R. L. Fernandez1, J. C. M. Dekkers1, J. Arango2, J. E. Fulton2, P. Settar3, N. P. O'Sullivan4 and D. J. Garrick5, 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. Weigend2, A. Weigend2, R. Preisinger2, M. Schmutz2, L. Roemisch-Margl3, R. Jonczyk4, M. C. Gülersönmez5, H. P. Piepho6, W. A. Malik7, F. Sittenstock8 and H. Simianer9, 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
A. M. G. Ibelli1, J. O. Peixoto1, J. A. P. Marchesi1, L. L. Coutinho1 and M. C. Ledur2, 1EMBRAPA Swine and Poultry, Concórdia, Brazil, 1Universidade do Contestado, Concórdia, Brazil, 2Universidade de São Paulo/Esalq, Piracicaba, Brazil

Detection of QTL Influencing Egg Quality Traits in Layers Receiving Various Diets.
H. Rome2,2, A. Varene1, F. Héraut1,2, H. Chaput1, C. Alleno2, P. Dehais5, A. Vignal1, T. Burlot1 and P. Le Roy1,2, 1INRA UMR 1348 PEGASE, Saint-Gilles, France, 2Agrocampus Ouest UMR 1348 PEGASE, Rennes, France, 3Novogen, Le Foëil, France, 4SYSAF, Nouzilly, France, 5Zootests, Ploufragan, France, 6INRA UMR 1388 GenPhySe, Castanet-Tolosan, France

Detecting Signatures of Selection in Lines of Broiler Chickens.
J. J. Stainton1,2, C. Grosse1, J. T. Howard2, F. Tiezzi1, K. A. Gray1, M. E. Cantão2, C. Marie-Etancelin1, 1JUT des Pays de l’Adour, UMR CNRS 5254 IPREM, Mont De Marsan, France, 2INRA UMR 1388 GenPhySe, Castanet-Tolosan, France

Detection Of Pleiotropic QTL Related To Protein Expression And Foie Gras Quality Traits.
Y. François1,2, C. Molette2, A. Vignal1, S. Davail1 and C. Marie-Etancelin1, 1INRA UMR 1388 GenPhySe, Castanet-Tolosan, France

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

Genome-Wide Association Analyses for Boar Taint Components in Different Pietrain Sired Crosses.
C. Grosse-Brinkhaus1, L. C. Storck1, C. Neuhoff1, L. Frieden1, K. Schellander1, C. Looft1 and E. Tholen1, Institute of animal science, University of Bonn, Bonn, Germany

Genome-Wide Association Study For Growth And Feed Intake in Duroc boars Utilizing Random Regression Models.
J. T. Howard1, F. Tiezzi1, S. Jiao1, K. A. Gray2 and C. Maltecca1, 1North Carolina State University, Raleigh, 2Smithfield Premium Genetics, Rose Hill, NC

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. Murani1, H. Reyers1, A. Göres1, A. Tuchschérer2, E. Kanitz2, S. Fonsuksil1 and K. Wimmers1, 1Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2Genetics and Biometry, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 3Behavioural Physiology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany

Genetic Associations of Farrowing Length in Two Maternal Lines of Pigs.
R. Zane1, A. M. G. Ibelli1, J. O. Peixoto1, M. E. Cantão1, M. V. G. da Silva1, P. F. Giachetto1, M. Freitas1, J. Lopes1 and M. C. Ledur1, 1EMBRAPA Swine and Poultry, Concórdia, Brazil, 2Embrapa Dairy Cattle, Juiz de Fora, Brazil, 3Embrapa Agricultural Informatics, Campinas, Brazil, 4BRF S/A, Curitiba, Brazil

Genome-Wide Association Study for Conformation Traits and Osteochondrosis in Pigs.
E. Grindflek1, H. Hamland1 and T. Aasmundstad2, Norsvin, Hamar, Norway

Studies of the Genetic Background of a Teat Defect in Pigs Born in Germany and Sweden.
E. Jonas1, H. Chalkias1, C. Neuhoff1, G. Lindgren1 and D. J. D. Koning2, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2Institute 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. Mäntysaari\textsuperscript{1}, MIT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

4:30 PM 080 Applications of Genomic Selection in Poultry.
A. Wole\textsuperscript{1,2}, A. Krans\textsuperscript{1}, J. Arango\textsuperscript{2}, P. Settar\textsuperscript{2}, J. E. Fulton\textsuperscript{2}, N. P. O'Sullivan\textsuperscript{2}, S. Avendaño\textsuperscript{2}, K. Watson\textsuperscript{2}, R. Preisinger\textsuperscript{1}, D. Habier\textsuperscript{1}, S. J. Lamont\textsuperscript{1}, R. L. Fernando\textsuperscript{1}, D. J. Garrick\textsuperscript{1} and J. C. M. Dekkers\textsuperscript{1}, \textsuperscript{1}Iowa State University, Ames, \textsuperscript{2}Hy-Line International, Dallas Center, IA, \textsuperscript{3}Aviagen Ltd, Edinburgh, United Kingdom, \textsuperscript{4}Aviagen Limited, Newbridge, United Kingdom, \textsuperscript{5}Lohmann Tierzucht GmbH, Cuxhaven, Germany

5:00 PM 081 Genomic Predictions in Aquaculture: Reliabilities in an Admixed Atlantic Salmon Population.
J. Ødegård\textsuperscript{1,5}, T. Moen\textsuperscript{1}, N. Santi\textsuperscript{1}, S. A. Korsvoll\textsuperscript{1}, S. Kjøglum\textsuperscript{1} and T. H. E. Meuwissen\textsuperscript{2}, \textsuperscript{1}AquaGen AS, Trondheim, Norway, \textsuperscript{2}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. Swalve\textsuperscript{1}, Martin Luther University Halle-Wittenberg, Wittenberg, Germany

4:30 PM 303 Genomic Feature Models.
P. Spørensen\textsuperscript{1}, S. M. Edwards\textsuperscript{2} and P. Jensen\textsuperscript{1}, \textsuperscript{1}Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, \textsuperscript{2}Center of 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. Cole\textsuperscript{1,2}, J. L. Hutchison\textsuperscript{2}, D. J. Null\textsuperscript{2}, P. M. VanRaden\textsuperscript{2}, G. E. Liu\textsuperscript{3}, S. G. Schroeder\textsuperscript{4}, T. P. L. Smith\textsuperscript{4}, T. S. Sonstegard\textsuperscript{2}, C. P. VanTassell\textsuperscript{2} and D. Bickhart\textsuperscript{7}, \textsuperscript{1}Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, \textsuperscript{2}Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, \textsuperscript{3}Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD, \textsuperscript{4}USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, \textsuperscript{5}USDA, ARS, BFGL, Beltsville, MD, \textsuperscript{6}Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD, \textsuperscript{7}USDA-ARS-AIPL, 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. Stothard\textsuperscript{1,2}, X. Liao\textsuperscript{3}, A. S. Arantes\textsuperscript{1}, M. De Paauw\textsuperscript{1}, C. Coros\textsuperscript{2}, G. S. Plastow\textsuperscript{3}, S. S. Moore\textsuperscript{1,3} and S. P. Miller\textsuperscript{1,4}, \textsuperscript{1}University of Alberta, Edmonton, AB, Canada, \textsuperscript{2}Delta Genomics Centre, Edmonton, AB, Canada, \textsuperscript{3}The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, \textsuperscript{4}AgResearch, Invermay, Mosgiel, New Zealand

4:30 PM 164 Using the Whole Read: Structural Variant Detection using NGS Data.
D. Bickhart\textsuperscript{1}, J. B. Cole\textsuperscript{2}, J. L. Hutchison\textsuperscript{2}, L. Xu\textsuperscript{2} and G. E. Liu\textsuperscript{3}, \textsuperscript{1}USDA-ARS-AIPL, Beltsville, MD, \textsuperscript{2}Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, \textsuperscript{3}Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, \textsuperscript{4}University of Maryland, College Park, \textsuperscript{5}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. Keeeler2, D. de Jong3 and J. de Vos4, 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. Woolliams4, 1Animal Health Trust, Suffolk, United Kingdom, 2University of Nottingham, Leicestershire, United Kingdom, 3Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

11:15 AM  282  Is Heterozygotie 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. Tetens1, S. Hedt1, E. Stamer2 and G. Thaller1, 1Institute of Animal Breeding and Husbandry, Kiel University, Kiel, Germany, 2TiDa GmbH, Westensee/Brux, Germany

11:45 AM  284  Influence Of Specialisation On Connectedness And Genetic Parameters In Dutch Warmblood Riding Horses.
              G. Rovere1,2, P. Madsen1, E. Norberg2, J. A. M. van Arendonk2 and B. J. Ducro2, 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. Johnston1 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. Larmer1, F. S. Schenkel2, S. P. Miller2 and P. G. Sullivan5, 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-Rodríguez1,2, M. A. Toró3, L. Varona3, M. J. Carabaño3, J. J. Cañas-Álvarez3, J. Altarriba1, T. B. R. Da Silva3,4, J. A. Baró3, A. Molina5 and C. J. Díaz5, 1University of Zaragoza, Zaragoza, Spain, 2ETS Ingenieros Agrónomos, Madrid, Spain, 3INIA, Madrid, Spain, 4Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 5UNESP-Jaboticabal, Brazil, Jaboticabal, Brazil, 4INIA, Spain, Madrid, Spain, 5Universidad de Valladolid, Palencia, Spain, 6Universidad de Córdoba, Córdoba, Spain

11:30 AM  256  Selection Signatures in Autochthonous Spanish Cattle Breeds using Site Frequency Spectrum Statistics.
S. Manilla12, A. González-Rodríguez3, E. F. Moussean4, J. J. Cañas-Álvarez3, J. Altarriba1, C. J. Díaz5, A. Molina5, P. Martínez Camblo6 and L. Varona3, 1University of 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. Lee3, K. D. Song3, J. Gibson4, S. W. Lee5 and C. Gondro5, 1University of New England, Armidale, Australia; 2The University of Queensland, School of Veterinary Science, Gatton, Australia; 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

10:00 AM  082  Genomic Relationships give Improved Prediction Ability for a Selection of Traits in Norsvin Landrace and Duroc.
Nordbø5,6, E. Gjerlaug-Enger1, T. Aasmandstad1 and E. Grindflek1, 1Norsvin, Hamar, Norway, 2Geno SA, Hamar, Norway

M. Koivula1, J. Strandén1, G. P. Aamand1 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. Ilsha1, A. Kranis1 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. Sonesson1, 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. Eding, 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, 1,2 The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Norwegian University of Life Sciences, Ås, Norway, 3Department 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, 1 MTT Agrifood Research Finland, Jokioinen, Finland, 2University of Edinburgh, Edinburgh, United Kingdom

T. H. E. Meuwissen, 1 A. K. Sonesson, 2 and J. Ødegård, 3 Norwegian University of Life Sciences, Ås, Norway, 2NOFIMA, Ås, Norway, 4AquaGen 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, 1 North Carolina State University, Raleigh

11:00 AM 312 Assembling a Reference Population – from Genetic Architecture to New Phenotypes.
K. Schoepke, 1 Martin-Luther-University Halle-Wittenberg, Halle, Germany

11:30 AM 313 How to Improve Genomic Predictions in Small Populations.
M. S. Lund, 1 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, 1 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, 1 K. A. Leymaster and M. L. Clawson, USA, 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, 1 J. C. McEwan, 2 M. A. Black, 3 M. E. Goddard, 4 B. Auvray 5 and K. G. Dodds, 6 AbacusBio Limited, Dunedin, New Zealand, 2AgResearch, Invermay, New Zealand, 3University of Otago, Dunedin, New Zealand, 4Department of Primary Industries, Melbourne, Australia, 5University of Melbourne, Melbourne, Australia, 6AgResearch, Mosgiel, New Zealand

11:45 AM 354 Inferring Ancestral Demography of Domestic and Wild Sheep using Whole-Genome Sequence.
S. Bolormaa, 12 J. Kijas, 1 D. Colman, 1 H. D. Daetwyler, 1,2 and I. M. MacLeod, 1 Department of Environment and Primary Industries, Bundoora, Australia, 2CRC for Sheep Industry Innovation, Armidale, Australia, 3CSIRO Animal, Food and Health Sciences, Brisbane, Australia, 4University of Alberta, Edmonton, AB, Canada, 5La Trobe University, Bundoora, Australia, 6University 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. Neuditschko1, M. S. Khaitark2 and H. W. Raadsma3, 1Agroscope - Swiss National Stud Farm, Avenches, Switzerland, 2Reprogen 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. Zhang1,2, B. Guldbrandsen3, M. Bosse3, M. S. Lund and G. Sahand1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Animal 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. Kogelman1, S. D. Pant1, J. Karjalainen1, L. Franke2, M. Fredholm1 and H. N. Kadarmideen1, 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

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. Sarup1, J. Jensen1, S. M. Edwards1, T. Østensen1, P. Sørensen1 and M. A. Henryson1, 1Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Pig Research Centre, Copenhagen, Denmark

2:30 PM 170 Regulatory and Coding Genome Regions are Enriched for Trait Associated Variants in Dairy Cattle.
L. Koufariotis1,2, Y. P. P. Chen1, S. Bolormaa2 and B. J. Hayes1, 1La Trobe University, Melbourne, Australia, 2Dairy Futures Co-operative Research Centre, Melbourne, Australia, 3Faculty of Science, Technology and Engineering, La Trobe University, Melbourne, CA, Australia, 4CRC for Sheep Industry Innovation, Armidale, Australia, 5The 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. Fleming1, J. E. Kohles2, E. Fritz-Waters3, J. M. Reecy2 and S. J. Lamont2, 1Iowa State University, Ames, 2Iowa 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. Visker1,2, S. van Engelen1,2, J. Dijkstra1, J. A. M. van Arendonk1 and H. Bovenhuis2, 1TI Food and Nutrition, Wageningen, Netherlands, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 3Animal 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 Engelen1, H. Bovenhuis2, J. Dijkstra1, J. A. M. van Arendonk1 and M. H. P. W. Visker1, 1TI Food and Nutrition, Wageningen, Netherlands, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 3Animal Nutrition Group, Wageningen University, Wageningen, Netherlands

2:00 PM 307 Strategies for Use of Reproductive Technologies in Genomic Dairy Cattle Breeding Programs.
J. R. Thomasen1,2 and A. C. Sørensen1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Viking Genetics, Assentoft, Denmark
2:15 PM 308 Inbreeding and Crossbreeding Parameters for Production and Fertility Traits in Holstein, Montbéliarde and Normande Cows.
C. Dezetter*, Groupe ESA, Angers, France; ONIRIS, Nantes, France; Coopex Montbéliarde, Rouans, France

2:30 PM 309 Genomic Predictions of Fertility Related Disorders in Norwegian Red using 30 Years of Data.
K. Haugaard*, B. Heringstad1,2 and M. Svendsen1,1Norwegian University of Life Sciences, Ås, Norway, 2Geno, Ås, Norway

2:45 PM 310 Milk Flow Traits of Friesian, Jersey and Friesian-Jersey Crossbred Cows Under Grazing Conditions in New Zealand.
N. Lopez-Villalobos*, J. P. Edwards and J. G. Jago1,1Massey University, Palmerston North, New Zealand, 2DairyNZ, Hamilton, New Zealand

Linear and Nonlinear Models: Inference
Chair: Daniel Gianola, University of Wisconsin
Bayshore Grand Ballroom D

1:30 PM 216 Selective Shrinkage of Genomic Effects using Synthetic Dependencies in Neighboring Chromosome Regions.
D. Wittenburg* and N. Reinsch, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany

1:45 PM 217 Improving REML Estimates of Genetic Parameters through Penalties on Correlation Matrices.
K. Meyer*, Animal Genetics and Breeding Unit, University of New England, Armidale, Australia

2:00 PM 218 Inferring the Ancestral Dynamics of Population Size from Genome Wide Molecular Data: An ABC Approach.
S. Boitard1,2 and S. Sochacki1,1GABI (INRA / AgroParisTech), Jouy-en-Josas, France, 2UMR 7205 ISYEB (MNHN / CNRS / EPHE / UPMC), Paris, France

B. D. Valente, G. Morota, G. J. M. Rosa, D. Gianola and K. A. Weigel, University of Wisconsin, Madison

2:30 PM 220 Using SNP Markers to Estimate Additive, Dominance and Imprinting Genetic Variance.
M. S. Lopes1,2, J. W. M. Bastiaansen1, L. Janss1, H. Bovenhuis1 and E. F. Knol1,1Animal 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

2:45 PM 221 Estimation of Single Locus Effects on Susceptibility, Infectivity and Recovery Rates in an Epidemic using Temporal Data.
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

Swine Breeding (2)
Chair: Brian P. Kinghorn, University of New England
Bayshore Grand Ballroom A

1:30 PM 378 Genetic Parameter for Litter Quality Traits.
H. R. Brandl*, Institute of Animal breeding and Genetics, Giessen, Germany

1:45 PM 379 Genetic Analysis of Birth Weight Uniformity in Pigs: Comparison of Methods.
E. Sell-Kubiak1, P. Bijma1, E. F. Knol2 and H. A. Mulder1,1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2TOPIGS Research Center IPG, Beuningen, Netherlands

2:00 PM 380 Social Genetic Effects for Litter Size of Sows Housed in Groups During Gestation.
K. L. Bunter*, Animal Genetics and Breeding Unit, UNE, Armidale, Australia
Most of the Long-Term Genetic Gains from Optimum- Contribution Selection can be Realised with Restrictions Imposed.

