35th International Society for Animal Genetics Conference

Salt Lake City, Utah

https://www.asas.org/meetings/isag2016
Welcome Letter..................................................................................................................................................................2
Notice to Attendees............................................................................................................................................................2
ISAG 2016 Organizing Committee....................................................................................................................................3
Workshop Chairs................................................................................................................................................................3
ISAG 2016 Sponsors..........................................................................................................................................................4
Exhibit Directory ...............................................................................................................................................................5
General Information ...........................................................................................................................................................6
    Registration.................................................................................................................................................................6
Hotel Information...............................................................................................................................................................6
Special Events.................................................................................................................................................................7
Public Transportation..........................................................................................................................................................7
Schedule of Events...........................................................................................................................................................8
Poster Schedule ................................................................................................................................................................9
Scientific Program...........................................................................................................................................................10
    Oral Sessions & Workshops......................................................................................................................................10
    Poster Presentations ................................................................................................................................................28

**Important Message**

In the event that protestors interrupt the meeting, please ignore them. Their goal is to attract attention. Any attention you give them will only help their cause. Convention staff have a plan to handle these situations, and they depend on attendee cooperation. If members of the media approach you for an interview, please politely decline and direct them to the convention’s media room, where spokespersons will be available.

Thank you for your cooperation.
Howdy!

It’s with great pleasure that the ISAG 2016 Local Organizing Committee welcomes you to Salt Lake City, Utah. We hope you will find the mountains and the Great Salt Lake a perfect backdrop for the conference. We have worked hard to insure that you will have time to network, educate, learn, relax and explore the city of Salt Lake and the surrounding area.

In a first for ISAG, we welcome our colleagues from the American Society of Animal Science to collaborate and attend our opening day of programming: Functional Annotation of Animal Genomes symposium. We would like to thank Drs. Deb Hamernik and Filipo Miglior for liaising with us to coordinate this crossover day. In addition, we need to give special recognition to the FAANG Communications Committee for their leadership in organizing the symposium. We identified the symposium’s topic as one of broad interest, and anticipate that members from both societies will enjoy the opportunity to exchange great science and camaraderie.

This conference would not be possible without the tremendous participation by our society’s membership, and the generous contributions of our sponsors, our invited speakers, and our workshop chairs who also served as the Scientific Program Committee. We have representation from 47 countries, and appreciate the great distances that some of you have travelled to join us. When you leave the conference, we hope you will take home wonderful memories from the excellent scientific program and fun social program we have planned.

Welcome and thank you!

Cheers,

Clare Gill on behalf of the 2016 Local Organizing Committee

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**Notice to Attendees**

Use of cameras, video cameras and cell phones (for calls or as cameras) is prohibited during oral and poster presentations to minimize disruption and unauthorized dissemination of data. Anyone found in violation of this policy will be asked to leave the session.
Committees

ISAG 2016 Local Organizing Committee
Clare Gill, Texas A&M University (Chair)
Noelle Cockett, Utah State University
Joan Lunney, USDA-ARS, Beltsville

ISAG Executive Committee
Ernie Bailey, University of Kentucky, USA (President)
Ingrid Olsaker, Norwegian School of Veterinary Science, Norway (Secretary)
Christian Looft, University of Bonn, Germany (Treasurer)
Noelle Cockett, Utah State University, USA
James Kijas, CSIRO, Australia
Stephen S. Moore, University of Queensland, Australia
Max Rothschild, Iowa State University, USA
Hans Lenstra, Utrecht University, Netherlands

ISAG 2016 Scientific Program Committee and Workshop Chairs

WORKSHOPS AND SYMPOSIA
Animal Forensic Genetics
Applied Genetics of Companion Animals
Applied Genetics and Genomics in other Species of Economic Importance
Applied Sheep and Goat Genetics
Avian Genetics and Genomics
Bovine Species Genomics Working Group
Cattle Molecular Markers and Parentage Testing
Companion Animal Genetics and Genomics
Comparative and Functional Genomics
Comparative MHC
Domestic Animal Epigenetics
Equine Genetics and Thoroughbred Parentage Testing
Functional Annotation of Animal Genomes Symposium
Genetically Engineered Livestock
Genetics and Genomics of Aquaculture Species
Genetics of Immune Response and Disease Resistance
Horse Genetics and Genomics
ISAG-FAO Genetic Diversity
Livestock Genomics for Developing Countries
Pig Genetics and Genomics
Publishing in Animal Genetics
Ruminant Genetics and Genomics

CHAIR
Guillermo Giovambattista
Leslie Lyons
Leanne van de Goor
Gesine Luehken
Richard Crooijmans
Hans Lenstra
Romy Morrin
Leslie Lyons, Tomas Bergstrom
Klaus Wimmers
Keith Ballingall
Hasan Khatib
Cecilia Penedo
Chris Tuggle
Bruce Whitelaw
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Stephen White
Rebecca Bellone, Teruaki Tozaki
Catarina Ginja
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Elisabetta Giuffra
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ISAG 2016 Sponsors

**Diamond Level**
Illumina, Inc.

**Platinum Level**
Affymetrix
International Foundation for Animal Genetics
International Society for Animal Genetics
Neogen/Geneseek
USDA-NIFA
Utah State University

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**Silver Level**
Ajinomoto Heartland
American Society of Animal Science
American Society of Animal Science Foundation
Dairy Research Institute/Innovation Center for US Dairy
USAID

**Bronze Level**
Cobb-Vantress
PLOS Genetics
Zoetis
Exhibit Floor Plan

- Service
- Posters
- Lobby

Rooms:
1. Lobby
2. Posters
3. Service
4. 4
5. 5
6. 6
7. 7
General Information

REGISTRATION

Friday, July 22, 2016
Salt Palace Convention Center, South Foyer
12:00-17:30

Saturday, July 23, 2016
Salt Palace Convention Center, South Foyer
7:00 – 16:30

Sunday, July 24, 2016
Hilton Salt Lake City Center, Grand Ballroom Foyer
7:00 – 17:30

Monday, July 25, 2016
Hilton Salt Lake City Center, Grand Ballroom Foyer
7:00 – 17:30

Tuesday, July 26, 2016
Hilton Salt Lake City Center, Grand Ballroom Foyer
7:00 – 12:00

Wednesday, July 27, 2016
Hilton Salt Lake City Center, Grand Ballroom Foyer
8:00 – 15:00

HOTEL INFORMATION

Hilton Salt Lake City Center
(ASAS/ISAG Headquarters Hotel)
255 South West Temple
Salt Lake City, UT 84101
(801) 328-2000

Salt Lake City Marriott
75 South West Temple
Salt Lake City, UT 84101
(801) 531-0800
Special Events

SATURDAY, JULY 23

Welcome Reception and Days of ‘47 Rodeo
The night will begin with a reception from 5:30 to 6:30 pm in the VIP Reception area. Following the reception, ISAG will be seated in a reserved section for all the rodeo action. The Welcome Reception and Days of ‘47 Rodeo is located at the Vivint Smart Home Arena in Salt Lake City at 301 West South Temple.

Monday, July 25

Western Social, sponsored by Utah State University
Immerse yourself in a evening of western dancing, music and culture at the Rice-Eccles Stadium, located on the University of Utah campus at 452 1400 E. in Salt Lake City.

TUESDAY, JULY 26

Afternoon Tours
Buses depart in front of the Hilton Lobby.

Antelope Island - Enjoy an afternoon exploring this beautiful island brimming with wildlife, scenic trails and picturesque views.

Historic Downtown Park City - Full of quaint shops, restaurants and museums, the tour option gives you the chance to explore all this remarkable mountain town has to offer.

Olympic Park Bus Tour - Explore the site of the 2002 Winter Olympics on a guided bus tour that will take you to the very top of the park and behind the scenes of some of the sensational event locations for the different Olympic events. Buses will depart from the Hilton and then take you to the Historic Downtown Park City afterwards, where you can take time to explore the shops or hop a bus to the Canyons Resort for some great additional activities on the mountain.

The Canyons Village - This phenomenal resort, located in the mountains above Park City, is chock full of great activities for the thrill seeker to the individual looking to visit the relaxing spa.

Gala Dinner, sponsored by Utah State University
Join us for an amazing evening of socializing, western entertainment and dinner at This is the Place Heritage Village. This historic village will take you back in time to the early settlers of the Salt Lake area. There will be a miniature train running during the evening to take you around the village to see all the historic homes, businesses and communities of yesteryear. Buses depart in front of the Hilton Lobby.

Public Transportation

TRAX/LIGHT RAIL SERVICE AND BUS
Public transportation to and from the Salt Lake City International Airport is provided by the Utah Transit Authority (UTA).

The TRAX/light rail Green Line leaves the airport every 15 minutes on weekdays and every 20 minutes on weekends. The TRAX stop is located at the south end of Terminal One. To locate the TRAX stop, visit our Airport Terminal Map. One-way fare for the bus and train is $2.50.
Schedule of Events

*All events take place at the Hilton Salt Lake City Center unless otherwise stated.

**SATURDAY, JULY 23, 2016**

08:30 Functional Annotation of Animal Genomes (FAANG) ASAS-ISAG Joint Symposium, Salt Palace Convention Center Grand Ballroom, sponsored by Illumina
11:55 FAANG Lunch, Salt Palace Convention Center Grand Ballroom, sponsored by Illumina
11:55 ASAS Breeding and Genetics ePosters and ISAG meeting ePosters viewing session, Salt Palace Convention Center South Foyer
17:30 Welcome Reception and Days of ’47 Rodeo, Vivint Smart Home Arena

**SUNDAY, JULY 24, 2016**

07:30 Poster session I, Alpine Ballroom
08:30 Plenary session: Epi/genotype to phenotype, Grand Ballroom A/B, sponsored by ISAG
10:30 Plenary session: Genome editing, Grand Ballroom A/B
12:00 Lunch, Grand Ballroom C
12:00 Workshop and standing committee chairs meeting, Topaz
13:00 Poster session II, Alpine Ballroom
14:00 Workshop: Animal forensic genetics, Canyon A
14:00 Workshop: Applied genetic and genomics in other species of economic interest, Canyon C, sponsored by Eurofins
14:00 Workshop: Genetically engineered livestock, Canyon B, sponsored by LGC Biosearch Technologies
14:00 Workshop: Genetics of immune response and disease resistance, Grand Ballroom B
14:00 Workshop: Horse genetics and genomics, Grand Ballroom A, sponsored by ASAS Foundation
14:00 Workshop: Bovine species genomics working group, Seminar Theater, sponsored by Zoetis

**MONDAY, JULY 25, 2016**

07:30 Poster session III, Alpine Ballroom
08:30 Workshop: Avian genetics and genomics, Canyon B, sponsored by Cobb-Vantress
08:30 Workshop: Comparative MHC, Canyon C, sponsored by Affymetrix
08:30 Workshop: Equine genetics and thoroughbred parentage testing, Canyon A, sponsored by ASAS Foundation
08:30 Workshop: ISAG-FAO genetic diversity, Grand Ballroom A, sponsored by FAO
08:30 Workshop: Ruminant genetics and genomics, Grand Ballroom B, sponsored by Illumina
12:00 Lunch, Grand Ballroom C
12:00 Meeting of associate editors and editorial board of *Animal Genetics*, Topaz
13:00 Poster session IV, Alpine Ballroom
14:00 Workshop: Cattle molecular markers and parentage testing, Canyon A, sponsored by Neogen
14:00 Workshop: Companion animal genetics and genomics, Canyon C, sponsored by ASAS Foundation
14:00 Workshop: Domestic animal epigenetics, Grand Ballroom A, sponsored by Eurofins
14:00 Havemeyer workshop on gene expression and annotation in horses, Seminar Theater, sponsored by Havemeyer
14:00 Workshop: Pig genetics and genomics, Grand Ballroom B, sponsored by Zoetis
14:00 Workshop: Publishing in *Animal Genetics*, Canyon B
21:00 Western social, sponsored by Utah State University

**TUESDAY, JULY 26, 2016**

07:30 Poster session V, Alpine Ballroom
08:30 Workshop: Applied genetics of companion animals, Canyon C
08:30 Workshop: Applied sheep and goat genetics, Canyon B
08:30 Workshop: Comparative and functional genomics, Grand Ballroom A
08:30 Workshop: Genetics and genomics of aquaculture species, Canyon A, sponsored by Illumina
08:30 Workshop: Livestock genomics for developing countries, Grand Ballroom B
12:00 Tours, Buses depart in front of the Hilton Lobby
18:00 Conference dinner, sponsored by Utah State University

**WEDNESDAY, JULY 27, 2016**

08:30 Plenary session: Genetic diversity and adaptation, Grand Ballroom A/B, sponsored by ISAG
10:30 Plenary session: Steve Bishop memorial session on animal disease genetics, Grand Ballroom A/B, sponsored by ISAG
12:00 Lunch, Grand Ballroom C
14:00 Award ceremony and business meeting, Grand Ballroom A/B
Poster Schedule

Poster sessions sponsored by: Eurofins, LGC Biosearch Technologies, Affymetrix, and Neogen/Geneseek

**SUNDAY, JULY 24, 2016**

**Poster session I: Authors present 7:30-8:30**
Bioinformatics, statistical genetics and genomic technologies I
  Functional genomics I
  Genetic diversity and polymorphisms I
  Genetics markers and selection I
  Genetics and disease I
  Genome editing and transgenic animals

**Poster session II: Authors present 13:00-14:00**
Bioinformatics, statistical genetics and genomic technologies II
  Functional genomics II
  Genetic diversity and polymorphisms II
  Genetics markers and selection II
  Genetics and disease II
  Epigenetics and epigenomics I

**MONDAY, JULY 25, 2016**

**Poster session III: Authors present 7:30-8:30**
Bioinformatics, statistical genetics and genomic technologies III
  Functional genomics III
  Genetic diversity and polymorphisms III
  Genetics markers and selection III
  Genetics and disease III
  Epigenetics and epigenomics II

**Poster session IV: Authors present 13:00-14:00**
Bioinformatics, statistical genetics and genomic technologies IV
  Functional genomics IV
  Genetic diversity and polymorphisms IV
  Genetics markers and selection IV
  Genetics and disease IV
  Epigenetics and epigenomics III

**TUESDAY, JULY 26, 2016**

**Poster session V: Authors present 7:30-8:30**
Bioinformatics, statistical genetics and genomic technologies V
  Functional genomics V
  Genetic diversity and polymorphisms V
  Genetics markers and selection V
  Genetics and disease V
  Structural and comparative genomics
ORAL SESSIONS & WORKSHOPS — Saturday, July 23

Functional Annotation of Animal Genomes (FAANG) ASAS-ISAG Joint Symposium
8:30 - 16:30

Chair: Chris Tuggle, Iowa State University
Sponsor: Illumina
Grand Ballroom A

8:30
Welcoming Remarks.