M. Henryon1,2, T. Ostersen1, B. Ask1, A. C. Sørensen1 and P. Berg1, 1Danish Agriculture and Food Council, Pig Research Center, Copenhagen, Denmark, Copenhagen, Denmark, 2School of Animal Biology, University of Western Australia, Crawley, Australia, Crawley, Australia, 1Pig Research Centre, Copenhagen, Denmark, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3Nordic Genetic Resource Centre, Ás, 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. Dekkers1, 1Iowa State University, Ames, 2North Dakota State University, Fargo


X. Guo1, O. F. Christensen1, T. Ostersen2, D. A. Sørensen1, Y. Wang3, M. S. Lund4 and G. Su4, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Pig Research Centre, Copenhagen, Denmark, 4College 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

Is There a Genetic Solution to Bovine Respiratory Disease Complex?


Disease Genetics: Successes, Challenges and Lessons Learnt.

S. C. Bishop1, 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. Mandonnet1, 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

Genomic Selection in Nelore Cattle in Brazil.

R. Carvalheiro1, Sao Paulo State University (UNESP), Jaboticabal, Brazil

Genome Wide Imputation in Canadian Beef Cattle.

F. S. Schenkel1, 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

Genetics of Trait Complexes - Lactation

Milking Efficiency – A Milkability Trait for Automatically Milked Cows.

P. Lovendahl1, J. Lassen2 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. Sargolzaei4,6, D. A. Grossi1, S. Nayeri1, S. S. Moore7, G. S. Plastow1, P. Stothard1 and F. S. Schenkel1, 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, 6The Semex Alliance, Guelph, ON, Canada, 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. Bovenhuis1 and N. Bédère2, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Wageningen 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. Gogignon-Gion1, M. Ferrand2, M. Gelé2, D. Pourcher3, M. N. Rossignol4, S. Friz5, M. Boussaha1, A. Capitan1, D. Rocha1, G. Miranda1, P. Martin1, M. Brochard2 and D. Boichard4, 1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2Idée, Paris, France, 3ECEL, Roulanx, France

5:00 PM 144 Genomic Regions Affecting Cheese Making Properties Identified in Danish Holsteins.
V. R. Gregersen1, H. P. Bertelsen1, N. A. Poulson1, L. B. Larsen1, F. Gustavsson1, M. Glantz1, M. Paulsson1, A. J. Buitenhuis1 and C. Bendixen1, 1Aarhus 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, 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, 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. Windig2,4, G. Leroy3, E. Verrier2,3, S. J. Hiemstra2, 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. Paiva2, B. P. Sollero1, P. Biegelmeier4, A. R. Caetano2 and F. F. Cardoso6, 1USDA-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. Hiemstra2,4 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
P. C. Muth\(^1\), A. Markemann\(^1\), L. T. T. Huyen\(^1\) and A. Valle Zárate\(^1\), \(^1\)University of Hohenheim, Stuttgart, Germany, \(^2\)National Institute of Animal Sciences, Hanoi, Vietnam

Assessing the Effects on Litter Size of Age of Inbreeding in an Ancient Line of Large White Pigs.
L. Silió\(^*\), J. Rodrigo\'n and M. C. Rodríguez, INIA, Madrid, Spain

An Observatory of the Genetic Variability of Ruminants and Equids Breeds.
C. Danchin-Burge\(^*\), E. Verrier\(^2,3\), D. Laloe\(^4\), R. Saintilan\(^1,4\) and G. Leroy\(^2,3\), \(^1\)Institut de l'Elevage, Paris, France, \(^2\)AgroParisTech, Paris, France, \(^3\)INRA UMR 1313 GABI, Jouy en Josas, France, \(^4\)UNCEIA, Paris, France

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

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

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

An Iterative Algorithm for Optimum Contribution Selection in Large Scale Breeding Programs.
B. S. Dagnachew\(^*\) and T. H. E. Meuwissen\(^*\), \(^1\)Norwegian University of Life Sciences, Aas, Norway, \(^2\)Norwegian University of Life Sciences, Ås, Norway

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

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

Diminishing Marginal Returns From Genomic Selection As More Selection Candidates Are Phenotyped.
T. O. Okeno\(^*\), M. Henry\(\textsuperscript{on}^\textsuperscript{1}\) and A. C. Sørensen\(^*\), \(^1\)Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, \(^2\)School of Animal Biology, University of Western Australia, Crawley, Australia, \(^3\)Crawley, Australia, \(^4\)Danish Agriculture and Food Council, Pig Research Center, Copenhagen, Denmark, \(^5\)Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Metabolomics: A Pathway for Improved Understanding of Genetic Modulation of Mammalian Growth and Tissue Deposition.
P. 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 ENVT, GenPhySE, Castanet-Tolosan, France, 2INRA, UR83, Recherches Avicoles, Nouzilly, France, 3INSERM, U846, INRA, USC1361, Institut Cellule Souche et Cerveau, Bron, France, 4UMR 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. McCarthy1,2, C. R. Gresham1, J. E. Koltes2, M. T. Arick2, E. Lyons1, M. W. Vaughn2, E. T. Dawson1, N. Hopkins1 and S. C. Burgess1, 1University of Arizona, Tucson, 2Mississippi State University, Starkville, 1Iowa State University, Ames, 2Texas Advance Computing Center, University of Texas, Austin, 2Texas 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. Fernando1,2, 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. Martinez4, G. C. Lamb5, D. O. Rae6, J. D. Wasdin7 and J. D. Driver8,
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-Waltl1 and C. Fuerst1, 1University of Natural Resources and Life Sciences, Vienna, Austria,
2University of Natural Resources and Life Sciences, Vienna, Austria, 3ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria

711 Imputation Accuracy using Flmpute and BEAGLE Software in Brazilian Synthetic Cow Breed.
T. C. S. Chud1, R. V. Ventura1,2, J. S. Schenkel1, R. Carvalheiro1, M. E. Buzanskas1, I. Urbinati1, L. C. Almeida Regitano1, C. R. Marcondes1 and D. P. Munari1, 1Univ Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil, 2University of Guelph, Guelph, ON, Canada, 3Beef Improvement Opportunities, Guelph, ON, Canada, 4Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 5Center for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 6Univ Estadual Paulista “Julio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 7Embrapa Southeast Livestock, Sao Carlos, Brazil, 8Brazilian Agricultural Research Corporation (Embrapa), Sao Carlos, Brazil, 9Universidade Estadual Paulista “Julio de Mesquita Filho”, Jaboticabal, Brazil

712 Selection Signatures in Canchim Beef Cattle.
I. Urbinati1, M. E. Buzanskas1, T. C. S. Chud2, F. B. Mokry2, L. C. Almeida Regitano3, R. H. Higa4 and D. P. Munari5, 1Univ Estadual Paulista Julio de Mesquita Filho, Jaboticabal, Brazil, 2University Federal de Sao Carlos, Sao Carlos, Brazil, 3Embrapa Southeast Livestock, Sao Carlos, Brazil, 4Embrapa Informática Agropecuária, Campinas, Brazil, 5Universidade Estadual Paulista “Julio de Mesquita Filho”, Jaboticabal, Brazil

713 Accuracy of Genomic Prediction for Tick Resistance in Braford and Hereford Cattle.
F. F. Cardoso1, B. P. Sollero2, H. B. Comin1, C. G. Gomes2, V. M. Roso2, R. H. Higa2, A. R. Caetano2, M. J. Yokoo2 and I. Aguilar2, 1Embrapa Southern Region Animal Husbandry, Bage, Brazil, 2Embrapa Southern Region Animal Husbandry, Ba­gé, Bage, Brazil, 3GenSys Consultores Associados, Porto Alegre, Brazil, 4Embrapa Informática Agropecuária, Campinas, Brazil, 5Embrapa Genetic Resources and Biotecnologia, Brasilia, Brazil, 6INIA, Las Brujas, Uruguay

714 Breed Additive and Heterosis Effects on Feedlot and Carcass Traits in Beef Cattle.
A. Theunissen1, M. M. Scholtz2, M. D. MacNeil3 and F. W. C. Nesar4, 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. Theunnissen
Northern Cape Department of Agriculture, Land Reform and Rural Development, Jan Kempdorp, South Africa

Accuracy of Genomic Prediction using Two Admixed Crossbred Populations.
A. Vallee
J. A. M. van Arendonk and H. Bovenhuis
Genes Diffusion,Douai, France
Animal 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. Grosso
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. Taniguchi
H. A. Hasegawa
I. Matsuno
Meiji University, Kawasaki, Japan

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

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

M. Méndez
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. Tizzoto
J. F. Taylor
E. Decker
C. F. Gromboni
M. A. Mudada
R. D. Schnabel
L. L. Coutinho
G. B. Mourão
R. T. Nassif
F. A. Donatoni Bressani
P. Tholon
T. S. Sonstegard
M. M. D. Alencar
R. R. Tullio
J. M. Reecy
A. R. Nogueira
L. C. Almeida Regitano
Federal University of São Carlos, São Carlos, Brazil
University of Missouri, Columbia
Instituto Federal de Educação, Ciência e Tecnologia da Bahia (IFBA), Valença, Brazil
Embrapa Pecuária Sudeste, São Carlos, Brazil
Universidade de São Paulo/Esalq, Piracicaba, Brazil
Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil
USDA, ARS, BFGL, Beltsville, MD
Iowa State University, Ames

Estimation Of Genetic Parameters Of Type Traits For Namibian Brahman Beef Cattle.
M. D. Fair
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. Neustäter
D. A. Gross
M. Jafarikia
M. Sargolzaei
and F. S. Schenkel
University of Guelph, Guelph, ON, Canada
Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada
Canadian Centre for Swine Improvement, Ottawa, ON, Canada
The Semex Alliance, Guelph, ON, Canada

Genomic Evaluation using 50K and Imputed HD Genotypes in Guzera (Bos indicus) Breed.
S. A. Boison
D. J. A. Santos
J. F. Garcia
J. Soelkner
M. G. C. D. Peixoto
and M. V. G. B. da Silva
University of Natural Resources and Life Sciences, Vienna, Austria
UNESP Univ Estadual Paulista, Jaboticabal, Brazil
Faculdade de Medicina
B. Greyling1, B. van Vuuren1, P. van Hooft1 and A. A. Maaiwashe1,2, 1Agricultural Research Council, Centurion, South Africa, 2University of Johannesburg, Johannesburg, South Africa, 3Resource Ecology Group, Wageningen University, Wageningen, Netherlands, 4University of the Free State, Bloemfontein, South Africa, 5ARC-Animal Production Institute, Irene, South Africa

454 Improving Predictive Ability of Selected Subsets of Single Nucleotide Polymorphisms in a Moderately Sized Dairy Cattle Population.
J. I. Weller1, E. Ezra2, E. Seroussi1, M. Shemesh2 and M. Ron1, 1ARO, The Volcani Center, Bet Dagan, Israel, 2Israel Cattle Breeders Association, Caesaria, Israel

455 Is the use of Formulas a Reliable way to Predict the Accuracy of Genomic Selection?
S. Brard1 and A. Ricard2, 1INRA, UMR 1388, Castanet-Tolosan, France, 2INRA, UMR 1313, Jouy-en-Josas, France

456 Association between GDF9, FecB and Prolactin Gene Polymorphisms and Prolificacy of Awassi Sheep.
K. I. Jawasreh1, A. Al-Qaïsi and F. T. Awawdeh, Jordan University of Science and Technology, Irbid, Jordan

457 The Role of Obesity Genes for Milk Fat Yield in Holstein Dairy Cattle.
L. G. Zielke1, R. H. Bortfeld1, J. Tetens1, G. Thaller4 and G. A. Brockmann1, 1Humboldt-Universität zu Berlin, Berlin, Germany, 2Department of Crop and Animal Sciences, Humboldt-Universität zu Berlin, Berlin, Germany, 3Institute of Animal Breeding and Husbandry, Christian-Albrechts-Universität zu Kiel, Kiel, Germany, 4Christian-Albrechts-Universität, Kiel, Germany

458 Accuracy of Genomic Prediction in French Charolais Cattle Population using High-density Chip.
T. Tribout1, M. Gunia1,2, R. Saintilan1, E. Vénot1,2, M. N. Fouilloux and F. Phocas1, 1INRA UMR 1313 GABI, Jouy-en-Josas, France, 2INRA UMR1388 GenPhySE, Castanet-Tolosan, France, 3INRA, UMR1313 GABI, Jouy-en-Josas, France, 4UNCEIA, Jouy-en-Josas, France, 5Institut de l'Elevage - Idele, Jouy-en-Josas, France

C. Hoze1, S. Fritz1,2, F. Phocas2, D. Boichard2, V. Ducrocq1 and P. Croiseau2, 1UNCEIA, Paris, France, 2INRA, UMR1313 GABI, Jouy-en-Josas, France

460 Estimation of Linkage Disequilibrium and Effective Population Size using Whole Genome Single Nucleotide Polymorphisms in Korean Native Pig and Landrace.
J. E. Park1,2, J. H. Lee3 and D. Lee4, 1Seoul National University, Seoul, South Korea, 2Hankyong National University, Anseong, South Korea

461 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. Knürr1, I. Strandén1, M. Koivula1, G. P. Aamand1 and E. A. Mäntysaari1, 1MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland, 2NAV Nordic Cattle Genetic Evaluation, Aarhus, Denmark

463 Imputation of Genotypes in Danish Two-Way Crossbred Pigs using Low Density Panels.
T. Xiang1,2, O. F. Christensen1, A. Legarra1 and T. Ostersen1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2INRA, Castanet-Tolosan, France, 3Pig Research Centre, Copenhagen, Denmark

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

465 Ancestral Haplotypes, Quantal Genomics and Healthy Beef.
E. J. Steele1, S. S. Lloyd2, S. Lester4, J. F. Williamson1, D. Bayard4 and R. L. Dawkins1,5, 1C.Y.O'Connor ERADE Village
Bias of Genetic Trend of Genomic Predictions Based on both Real and Simulated Dairy Cattle Data.
P. Ma1, M. S. Lind2, U. S. Nielsen2, G. P. Aamand4, A. C. Sørensen1 and G. Su1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, 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. Schenkel2, R. Carvalheiro1, P. Tholon2, J. A. Oliveira1 and S. A. Queiroz2, 1Universidade Estadual Paulista, Jaboticabal, Brazil, 2GenSys Associated Consultants, Porto Alegre, Brazil

Non-Hierarchical Cluster Analysis with the Breeding Values for Reproductive and Productive Traits in Beef Cattle.
C. C. P. Paç1,2, H. L. Moreira1, R. P. Savegnago1, M. E. Buzanska2, R. B. Lôbo2 and D. P. Munari1, 1Universidade do Estado de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 2Universidade Estadual Paulista - Júlio de Mesquita Filho, Faculdade de Ciências Agrárias e Veterinárias, Departamento de Ciências Exatas, Jaboticabal, Brazil, 3Embrapa Pecuária Sudeste, São Carlos, Brazil

Accuracy of Genotype Imputation with Different Low Density Panels in Braford and Hereford Cattle.
M. L. Piccoli1,2,3, J. Braccini Neto1, F. F. Cardoso1, M. Sargolzaei4,5 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. Piper1, J. M. Seddon1, M. R. Fortes1 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, 3The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 4The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia

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. Sada1, Miyagi University, Sendai, Japan

Across-Country Genetic Parameters in Beef Cattle for Interbull Weaning Weight Genetic Evaluation.
T. Pabion1, M. Nilforooshan1, D. Laloe1, E. Hjerpe2 and E. Venot4, 1Irish Cattle Breeding Federation, Cork, Ireland, 2Interbull center, Uppsala, Sweden, 3INRA GABI, Jouy en Josas, France, 4INRA UMR 1315 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. Pabion4, 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. Queiroz, E. F. M. Paterno, A. F. D. A. Fernandes, H. H. R. Neves, J. A. Oliveira and R. Carvalheiro, Universidade Estadual Paulista, Jaboticabal, Brazil, GenSys Associated Consultants, Porto Alegre, Brazil, Universidade 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. Moreira, M. A. Prata, A. E. Vercesi Filho, M. L. P. Lima, R. B. Lóbo and C. C. P. Paz, Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CENA/USP, Piracicaba-SP, Brazil, SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Serdâo-zinho-SP, Brazil

Analysis of Copy Number Variation Regions in a Nellore Population Evaluated for Feed Efficiency.
G. A. Oliveira Junior, F. S. B. Rey, M. V. G. B. da Silva, M. H. A. Santana, P. A. Alexandre, J. P. Eler and J. B. S. Ferraz, INAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, Sao Paulo State University (UNESP), Jaboticabal, Brazil, Embrapa Dairy Cattle, Juiz de Fora, Brazil

Genetic and Phenotypic Correlation between Gestation Period and Growth Traits Pre and Post Weaning.
H. L. Moreira, E. B. Canova, A. E. Vercesi Filho, M. L. P. Lima and C. C. P. Paz, Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CENA/USP, Piracicaba-SP, Brazil, SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Serdâo-zinho-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. Ramos, S. L. Caetano, R. B. Lóbo, L. A. F. Bezerra, A. Bonjácio and D. P. Munarí, UNESP, Jaboticabal, Brazil, Centro Universitário de Barretos, Barretos, Brazil, Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, Centro de Energia Nuclear na Agricultura, Universidade São Paulo, CENA/USP, Piracicaba-SP, Brazil, SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Serdâo-zinho-SP, Brazil

Genetic Architecture Of Birth And Weaning Traits In Charolais Beef Cattle.