8:35
Introductory Remarks.

8:40
Sponsor’s Remarks.
André Eggen, Illumina

8:45
S0100
Important lessons from complex genomes.

9:25
Discussion.

9:40
S0101
Causal inference of molecular networks integrating multi-omics data.
F. Peñagaricano*, University of Florida, Gainesville

10:05
Break.

10:35
S0102
Genotypes to phenotypes: Lessons from functional variation in the human genome and transcriptome.
B. E. Stranger*, Section of Genetic Medicine, Department of Medicine, Institute of Genomics and Systems Biology, Center for Data Intensive Sciences, University of Chicago, Chicago, IL

11:20
Discussion.

11:35
S0103
Recurrent chimeric transcripts in human and mouse.
S. Djebali1,2,3, B. Rodriguez Martín2,3, E. Palumbo2,3, D. D. Pervouchine1, A. Breschi2,3, C. Davis4, A. Dobin4, G. Alonso5, A. Rastirojo1, B. Aguado2, T. R. Gingeras4, and R. Guigó2,3, 1GenPhySE, INRA, Castanet-Tolosan, France, 2Universitat Pompeu Fabra (UPF), Barcelona, Spain, 3Bioinformatics and Genomics Programme, Centre for Genomic Regulation (CRG), Barcelona, Spain, 4Cold Spring Harbor Laboratory, Functional Genomics, Cold Spring Harbor, NY, 5Centro de Biología Molecular Severo Ochoa (CSIC - UAM), Madrid, Spain

12:00
Lunch and Poster Viewing.

13:00
S0104
Improving genomic selection across breeds and across generations with functional annotation.
B. Hayes1,2, A. J. Chamberlain1, H. Daetwyler3, C. J. Vander Jagt2, and M. E. Goddard4, 1Department of Economic Development, Melbourne, Australia, 2Dairy Futures Cooperative Research Centre, Bundoora, Australia, 3Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, 4Department of Primary Industries, Melbourne, Australia

13:40
Discussion.

13:55
S0105
Integrating dynamic omics responses for universal personalized medicine.
G. I. Mias*, Michigan State University, East Lansing

14:35
Discussion.

14:50
Break.

15:20
S0106
A review of sequencing and assembly methods that enhance computational use.
W. C. Warren*, McDonnell Genome Institute, Washington University School of Medicine, St Louis, MO

16:00
Updates on Ongoing FAANG Activities.
Plenary Session: Epi/Genotype to Phenotype  
8:30 - 10:00
Chairs: Rebecca Bellone, University of California-Davis; Hasan Khatib, University of Wisconsin-Madison  
Sponsor: ISAG  
Grand Ballroom A/B

8:30  S0107  Environmentally induced epigenetic transgenerational inheritance of disease: Ancestral ghosts in your genome.  
M. K. Skinner*, Washington State University, Pullman

9:15  S0108  Genetic background-dependent effects of diet on health and production traits.  
D. Threadgill*, Texas A&M University, College Station

Plenary Session: Genome Editing  
10:30 - 12:00
Chairs: Bruce Whitelaw, The Roslin Institute and R(D)SVS, University of Edinburgh; Teruaki Tozaki, Laboratory of Racing Chemistry  
Sponsor: ISAG  
Grand Ballroom A/B

10:30  S0109  Engineering the genome to investigate disease mechanisms.  
R. J. Platt*, Broad Institute, Cambridge, MA

11:15  S0110  Gene editing in livestock.  
S. C. Fahrenkrug*, Recombinetics, Inc, St Pual, MN

Workshop: Animal Forensic Genetics  
14:00 - 17:30
Chair: Guillermo Giovambattista, National University of La Plata  
Canyon A

14:00  Welcoming Remarks.

14:15  P6053  Domestic animal forensics at the UC Davis Veterinary Genetics Laboratory.  
R. A. Grahn1, C. D. Lindquist1, and C. Peneda1, 1University of California-Davis, Veterinary Genetics Laboratory Forensics Unit, 2Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis

14:30  P4056  Evaluation of single nucleotide polymorphism (SNP) markers for canine parentage analysis.  
J. Qiu1, B. Simpson1, L. Kock1, J. Donner2, C. Cole1, S. Davison1, M. Dunn1, D. Bannasch1, and A. Boyko8, 1GeneSeek, a Neogen Company, Lincoln, NE, 2Genoscooper Laboratories, Helsinki, Finland, 3Mars Veterinary, Portland, OR, 4American Kennel Club, Raleigh, NC, 5School of Veterinary Medicine, University of California-Davis, 6Cornell University, Ithaca, NY

14:45  P5005  Hitchhiking effects influence allele frequencies and exclusion probabilities of microsatellites used for parentage control in Holstein Friesian cattle.  
B. Brenig and E. Schütz, Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany

15:00  P4043  Construction of the SNP panel for Hucul horse parentage control based on the OpenArray platform.  
A. Fornal1, A. Pietrzynska-Kajtoch2, and A. Radko2, 1National Research Institute of Animal Production, Balice, Poland, 2National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland

15:15  P1027  Application of analysis tools from Affymetrix on Eureka™ Genotyping Solution to provide accurate and automated animal genotypes.  
S. Nohzadeh-Malakshah, V. Joshi, and A. Pirani8, Affymetrix Inc., Santa Clara, CA
15:30  Break.
16:00  Proposals for the Animal Forensic Genetics Committee for the coming years.
16:15  Business meeting.

**Workshop: Applied Genetics and Genomics In Other Species of Economic Interest**

14:00 - 17:30

Chair: Leanne Van de Goor, VHLGenetics
slin Institute and R(D)SVS, University of Edinburgh
Sponsor: Eurofins
Canyon C

14:00  Welcoming remarks.
14:05  Dromedary comparison test.
14:30  Alpaca/Llama comparison test.
15:00  Pigeon comparison test.
15:30  Break.
16:00  Selection of new Duty Labs for 2018-2019 comparison tests.
16:15  Election of Committee & any other Business.

**Workshop: Genetically Engineered Livestock**

14:00 - 17:30

Chair: Bruce Whitelaw, The Roslin Institute and R(D)SVS, University of Edinburgh
Sponsor: LGC Biosearch Technologies
Canyon B

14:00  Introductory remarks, Bruce Whitelaw: The new era of genome editing.
14:15  S0119  CD163- A gatekeeper for susceptibility to porcine reproductive and respiratory syndrome virus.
      R. S. Prather*, University of Missouri, Columbia
14:45  P7008  Characterization of CD163 modification pig for PRRSV resistance.
      J. Chen*, N. Li, Y. Zhao, X. Hu, and Y. Xing, China Agricultural University, Beijing, China
15:00  P7003  Heritable multiplex gene editing via CRISPR/Cas9 exhibits no detectable genome-wide off-target effects in sheep.
      X. Wang* and Y. Chen, Northwest A&F University, Yangling, China
15:30  Break.
16:00  P7010  Generation of a novel glycosylated anti-CD20 monoclonal antibody in milk of transgenic cattle.
      R. Zhang*, Y. Dai, J. Wang, B. Tang, and N. Li*, 'China Agricultural University, Beijing; 'Beijing Genprotein Biotechnology Company, Beijing, China
16:15  P7002  Skin-specific transgenic expression of ovine β-catenin in mice.
      J. Wang*, K. Cui, D. Han, Z. Yang, and X. Deng, 'College of Animal Science and Technology, China Agricultural University, Beijing, China; 'China Agricultural University, Beijing, China; 'Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing
16:30  P7007  Targeted IGF1 promoter modification in mice using small intestine-specific regulatory element binding sites.
      Y. Zheng*, R. Zhang, Z. Yu, and N. Li, China Agricultural University, Beijing, China
16:45  Concluding remarks, Bruce Whitelaw: Should the differences between transgenic and genome editing matter from a scientific and regulatory perspective.
Workshop: Genetics of Immune Response & Disease Resistance  
14:00 - 17:30

Chair: Stephen White, USDA ARS Animal Disease Research Unit; Washington State University
Sponsor: Zoetis

Grand Ballroom B

14:00 S0121  Are we loosing our 6th sense?  
D. Werling*, Royal Veterinary College, Hatfield, United Kingdom

14:30 P6002  Evaluating the metagenome of nasal samples from cattle with bovine respiratory disease complex (BRDC).  
T. G. McDaneld*, L. A. Kuehn, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

14:45 P6011  Transcriptome profiling of the peripheral blood mononuclear cells following PRRSV vaccination in Pietrain pig.  
A. Islam1, C. Neuhoff*2, C. Große-Brinkhaus2, M. J. Pröll1, M. J. Uddin1, S. Agter Rony1, D. Tesfaye1, E. Tholen2, M. Hölker1, and K. Schellander2, 1Institute of animal science, University of Bonn, Bonn, Germany, 2Institute of Animal Science, University of Bonn, Bonn, Germany, 3School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia

15:00 P6013  Identifying driver mutations for Marek’s disease lymphomas in chicken using integrated genomic screens.  
A. Steep1, H. Xu1, Y. Zhang1, A. Black Pyrkosz1, M. E. Delany2, D. Frishman3, and H. H. Cheng4, 1Michigan State University, East Lansing, 2Technische Universität München, Freising, Germany, 3USDA, ARS, ADOL, East Lansing, MI, 4University of California-Davis

15:15 P6025  Network-based Integration of Gene Expression and Genome-wide Association Data to Prioritize Genomic Variants Associated with Susceptibility to Bovine Tuberculosis.  
K. E. Killick1, K. E. McLaughlin1, N. C. Naipar1, L. Burkitt-Gray1, I. W. Richardson1, H. L. Wienco1, D. A. Magee1, J. A. Browne1, B. Villarreal-Ramos1, H. M. Vordermeier1, D. P. Berry1, D. G. Bradley1, E. Gornley1, S. V. Gordon1, and D. E. MacHugh1, 1School of Agriculture and Food Science, University College Dublin, Ireland, 2Proteome Center, University of Tubingen, Germany, 3Department of Genetics, Trinity College Dublin, Ireland, 4Equinome Ltd., NovaUCD, Dublin, Ireland, 5Animal and Plant Health Agency, Weybridge, Surrey, United Kingdom, 6Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 7School of Veterinary Medicine, University College Dublin, Ireland

15:30 Break.

16:00 P6032  Identification and characterization of a novel pathogen causing bovine abortion.  
B. T. Welly, M. R. Miller, J. L. Stott, M. T. Blanchard, A. Islas-Trejo, S. M. O’Rourke, A. E. Young, J. F. Medrano, and A. L. Van Eenennaam*, University of California-Davis

16:15 P6033  Genome association of domestic sheep eosinophils with known parasite resistance QTL.  
M. R. Mousel1, S. N. White1,2, M. V. Gonzalez2,3, J. O. Reynolds2, and D. P. Knowles1,2, 1USDA, ARS, Animal Disease Research Unit, Pullman, WA, 2Washington State University, Pullman, 3Center for Applied Genomics, The Children’s Hospital of Philadelphia, PA, 4USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID

16:30 P5045  A genome-wide association study for natural antibodies measured in blood of Canadian Holstein cows.  
B. de Klerk1, K. A. Thompson-Crispi2, M. Sargolzaei1, J. J. van der Poel1, B. J. Ducro1, J. A. M. van Arendonk1, and B. Mallard1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Trouw Nutrition Agresearch, Guelph, ON, Canada, 3Semex Alliance, Guelph, ON, Canada, 4Dept of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada

16:45 P6041  Microarray analysis of genomic aberrations of horse sarcoids.  
K. Pawlina1, A. Gurgul1, J. Klukowska-Rötzler1, C. Koch1, K. Mählmann1, and M. Bugno-Poniewierska1, 1National Research Institute of Animal Production, Balice, Poland, 2University of Bern, Switzerland, 3University of Veterinary Medicine Hannover, Hannover, Germany

17:00 P7009  Precancerous molecular features committing development of colon polyps revealed by studies on the porcine model of human familial adenomatous polyposis.  
T. Flisikowska1, M. Stachowiak2, C. Wander1, A. Wagner1, C. Wurmser1, A. Perkowska1, F. Bruening1, S. Bauersachs1, A. Kind1, R. Fries2, M. Switonski2, D. Saur1, K. Flisikowski1, and A. Schnieke1, 1Chair of Livestock Biotechnology, Technische Universität München, Freising, Germany, 2Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poznan, Poland, 3Chair of Animal Breeding, Technische Universität München, Freising, Germany, 4Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland, 5Klinikum Rechts der Isar II, Technische Universität München, Munich, Germany
Workshop: Horse Genetics & Genomics
14:00 - 17:30

Chair: Rebecca Bellone, University of California-Davis; Teruaki Tozaki, Laboratory of Racing Chemistry
Sponsor: ASAS Foundations
Grand Ballroom A

14:00 Welcoming Remarks.