Genetic Parameters of Body Condition Score and Growth Traits of Nellore Cows.
A. F. D. A. Fernandes, H. H. R. Neves, N. Hurtado-Lugo, R. Carvalheiro, J. A. Oliveira and S. A. Queiroz, Universidade Estadual Paulista, Jaboticabal, Brazil, GenSys Associated Consultants, Porto Alegre, Brazil, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 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-Alvarez, A. González-Rodríguez, S. Muñilla, L. Varona, C. J. Díaz, J. A. Baró, C. Moreno, A. Molina and J. Piedrafita, Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, Universidad de Zaragoza, Zaragoza, Spain, INIA, Madrid, Spain, Universidad de Valladolid, Palencia, Spain, 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. Manfredi, C. Carre and M. A. Toro, INRA, Toulouse, France, IMT Université Paul Sabatier, Toulouse, France, 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.
Estimating Rate of Inbreeding and Effective Population Size using Genomic Data in Norwegian Red Cattle.
B. Hillestad¹, J. A. Woolliams², T. H. E. Meuwissen², D. I. Våge¹ and G. Kleemetsdal¹, ¹Norwegian University of Life Sciences, Ås, Norway, ²The Roslin Institute and (D)SVS, University of Edinburgh, Midlothian, United Kingdom

Quality Control of Genomic regions Having Heritability Estimates of Gene Content.
N. S. Forneris¹, A. Legarra³, Z. G. Vitezica³, S. Tsuruta³, I. Aguilar³, R. J. C. Cantel¹ and I. Misztal¹, ¹Department of Animal Science, University of Buenos Aires, Buenos Aires, Argentina, ²INRA, Castanet-Tolosan, France, ³University of Georgia, Athens, ¹INIA, Las Brujas, Uruguay, ²CONCET, Buenos Aires, Argentina

Impact of Adding Foreign Genomic Information on the Mexican Holstein Imputation Process.
M. Nishio¹ and M. Satoh, ¹NARO Institute of Livestock and Grassland Science, Tsukuba, Japan

Towards Genomic Selection in Danish Warmblood Horses: Expected Impacts and Selective Genotyping Strategy.
T. Mark¹, L. Jönsson¹, M. Holm¹ and K. Christiansen¹, ¹University of Copenhagen, Frederiksberg C, Denmark, ²Danish Warmblood Association, Maarslet, Denmark, ³Knowledge Centre for Agriculture, Aarhus, Denmark

Compressing Efficiency Relationship Matrix: Developing New Methods to Determine Genomic Relationships for Improved Breeding.
N. J. Hudson¹, J. Kijas³, L. R. Porto-Neto³ and A. Reverter-Gomez³, ¹CSIRO, Brisbane, Australia, ²CSIRO Animal, Food and Health Sciences, Brisbane, Australia, ³CSIRO Food Futures Flagship, Brisbane, Australia

Genomic Evaluation of Both Purebred and Crossbred Performances.
O. F. Christensen¹, B. Nielsen¹, P. Madsen¹ and G. Su¹, ¹Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ²Pig Research Centre, Copenhagen, Denmark

Genome-Wide Association using High Density Genotypes for Calving Difficulty in Dairy and Beef Cattle.
D. Purfield¹, D. Bradley³, F. Kearney³, R. Evans³ and D. P. Berry³, ¹Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co.Cork, Ireland, ²Department of Genetics, Trinity College Dublin, Dublin, Ireland, ³Irish Cattle Breeding Federation, Co. Cork, Ireland

Impact of Relationships between Test and Reference Animals and between Reference Animals on Reliability of Genomic Prediction.
X. Wu¹², M. S. Lund¹, D. Sun², Q. Zhang³ and G. Su¹, ¹Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ²College of Animal Science and Technology, China Agricultural University, Beijing, China, ³China Agricultural University, Beijing, China

Towards Genomic Selection in Danish Warmblood Horses: Expected Impacts and Selective Genotyping Strategy.
T. Mark¹, L. Jönsson¹, M. Holm¹ and K. Christiansen¹, ¹University of Copenhagen, Frederiksberg C, Denmark, ²Danish Warmblood Association, Maarslet, Denmark, ³Knowledge Centre for Agriculture, Aarhus, Denmark

Polymorphism Of Three Milk Protein Genes in Mexican Jersey Cattle.
J. L. Zepeda-Batista¹, B. Alarcon-Zuniga¹, A. Ruiz-Flores¹, R. Nunez-Dominguez¹ and R. Ramirez-Valverde², ¹UNIVERSIDAD AUTONOMA CHAPINGO, TEXCOCO, Mexico, ²Universidad Autónoma Chapingo, Chapingo, Mexico

Impact of Adding Foreign Genomic Information on the Mexican Holstein Imputation Process.
F. J. Ruiz-Lopez¹, A. García-Ruiz¹, G. R. Wiggans¹, C. P. VanTassell¹ and H. H. Montaldo¹, ¹Natl. Cent. for Research on Physiology and Animal Breeding INIFAP, Queretaro, Mexico, ²National Autonomous University of Mexico (UNAM), Mexico, ³Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, ⁴Bovine Functional Genomics Laboratory ARS-USDA, Beltsville, MD, ⁵Universidad Nacional Autónoma de México, DF, Mexico

Genome Regions Associated to Milk Production Traits and Somatic Cell Score in the Mexican Holstein Population.
A. García-Ruiz¹, F. J. Ruiz-Lopez¹, C. P. VanTassell¹ and H. H. Montaldo¹, ¹National Autonomous University of Mexico (UNAM), Mexico, ²INIA, Las Brujas, Uruguay, ³CONCET, Buenos Aires, Argentina

Compression Efficiency Relationship Matrix: Developing New Methods to Determine Genomic Relationships for Improved Breeding.
N. J. Hudson¹, J. Kijas³, L. R. Porto-Neto³ and A. Reverter-Gomez³, ¹CSIRO, Brisbane, Australia, ²CSIRO Animal, Food and Health Sciences, Brisbane, Australia, ³CSIRO Food Futures Flagship, Brisbane, Australia

Genomic Evaluation of Both Purebred and Crossbred Performances.
O. F. Christensen¹, B. Nielsen¹, P. Madsen¹ and G. Su¹, ¹Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ²Pig Research Centre, Copenhagen, Denmark
Metabolism of CLA Isomers, c9,t11- & t10,c12 in Adipocyte Cultures and their Effect on Delta-6 Desaturase Expression.
W. J. Meadus, Agriculture & Agri-Food Canada, Lacombe, AB, Canada

Association of SNPs and Haplotypes in Adiponectin and Adiponectin Receptors with Pig Meat Quality Traits.
M. F. Palint, M. Jafarkia, C. Gariépy, F. Fortin, L. Maigne, S. Wyss and B. Sullivan, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, Canadian Centre for Swine Improvement, Ottawa, ON, Canada, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada, Centre de développement du porc du Québec, Québec, QC, Canada

The Effect of Inbreeding on the Prediction of Genomic Values.
R. P. Savegnago, Univ. Estadual Paulista – FCAV/UNESP, Jaboricabal, 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. Connolly, A. Cromie and D. P. Berry, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, Irish 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. Chardulo, W. A. Baldassini, L. G. Albuquerque, H. N. Oliveira, J. A. Silva and P. M. Padilha, FMVZ - São Paulo State University, Botucatu, Brazil, ESALQ - São Paulo University, Piracicaba, Brazil, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboricabal, Brazil, Universidade Estadual Paulista, Botucatu, Brazil, IBB - São Paulo State University, Botucatu, Brazil

Analysis of Copy Number Variants in Spanish Autochtonous Beef Cattle Breeds.
T. B. R. Da Silva, A. González-Rodríguez, C. Aviles, E. F. Mrousan, J. J. Cañas-Álvarez, L. Varona, M. J. Carabaño, P. Martínez-Cambor and C. J. Díaz, INIA, Spain, Madrid, Spain, UNESCO-Jaboticabal, Brazil, Jaboticabal, Brazil, Universidad de Zaragoza, Zaragoza, Spain, Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, INIA, Madrid, Spain, Universidad de Oviedo, Oviedo, Spain

Phenotypic and Genetic Ties Between Growth Traits and Marrow Traits in Nellore Cattle.
R. L. Tomussi, A. F. B. Magalhães, R. Espigolan, D. G. M. Gordo, W. B. Andrade, G. C. Venturini, L. A. L. Chardulo, L. G. Albuquerque and F. S. B. Rey, Sao Paulo State University (UNESP), Jaboticabal, Brazil, Universidade Estadual Paulista, Jaboricabal, Brazil, Sao Paulo State University (UNESP), Botucatu, Brazil, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Analysis of Age at First Calving Dealing with Censored Data.
D. Anastasio Garcia, R. Carvalheiro, G. J. M. Rosa, B. D. Valente and L. G. Albuquerque, Sao Paulo State University (UNESP), Jaboticabal, Brazil, Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboricabal, Brazil, University of Wisconsin, Madison, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Genetic Analysis of Feet and Legs in Nellore Cattle.
G. Vargas, H. H. R. Neves, V. Cardoso, D. P. Munari and R. Carvalheiro, Sao Paulo State University, Jaboticabal, Brazil, GenSys Associated Consultants, Porto Alegre, Brazil, Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, Brazil, Universidade 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 Magalhães, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São 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, R. K. Oto, M. Marques Farah1, L. O. Duitama Carreto1 and R. da Fonseca1, 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

K. Inoue1,2, B. D. Valente1, N. Shoji1, T. Honda1, K. Oyama1 and G. J. M. Rosa1, 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. Coros1, M. DePauw1, G. S. Plastow1, S. S. Moore1, S. P. Miller1 and P. Stothard1, 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.  
J. A. Hidalgo1,2, R. Núñez-Domínguez1, R. Ramírez-Valverde1, J. Domínguez-Viveros1 and F. A. Rodríguez-Almeida1, 1Universidad Autónoma Chapingo, Chapingo, Mexico, 2Universidad Autónoma de Chihuahua, Chihuahua, Mexico

Monoallelic Expression of NNAT Gene in Nelore Steers Skeletal Muscle.  
M. M. Souza1,2, A. Zerlotini1, P. C. Tizzio1, P. S. N. Oliveira1, A. L. Somavilla1, F. B. Mokry1, A. S. M. Cesar1, W. J. S. Diniz1, M. A. Madadu1, S. C. M. Nicuara1, 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 São 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 Braford Breeds.  
P. Bieglmeyer1,2, M. M. Oliveira2,3, L. L. Cardoso2,3, C. G. Gomes2, R. H. Higa4, N. L. Dionello4, A. R. Caetano4, J. P. Steibel5 and F. F. Cardoso1, 1Federal University of Pelotas, Pelotas, Brazil, 2Embrapa Southern Region Animal Husbandry, Bage, 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. Albuquerque2, G. Moraes3 and L. F. Souza4, 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. Queiroz3, 1GenSys Associated Consultants, Porto Alegre, Brazil, 2Universidade Estadual Paulista “Júlio de Mesquita Filho”-UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 3Universidade Estadual Paulista, Jaboticabal, Brazil

Evaluation of the Protein Change in the Meat of Nellore Beef Cattle with Contrasting Shear Force.  
M. E. Carvalho1, G. Gasparin1, J. P. Eler1, J. C. D. C. Balieiro1, L. C. A. Regitano1, J. B. S. Ferraz2 and L. L. Coutinho2, 1NAP-GMABT - Dep. of Veterinary Medicine, University of São Paulo - FZEA, Pirassununga, Brazil, 2Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, 3NAP-GMABT/FZEA/University of São Paulo, Pirassununga, Brazil, 4University of São 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. Zhang1,2, J. M. Young1, C. Wang1, X. Sun1, 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. Sargolzaei1,2, L. R. Schaeff3, J. P. Chenaux1, G. Kistemaker1, G. R. Wiggans4 and F. S. Schenkel1, 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. Poole1, E. O. Rege1, 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. Petukhov1, Novosibirsk State Agrarian University, Novosibirsk, Russia

Do Rare Variants Contribute to the Genomic Prediction Accuracy?  
T. Sachocki1, J. Szyda2 and A. Zarnecki1, 1Wroclaw University of Environmental and Life Sciences, Wroclaw, Poland, 2National Research Institute of Animal Production, Cracow-Balice, 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. Wu2, X. Xu2, Y. Zhang2 and H. Tulaftu2, 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. Gulbrandsen1, C. Høje2, R. F. Brondum1, D. Boichard1 and M. S. Lund1, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, 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. Park1,2 and D. Lee2, 1Hankyong 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. Mrode1 and M. P. Coffey2, 1Scotland's Rural College, Edinburgh, United Kingdom, 2SRUC, Edinburgh, United Kingdom

A. Baur1,2, S. Fritz1, J. Promp3, O. Bulo4, D. Boichard5, V. Ducrocq6 and P. Croiseau7, 1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2UNCEIA, Paris, France, 3IDEE, 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 Wolde4, W. Van Berkel5 and B. Sullivan6, 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. Schwarzenbacher1, 2 and H. Pausch3, Zuchtdaten EDV-Dienstleistungen GmbH, Vienna, Austria, 1Chair of Animal Breeding, Technische Universität München, Freising, Germany

H. E. Theron1, 2, R. R. van der Westhuizen1, 2, E. van Marle-Koster2 and J. van der Westhuizen1, 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. Varona1, Z. G. Vitezica2, S. Munilla1 and A. Legarra1, 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 Nellore cattle.
F. Baldi1, 3, F. Feitosa2, A. S. C. Pereira2, G. C. Venturini1, R. L. Tonussi1, R. Espigolan1, D. G. M. Gordo1, G. M. de Camargo1, L. A. L. Chardulo4 and L. G. Albuquerque5, 1Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, Faculdade de Ciências Agrárias e Veterinárias, 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. Gomes1, R. A. A. Torres Júnior2, G. R. D. O. Menezes2, J. V. F. Battistelli2, T. F. Rocha2, M. R. Reggiori2 and M. E. Buzanska2, 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. Bertipaçá1, L. O. Duítama Carreño1, R. R. Aspilcueta Borquis2, A. A. Boligon1, R. da Fonseca1, M. M. Farah1, G. C. Venturini1 and F. Baldi1, 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 Nellore Cattle.
A. P. Nascimento Terakado, Universidade Estadual de São Paulo, Jaboticabal, Brazil

Racial Composition of Composite Bovine for Mating with Different Female Genetic Groups.
R. S. Bueno1, G. B. Mourão2, E. C. Mattos3, J. C. D. C. Balieiro1, J. P. Eler4 and J. B. S. Ferraz4, 1University 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 São 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. Ulhôa Magnabosco³, M. Correa da Silva⁴, R. B. Lôbo⁵, F. Nakagawa⁶ and F. B. Lopes⁷,
¹Federal University of Goiás, Goiânia, Brazil, ²University of California, Davis, ³Embrapa Cerrados, Brasília, Brazil, ⁴University of California, Davis, ⁵Embrapa Cerrados, Brasília, Brazil, ⁶University of Goiás, Goiânia, Brazil, ⁷ANCP-Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, ⁸OB 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. Ulhôa Magnabosco², R. D. Sainz³, C. Ubirájara Faria³, R. B. Lôbo⁴, F. Nakagawa⁵ and F. B. Lopes⁶,
¹Federal University of Goiás, Goiânia, Brazil, ²Embrapa Cerrados, Brasília, Brazil, ³University of California, Davis, ⁴Embrapa Brazilian Agriculture Research Corporation, Brasília, Brazil, ⁵Federal University of Uberlândia, Uberlândia, Brazil, ⁶OB Brand, Pontes e Lacerda, Brazil

Genomic analysis of Canadian Simmental Population.
N. Zare¹, G. VanderVoorst², M. Sargolzaei², D. Lu¹ 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. Keenan¹ 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. Kallenbach¹, R. Lock² and C. J. Kojima³,
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,
¹NIAS, Chonan, South Korea

Relationship between Beef Heifer Residual Feed Intake and Productivity as Cows.
C. D. Callum¹,
¹University 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,
¹Universidade 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. Moresan¹, S. Munilla²³, C. J. Díaz²³, A. González-Rodríguez³, J. Piedrafita¹, C. Aviles², J. A. Baro³, 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
502 Linkage Disequilibrium and Persistence of Phase in Five Spanish Local Beef Cattle Breeds.
J. J. Cañas-Alvarez, E. F. Mouresan2, L. Varona2, C. J. Díaz2, C. Aviles3, J. A. Baró3, J. Altarriba4, J. Casellas4 and J. Piedrafitat5, 1Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, 2Universidad de Zaragoza, Zaragoza, Spain, 3INIA, Madrid, Spain, 4Universidad de Córdoba, Cordoba, Spain, 5Universidad de Valladolid, Palencia, Spain

503 Generalization of Henderson's T-inverse to Include Genomic Data.
A. A. Mauwase1, ARC-Animal Production Institute, Irene, South Africa; University of the Free State, Bloemfontein, South Africa