14:02 P6015 An Intronic MBTPS2 Variant Results in a Splicing Defect in Horses with Brindle Coat Texture.
L. Murgiano1, D. Waluk2, R. Towers3, N. Wiedemaar4, J. Dietrich1, V. Jagannathan5, M. Drögemüller1, T. Druet1, A. Galichet6, M. C. Penedo7, E. Müller2, P. Roosje8, M. Welle8, and T. Leeb*1, 1Institute of Genetics, University of Bern, Switzerland, 2Department of Dermatology, University Hospital of Bern, Switzerland, 3Institute of Medical Genetics, Cardiff University, United Kingdom, 4University of Liège, Belgium, 5Department of Dermatology, University Hospital of Bern, Switzerland, 6Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, 7Division of Clinical Dermatology, Department of Clinical Veterinary Medicine, University of Bern, Switzerland, 8Institute of Animal Pathology, University of Bern, Switzerland

14:15 P5032 A genome-wide association study of young horse test traits in Swedish Warmblood.
S. Eriksson, Å. Viklund, and S. Mikko*, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

14:30 P8004 A comprehensive gene catalogue of the horse Y chromosome.
J. Janečka1, L. Orlando2, M. Schubert1, S. Ghosh3, T. A. Stout4, B. P. Chowdhary5, and T. Raudsepp*4, 1Duquesne University, Pittsburgh, PA, 2Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark, 3University of Kentucky, Lexington, KY, 4KU Leuven, Leuven, Belgium, 5Natural History Museum of Denmark Copenhagen University, Copenhagen, Denmark, 6Texas A&M University, College Station, 7Utrecht University, Utrecht, Netherlands, 8Qatar University, Doha, Qatar

14:45 S0122 Improving the structural and functional annotation of the equine reference genome.
J. N. MacLeod5, M. S. Hestand2, L. Orlando1, and T. S. Kalbfleisch6, 1University of Kentucky, Lexington, KY, 2KU Leuven, Leuven, Belgium, 3Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark, 4Texas A&M University, College Station, 5Utrecht University, Utrecht, Netherlands, 6Qatar University, Doha, Qatar

15:15 Discussion on EquCab 3.0 Led by J. N. MacLeod, & T. S. Kalbfleisch.

15:30 Break.
16:00 P6010  Identification of novel genetic variants in the equine collagenous lectin genes through targeted, next generation re-sequencing.
R. S. Fraser*, A. Meyer, L. G. Arroyo, J. D. Hampermiller, and B. N. Lillie, 1Department of Pathobiology, University of Guelph, Guelph, ON, Canada, 2Ontario Institute for Cancer Research, Toronto, ON, Canada, 3Department of Clinical Studies, University of Guelph, Guelph, ON, Canada

16:15 P2021  Age-related methylation patterns of equine blood leukocytes.
T. Ząbek*, E. Semik, T. Szmatoła, A. Gurgul, A. Fornal, and M. Bugno-Poniewierska, National Research Institute of Animal Production, Balice, Poland

16:30 P3002  Functional annotation of the equine genome.
C. J. Finno*, J. L. Petersen, R. Bellone, and J. N. MacLeod, 1University of California, Davis, Davis, CA, 2University of Nebraska-Lincoln, 3University of California-Davis, 4University of Kentucky, Lexington

16:45  Panel Discussion: C. J. Finno, J. L. Petersen, R. Bellone, and J. N. MacLeod.

17:15  Business Meeting.

Workshop: Bovine Species Genomics Working Group
14:00-17:30
Chair: Hans Lenstra, Utrecht University
Informal discussion of the genomes of bovine species other than the well-studied Bos taurus: zebu, banteng, gaur, gayal, yak, bison, wisent and water buffalo.

ORAL SESSIONS & WORKSHOPS — Monday, July 25

Workshop: Avian Genetics & Genomics
8:30 - 12:00
Chair: Richard Crooijmans, Wageningen University
Sponsor: Cobb-Vantress
Canyon B

8:30 P1003  MiRNAs expression profiling of Myostatin transgenic and wild type littermate mice by Solexa deep sequencing.
R. Javed*, Huazhong Agricultural University, Wuhan, China

8:45 P5011  Fine mapping the QTL for growth traits in outbred chicken advanced intercross lines by improved ddGBS.
Y. Wang*, X. Cao, X. Gu, and X. Hu, China Agricultural University, Beijing, China

9:00 P3005  Genome-wide transcriptomic analysis of liver in sex-linked Dwarf and wild type chickens.

9:15 P3020  The potential relationship between comb color and egg production revealed by GWAS in Blue-shelled chicken.
X. Dong*, J. Li, Y. Zhang, X. Deng, and C. Wu, Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing

9:30 P1019  Genetic introgression through selection in domestic chickens: Insight from whole genome sequence analysis.
R. A. Lawal*, D. Wragg, P. Silva, K. Vanmechelen, A. Vereijken, D. D. Wu, R. M. Al-Atiyat, and O. Hanotte, 1School of Life Sciences, University of Nottingham, University Park, Nottingham, United Kingdom, 2Institut National de la Recherche Agronomique (INRA), UMR 1338 GenPhySE, 31326, Castanet Tolosan, France, 3Department of Animal Science, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka, 4Open University of Diversity, Hasselt, Belgium, 5Hendrix Genetics, Boxmeer, Netherlands, 6State Key Laboratory of Genetic Resources and Evolution, Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Science, Kunming, China, 7King Saud University, Riyadh, Saudi Arabia, 8School of Life Sciences, University of Nottingham, United Kingdom
9:45 P5035  Fine mapping of a distal chromosome 4 QTL affecting growth and muscle mass in a chicken advanced intercross line.  
S. Lyu1, D. Arends1, M. K. Nassar1,2, and G. A. Brockmann1, 1Albrecht Daniel Thaer-Institut for Agricultural and Horticultural Sciences, Faculty of Life Sciences, Humboldt-Universität zu Berlin, Germany, 2Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt

10:00 Break.

10:30 P1033  Relaxation of purifying selection is prevalent among domesticated animals.  
J. Chen1*, X. Du1, C. Zhang1, and S. Zhao1, 1Huazhong Agricultural University, Wuhan, China, 2Kib, Kunming, China

10:45 P5047  Wide genome involvement in response to long-term selection for antibody response in an experimental population of White Leghorn chickens.  
M. Lillie*, Swedish University of Agricultural Sciences, Uppsala, Sweden

11:00 P2025  Identification of tissue-specific promoters in chickens.  
C. Kern1*, P. Saelao1, Y. Wang1, M. Halstead1, J. Chitwood1, T. Kim1, P. J. Ross1, I. Korf1, M. E. Delany1, H. Cheng1, and H. Zhou1, 1University of California-Davis, 2USDA-ARS Avian Disease and Oncology Laboratory, East Lansing, MI

11:15 P2024  Profiling of open chromatin in chicken tissues using ATAC-seq.  
M. Halstead1, C. Kern1, P. Saelao1, Y. Wang1, H. Zhou1, and P. J. Ross1, University of California-Davis

11:30 P3052  Characterization of circular RNAs in relation to embryonic muscle development in chicken.  
H. Ouyang1, Q. Nie2, and X. Zhang1, 1College of Animal Science, South China Agricultural University, Guangzhou, China, 2South China Agricultural University, Guangzhou, China

11:45 P1046  Deciphering chicken fatness trait with integrative genetics and genomics approaches.  
C. K. Khoo1,2*, A. Gheyas1, R. Kuo1, L. Eory1, P. M. Hocking1, and D. Burt1, 1The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, United Kingdom, 2Department of Veterinary Services, Ministry of Agriculture & Agro-Based Industry Malaysia, Putrajaya

Workshop: Comparative MHC  
8:30 - 12:00

Chair: Keith Ballingall, Moredun Research Institute; Sam Ho, Gift of Life Michigan

Sponsor: Affemetrix

Canyon C

8:30  Introductory Remarks.