504 Genome-Assisted Multiple-Trait Analysis of Carcass Traits in Nellore Cattle.
G. A. Fernandes Júnior2,3, G. J. M. Rosa2, R. B. Costa2, R. Carvalheiro1, L. A. L. Chardulo1, D. G. M. Gordo1, F. Baldi1, H. N. Oliveira1, H. Tonhati2, L. G. Albuquerque2 and R. M. O. Silva1, 1Sao 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

505 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. Hayr2, M. Saatchi1, R. Sherlock2, D. Johnson2 and D. J. Garrick1, 1Iowa State University, Ames, 2LIC, Hamilton, New Zealand

506 Genomics Tools for Improving Health and Production Performance of Canadian Pigs.
M. Jafarikia1,2 and B. Sullivan1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Centre for Swine Improvement, Ottawa, ON, Canada

507 Comparison of Breeding Values from Single-Step and Bivariate Blending Methods.
M. Taskinen1,2, E. A. Mäntysaari2, G. P. Aamand2 and I. Strandén2, 1MTT Agrifood Research Finland, Jokioinen, Finland, 2Nordic Cattle Genetic Evaluation, Aarhus, Denmark, 3MTT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

508 Implementation of Genomic Selection in Norsvin Genetic Program; Genetic Gain in Production and Maternal Traits in Norsvin Landrace.
I. Andersen-Ranberg1,3 and E. Grindflek2, 1Norsvin, Aas, Norway, 2Norsvin, Hamar, Norway

509 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. Fragomeni1,2, J. Miszta1, D. Lourenco1, S. Tsuruta1, Y. Masuda1,2 and T. J. Lawlor2, 1University of Georgia, Athens, 2Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, 3Holstein Association USA Inc., Brattleboro, VT

510 Use of Field Data in Genomic Reference Populations for Pig Breeding.
M. Lillehammer1, T. H. E. Meuwissen2 and A. K. Sonesson1, 1Nofima As, Ås, Norway, 2Norwegian University of Life Sciences, Ås, Norway, 3NOFIMA, Ås, Norway

511 Different Strategies for Genomic Prediction of Average Daily Weight Gain in Nellore Finishing Steers.
A. L. Somavilla1, L. C. A. Regitano2, F. B. Mokry1, M. A. Mudaudi1, R. R. Tullio1, M. L. Nascimento1, L. L. Coutinho2 and D. P. Munari1, 1Universidade 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

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

513 Accuracy of Molecular Breeding Values for Production and Efficiency Traits of Canadian Crossbred Beef Cattle using a Cross-Validation Approach.
E. C. Akanno1, G. Plastow1, C. Li1,2, S. P. Miller1,3 and J. A. Basarab4, 1University 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

514 Flexibility of Bayesian LASSO under Different Genetic Structure.
L. O. Dutíama1, 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

Presentation Time: 9:30 AM – 10:00 AM

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

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. Kawahara1, 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. Stoop1, 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. Zakizadeh1 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. Sasaki1, 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

Poster Session: 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. Mohammadi1, University of Tabriz, Tabriz, Iran

M. N. Bemji1, 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. Astruc2, J. Palhière2, S. Lemarié2 and A. Fugeray-Scarbel5,
1INRA, Castanet tolosan, France,
2INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France,
3Idele, Castanet tolosan, France,
4idele, Castanet tolosan, France,
5INRA, grenoble, 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. Fuerst-Wall1,2 and C. Fuers1,1 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. Lobo1,2, S. R. Paiva1 and R. N. B. Lobo1,1 Embrapa Goats and Sheep, Sobral, Brazil, 2Embrapa Secretariat of International Affairs, Brasilia, Brazil, 1Federal University of Ceará, Fortaleza, Brazil

QTL Affecting Skin Traits on CHI19 in an Angora x Creole Goat Backcross Population.
M. Poli1, Instituto de Genética CICVYa-INTA, Buenos Aires, Argentina

Genetic Analysis of Daily Maximum Milking Speed by a Random Walk Model in Dairy Cows.
B. Karacaören1, L. Janss1 and H. N. Kadarmideen1, Section of Biometry and Genetics, Department of Animal Science, Akdeniz

Effects of Housing type × Feeding System on Milk Yield of Holstein Cows.
K. Hagiy2,3, S. Yamaguchi2, K. Hayasaki1, T. Yamazaki1, T. Osawa1, H. Abe1, S. Nakagawa2, T. Kawahara1 and M. Suzuki1, 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, 5Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan

Genetic Analysis of Wool Shedding Scores of Ewes from a Composite Flock using a Threshold Model, G. Ciappesoni1, G. Banchero1 and A. Vázquez1, INIA, Rincón del Colorado, Uruguay, 2INIA, Colonia, Uruguay

Impact Of The Hypermuscularity GDF8 Gene On Sheep Maternal Abilities Traits.
D. Francois1, D. Carpenter1, Y. Bourdillon1, D. Grasset4, F. Tortereau2 and J. Raoul1, INRA, Toulouse, France, 2INRA, Toulouse, France, 3INRA UE0322, La Sapinière, Bourges, France, 4GID Lacune, Lauras, France, 5Idele, Castanet tolosan, France

Characterization of Linkage Disequilibrium and Consistency of Gametic Phase in Canadian Goats.
L. F. Brito1,2, M. Jafarikia1, D. A. Grossi3, L. Maignel4 and A. Vázquez1, 1INIA, Colonia, Uruguay, 2University of Natural Resources and Life Sciences (BOKU), Vienna, Austria, 3INIA, Rincón del Colorado, Uruguay, 4INRA, Toulouse, France

S. Andonov1, G. Klemetsdal2 and T. Ádnøy3, 1Faculty of Agricultural Sciences and Food, Skopje, Macedonia, 2Norwegian University of Life Sciences, Ås, Norway, 3Norwegian University of Life Sciences, Ås, Norway

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

Genetic Analysis of Wool Shedding Scores of Ewes from a Composite Flock using a Threshold Model and Bayesian Methodologies.
N. Vargas Jurado1,2, 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 Swalte, Martin Luther University Halle-Wittenberg, and Christian Maltecca, North Carolina State University

Effects of Housing type × Feeding System on Milk Yield of Holstein Cows.
K. Hagiy2,3, S. Yamaguchi2, K. Hayasaki1, T. Yamazaki1, T. Osawa1, H. Abe1, S. Nakagawa2, T. Kawahara1 and M. Suzuki1, 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, 5Obihiro 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. Karacaören1, L. Janss1 and H. N. Kadarmideen1, Section of Biometry and Genetics, Department of Animal Science, Akdeniz
Comparison of Natural Antibodies Measured in Milk and Blood Samples of Dutch Dairy Cattle.

B. de Klerk1, B. J. Ducro2, H. C. Heuven3, I. den Uyl4, J. A. M. van Arendonk5, H. K. Parmentier6 and J. J. van der Poel7,
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. Bruneli6,
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. Rodríguez-Ramírez1, J. Fernández1, M. A. Toro2, D. Hernández2 and B. Villanueva1,
1INIA, Madrid, Spain,
2ETS Ingenieros Agrónomos, Madrid, Spain

Estimates of Genetic Parameters for Test Day and 305-day Milk Yield in First Lactation of Mambí de Cuba Cows.

A. Hernández1, Instituto de 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. Amer1 and C. V. Pflühli1, AbacusBio Limited, Dunedin, New Zealand,
2DairyNZ, Hamilton, New Zealand


A. Nishiura1, O. Sasaki1, M. Aihara2, H. Takeda2 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. P. M. Gama1, M. H. Lidauer1, G. P. Aamand2 and C. V. Phyn3,
1MPI Bio Limited, Dunedin, New Zealand,
2DairyNZ, Hamilton, New Zealand

New Simulation Method to Create Data Sets With a Desired Genetic Trend.

A. M. Tyrissevi1, M. H. Lidauer1, G. P. Aamand2 and E. A. Mäntysaari3,
1MIT Agrifood Research Finland, Jokioinen, Finland,
2Nordic Cattle Genetic Evaluation, Aarhus, Denmark

Genetic Parameters for Rank of Dairy Gir Cattle in Agricultural Shows using Thurstonian Procedures.

1Univesidade 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,
3São Paulo State University (UNESP), Jaboticabal, Brazil,
4Associação Brasileira de Criadores de Gir Leiteiro, Uberaba-MG, Brazil

Descriptive Analysis of Copy Number Variation Regions in a Population of Dairy Gyr Cattle.

1Embrapa Dairy Cattle, Juiz de Fora, Brazil,
2NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil,
3São 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. Lidauer, 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. Taddeo1, EEA Bariloche-INTA, San Carlos de Bariloche, Argentina

Genetic Improvement Of Sheep In Ireland.
T. Pabiou1, T. Byrne2, E. Wall2 and N. McHugh4, 1Irish Cattle Breeding Federation, Bandon, Ireland, 2AbacusBio ltd, Dunedin, New Zealand, 3SheepIreland, Bandon, Ireland, 4Teagasc Moorepark, Fermoy, Ireland

W. Olivier1, Grootefontein ADI, Middelburg, South Africa

ASIP and MC1R Mutations Causing Black Coat Colour in Five Swedish Sheep Breeds.
C. M. Rochus1,2,3, S. Mikko1, A. Näsholm1 and A. M. Johansson1, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2AgroParisTech, Paris, France, 3GenPhySE, INRA, Castanet-Tolosan, France

Relationships of Faecal Worm Egg Count with Body Weight and Male Fertility In South African Merinos.
P. A. M. Matebesi-Ranthimo1,2, S. W. Cloete3,4, J. B. van Wyk5 and J. J. Olivier3, 1National University of Lesotho, Maseru, Lesotho, 2University of the Free State, Bloemfontein, South Africa, 3Directorate Animal Sciences, Elsenburg, South Africa, 4Universitats of Stellenbosch, Elensburg, South Africa

Null Genetic Differentiation among Flocks Contributing to the Ripollesa Sheep Herdbook.
J. Casellas1, M. Fina1, R. Bach2 and J. Piedrafit2, 1Universitat Autònoma de Barcelona, Bellaterra, Spain, 2ANCRI, Monells, Spain, 3Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain

Breech Strike Indicator Traits for Merino Sheep in Non-Seasonal Rainfall Environments.
T. L. Bird-Gardiner1,2,3, D. J. Brown4, J. L. Smith4, S. Mortimer4 and G. Refshauge5, 1Cooperative Research Centre for Sheep Industry Innovation, Armidale, Australia, 2University of New England, Armidale, Australia, 3NSW Department of Primary Industries, Trangie, Australia, 4Animal Genetics and Breeding Unit, UNE, Armidale, Australia, 5CSIRO Animal, Food and Health Sciences, Armidale, Australia, 6NSW DPI, Trangie, Australia, 7NSW Department of Primary Industries, Cowra, Australia

Genetic Parameters and QTL Detection for Milking Speed in Dairy Alpine and Saanen Goats.
I. Palhière1, H. Larroque2, C. Virginie3, G. Tosser4 and R. Rachel5, 1INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, 2Institut de l’Elevage, Castanet-Tolosan, France, 3INRA, UMR 1388 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 Wyk3, S. W. Cloete4 and B. J. Olivier4, 1University of the Free State, Bloemfontein, South Africa, 2Directorate Animal Sciences, Elsenburg, South Africa

Effects of Buck and Doe Size on the Growth Performance and Survival of their Progeny.
D. R. Kagonza1, M. F. Rothschild2 and K. J. Stalder3, 1Department of Agricultural Production, College of Agricultural and Environmental Sciences (CAES), Makerere University, Kampala, Uganda, 2Iowa State University, Ames, 3Department 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
Genetics of Sheep Health Traits.
N. McHugh1, S. Potterton2, E. Wall3 and T. Pabion2, 1Teagasc Moorepark, Fermoy, Ireland, 2Sheep Ireland, Co. Cork, Ireland, 3Sheep Ireland, Bandon, Ireland, 4Irish Cattle Breeding Federation, Cork, Ireland

Genetic Association between Body Measurements and Weight in Santa Inês Sheep.
E. J. Oliveira1,1, El Faro2, A. P. Freitas2, F. F. Similli2, A. E. Vercesi Filho2, M. L. P. Lima2, R. L. D. Costa2 and C. C. P. Paz1,2, 1Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto - Departamento de Genética (USP/FMRP), Ribeirão Preto-SP, Brazil, 2SA/A/PTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Genomic Breeding in French Lacaune and Manech Dairy Sheep: Design and Expected Genetic Gain.
D. Buisson1,2,3, G. Lagriffoul4, G. Baloche1, X. Aguerre1, P. Boulenc5, F. Fidelle5, G. Fregeat5, B. Giral-Viala5, P. Guibert5, P. Panié, C. Soulas1, J. M. Astruc1 and F. Barillet1, 1INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France, 2OS Upa Lacaune, Rodez, France, 3CDEO, Ordiarp, France, 4Izele, Toulouse, France, 5Ovitest, Rodez, France, 6Confédération Générale de Roquefort, Millau, France

M. Tolone1, J. M. Yáñez2, A. M. Satera1, L. M. Scatassa1 and B. Portolano1, 1Università degli Studi di Palermo, Palermo, Italy, 2University of Chile, Santiago, Chile, 3IZS della Sicilia “A. Mirri”, Palermo, Italy

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

Genetic Evaluations of Milkability in Norwegian Red Based on Data from Automatic Milking Systems.
B. Heringsstad1,2 and H. K. Bagten1, 1Geno, Ås, Norway, 2Norwegian University of Life Sciences, Ås, Norway

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

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

Trend Validation Procedures Applied by Interbull – A Historical Overview.
V. Paucci1 and J. W. Dürr, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

Genetic Analysis of Milk Fat Globule and Casein Micelle Size in Canadian Holsteins.
A. Fleming1, A. Koek1, F. Miglior2, M. Corredig3, J. Chen2, B. Mallard4, A. Ali4 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, 4Dept of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada, 5Dept of Mathematics and Statistics, University of Guelph, Guelph, ON, Canada

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

Multivariate Outlier Detection in Genetic Evaluation in Nordic Jersey Cattle.
H. Gao1, P. Madsen1, J. Pösö2, J. Pedersen2, M. H. Lidauer3 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. Bykov3 and M. Kargo4, 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 Admixtue by Quantifying Breed Composition to Gain Historical Perspective on Dairy Cattle in Canada.
S. G. Larmer*, 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. Hansen2, 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. Gonçalves*, 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. Candá2, F. A. T. Bruneli3, G. G. Santos4, C. H. C. Machado5, P. S. Lopes6 and M. G. C. D. Peixoto7, 1Embrapa Dairy Cattle, Juiz de Fora, Brazil, 2Universidade Eduardo Mondlane, Vilanculos, Mozambique, 3Associação Brasileira de Criadores de Zebu, Uberaba, Brazil, 4Univerridade Federal de Viçosa, Viçosa, Brazil

Phenotypic and Genetic Trends for Growth and Milk Traits of Guzera Breed in Dual Purpose Herds.
T. M. Gonçalves*, R. A. Canda*, G. G. Santos2, A. D. Catão3, M. G. C. D. Peixoto4, B. Villanueva5, C. H. C. Machado6, P. S. Lopes7, 1Embrapa Dairy Cattle, Juiz de Fora, Brazil, 2Universidade Eduardo Mondlane, Vilanculos, Mozambique, 3AbcZ, Uberaba, Brazil, 4Universidade Federal de Viçosa, Viçosa, Brazil

Genomic Estimates of Inbreeding and Coancestry in Austrian Brown Swiss Cattle.
F. Gómez-Romano1, J. Soelkner2, B. Villanueva3, G. Mészáros4, A. Correa5, 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. Smith*, 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. Massiga5, F. C. Muchadeyi6, J. Rees7, B. Sayre8, A. R. Elbehay9, M. F. Rothschild10, D. F. Mujib11, O. Mwav12, S. Kemp13, L. Colli14, P. Ajmone-Marsan15, P. Crepaldi16, J. Soelkner17, C. P. VanTassel18 and S. Abegaz19, 1Cornell University, Ithaca, NY, 2USDA, ARS, BFGL, Beltsville, MD, 3USDA-ARS, Beltsville, MD, 4ASARECA, 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, 10Universita 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
Lambing Ease is Heritable but not Correlated to Litter Size in Danish Meat Sheep Breeds.
A. C. Sørensen1, P. Valasek2, J. Pedersen2 and E. Norberg2, 1Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Czech University of Agriculture, Prague, Czech Republic

Characterization of a New Allele Encoding $\alpha_{s2}$-casein in the Lacaune Dairy Sheep: Possible Phylogeny Relationship among CSN1S2 Alleles.
Z. H. Fang1,2,3, G. Miranda1,2 and P. Martin1,2, 1INRA, UMR1313 GABI, Jouy-en-Josas, France, 2Agroparistech, UMR 1313, GABI, Jouy-en-Josas, France, 3Wageningen University, Animal Breeding and Genomics Centre, Jouy-en-Josas, Netherlands

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

Targeted Association Mapping in Merinoland Crossbred Lambs.
K. Schiller1,2, P. Stratz2, S. Preuss2 and J. Bennewitz3, 1Institute for Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany, 2Institute for Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany, 3Institute for Animal Husbandry and Breeding, University of Hohenheim, 70599 Stuttgart, Germany

Genomic Analysis of the Spring Leg Defect in the Canadian Dorset Sheep Breed.
J. Cameron1, M. Jalaliria1, 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, 3Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

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

Breed Variation in Wool Quality, Growth and Plasma Metabolites of Prime Lambs Fed Degummed Canola.
A. E. Malan-Adl1,2, P. D. McEvoy1, D. Parsons1 and P. A. Lane1, 1University of Tasmania, Hobart, Tasmania, Australia, 2James Cook University, Townsville, Australia

Screening for Footrot Resistant Gene Markers and White Blood Cell Types in Katahdin and Katahdin Crossbred Sheep.
T. Wuliji1, W. R. Lamberson2, 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

Genetic Parameters of Objectionable Fibres, Skin Spots and Halo-hair in Corriedale Sheep.
A. Sanchez1,2, J. J. Urioste2, F. Peñagaricano2, K. Neimaur1, J. Sienra1 and R. Kremer1, 1Universidad de la República, Montevideo, Uruguay, 2University of Wisconsin, Madison

Situation Analysis for the Performance Recording of Australian Meat Goats.
M. N. Aldridge1, D. J. Brown2, T. Hooke1 and W. S. Pitchford1, 1School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia, 2Animal Genetics and Breeding Unit, UNE, Armidale, Australia

Effects of Selection Accuracy, Risk and Young Ewe Fertility on Breeding Program Design.
J. E. Newton1,2,3, D. J. Brown1, A. A. Swan2, S. Dominik2 and J. van der Werf1, 1Animal Genetics and Breeding Unit, UNE, Armidale, Australia, 2CSIRO Animal Food and Health Sciences, Armidale, Australia, 3University of New England, Armidale, Australia

The Relationship of OPP Infection to TMEM154 Genotype in a Midwestern Sheep Flock.
T. W. Murphy1, D. L. Thomas1, T. A. Taylor2, M. J. Maroney1 and K. M. Nelson1, 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.†, A. S. Nguluma†, L. Wang†, J. L. Groves† and M. L. Leite-Browning†, †Tennessee State University, Nashville, TN, ‡Alabama A&M University, Huntsville

Transcriptome Comparison between the Pubertal and Adult Testis in Goats.
Z. Liu†, J. Li‡, H. Xiao†, W. Liu†, X. Yue† and Y. Ma†, †Inner Mongolia Agriculture University, Hohhot, China, ‡Inner Mongolia Agriculture University, Hohhot, China, ‡The 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. Lipkin†, M. A. Dolezal†, A. Bagnato, J. E. Fulton, N. P. O’Sullivan†, E. Santus†, D. Burt† and M. Soller†, †Hebrew University of Jerusalem, Jerusalem, Israel, ‡Università degli Studi di Milano, Milano, Italy, §Hy-Line International, Dallas Center, IA, ¶ANARB, Italian Brown Cattle Breeders’ Association, Bussolengo (VR), Italy, †The 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. Kargo†,‡, J. Ettema†, L. H. Sørensen†, M. Fjordside† and L. Hjortø†, †Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ‡Knowledge Center for Agriculture, Aarhus, Denmark, §SimHerd Inc., Tjele, Denmark, ¶Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, †VikingDenmark, Viborg, Denmark, ‡Knowledge Centre for Agriculture, Aarhus, Denmark

Use of DNA Markers in Parentage Testing in Mexican Jersey Cattle.
R. Cuevas-Pat, R. Niñez-Domínguez*, 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. Winkelman*, 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. Kheirabadi†, S. O. Peters*, I. G. Imumorin† and M. Ghaderi-Zefrehel†, †University of Yasouj, Yasouj, Iran, ‡Berry College, Mount Berry, GA, §Cornell 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. Dechow* and I. W. Haagen, Pennsylvania State University, University Park

An Approach to Genomic Analysis of Longitudinal Data using Random Regression.
D. J. A. Santos‡, S. A. Boisson†, A. H. Utsunomiya†, M. G. C. Peixoto†, H. Tonhati†, J. Sölkner* and M. V. G. B. de Silva†, †State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, ‡University of Natural Resources and Life Sciences, Vienna, Austria, §UNESP Univ Estadual Paulista, Jaboticabal, Brazil, ¶Embrapa 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-Enciso¹, Universitat Autònoma de Barcelona, Bellaterra, Spain

660  High Imputation Accuracy in Layer Chicken from Sequence Data on a Few Key Ancestors.
M. Heidaritabar¹, M. P. L. Calus², A. Vereijken³, M. A. Groenen¹ and J. W. M. Bastiaansen², Wageningen University, Wageningen, Netherlands, ³Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, ¹Hendrix Genetics, Boxmeer, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

661  Imputation of Sequence Level Genotypes in the Franches-Montagnes Horse Breed.
M. Frischknecht¹,²,³, M. Neuditschko¹,², V. Jagannathan¹,², C. Drögemüller²,³, J. Tetens², G. Thaller⁴ and S. Rieder¹,³, ¹Agroscope - Swiss National Stud Farm, Avenches, Switzerland, ²Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, ³Swiss Competence Center of Animal Breeding and Genetics, Bern, Switzerland, ⁴Graduate School for Cellular and Molecular biology, University of Bern, Bern, Switzerland, ¹Institute of Animal Breeding and Husbandry, Christian-Albrechts-Universität zu Kiel, Kiel, Germany, ¹Institute 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.
R. van Binsbergen¹,²,³, M. P. L. Calus¹, M. C. A. M. Bink¹, C. Schrooten¹, F. A. van Eeuwijk¹ and R. F. Veerkamp¹, ¹Wageningen University, Wageningen, Netherlands, ²Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ³CRV, Arnhem, Netherlands

665  Characterization of Genetic Variation in Icelandic Cattle.
L. E. Holm¹,², A. Das¹, J. Momeni¹, F. Panitz¹, C. Bendixen¹ and E. Eythorsdottir², ¹Dept. Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, ²Faculty 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. Das¹, 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. Li¹,², M. Sargolzaei¹,² and F. S. Schenkel¹, ¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²The Semex Alliance, Guelph, ON, Canada

668  Comparison of Variant Calling Methods for Whole Genome Sequencing Data in Dairy Cattle.
C. F. Baes¹,²,³, M. A. Dolezal⁴,⁵, E. Fritz-Waters⁶, J. E. Koltes⁶, B. Baps⁶, C. Flury⁶, H. Signer-Hasler⁶, C. Stricker⁶, R. L. Fernando⁶, F. Schmitz-Hsu⁶, D. J. Garrick⁶ and B. Gredler⁶, ¹Bern University of Applied Sciences, School of Agriculture, Forest and Food Sciences, Zollikofen, Switzerland, ²Qualitas AG, Zug, Switzerland, ³University of Veterinary Medicine Vienna, Vienna, Austria, ⁴Università degli Studi di Milano, Milano, Italy, ⁵Iowa State University, Ames, ⁶Bern University of Applied Sciences, School of Agricultural, Forest and Food Sciences, Zollikofen, Switzerland, ²Bern University of Applied Sciences, School of Agriculture, Forest and Food Sciences, Zoll, Switzerland, ³agn-genetics, Davos, Switzerland, ⁴swisssgenetics, Zollikofen, Switzerland

Posters: Statistical and Genomic Tools for Mapping QTL and Genes (Group 2)
Chair: Michael E. Goddard, Department of Environment and Primary Industries
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. Böttard4,5, S. Mercier6,7, D. Robelin1, T. Faraut1, C. Arnould6, E. Lebihan9, J. Recocoquillay8, G. Salin4,10, P. Dehais11,12, F. Pêtel13, C. Leterrier2 and M. SanCristobal7,14, 1Institute Pasteur Montevideo, Montevideo, Uruguay, 2IMERL, Facultad de Ingeniería, Universidad de la República, 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 ENV, GenPhySE, Castanet-Tolosan, France, 14INSA Toulouse, GMM, Toulouse, France

A New Method to estimate Recombination Rate Based on SNP Allelic Dosage Data.
T. Yang1, 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. Heuer2 and G. Thaller2,1, Institute 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. Sarup3 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, 3Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark

Accounting for Population Structure and Haplotype Diversity in Whole Genome Scans for Selection Signatures.
B. Servin1, S. Böttard4, C. Chevalier1, M. I. Fariello2, F. Phoca5 and M. SanCristobal6, 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. Stella1, 1Fondazione Parco Tecnologico Padano, Lodigiano, Italy, 2Parco Tecnologico Padano (PTP), Lodigiano, Italy

Haplo-Block Structure of Southern African Village Chicken Populations.
K. S. Khanyile1,2, E. F. Dzomba3 and F. C. Muchadeyi4, 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. Knot3, C. Hayward4, V. Vitart5, I. Rudan6, H. Campbell7, N. Hastie1, A. F. Wright1, P. Navarro1 and C. Haley2,3, 1MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothan, 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. Bertoni1, M. V. A. Lemos2, C. Aboujiaoudé2, G. M. de Camargo1, L. A. L. Chardona1, L. G. Albuquerque3 and F. Baldi4, 1State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, 2Jaboticabal, Brazil, 3Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, 4State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, 5State University of São Paulo, Botucatu, São Paulo, Brazil, Botucatu, Brazil

Bayes U: A Genomic Prediction Method Based on the Horseshoe Prior.
R. Pong-Wong1 and J. A. Woolliams, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothan, United Kingdom

PREGSF90 – POSTGFS90: Computational Tools for the Implementation of Single-Step Genomic Selection and Genome-Wide Association with Ungenotyped 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,1,2, O. Facó,1 and A. M. B. O. Lobo,1, Embrapa Goats and Sheep, Sobral, Brazil, 2Federal University of Ceará, Fortaleza, Brazil, 3Federal University of Maranhão, Imperatriz, Brazil

R. I. Cuelmos,1, W. F. Meuwissen2, A. Sewalem,3, A. Taton,4, D. M. Lefebvre,5,6, R. Lacroix,4, E. Bouchard,4, D. Haine,5 and J. Dubuc,5,6, McGill University, Department of Animal Science, Ste-Anne-de-Bellevue, QC, Canada, 2McGill University, vide Sainte Anne de Bellevue, QC, Canada, 3Agriculture and Agrifoods Canada, Guelph, ON, Canada, 4Valacta, Ste-Anne-de-Bellevue, QC, Canada, 5University of Montreal, Saint-Hyacinthe, QC, Canada

386 Approximate Multivariate Genetic Evaluation of Functional Longevity and Type Traits in Austrian Fleckvieh Cattle.
C. Pfeiffer,1,2, B. Fuerst-Waltl,2, V. Duroc,1 and C. Fuerst,1, University 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, H. Luis Moreira,2, R. D. Silva Verneque,2, A. Eugênio Vercesi Filho,3, M. G. Campolina Diniz Peixoto,1, L. El Faro,4 and V. Lúcia Cardoso,1, Universidade de São Paulo, Faculdade de Medicina de Ribeirão Preto-Departamento de Genética,
**Consumers' Preference for “Bicycle Poultry” in Bénin: Implication for Designing Breeding Schemes.**
E. Sodjinou¹, A. Hemmingsen², D. O. Kouadnandé³, 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. Nesser¹,² and S. D. Mulageta¹, 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. Nesser¹,², N. A. Malwashes¹ and Z. King¹, ¹University of the Free State, Bloemfontein, South Africa, ²ARC-Animal Production Institute, Irene, South Africa

**Incorporating Risks in Economic Values for Pigs in Smallholder Production Systems in Kenya.**
J. Mbathia¹, T. Rewe², T. Okeno² and A. Kahi¹, ¹Egerton University, Njoro, Kenya, ²Pwani University, Kilifi, Kenya, ³Aarhus University, Tjele, Denmark

**Estimating the Economic Value of using a Panel of Tenderness Markers to Select for Improved Consumer Palatability Scores.**
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, Ås, Norway

**Optimization of a Meat Index for Austrian Land Sheep.**
L. Grill, A. Willam¹ 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. Knox², M. D. MacNeil² and S. L. Rodriguez Zas², ¹University of Illinois, Urbana, ²University of the Free State, Bloemfontein, South Africa

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

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**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. Flores¹² and J. van der Werf¹, 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
Initial RNA-Seq Analysis on the Milk Transcriptional Profiling of Two Sheep Breeds.
A. Suarez-Vega1, B. Guiterrez-Gil2, C. Esteban5 and J. J. Aranz3,1, Universidad de León, Leon, Spain, 2Universidad de León, León, Spain, 3Supercomputing Center of Castile and León, León, Spain

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. Tonhati4, 1Universidade Estadual Paulista “Júlio de Mesquita Filho” (FCAV-UNESP), Jaboticabal, Brazil, 2CAPES Foundation, Ministry of Education of Brazil, Brasília – DF 70.040-020, Brasília, Brazil, 3University of Georgia, Athens, 4State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Fine-Mapping of a Candidate Region Associated with Milk-Fat Composition on Bos Taurus Autosome 17.
S. I. Duchemin1,2, M. H. P. W. Visker1, 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, 3TI Food and Nutrition, Wageningen, Netherlands

Comparison of Genetic Parameters Estimation of Fatty Acids from Gas Chromatography and FT-IR in Holsteins.
N. A. Poulsen1, C. E. Eskildsen2, T. Skov3, L. B. Larsen1 and A. J. Buitenhuis1, 1Aarhus University, Food Science, Tjele, Denmark, 2University of Copenhagen, Food Science, Copenhagen, Denmark, 3Aarhus University, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Tjele, Denmark

Estimation of Genetic Parameters for the Protein Profile in Danish Holstein Milk.
A. J. Buitenhuis1, N. A. Poulsen2 and L. B. Larsen3, 1Aarhus University, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Tjele, Denmark, 2Aarhus University, Food Science, Tjele, Denmark

QTL Detection for Milk Fatty Acids in French Dairy Cattle.
A. Govignon-Gion1, S. Fritz1,2, H. Larroque1, M. Brochard1, C. Chantry6, F. Lahalle7,8 and D. Boichard2, 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, 5Idale, Paris, France, 6LABOGENA, Jouy-en-Josas, France, 7Institut de l’Elevage, Paris, France, 8CNIEL, Paris, France

Genetic Parameters of Average Milk Flow Recorded Electronically from Milking Parlours and Automatic Milking Systems in Estonian Holstein Dairy Cows.
D. Pretto1, A. Tännavõts2, H. Kiiman1,2, E. Pärna1,2, H. Viinalass1,2 and T. Kaart3,2, 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

QTL Detection for Fat Yield on BTA14 using Linkage Disequilibrium Based Methods.
M. J. Beribe1, H. A. Carignano1, N. Lopez-Villalobos2, M. Poli1 and D. L. Roldan1, 1Instituto de Genética CIVyA-INTA, Buenos Aires, Argentina, 2Massey University, Palmerston North, New Zealand

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

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

Genetic Relationship between Lactation Curve Traits in Dairy Cattle.
C. B. Wasike1, K. J. Peters2 and A. K. Kah2, 1Department of Animal Science, Maseno University, Maseno, Kenya, 2Sheep and Goat Association of Berlin- Brandenburg, Berlin, Germany

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. Pétille1, L. D. Cassoli1, P. F. Machado1, L. L. Coutinho2 and G. B. Mourao1,
Random Regression Model Analysis for Total Milk Solids in First Lactation Dairy Cattle.
A. Zampar1, F. S. Cavalcante1, P. F. Machado2, L. E. Bastos3, A. B. Fraga1 and G. B. Mourão2,1Federal 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. Li2,3, F. Beaudoin1, X. Zhao2, C. Lei2 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-Díaz2, S. F. N. Pertile1, J. Petrini1, M. Salvian2, M. A. P. Rodríguez1, R. R. Lima2, P. F. Machado1, L. L. Coutinho1 and G. B. Mourao1,1Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil,2Federal University of Lavras, Lavras, Brazil,1University 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, 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,1Iowa State University, Ames
R. B. Onzima1, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands; Kachwekano 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. Fuerst2 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. Canario1,3, M. Sourdoux1, D. Bahon3, J. Riquer1 and L. Flatres-Grall1,4GENE+, 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. Scales2, D. J. A. Santos3, M. G. Campolina Diniz Peixoto1 and A. Eugênio Vercesi Filho1,1Embrapa Dairy Cattle, Juiz de Fora, Brazil,2State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil,1UNESP 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. Cassandra1,2, D. Pretto2, 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,1Massey 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 Filho2, R. L. R. Carneiro1, R. C. Sesana2 and L. El Faro2,1Apta Regional - PRDTA Centro Leste SAA/SP, Ribeirão Preto-SP, Brazil,2Instituto de Zootecnia APTA SAA/SP, Sertãozinho-SP, Brazil,1SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil,2CRV-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. Lendenbauer¹, 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, ²University of California, Davis

Development of Selection Indexes for a Beef Cattle Production System from Available EPDs.
M. I. Pravia¹,², O. Ravagnolo³ and J. Urioste³,¹
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. Clark¹, D. Brown² and J. van der Werf³,
¹University of New England, Armidale, Australia,
²Animal Genetics and Breeding Unit, Armidale, Australia

Optimising Current Generation Gains to Supplement Genetic Gain in Commercial Sheep Flocks.
J. S. Richards¹,², B. P. Kinghorn¹ and K. D. Atkins²,
¹University of New England, Australian Cooperative Research Centre for Sheep Industry Innovation, NSW Department of Primary Industries, Orange, Australia,
²University of New England, Armidale, Australia,
³Shoal Bay, Australia