8:31 P4020  Diversity analysis of transcribed MHC class Iβ loci in Japanese quail.  
S. Asaji1, S. Suzuki1, T. Ishige1, K. Hosomichi1, T. Shinoda1, H. Hara1, T. Hirano1, and K. Hanzawa1, 1Tokyo University of Agriculture, Atsugi, Japan, 2Tokai University School of Medicine, Isehara, Japan, 3Tokyo University of Agriculture, Setagaya, Japan, 4Kanazawa University, Kanazawa, Japan

8:45 P6018  Revealing the importance of SLA-DRB1 to post-weaning piglet survivability by a case-control analysis and subsequent validation using in silico epitope binding analysis and molecular structural modeling.  
M. T. Lc1, H. J. Lee1, J. Lee2, and C. Park1, Konkuk University, Seoul, The Republic of Korea

9:00 P5034  Differential proportion of ancestral MHC haplotypes in Brangus breed.  
D. Goszczynski1, C. Corbi1, H. Morales1, D. Poski1, E. Villegas Castagnasso1, S. Munilla2, P. Peral Garcia1, A. Rogberg2,3, R. J. C. Canter2,3, and G. Giovambattista1, 1IGEVET – Instituto de Genetica Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, 2Departamento de Produccion, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina, 3INPA – Unidad Ejecutora UBA-CONICET de Investigaciones en Produccion Animal, Buenos Aires, Argentina

S. Ho1, J. H. Lee2, A. Ando1, C. Rogel-Gaillard4, L. B. Schook1, D. M. Smith5, J. K. Lunney1, and S. E. Hammer6, 1Gift of Life Michigan, Ann Arbor, MI, 2Chungnam National University, Daejeon, The Republic of Korea, 3Tokai University School of Medicine, Isehara, Kanagawa, Japan, 4GABI, INRA, AgroParisTech, Université© París-Saclay, Jouy-en-Josas, France, 5University of Illinois at Urbana-Champaign, 6University of Michigan, Ann Arbor, 7USDA ARS BARC APDL, Beltsville, MD, 8University of Veterinary Medicine Vienna, Austria

16 • ISAG 2016 PROGRAM
The Ovar-DRB1 *0404 haplotype is associated with growth and lifetime prolificacy ewe traits.
1Washington State University College of Veterinary Medicine, Pullman, 2Erciyes University Faculty of Agriculture, Kayseri, Turkey, 3USDA, ARS, Animal Disease Research Unit, Pullman, WA, 4USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID, 5Washington State University, Pullman, 6Center for Reproductive Biology, Washington State University, Pullman

Limited MHC diversity and an exotic virus may have contributed to the decline of red squirrels in the United Kingdom.
K. Ballingall1, A. McIntyre2, Z. Lin1, and C. J. McInnes2, 1Moredun Research Institute, Edinburgh, United Kingdom, 2Moredun Research Institute, Penicuik, United Kingdom

The gene duplication of beta-2 microglobulin in artiodactyla and remains intact only in pigs.
M. T. Le, M. K. Choi, H. Cho, and C. Park*, Konkuk University, Seoul, The Republic of Korea

Evaluating the accuracy of imputation in the highly polymorphic MHC region of genome.
M. Emam1, M. Sargolzaei2, S. Tabatabaei1, S. L. Cartwright1, F. S. Schenkel2, F. Miglior1, J. P. Chesnais1, and B. Mallard1, 1Department of Pathobiology, University of Guelph, Guelph, ON, Canada, 2Semex Alliance, Guelph, ON, Canada, 3University of Guelph, Guelph, ON, Canada, 4Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada

Extensive functional class I MHC diversity in sheep.
K. Ballingall1, S. Golf1, J. M. Pemberton1, and K. Dicks1, 1Moredun Research Institute, Edinburgh, United Kingdom, 2Royal Veterinary College, Hatfield, United Kingdom, 3The University of Edinburgh, United Kingdom

Workshop: Equine Genetics & Thoroughbred Parentage Testing
8:30 - 12:00
Chair: Cecilia Penedo, University of California-Davis
Sponsor: ASAS Foundation
Canyon A

Welcome Remarks.
8:35 Horse Comparison Test (Standing Committee).
9:30 ISBC Directives and Lab Performance (Cecilia Penedo).
10:00 Break.
10:30 Development and evaluation of a set of 100 SNP markers for DNA typing in the domestic horse.
H. Holl1, J. Vanhnsy2, R. Everts2, D. Cook1, S. Brooks2, M. Carpenter2, C. Bustamante2, and C. Lafayette2, 1Etalon Inc., Menlo Park, CA, 2Agena Bioscience, San Diego, CA
10:45 Election of Committee Members and Other Business.
Workshop: ISAG-FAO Genetic Diversity
8:30 - 12:00

Chair: Catarina Ginja, University of Porto
Sponsor: FAO
Grand Ballroom A

8:30  S0123  The adaptation of farm animals to northern and Arctic environments.
J. Kantanen*, Natural Resources Institute Finland (Luke), Jokioinen, Finland

9:00  P4008  Genome-wide copy number variation in the bovine genome detected using low coverage sequence of popular beef breeds.
B. N. Keel*, W. M. Snelling, and J. W. Keele, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

9:15  P4027  Systematic profiling of short tandem repeats in the cattle genome.
L. Xu1, R. Haas2, J. Sun1, Y. Zhou1, D. Bickhart4, J. Li1, J. Song1, T. Sonstegard5, C. P. VanTassell1, H. Levin7, and G. E. Liu5*, 1Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, 2University of Wisconsin–Platteville, 3South China Agricultural University, Guangzhou, China, 4Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China, Beijing, China, 5University of Maryland, Animal Science and Avian, College Park, 6Recombinetics, Inc., St Paul, MN, 7University of California-Davis, Department of Evolution and Ecology

9:30  P4014  Global and local admixture analyses of Baladi cattle.
A. Shabtay1, M. Soller2, J. Sölken3, G. Mészáros3, T. Sonstegard5, E. O. Ünal5, H. J. Huson6, Y. T. Utsunomiya7, and E. Lipkin2*, 1Department of Ruminant Sciences, Agricultural Research Organization (ARO), Newe Ya’ar Research Center, Ramat Yishay, 30095, Israel, 2Hebrew University of Jerusalem, Jerusalem, Israel, 3University of Natural Resources and Life Sciences, Vienna, Austria, 4Recombinetics, Inc., St Paul, MN, 5Namik Kemal University, Agriculture Faculty, Department of Animal Sci., Tekirdag, Turkey, 6Cornell University, Ithaca, NY, 7UNESP Univ Estadual Paulista, Jaboatocabal, Brazil

9:45  P4029  Launching SheepGenomesDB: 100 million variants from nearly 500 sheep genomes.
J. Kijas*, R. Brauning2, S. M. Clarke3, A. McCulloch3, N. E. Cockett4, G. Saunders5, M. Naval Sanchez2, S. McWilliam1, and H. Daetwyler6, 1CSIRO Agriculture, Brisbane, Australia, 2AgResearch, Mosgiel, New Zealand, 3AgResearch Limited, Mosgiel, New Zealand, 4Utah State University, Logan, UT, 5EMBL-EBI, Hinxton, United Kingdom, 6Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia

10:00 Break.