Poster: 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. Mark³,
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. Hellinga³, P. A. J. Leegwater³, W. Back³,², J. W. M. Bastiaansen³ and B. J. Ducro³,
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

Genetic Analysis Of Hunting Traits In Norwegian Elkhounds.
M. Wetten¹ and T. Aasmundstad²,
¹Geninova, Hamar, Norway,
²Norsvin, Hamar, Norway

Genetic Analysis Of Hunting Trails 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. Clements², 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
The Genetics of Aggression, Fear and Sociability in Everyday Life of Swedish Dogs.  
H. Eken Asp, P. Arvelius, W. F. Fikse, K. Nilsson 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.  
B. J. Ducro1, J. J. Windig1, H. Bovenhuis1, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, Koninklijke Vereniging “Het Friesch Paarden-Stamboek”, Drachten, Netherlands

Model Assessment for Ranking Traits of Criollo Horses Participating in Endurance Trials.  
R. López-Correa1, F. Peñagaricano2, G. Rovere3 and J. I. Urioste1, Universidad de la República, Montevideo, Uruguay, 2University of Wisconsin, Madison, 3Wageningen University, Wageningen, Netherlands

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**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. Ferdosi1, J. van der Werf1, B. Tier2 and C. Gondro4, 1School of Environmental and Rural Science, University of New England, Armidale, Australia, 2University of New England, Armidale, Australia, 3Animal Genetics and Breeding Unit, Armidale, Australia, 4School of Environmental & Rural Science, University of New England, Armidale, Australia

Sequence Analyses of Bovine PAG-1 Gene.  
M. O. Ozoje1, S. O. Durosaro1, P. E. Esada1 and S. O. Peters2, 1Federal University of Agriculture, PMB 2240, Abeokuta, Nigeria, 2New Mexico State University, Mount Berry, GA

Inferring a Core Transcriptional Regulatory Network in Cows.  
S. Strunz1, T. Kacprowski2, N. Melzer3, J. Friedrich4 and A. de la Fuente1, Leibniz-Institute for Farm Animal Biology, Dummerstorf, Germany, 2University Medicine Greifswald, Greifswald, Germany, 3University of Rostock, Rostock, Germany

Copy Number Variation in Brown Swiss Dairy Cattle.  
M. A. Dolezal1,2, A. Bagnato1, F. Schiavini2, E. Santus3, L. E. Holm4, C. Bendixen4 and F. Panitz2, 1Università degli Studi di Milano, Milano, Italy, 2University 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. Cortet³, A. Blanchard-Letort⁴, F. Guégnard⁴, D. Francois⁵, Y. Bourdillon⁴, C. Grisè⁵, F. Prevot⁵, A. Averardère⁶, J. Demars⁶, J. Sarry⁶, A. Stellé⁶, F. Woloszyn⁶, K. Canale-Tabet⁴, J. Cabaret⁴, G. Tosser-Klopp⁴ and G. Salle⁴, ¹INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, ²ENVIT-INRA IHAP, 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, ²INRA GenPhySE UMR1388, Toulouse, France, ¹Fondazione 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. Farid¹, 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. Cockram¹, J. Salak-Johnson¹, C. Chase¹, M. G. Thomas¹, R. K. Pee¹ 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 STAT5A/B 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, G. Bramis¹, G. Arsenos¹ and G. Banos¹, 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. Emam¹, M. A. Paibomesai¹, K. A. Thompson-Crispi¹, F. S. Schenkel¹, F. Miglior², M. Sargolzaei² and B. Mallard², 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-Valladares² and B. Gutierrez-Gil², 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-Ismail¹, A. Koeck¹, S. P. Miller¹,²,³ P. Stothard¹, G. S. Plastow⁴, F. Miglior¹,²,³ S. S. Moore⁴, M. Sargolzaei⁴ and F. S. Schenkel¹, ¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²Animal and Poultry Science, Dumanhour University, Dumanhour, 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. Sollero¹2, C. G. Gomes¹, V. M. Roso¹, R. H. Higa¹, M. J. Yokoo¹, L. L. Cardoso⁶, A. R. Caetano⁶ and F. F. Cardoso⁶, 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, Brazil, ⁴Gensys Consultores Associados, Porto Alegre, Brazil, ⁵Embrapa Informática Agropecuária, Campinas, Brazil, ⁶Embrapa Southern Region Animal Husbandry, 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. Lewis¹2, P. B. Siegel³ and I. Kyriazakis¹, 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, P. J. Griebel² and S. M. Schmutz³, 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 Immunoresponders.
K. Fleming¹1, K. A. Thompson-Crispi¹2, D. C. Hodgins¹, F. Miglior¹2³ and B. Mallard²1, 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, M. C. Niederwerder¹, N. V. L. Serado¹, M. A. Kerrigan¹, R. R. R. Rowland¹, J. K. Lunney¹ and J. C. M. Dekkers¹, ¹Iowa State University, Ames, ²Kansas State University, Manhattan, ³USDA, ARS, BARC, APDL, , Beltsville, MD

Analysis Of Biological Pathways Associated With Immune-capacity Traits In Pig.
T. Okamura¹2, Y. Takahagi¹, T. Matsumoto¹, H. Uenishi¹, K. Suzuki¹ and M. Satoh¹, 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. Waters¹, ¹School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, ²Teagasc Grange, Meath, 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. Fukumasa¹ and J. B. Sterman Ferraz¹, 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, ³University of Sao Paulo, Pirassununga, Brazil, ⁴CNPGC/EMBRAPA, Campo Grande, Brazil, ⁵UNESP Univ Estadual Paulista, Jaboticabal, Brazil, ⁶Faculdade de Ciências Agrárias e Veterinárias – UNESP, Jaboticabal, Brazil, ⁷UNESP Univ Estadual Paulista, Araçatuba, Brazil, ⁸University of Sao Paulo, Pirassununga, Brazil

Genetic Parameters and Accuracy of Recording Dry Matter Intake in First Parity Holstein-Friesian Cows.
C. I. V. Manzanilla Pech¹2, R. F. Veerkamp¹2, M. P. L. Calus¹, J. E. Pryce¹ and Y. de Haas¹, ¹Animal Breeding and Genomics
Positional Candidate Genes for Residual Intake and Gain in Nellore Beef Cattle.
P. S. N. Oliveira1, A. S. M. Cesar2, M. L. Do Nascimento1, M. M. Souza1, R. R. Tullio1, D. P. Lanna1, G. B. Mourão3, J. M. Reecy4, D. J. Garrick4, M. A. Mudadi5, L. L. Coutinho6 and L. C. Almeida Regitano1, 1Federal University of São Carlos, São Carlos, Brazil, 2LZT/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. Plastow3 and J. C. M. Dekkers1, 1Iowa State University, Ames, 2Genesis Inc, Lethbridge, AB, Canada, 3University of Alberta, Edmonton, AB, Canada

Life cycle Biological Efficiency of Mice Selected for Heat Loss.
A. Bhatnagar1 and M. K. Nielsen2, 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. Cundiff*, USDA-ARS, U.S. MARC, Clay Center, NE

Feed Intake Variation in Crossbred Lambs Supplemented with Spirulina.
B. W. Holman1 and A. E. Malau-Aduli2, 1NSW Dept of Primary Industries, COWRA, Australia, 2University of Tasmania, Hobart, Tasmania, Australia

P. A. Alexandre1, M. H. A. Santana1, J. P. Eler1, H. Fukumasu1, G. A. Oliveira Jr. and J. B. S. Ferraz, 1NAP-GMABT/FZEA/University of Sao Paulo, Pirassunungu, Brazil

Selection for Postweaning Weight and Residual Feed Intake in Nellore Cattle.
M. E. Z. Mercadante1, T. M. Ceacero1, M. Morelli1, J. N. S. G. Cyrillo1, F. M. Monteiro1 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. Garreau1 and J. Raesche1, 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. Morganz2 and A. Vignau1, 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 Purebred Sire Lines.
N. Duijvestein1, E. F. Knol2 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. Nyholm1, A. Sairanen1, T. Pitkänen1, E. A. Mäntysaari1 and M. H. Lidauer1, 1MTT Agrifood Research Finland, Jokiotien, 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. Serão2, R. K. R. Rowland3, 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

### Predicting MHC Haplotypes from High-Density SNP Genotypes in Pigs.

J. Dunkelberger§, S. Ho, A. 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

### The Homology Modeling Study of the Bovine \( \beta \)-calpain Inhibitor-Binding Domains.

H. H. Chai*, Animal Genome & Bioinformatics Division, National Institute of Animal Science, Suwon, South Korea

### Genetic and Non-Genetic Indirect Effects for Bite Mark Traits in Group Housed Mink.

S. W. Alemu, P. Berg, L. Janss, S. H. Moller and P. Bijma, 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

### 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

### 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

### 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

### 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. Hayess and B. N. Lillies, Department of Pathobiology, University of Guelph, Guelph, ON, Canada, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada

### 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. Walle, Scotland's Rural College, Edinburgh, United Kingdom, Moredun Research Institute, Edinburgh, United Kingdom, SRUC, Edinburgh, United Kingdom

### 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

### 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

### Genetics of Susceptibility to Bovine Viral Diarrhea, Infectious Bovine Respiratory Disease, and Liver Fluke in Cattle.

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

568 Estimation of Additive Genetic and Maternal Genetic Effects in Mice Selected for High and Low Oxygen Consumption.
K. Suzuki\(^*\), Tohoku University, Aoba-ku, Sendai City, Japan

569 Genetic Structure of Quantitative Traits for Effective Feeding during the Growing to Finishing Phases in Landrace Pigs.
M. Taniguchi\(^*\), A. Arakawa\(^*\), K. Hirose\(^*\), S. Nakaizato\(^*\), T. Matsumoto\(^*\), A. Ishida\(^*\), T. Ito\(^*\), K. Fukawa\(^*\) and S. Mikawa\(^*\), University of Aomori, Aomori, Japan, S. Suzuki\(^*\), Bioforsk, Tingvoll, Norway

570 Preliminary Investigation into Genetic Parameters for Feedlot Traits of Angus Cattle in South Africa.
J. Hendriks\(^*\), Agricultural Research Council, Pretoria, South Africa; University of the Free State, Bloemfontein, South Africa

571 Whole Genome Characterization and Associations Studies in Two Divergent Pig Lines Selected on Residual Feed Intake.
J. Riquet\(^*\), Y. Labrunie\(^*\), K. Feve\(^*\), Y. Billon\(^*\) and H. Gilbert\(^*\), INRA UMR1388, F-31326 Castanet-Tolosan, France; INRA UE1372, F-17700 Surgères, France

572 Prediction of Body Weight of Primiparous Dairy Cows Throughout Lactation.
M. L. Vanrobays\(^*\), J. Vandenberg\(^*\), H. Hammami\(^*\) and N. Gengler\(^*\), University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium; National Fund for Scientific Research, Brussels, Belgium

573 Variation among Dairy Cows in Rumen Liquid Fermentation Characteristics.
J. Lassen\(^*\), P. Lovendahl\(^*\), L. Kristensen\(^*\), Z. Zhu\(^*\), O. Højberg\(^*\), M. Poulsen\(^*\) and S. J. Noel\(^*\), Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark; Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjøle, Denmark; Department of Molecular Biology and Genetics, Aarhus University, Tjøle, Denmark; Department of Animal Science, Aarhus University, Tjøle, Denmark; Dept. Animal Science, Aarhus University, Tjøle, Denmark; Dept. Animal Science, aarhus University, Tjøle, Denmark
The Value of Group Records in Predicting Breeding Values for Individual Feed Intake in Pigs.
J. P. Sanchez¹, J. M. Paibomesai², M. A. Emam², M. A. Paibomesai¹, J. Reisach³ and R. Quintanilla³, ¹IRTA, Caldes de Montbui, Spain, ²IRTA, Monells, Spain, ³Selección Batallé, Riudarenes, Spain

Genetic Parameters for Dry Matter Intake at Different Lactation Stages among Primiparous Holstein, Jersey and Red Cows.
B. LI¹, Swedish University of Agricultural Sciences, Uppsala, Sweden

Genetic Variation in Efficiency to Deposit Lean Meat and Fat in Norwegian Landrace Pigs.
K. H. Martinsen¹, J. Ødegård², D. Olsen² and T. H. E. Meuwissen¹, ¹Norwegian University of Life Sciences, Ås, Norway, ²AquaGen, Ås, Norway

Increased Fat EBVs Reduce Need for Supplementary Feeding.
W. S. Pitchford¹ and S. F. Walkom², ¹School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia, ²School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy SA 5351, Australia

Residual Feed Intake in Beef Cattle; Genes, Metabolites and Beyond.
B. K. Karisa¹, J. M. Thomson² and G. S. Plastow², ¹University of Alberta, Edmonton, AB, Canada, ²Montana State University, Bozeman, MT

Genomic Selection for Feed Intake and Weight Gain Assuming Different Prior Distributions in Nellore Beef Cattle.
F. M. Rezende¹, M. H. A. Santana¹, G. A. Oliveira Junior², F. Baldí³, A. S. M. Cesar³, E. C. Mattos³, J. B. S. Ferrez³ and N. Ibáñez-Escriche¹, ¹Federal University of Uberlândia, Patos de Minas, Brazil, ²NAP-GMABT/FZEA/University of Sao Paulo, Pirassununga, Brazil, ³Universidade Estadual Paulista “Júlio de Mesquita Filho”- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, ¹University of Sao Paulo, Piracicaba, Brazil, ¹IRTA - Cataluña, Lleida, Spain

Rumen Microbial Taxa and By-products Associated with Feed Efficiency in Sheep.
K. M. Cammack¹, M. Ellisson², G. C. Conant², W. R. Lamberson³ and K. J. Austin¹, ¹Department of Animal Science, University of Wyoming, Laramie, WY, ²University of Wyoming, Laramie, WY, ³University of Missouri, Columbia

Genetics of Alternative Definitions of Feed Efficiency in Grazing Lactating Dairy Cows.
A. M. Harley¹, S. McParland², E. Kennedy², E. Lewis², M. O'Donovan², N. Lopez-Villalobos¹ and D. P. Berry¹, ¹Massey University, Palmerston North, New Zealand, ²Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ³Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

Functional Cluster Analysis of Genome Wide Associations for Energy Balance for Cows in Experimental Herds in Four European Countries.
A. Tolkamp¹, M. P. Coffey², E. Wall², D. P. Berry³, E. Strandberg¹ and R. F. Veerkamp⁴, ¹Scotlands Rural College (SRUC), Edinburgh, United Kingdom, ²SRUC, Edinburgh, United Kingdom, ³Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ⁴Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Increased Fat EBVs Reduce Need for Supplementary Feeding.
W. S. Pitchford¹ and S. F. Walkom², ¹School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia, ²School 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. Johnson¹, 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-Lesperance¹, D. C. Hodgkins², M. Enam¹, M. A. Paibomesai¹ and B. Mallard², ¹University of Guelph, Guelph, ON, Canada, ²Dept Pathobiology, University of Guelph, Guelph, ON, Canada, ¹Center 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 Laan1,2, B. Bed'Hom3, N. Bruneau4, O. Cházara5 and B. Besbes5, INRA, UMR1313 GABI, Jouy-en-Josas, France, 1INRA UMR1313 GABI, Jouy-en-Josas, France, 2Department of Pathology, University of Cambridge, Cambridge, United Kingdom, 3FAO, Roma, Italy

Predicting Susceptibility to Johne's Disease in New Zealand Dairy Cattle.
R. G. Sherlock1, Livestock Improvement Corporation, Hamilton, New Zealand

Genetic Parameters for Natural Antibodies in a Chicken Layer Line.
T. V. Berghof1,2, J. J. van der Poel1, J. A. Arts3, S. van Engelen4, H. K. Parmentier2 and H. Bovenhuis1, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Adaptation 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 Camargo1, State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

Genetic Parameters of Atypical Progesterone Profiles in Holstein-Friesian Cows using Data from Four European Experimental Research Herds.
S. Nyman1, K. Johansson1, D. J. D. Koning1, D. P. Berry1, R. F. Veerkamp1, E. Wall2 and B. Berglund1, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2Växa Sverige, Uppsala, Sweden, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, 3SRUC, Edinburgh, United Kingdom

Bayesian Estimates of Genetic Parameters for Reproductive Traits in Nellore Cows Raised on Pasture in the Tropics.
F. B. Lopez1, C. U. Magnabosco1, M. M. S. Mamede2, L. C. Moreira2, F. M. Souza2, M. G. Narcizo2, R. B. Lôbo3, G. J. M. Rosa3 and R. D. Sainz3, 1Embrapa Cerrados, Brasília, Brazil, 2Federal University of Goiás, Goiânia, Brazil, 3Brazilian Society of Breeders and Researchers, Ribeirão Preto, Brazil, 4University of Wisconsin, Madison

Assessment of Genetic and Non-Genetic Factors Related to Survival Probabilities of Farmed White-Tailed Deer Neonates.
M. Parra-Bracamonte1, 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. Ismael1,2, M. Kargo3, A. Fogh4, E. Strandberg1, P. Lovendahl1, 1Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 3Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 4Knowledge Center for Agriculture, Aarhus, Denmark

Genome-Wide Scan for Reproductive Traits of Beef Heifers using High Density SNP Panels.
A. Michenet1, F. Phocas1, R. Saintilan2 and E. Venot1, MIDATEST, Sosu, France, 2INRA, UMR1313 GABI, Jouy-en-Josas, France, 3INRA UMR 1313 GABI, Jouy-en-Josas, France

Effect of Selection for Residual Variance of Litter Size on Hematology Parameters as Immunology Indicators in Rabbits.
M. J. Argente1, M. D. L. L. García1 and A. Blasco4, 1Universidad Miguel Hernández de Elche, Orihuela, Spain, 2Universidad 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 García1, 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. Bodin¹, S. Fabre 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*, 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 PigsRaised Extensively.
L. T. Gama¹, F. David² and H. Paixim², ¹FMV - University of Lisbon, Lisbon, Portugal, ²ACEPA, Évora, Portugal

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. Estany² and M. F. Rothschild¹, 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. Taniguchi¹, I. Matsuno¹ and Y. Mizoguchi¹, ¹Meiji University, Kawasaki, Japan, ²Meiji University, Kawasaki, Japan

Genome-Wide Association Studies on Piglet Splay leg Syndrome.
X. Hao¹*, G. S. Plastow², C. Zhang¹, Z. Hu², H. Yang¹, W. Li², Z. Wang¹, Z. Wang² and S. Zhang¹, ¹Huazhong Agricultural University, Wuhan, China, ²University of Alberta, Edmonton, AB, Canada, ³Wuhan Tianzhong Stock Corporation, Wuhan, China
924  Genome-Wide Association Studies (GWAS) Identify a QTL Close to PRKAG3 Affecting Meat pH and Colour in Crossbred Commercial Pig Lines.

t. Zhang	extsuperscript{1}, Z. Wang	extsuperscript{1}, H. Bruce	extsuperscript{2}, R. A. Kemp	extsuperscript{3}, P. Charagu	extsuperscript{1}, Y. Miar	extsuperscript{4}, T. Yang	extsuperscript{1} and G. S. Plastow	extsuperscript{5}, 1University of Alberta, Edmonton, AB, Canada, 2Genesis Inc, Lethbridge, AB, Canada, 3Hypor Inc, Regina, SK, Canada

925  Strategies to Implement Genomic Selection in Pig Breeding using Very Low Marker Density.

P. Stratz	extsuperscript{1}, R. Wellmann	extsuperscript{2} and J. Bennewitz	extsuperscript{3}, 1Institute of Animal Husbondry and Breeding, University Hohenheim, Hohenheim, Germany, 2Institute of Animal Husbandry and Breeding, University Hohenheim, Stuttgart, Germany

926  Reliability of Genomic Selection of Reproduction Traits in Finnish Yorkshire Pig Breed.

P. Uimari	extsuperscript{1}, M. L. Sevon	extsuperscript{2} and T. Serenius	extsuperscript{3}, 1University of Helsinki, Helsinki, Finland, 2MTT Agrifood Research Finland, Jokioinen, Finland, 3Figen Ltd, Seinäjoki, Finland

927  Crossbreeding Effects and Genetic Parameters on Piglet Survival from Three Iberian Strains.

N. Ibanez-Escriche	extsuperscript{1}, L. Varona	extsuperscript{2}, E. Magallón	extsuperscript{1} and J. L. Noguera	extsuperscript{1}, 1IRTA, Lleida, Spain, 2Universidad de Zaragoza, Zaragoza, Spain, 3Inga Food, Zaragoza, Spain

928  Genetic and Epigenetic Analysis of FUT1 (fucosyltransferase 1) Transgenic Cloned Yorkshire Piglets.

Y. Yu	extsuperscript{1} and Y. Dong	extsuperscript{1}, 1College of Animal Science and Technology, China Agricultural University, Beijing, China, 2China Agricultural University, Beijing, China

929  Genome-Wide Association Study for Intramuscular Fat Content and Composition in Duroc Pigs.

R. Ros-Freixedes	extsuperscript{1}, S. Gol	extsuperscript{2}, R. N. Pena	extsuperscript{1}, M. Tor	extsuperscript{1}, J. C. M. Dekkers	extsuperscript{2} and J. Estany	extsuperscript{1}, 1Universitat de Lleida, Lleida, Spain, 2Iowa State University, Ames

930  Genetic Correlations of Intramuscular Fat and Oleic Acid Content among Muscles and with Subcutaneous Fat in Duroc Pigs.

R. Ros-Freixedes	extsuperscript{1}, E. Henríquez	extsuperscript{1}, J. Reixach	extsuperscript{2}, M. Tor	extsuperscript{1} and J. Estany	extsuperscript{1}, 1Universitat de Lleida, Lleida, Spain, 2Selección Batallé, Riudaretanes, 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

637  Genetic Correlations among Detailed Reproductive Traits, Traditional Reproductive Traits and Milk Production in Irish Dairy Cows.

T. R. Carthy	extsuperscript{1}, D. P. Berry	extsuperscript{2}, R. Evans	extsuperscript{1} and D. P. Ryan	extsuperscript{4}, 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

638  Effects of the FecL Major Gene on Mean and Variance of Litter Size in the Lacanue Meat Sheep Population.

L. Bodin	extsuperscript{1}, P. M. Martin	extsuperscript{2} and J. Raoul	extsuperscript{2}, 1INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 2Idele, Castanet tolosan, France

639  Single Nucleotide Polymorphisms in Candidate Genes Related to Daughter Pregnancy Rate in Holstein Cows.

M. S. Ortega	extsuperscript{1}, A. C. Denicol	extsuperscript{1}, D. J. Null	extsuperscript{2}, J. B. Cole	extsuperscript{2} and P. J. Hansen	extsuperscript{1}, 1Department of Animal Sciences, University of Florida, Gainesville, 2Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD

640  The Fertility of South African Holstein and Jersey Heifers.

C. J. Muller	extsuperscript{2}, Directorate Animal Sciences, Elsenburg, South Africa

641  Follicular Dynamics and Uterine Environment Associations with Production and Performance Traits in Irish Dairy Cows.

A. Fitzgerald	extsuperscript{1}, D. P. Berry	extsuperscript{2} and D. P. Ryan	extsuperscript{1}, 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, I. D. P. S. Diaz², N. Irano², L. Takada³, R. Carvalheiro³, F. Baldi¹, H. N. Oliveira¹, H. Tonhati³ and L. G. Albuquerque¹, 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.

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. Fernando³, J. M. Reecy³, I. G. Imumoni³ and M. G. Thomas³, ¹Berry College, Mount Berry, GA, ²Adnan Menderes University, Aydin, Turkey, ³Iowa State University, Ames, ¹Cornell University, Ithaca, NY, ²Colorado 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. Ytournel¹, E. Brunet¹, P. Derks¹ and A. Huisman¹, ¹Hypor, Boxmeer, Netherlands, ²France Gênes, Saint Gérand, France, ³Hendrix Genetics, Boxmeer, Netherlands.

645 Genome-Wide Association Study on Long-Yearling Scrotal Circumference in Canchim Cattle.
M. E. Buzanskas¹, D. A. Grossi², R. V. Ventura², T. C. S. Chud³, I. Urbinati³, S. Meirelles³, F. B. Mokry³, F. S. Schenkel³, I. Regitano⁴, M. M. D. Alencar⁴ and D. P. Munari⁴, 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, ⁴Federal University of Lavras, Lavras, Brazil, ¹Universidade Federal de São Carlos, São Carlos, Brazil, ²Embrapa Pecuária Sudeste, São Carlos, Brazil, ³Embrapa Southeast Livestock, Sao Carlos, Brazil, ⁴Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil.

646 Genetic Parameters of Days Open and Protein Yield Across Lactations for the Uruguayan Holstein Population.
N. Frioni¹, Facultad de Agronomía, Uruguay, Montevideo, Uruguay.

647 Genome Wide Scan for Age at First Calving in Gyr Dairy Cattle.
A. T. H. Utsunomiya¹, S. A. Boison², D. J. A. dos Santos³, Y. T. Utsunomiya¹, M. A. Machado⁴, R. S. Verneque⁵, J. Sölkner⁶, J. F. García⁷, 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, ⁵Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ⁶Federal University of Lavras, Lavras, Brazil, ⁷Universidade Federal de São Carlos, São Carlos, Brazil, ⁸Embrapa Pecuária Sudeste, São Carlos, Brazil, ⁹Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil.

648 Genome Wide Association Study for Calving Interval in Gyr Dairy Cattle.
M. A. Machado¹, A. T. H. Utsunomiya¹, S. A. Boison², D. J. A. dos Santos³, Y. T. Utsunomiya¹, R. da Fonseca³, J. Sölkner³, J. F. García³, R. S. Verneque¹ and M. V. G. B. da Silva³, ¹Embrapa Dairy Cattle, Juiz de Fora, Brazil, ²Unesp-Univ Estadual Paulista, Araçatuba, Brazil, ³São Paulo State University "Júlio de Mesquita Filho", Dracena, Brazil.

649 Mapping of a Major Gene for Bovine Ovulation Rate.
B. W. Kirkpatrick¹ and C. A. Morris², ¹University of Wisconsin, Madison, ²AgrResearch, 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, I. Baltenweck², J. Poole³, E. O. Rege¹, C. Gondro⁴, S. Weerasinghe⁵, J. Gibson⁶, 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.

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. Dafrasne1, 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. Dube1, A. Davids and K. Dzama, University of Stellenbosch, Stellenbosch, South Africa

Candidate Genes Network for Number of Teats in Pigs.
S. E. Guimaraes1,2, L. L. Verardo1, 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, Beuningen, Netherlands

Tracking Footprints of an Experiment of Selection in Iberian Pigs.
M. C. Rodríguez1, Y. Nuñez, A. Fernandez, A. Fernandez, C. Barragan and L. Silió, INIA, Madrid, Spain

Genomic Selection in Pig Breeding for Improved Meat Quality.
E. Gjerlaug-Enger1, Nordbo5 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. Lopes2,3, J. W. M. Bastiaansen2 and B. Harlizius2, 1TOPIGS Research Center IPG BV, Beuningen, Netherlands, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 3TOPIGS Research Center IPG, Beuningen, Netherlands

Effectiveness of genomic prediction of boar taint components in different Pietrain sired breeding populations.
C. Grosse-Brinkhaus, C. Neuhoff, K. Schellander, C. Looft and E. Tholen1, 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. Tenesa5 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. Huang2 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. Lucoat1, S. D. Kachman1, R. K. Johnson1 and D. C. Ciobanu1, 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, 1Genesis Inc, Oakville, MB, Canada, 2Genesis Inc, Lethbridge, AB, Canada

Genetic Association between Leg Conformation in Young Pigs and Longevity of Yorkshire Sows.
H. T. Le1,2, K. Nilsson1, E. Norberg1 and N. Lundeheim1, 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. Ishii1 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. Gebeyehu*, 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*, Institute of 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*, Institute of 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*, 1M. C. Rodríguez and L. Silió, 1INIA, Zafra, Spain, 2INIA, Madrid, Spain

A. Hamrouni*, M. Djemali* and S. Bendhiaf, 1Institut National Agronomique de Tunis, Rude de kornich Chot El Salem Gabès, Tunisia, 2Carthage University-INAT-TUNISIA, Laboratoire des Ressources Animales et Alimentaires, 1082 Cité Mahrajène, Tunisia, Tunis, Tunisia, 3Institut National de Recherche Agronomique de Tunis, Tunis, Tunisia

422 Influences of Environmental Descriptor 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.
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*, National Research Institute of Animal Genetics and Breeding, St. Petersburg, Russia

851 The Effect of Inbreeding on Linkage Disequilibrium. G. B. Nascimento¹, R. P. Savegnago¹, R. V. Ventura², M. C. Ledur² and D. P. Munari³, ¹Univ. Estadual Paulista – FCAV/UNESP, Jaboticabal, Brazil, ²University of Guelph, Guelph, ON, Canada, ³Bee Improvement Opportunities, Guelph, ON, Canada, ⁴Embrapa Suínos e Aves, Concórdia, Brazil, ⁵Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil

852 Impact of Egg Weight Selection on Body Weight of Japanese Quail. A. E. Eldlebshany*, Alexandria University, Alexandria, Egypt

853 Improving Analysis of Direct and Indirect Genetic Effects on Survival Data in Laying Hens. T. Brinker¹, E. D. Ellen¹, J. Visscher² and P. Bijma², ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Institut 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*, 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. Cruz¹, R. P. Savegnago², G. S. Schmidt³, M. C. Ledur³ and D. P. Munari³, ¹São Paulo State University, Jaboticabal, Brazil, ²Univ. Estadual Paulista – FCAV/UNESP, Jaboticabal, Brazil, ³Embrapa Suine and Poultry, Concórdia, Brazil, ⁴Embrapa Suínos e Aves, Concórdia, Brazil, ⁵Universidade 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. Peeters¹, J. Visscher² and P. Bijma², ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Institut 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*, 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 3, M. Chabault-Dhuit 4, F. D'Abbadie 4, E. Le Bihan-Duval 4 and O. Demeure 1,2, INRA, UMR1348 PEGASE, Saint-Gilles, France, 1 Agrocampus Ouest, UMR1348 PEGASE, Rennes, France, 4 Université Européenne de Bretagne, RENNES, France, 5 INRA UR83, Nouzilly, France, 6 SASSO, Sabres, France

Genetic Analysis of Meat-Type Qauli 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, 1 Universidade Federal do Ceará, Fortaleza, Brazil, 2 Universidade Federal de Viçosa, Viçosa, Brazil

Genetic Parameters for Early Reproduction Traits in Ostriches.
S. W. Cloete 1 and Z. D. Brand 2, 1 Directorate Animal Sciences, ELSenburg, South Africa, 2 Directorate 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 1, J. R. Pandolfi 3, M. E. Cantão 1, J. O. Peixoto 1, L. L. Coutinho 2 and M. C. Ledur 1, 1 EMBRAPA Swine and Poultry, Concórdia, Brazil, 2 University of Sao Paulo, Piracicaba, Brazil, 3 Universidade 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. Ibelli 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, 1 EMBRAPA Swine and Poultry, Concórdia, Brazil, 2 Universidade de Sao Paulo/Esalq, Piracicaba, Brazil, 3 Santa Catarina State University, Lages, Brazil

Variations Of The Melanocortin 1 Receptor Gene Associated With Partridge Phenotypes In Wenchang Chickens.
X. Zhang, South China Agroicultural University, Guangzhou, China

Genetic Evaluation of Body Weight and Tibia Resistance in Broilers.
J. O. Peixoto 1, V. L. Kawski 1, A. M. G. Ibelli 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, 1 EMBRAPA Swine and Poultry, Concórdia, Brazil, 2 Universidade Estadual Paulista "Júlio de Mesquita Filho", Concórdia, Brazil, 3 Universidade 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 2, G. Gasparin 2, M. Paduan 1, S. C. S. Andrade 1, H. Montenegro 1, D. Burri 1, M. C. Ledur 1 and L. L. Coutinho 2, 1 Department of Animal Science, University of Sao Paulo/ESALQ, Piracicaba, Brazil, 2 The Roslin Institute and Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom, 3 Department of Genetics, University of Sao Paulo (ESALQ), Piracicaba, Brazil, 4 EMBRAPA Swine and Poultry, Concórdia, Brazil, 5 Universidade de Sao Paulo/Esalq, Piracicaba, Brazil

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 1, 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 3, N. F. Berge 1, J. M. Neary 1, F. B. Garry 2, T. N. Holt 4, H. D. Blackburn 4, S. E. Speidel 4, D. J. Garrick 2, R. M. Enns 1 and M. G. Thomas 1, 1 Colorado State University, Department of Animal Sciences, Fort Collins, 2 Virginia Polytechnic Institute and State University, Blacksburg, 3 Colorado State University, College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO, 4 USDA-ARS-National Animal Germplasm Program, Fort Collins, CO, 5 Iowa State University, Ames

Relationship of Endocrine Pathway SNP and Molecular Breeding Value with Milk Production in Heat Stressed Holstein Cows.
A. I. Hernandez 1, P. Luna 2, G. Rincon 1, J. F. Medrano 1, R. M. Enns 1 and M. G. Thomas 1, 1 Colorado State University, Fort Collins, 2 Instituto Tecnologico de Sonora, Ciudad Obregon, Mexico, 3 Zoetis Inc., Kalamazoo, MI, 4 University of California, Davis, 5 Colorado 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. Berge1, S. E. Speidel, X. Zeng, M. M. Calibertson, 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.
T. Dessie1, G. Gebreyesus2, G. Mekuriaw3, T. Woldaa4, T. Jemberé5, M. Agaba6 and A. M. Okeya7, 1International Livestock Research Institute, Addis Ababa, Ethiopia, 2International Livestock Research Institute, Addis Ababa, Ethiopia, 3Addis Ababa University, Addis Ababa, Ethiopia, 4The Finnish Game and Fisheries Research Institute, Tervo, Finland, 5Hohenheim University, Stuttgart, Germany, 6Haramaya University, Haramaya, Ethiopia, 7Biosciences eastern and central Africa - International Livestock Research Institute Hub, Nairobi, Kenya, 1International Livestock Research Institute, Nairobi, Kenya