10:30 Overview of the latest FAO-Report on the diversity and management of Farm Animal Genetic Resources.

M. Yaro1, K. A. Munyard2, E. Morgan3, R. J. Allcock2, M. J. Stear4, and D. M. Groth1*, 1Curtin University, Perth, Australia, 2University of Western Australia, Perth, Australia, 3University of Glasgow, Glasgow, United Kingdom

11:00  P4060  Runs of homozygosity reveal natural selection footprints of some African chicken breeds and village ecotypes.
A. R. Elbeltagy1,2, D. S. Fleming1, F. Bertolini1, A. G. Van Goor1, C. M. Ashwell3, C. J. Schmidt4, S. J. Lamont1, and M. F. Rothschild1, 1Department of Animal Science, Iowa State University, Ames, 2Department of Animal Biotech. Animal Production Research Institute, Cairo, Egypt, 3Department of Poultry Science, North Carolina State University, Raleigh, 4Department of Animal and Food Sciences, University of Delaware, Newark

11:15  P4066  Genetic diversity of pig populations from the US mainland, Pacific islands and China: Autosomal SNP evaluation.

11:30  P4016  Paternal genetic characterization of wild boars and domestic pigs in Japan, based on SRY and TSPY gene haplotypes.
Y. Sato*, K. Sato, and Y. Mizoguchi, School of Agriculture, Meiji University, Kawasaki, Japan

11:45  P4059  Origins and genetic structure of Creole cattle inferred from Y-chromosomal variation.
C. Ginja1, C. Penedo2, O. Cortês3, I. Martin-Burriel1, A. Egito3, L. T. D. Gama3, J. V. Delgado Bermejo3, B. Consortium3, A. Martinez-Martinez2, 1CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal, 2Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, 3Universidad Complutense de Madrid, Madrid, Spain, 4Laboratorio de Genética Bioquímica, Universidad de Zaragoza, Zaragoza, Spain, 5Embrapa-Laboratório de Genômica e Melhoramento Animal, Campo Grande, Brazil, 6Faculdade de Medicina Veterinaria, Universidade Técnica de Lisboa, Lisboa, Portugal, 7Departamento de Genética, Universidad de Cordoba, Cordoba, Spain
Workshop: Ruminant Genetics & Genomics
8:30 - 12:00
Chair: James Kijas, CSIRO Agriculture
Sponsor: Illumina
Grand Ballroom B

8:30 P1009  Sheep reference genome sequence updates: Texel improvements and Rambouillet progress.
Y. Liu1, S. C. Murafi2, R. A. Harris3, A. C. English4, X. Qin1, E. Skinner5, S. Richards6, J. Rogers7, Y. Han8, V. Vee7, M. Wang9, Q. Meng1, M. P. Heaton12, T. P. L. Smith12, B. P. Dalrymple12, J. Kijas1, N. E. Cockett10, E. A. Boerwinkle11, D. M. Muzny12, R. A. Gibbs12, and K. C. Worley*12, 1Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, 2Iowa State University, 3CSIRO Agriculture, Brisbane, Australia, 4Utah State University, Logan, 5University of Texas Health Science Center at Houston

8:45 P3040  Large-scale gene co-expression network as a source of functional annotation for bovine genes.
H. Beiki1, J. M. Reecy*2, A. Pakdel3, A. Nejati Javaremi4, and A. Masoudi Nejad5, 1Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran (Islamic Republic of), 2Iowa State University, Ames, 3Isfahan University of Technology, Isfahan, Iran (Islamic Republic of), 4University of Tehran, Karaj, Iran (Islamic Republic of), 5University of Tehran, Tehran, Iran (Islamic Republic of)

9:00 P3003  The extent of cis-regulation of gene expression and its influence on complex trait variation in cattle.
A. J. Chamberlain12, M. Khansefid12, C. J. Vander Jagt12, B. J. Hayes12, L. C. Marett1, Y. Chen4, S. Bolormaa1, C. A. Millen1, T. T. Nguyen1, and M. E. Goddard1, 1Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, 2Dairy Futures Cooperative Research Centre, Bundoora, Australia, 3University of Melbourne, Parkville, Australia, 4La Trobe University, Bundoora, Australia, 5Department of Economic Development, Jobs, Transport and Resources, Ellinbank, Australia, 6NSW Department of Primary Industries, Menangle, Australia

9:15 P5060  The effect of selection over years on breed composition in tropical composite cattle.
L. R. Porto-Neto1, S. Harburg2, R. Bunch2, R. E. Lyons3, S. A. Lehnert1, and A. Reverter1, 1CSIRO Agriculture, Brisbane, Australia, 2North Australian Pastoral Company, Brisbane, Australia, 3University of Queensland, Gatton, Australia

9:30 S0125  Changing patterns of genomic variability following domestication of sheep.
M. Naval Sanchez1, R. Brauning2, S. M. Clarke2, Q. Nguyen3, A. McCulloch4, N. E. Cockett5, W. Zamani6, F. Pompanon7, P. Taberlet8, S. M. Clarke9, H. Daetwyler10, and J. Kijas11, 1CSIRO Agriculture, Brisbane, Australia, 2AgResearch, Mosgiel, New Zealand, 3AgResearch Limited, Mosgiel, New Zealand, 4Utah State University, Logan, UT, 5Department of Environmental Sciences, Tarbiat Modares University, Noor, Iran (Islamic Republic of), 6Laboratoire d’Ecologie Alpine, Universite Grenoble Alpes, Grenoble, France, 7Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia

10:00 Break.

10:30 P6019  Host genetics of resistance to bovine tuberculosis infection in dairy cows.
S. Wilkinson1, S. C. Bishop1, A. R. Allen2, S. H. McBride2, R. A. Skuce3,4, M. Bermingham1, J. A. Woolliams1, and L. J. Glass5, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush EH25 9RG, United Kingdom, 2Agri-Food and Biosciences Institute Stormont, Belfast BT4 3SD, United Kingdom, 3Queen’s University Belfast, Belfast BT9 7BL, United Kingdom

10:45 P5056  Genome-wide association study for stayability measures in Nellore-Angus crossbred cows.
B. N. Engle6, A. D. Herring, J. E. Sawyer, D. G. Riley, J. O. Sanders, and C. A. Gill, Department of Animal Science, Texas A&M University, College Station

11:00 P6038  Tackling the itch: GWAS-based candidate genes for psoroptic mange sensitivity in Belgian Blue cattle.
A. Coussé1, M. Elansary2, R. Abos2, C. Sarre3, L. Francois1, X. Hubin1, A. Stinckens1, C. Saegerman2, T. Druet2, B. Losson2, E. Claerebout1, M. Georges2, and N. Buys1, 1KU Leuven, Leuven, Belgium, 2University of Liège, Liège, Belgium, 3Ghent University, Ghent, Belgium, 4AWE asbl, Ciney, Belgium