E. Akanno1, V. Okoro2, 1, S. N. Ibe3, O. O. Emenalom4, N. O. Aladi5, E. B. Etuk6, U. E. Ogundu7, J. N. Okeudo1, M. O. Obike2, H. O. Obikaonu1 and C. I. Okoli1, 1Federal University of Technology, Owerri, Nigeria, 2Michael Okpara University of Agriculture, Umudike, Nigeria

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

Experimental Designs for Genetic Parameters and Response to Selection of Social Interaction Traits in Aquaculture.
P. Sae-Lim1 and P. Bijma2, 1Nofima, Ås, Norway, 2Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands

Indirect Genetic Effects for Harvest Weight in Nile Tilapia (Oreochromis niloticus).
H. L. Khaw1,2, R. W. Ponzoni3, H. Y. Yee4, M. A. Aziz5 and P. Bijma1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2The WorldFish Center, Penang, Malaysia, 3WorldFish, Penang, Malaysia

Sexual Maturation of 1 and 2 Year Old Farmed Atlantic Cod – Prevalence and Heritability Estimates.
T. M. K. Drangsholt1, H. M. Nielsen2, R. Bangera1, V. Puvanendran3, 1Nofima, Tromsø, Norway, 2Nofima, Ås, Norway, 3Norwegian 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 (Oncorhynchus mykiss).
M. Dupont-Nivet1, M. Crusol1, D. Rigaudreau1 and E. Quiller1, 1INRA, UMR 1313 GABI, Jouy en Josas, France, 2INRA, UE 907 IERP, Jouy en Josas, France

Effect of Family Structure and Size on Genomic Selection Accuracy in Aquaculture Breeding.
K. G. Nirea1, A. K. Sonesson2, M. Lillehammer1 and T. H. E. Meuwissen3, 1Norwegian University of Life Sciences, Ås, Norway, 2Nofima, Ås, Norway, 3INRA, Jouy en Josas, France

Correcting for Early Within-Family Pre-Selection in Genetic Evaluation - A Simulation on Rainbow Trout Growth.
M. Janhunen4, A. Kause4, H. Vehviläinen4, H. Koskinen4 and A. Nousiainen2, 1MIT Agrifood Research Finland, Jokioinen, Finland, 2Finnish 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. Lowe1, M. Bekker2, S. C. Bishop1, J. E. Bron2, J. B. Taggart2 and R. D. Houston1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Institute 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. F. Hely\textsuperscript{1}, P. Amer\textsuperscript{1}, S. Walker\textsuperscript{1} and J. Symonds\textsuperscript{2}, \textsuperscript{1}AbacusBio Limited, Dunedin, New Zealand, \textsuperscript{2}NIWA, Ruakaka, New Zealand

Improving Uniformity of Growth by Mating and Selection Strategies in Rainbow Trout. A. Kause\textsuperscript{1}, M. Janhunen\textsuperscript{1}, H. Vehviläinen\textsuperscript{1}, H. Koskinnen\textsuperscript{1} and A. Nousiainen\textsuperscript{2}, \textsuperscript{1}MTT Agrifood Research Finland, Jokioinen, Finland, \textsuperscript{2}Finnish Game and Fisheries Research Institute, Tervo, 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\textsuperscript{1}, SYSAAF, Rennes, France

Genome-Wide Association Study (GWAS) for Growth Rate and Sexual Maturation in Atlantic Salmon (Salmo salar). A. P. Gutierrez\textsuperscript{1}, J. M. Yañez\textsuperscript{1}, S. Fukai\textsuperscript{1}, B. Swift\textsuperscript{4} and W. S. Davidson\textsuperscript{5}, \textsuperscript{1}Simon Fraser University, Burnaby, BC, Canada, \textsuperscript{2}University of Chile, Santiago, Chile, \textsuperscript{3}Cermaq, Campbell River, BC, Canada, \textsuperscript{4}TRI-GEN Fish Improvement Ltd., Agassiz, BC, Canada, \textsuperscript{5}Simon Fraser University, Burnaby, BC, Canada

Posters: Genetics of Trait Complexes: Growth and Development (Group 1)
Chair: Michael D. MacNeil, Delta G
Presentation Time: 10:00 AM – 10:30 AM

A Co-association Network Analysis of the Genetic Determination of Pig Growth and Shape. A. M. Puig Oliveras\textsuperscript{1}, 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\textsuperscript{1}, Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan

A Genome-Wide Association Study for Morphometric Traits in Quarter Horse. R. A. Curi\textsuperscript{1}, Universidade Estadual Paulista, Botucatu, Brazil

Heritability Estimates of Conjugated Linoleic Acid Isomers in Brisket Adipose Tissue of Canadian Crossbred Beef Steers. C. Li\textsuperscript{1}, Agriculture and Agri-Food Canada, Edmonton, AB, Canada

Growth Curves Changes in Nellore Males Selected for Postweaning Weight. S. F. M. Bonilha\textsuperscript{1}, C. C. Coutinho\textsuperscript{1}, M. E. Z. Mercadante\textsuperscript{1}, A. M. Jorge\textsuperscript{2}, L. El Faro\textsuperscript{3}, C. C. P. Paz\textsuperscript{1}, J. N. S. G. Cyrillo\textsuperscript{1} and R. H. Branco\textsuperscript{1}, \textsuperscript{1}Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil, \textsuperscript{2}Faculdade de Medicina Veterinaria e Zootecnia, Universidade Estadual Paulista, Botucatu-SP, Brazil, \textsuperscript{3}SAA/APTA/Instituto de Zootecnia-Centro de Bovinos de Corte, Sertãozinho-SP, Brazil

Identification of Selection Footprints in a Brown Hanwoo (Korean cattle) Population for Production Traits. D. Lim\textsuperscript{1}, Animal Genomics & Bioinformatics Division, NIAS, RDA, Suwon, South Korea

Induction of Differentiation by AAV2-Mediated Follistatin Overexpression in Ovine Primary Myoblasts. M. Nazari\textsuperscript{1} and L. Zhang, Animal science, Beijing, China

Regional Heritability Mapping of Age-Dependent Loci Affecting Growth Traits in Scottish Blackface Lambs. G. Hadjipavlou\textsuperscript{1}, V. Riggio\textsuperscript{2}, R. Pong-Wong\textsuperscript{3}, O. Matika\textsuperscript{1} and S. C. Bishop\textsuperscript{1}, \textsuperscript{1}Agricultural Research Institute, Lefkosia, Cyprus, \textsuperscript{2}The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Investigation of Candidate Regions Associated With Fat Deposition in Thin and Fat Tail Sheep Breeds. M. H. Moradi\textsuperscript{1}, Arak University, Arak, Iran

Genetic Parameter Estimation of Body Size and Birth Weight in Chinese Holstein Cows. X. Zhang\textsuperscript{1}, Y. Wang\textsuperscript{1}, G. Guo\textsuperscript{2}, Y. Yu\textsuperscript{1}, X. Li\textsuperscript{2}, X. Wang\textsuperscript{2} and F. Wang\textsuperscript{2}, \textsuperscript{1}College of Animal Science and Technology, China
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. Setter2, J. E. Fulton2, N. P. O’Sullivan1 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

Animal Genetic Resources in Slovakia.
P. Chrenek*, Slovak University of Agriculture, Nitra, Slovakia

Genetic Diversity of the Afrikaner Cattle Breed.
L. Pienaar*, 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. Chapuis*, 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. Santos2, F. A. T. Bruneli2, R. B. Teixeira1, L. G. D. Castro4, D. R. L. Reis1, 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. Diaz2, A. G. Drucker3, M. J. Carabaño2 and K. Zander4,5, 1AbacusBio Ltd., Dunedin, New Zealand, 2INIA, Madrid, Spain, 3Bioversity International, Rome, Italy, 4The Northern Institute, Darwin, Australia, 5Research 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. Aguilar2, N. Grasso2, F. Pieruccioni2 and G. Ciappesoni2, 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. Pong-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. Maiwashe2, 1Agricultural Research Council, Pretoria, South Africa, 2University of Pretoria, Pretoria, South Africa

Genetic Diversity in the Ramo Grande Cattle Breed Assessed by Pedigree Information and Microsatellite Markers.
A. L. Pavão1, C. Ginja2 and L. T. Gama1, 1Direcção 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. Samaraweera1, P. Silva2, N. Abeykone1, M. N. M. Ibrahim1, A. M. Okeyo1 and J. Han1, 1Faculty of Animal Science and Export Agriculture, Uva Wellassa 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. Rönnergård1,2, M. Fellek1,2, M. Alam1 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. Fikse1, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden
Aggregation of Methods for Genetic Prediction.
C. Carre1,2, L. Tusell2, S. Formi1, F. Gamboa1, D. Gianola1 and E. Manfredi2, 1IMT Université Paul Sabatier, Toulouse, France, 2INRA, Toulouse, France, 3Genus Plc, Hendersonville, TN, 4University of Wisconsin, Madison

Bayesian Analysis of Heterogeneous Residual Variance in Canine Behaviour.
S. M. van den Berg1, I. Schwabe2, F. Fikse3, H. C. Heuven1 and C. A. Glas1, 1University of Twente, Enschede, Netherlands, 2University of Twente, Enchede, Netherlands, 3Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 4University of Utrecht, Utrecht, Netherlands

Influence of Family Structure on Variance Decomposition.
S. M. Edwards1, P. M. Sarup1 and P. Sørensen2, 1Center of Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 2Center 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. Nath1, C. M. Pooley2, S. C. Bishop2 and G. Marion1, 1Biomathematics and Statistics Scotland, Edinburgh, United Kingdom, 2The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom

Variational Bayesian Method to Estimate Variance Components.
A. Arakawa1, M. Tamiguchi1, T. Hayashi1 and S. Mikawa1, National Institute of Agrobiological Sciences, Tsukuba, Japan, 2NARO Institute for Agricultural Research Center, Tsukuba, Japan

Parallel Computing to Speed up Whole-Genome Analyses using Independent Metropolis-Hastings Sampling.
H. Cheng1, R. L. Fernando and D. J. Garrick, Iowa State University, Ames

Results of Genome Wide Association Studies Improve the Accuracy of Genomic Selection.
Z. Zhang1, J. He1, H. Zhang1, P. Gao1, M. Erbe1, H. Simianer2 and J. Li1, 1South China Agricultural University, Guangzhou, China, 2Georg-August University, Göttingen, Germany

Estimation of Genetic Parameters and Breeding Values in Honey Bees.
E. W. Brascamp1, 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. Blank1 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. Matilainen1, J. Strandén and E. A. Mäntysaari, MT Agrifood Research Finland, Biotechnology and Food Research, Jokioinen, Finland

DMU - A Package for Analyzing Multivariate Mixed Models in quantitative Genetics and Genomics.
P. Madsen1, 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. Hu1 and R. C. Yang1,2, 1University of Alberta, Edmonton, AB, Canada, 2Alberta Agriculture and Rural Development, Edmonton, AB, Canada

Genetic Analysis of Micro-environmental Plasticity in Drosophila melanogaster.
F. Morgante1,2, D. A. Sorensen2, P. Sorensen1, C. Maltecca1 and T. F. Mackay1, 1Department of Biological Sciences, North Carolina State University, Raleigh, 2Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, 3North 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 Peneaus (Litopenaeus) vannamei.
L. De los Ríos-Pérez1, G. R. Campos-Montes2, A. Martínez-Ortega3, 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. Nielsen1 and P. Sue-Lim, Nofima, Ås, Norway

Genetic Bases of Resistance versus Susceptibility to Flavobacterium psychrophilum in Rainbow Trout.
E. Quillet1, N. Dechamps2, C. Herve3, F. Krieg1, C. Chantry-Darmon1, M. Boussaha3, A. Bérard3, V. Laurens2, T. Rochat10, E. Duchaud8, P. Boudinot51, J. F. Bernardet8 and C. Michel51, INRA, 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 Génomypage, Evry, France, 8INSERM UMR 866, Dijon, France, 9Université de Bourgogne, Institut Fédératif de Recherche Santé STIC, Dijon, France, 10INRA, UR 892 VIM, Jouy-en-Josas, France

O. O. T. Agbébi 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. Meier1, 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. Bruun1, C. B. Jørgensen1, T. H. E. Meuwissen, H. N. Kadarmideen1 and M. Fredholm1, 1Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 2Department of Animal and Aquacultural Sciences, University of São Paulo, Piracicaba, Brazil, 3Embrapa Pecuária Sudeste, São Carlos, Brazil, 4Iowa State University, Ames, 5University of São Paulo/ESALQ, Piracicaba, Brazil, 6Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, 7University of São Paulo / ESALQ, Piracicaba, Brazil

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-Waters1, G. Gasparin4, G. B. Mourao5, D. P. D. Lanna6, J. M. Reecy7 and L. L. Coutinho8, 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 São 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. Martinez-Alvaro*, Universitat Politecnica de Valencia, Valencia, Spain

Genome-Wide Association Study on Body Weight Reveals Major Loci on OAR6 in Australian Merino Sheep.

H. A. Al-Mamun*, S. Clark†, P. Kwan* and C. Gondro*, University of New England, Armidale, Australia, School of Environmental & Rural Science, University of New England, Armidale, Australia

Genome-Wide QTL Mapping of Body Composition and Bone Mineral Density Traits in Pigs.

S. Rothammer‡, P. V. Kremer*, M. Bernau*, I. Fernandez-Figares Ibanez‡, J. Pfister-Schür*, I. Medugorac and A. M. Scholz‡, Chair of Animal Genetics and Husbandry, LMU, Munich, Germany, University of Applied Sciences Weihenstephan-Triesdorf, Weidenbach, Germany, Livestock Center of the Faculty of Veterinary Medicine, LMU, Munich, Germany, CSIC, Estación Experimental del Zaidín, Granada, Spain

MyoD1 Expression Levels Affect Meat Tenderness in Nellore Beef Cattle.

P. C. Tizóto*, G. Gasparini*, L. L. Coutinho*, G. B. Mourao*, M. A. Mudadu†, M. M. Souza†, W. Malagó Jr†, F. A. Donatoni Bressani†, R. R. Tullio†, R. T. Nassu† and L. C. A. Regitano‡, University of São Paulo/ESALQ, Piracicaba, Brazil, University of São Paulo/ESALQ, Piracicaba, Brazil, Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, Embrapa Pecuária Sudeste, São Carlos, Brazil, Embrapa Southeast Livestock, SAO CARLOS, Brasil, Embrapa Southeast Livestock, São Carlos, Brazil

Estimation Of Genetic Parameters For Body Weight From Birth To 10 Years Old In Nellore Females.

J. N. S. G. Cyrillo*, J. V. Portes*, M. E. Z. Mercadante*, S. F. M. Bonilha†, L. T. Dias* and R. H. Branco*, Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil, Universidade Federal do Paraná, Curitiba, Brazil

A Novel SNP Polymorphism in the Ovine Leptin Gene Related to Back Fat Depth.

F. A. Rodríguez*, D. E. Briones, M. E. Burrola-Barraza, J. A. Grado Ahuir and I. A. García-Galicia, Universidad Autónoma de Chihuahua, Chihuahua, Mexico

Estimation of Genetic (Co)variances of von Bertalanffy and Gompertz Growth Function Parameters in Pigs.

J. M. Coyne†, M. L. Sevon-Aimonen†, D. P. Berry†, E. A. Mäntysaari†, J. Juga§ and N. McHugh‡, Teagasc Moorepark, Fermoy, Cork, Ireland, Agrifood Research Finland, Jokioinen, Finland, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland, Teagasc Moorepark, Fermoy, Ireland

Genome Wide Association for Growth Curve Parameters in Brahman Cattle.

A. Camporez Crispim†, M. J. Kelly‡, F. F. Silva‡, M. R. Fortes*, S. E. Guimarães*, P. S. Lopes* and S. S. Moore‡, Universidade Federal de Viçosa, Viçosa, Brazil, The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia, The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia

Genetic Analysis of Growth in Performance Tested Young Bulls accounting for Indirect Genetic Effects.

C. Sartori†, 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. Kramer*, 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. Li*, 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. Dematawewa¹, University of Peradeniya, Peradeniya, Sri Lanka

Assessment of Generation Interval and Inbreeding in a Peruvian Alpaca Population.
J. Vilela¹ and V. Montenegro², ¹Universidad Nacional Agraria La Molina, Lima, Peru, ²D-Agos 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.
J. Zeng³, Iowa State University, Ames

Y. Masuda¹,², I. Aguilar³, S. Tsuruta¹ and I. Misztal³, 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. Chen⁴, 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. Yokoo¹, G. de los Campos², G. J. M. Rosa², F. F. Cardoso², B. P. Sollero², L. L. Cardoso², R. B. Lôbo³ and L. G. Albuquerque³, 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), Brasilia, 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.
J. Jiang, Q. Zhang and J. F. Liu, China Agricultural University, Beijing, China

Efficient Approximations of the Inverse of a Part of the Additive Relationship Matrix.
P. H. Faux¹ and N. Gengler², ¹University of Liège, Gembloux, Belgium, ²University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium

P. Croiseau¹, M. N. Fouilloux², D. Jonas¹,², S. Fritz², A. Baur², V. Ducrocq¹, F. Phocas¹ and D. Boichard¹, ¹INRA, UMR1313 GABI, Jouy-en-Josas, France, ²Institut de l’Elevage - Idéle, Jouy-en-Josas, France, ³AgroParisTech, Paris, France, ⁴UNCEIA, Paris, France