11:15 P5021  Indel polymorphism in 3'-UTR of RXFP2 does not segregate with horns status in sheep breeds with a variable and/or sex-limited horns status.
G. Lühken1, S. Krehb1, S. Rothhammer1, J. D. Küpper1, B. Mioč2, I. Medugorac3, 1Department of Animal Breeding and Genetics, Justus Liebig University, Gießen, Germany, 2Department of Functional Genome Analysis, Gene Center, Ludwig Maximilians University, Munich, Germany, 3Chair of Animal Genetics and Husbandry, Ludwig Maximilians University, Munich, Germany, 4Department of Animal Breeding and Genetics, Justus Liebig University of Gießen, Gießen, Germany, 5Department of Animal Science and Technology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia, 6Tierzuchtforshung e.V. München, Grub, Germany
Holstein Friesian lethal haplotype 5 is caused by a 138kbp deletion on chromosome 9.
C. Wehrhahn1, E. Schätz2, M. Wanek2, R. Borfeld2, J. Beck2, and B. Brenig3, 1Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, 2Institute for Livestock Reproduction GmbH, Schönow, Germany, 3Chronix Biomedical GmbH, Göttingen, Germany

Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with high-altitude pulmonary hypertension.
M. P. Heaton1, T. P. L. Smith1, J. K. Carnahan1, V. Basnayake2, J. Qiu2, B. Simpson2, and T. S. Kalbfleisch3, 1USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 2GeneSeek, a Neogen Company, Lincoln, NE, 3University of Louisville, KY

**Workshop: Cattle Molecular Markers & Parentage Testing**
**14:00 - 17:30**

Chair: Romy Morrin, Weatherbys DNA Laboratory

Sponsor: Neogen
Canyon A

14:00 Welcoming Remarks.
14:03 Cattle STR/SNP Comparison Test 2015-2016.
14:05 Presentation by Duty Lab.
14:20 Presentation of the STR results.
14:35 Evaluation of results by the Chair.
14:50 Presentation of SNP results.
15:05 SNP standardised nomenclature discussion.
15:30 Break.
16:00 Genomic evaluations in dairy cattle, beef cattle and sheep in Ireland.
D. P. Berry1, F. Kearney2, R. Evans2, E. Wall2, and A. Cromie1, 1Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 2Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland

16:30 Effectively managing bovine genetic disease risk via genotyping the Irish national herd.
M. C. McClure1, M. Mullen2, S. M. Waters3, F. Kearney4, J. McClure4, P. Flynn4, and R. Weld5, 1Irish Cattle Breeding Federation, Bandon, Ireland, 2Athlone Institute of Technology, Athlone, Ireland, 3Teagasc Grange, Meath, Ireland, 4Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, 5Weatherbys Ireland, Naas, Ireland

16:45 Next Comparison Test 2017.
16:55 Election of Committee.
17:10 AOB.

**Workshop: Companion Animal Genetics & Genomics**
**14:00 - 17:30**

Chairs: Leslie Lyons, University of Missouri - Columbia; Tomas Bergstrom, University of Gothenburg

Sponsor: ASAS Foundation
Canyon C

14:00 Welcoming Remarks.
14:01 Study of the mutant MDRI allele in four Collie breeds in Italy.
S. P. Marelli1, G. Minozzi1, M. Longeri2, R. Rizzi2, G. Gandini2, and M. Polli2, 1Università degli Studi di Milano, Milan, Italy

14:15 Around the tail of the Khmer cat.
A. Cristalli1, S. P. Marelli1, P. Valialet1, F. Genova1, and M. Longeri1, 1DVM, PhD, Arezzo, Italy, 2Università degli Studi di Milano, Milan, Italy

14:30 Runs of homozygosity highlight candidate genes and biological pathways related to athletic performance in Alaskan sled dogs.
H. J. Huson1, A. Valenti1, and A. Bayko1, Cornell University, Ithaca, NY
14:45  P6046  Precision medicine and the 99 lives cat genome sequencing initiative.
L. Lyons*, Department of Veterinary Medicine & Surgery, College of Veterinary Medicine, University of Missouri-Columbia

15:00  P4062  DNA sequencing and genetic polymorphism discovery in the canine monoamine oxidase A (MAOA) gene.
J. Sacco*, A. Ruplin, P. Skonieczny, and M. Ohman, Drake University, Des Moines, IA

15:15  P6030  Three diverse mutations underlying canine xanthine urolithiasis.
N. M. Tate*, K. M. Minor, J. R. Mickelson, K. Peterson, J. P. Lulich, and E. Furrow, University of Minnesota, Saint Paul

15:30  Break.

16:00  P6000  Whole genome sequencing of canine family trios to identify rare alleles for Mendelian diseases.
S. Mäkeläinen*, G. Andersson, and T. F. Bergström, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

16:15  Cat Genome Assembly Improvements update.

16:30  Felid Genomes.

16:45  Dog 10K Genomes update.

17:00  Break.

17:15  Selection of 2016 - 2019 committee members.

17:25  Concluding Remarks.

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**Workshop: Domestic Animal Epigenetics**

**Chair: Hasan Khatib, University of Wisconsin-Madison**

**Sponsor: Eurofins**

**Grand Ballroom A**

14:00 - 17:30

14:00  S0118  A hierarchy of epigenetic changes in the developmental transition from brown to white perirenal adipose tissue.
T. Vuocolo1, A. Statham2, D. C. Bauer3, S. McWilliam1, S. S. Nair4, J. L. Morrison5, S. Zhang6, M. Buckley7, I. C. McMillen8, S. J. Clark2, and R. L. Tellam9, 1CSIRO Agriculture, Brisbane, Australia, 2The Garvan Institute of Medical Research, Sydney, Australia, 3CSIRO Data61, Sydney, Australia, 4Garvan Institute for Medical Research, Sydney, Australia, 5The University of South Australia, Adelaide, Australia, 6The University of Newcastle, Newcastle, Australia

K. M. Schachtschneider1,2, M. F. Derks3,4, O. Madson1, V. N. Laine1, L. B. Schook2, M. A. Groenen1, K. J. Verhoeven1, and K. van Oers1, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Department of Animal Sciences, University of Illinois at Urbana-Champaign, 3Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands, 4Bioinformatics Group, Wageningen University, Wageningen, Netherlands, 5Department of Terrestrial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands

15:15  Business meeting and elections.

15:30  Break.

16:00  P2022  Mining functional genomics and epigenetics data with livestock EpidB.
E. Fritz-Waters1, M. W. Vaughn2, J. P. Carson1, J. M. Reecy1, and J. E. Koites3,1, 1Iowa State University, Ames, 2Texas Advance Computing Center, University of Texas, Austin, 3University of Arkansas, Fayetteville

16:30  P2026  Polar overdominance and maternal genome effects in placenta drive heterosis in utero.
C. A. S. Estrella1,2, K. L. Kind1,2, M. Ghanipoor-Samami2,3, A. Javadmanesh1,2, C. T. Roberts1,4, and S. Hiendleder1,2, 1Robinson Research Institute, The University of Adelaide, Adelaide, Australia, 2JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia, 3School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia, 4Discipline of Obstetrics and Gynaecology, School of Medicine, The University of Adelaide, Adelaide, Australia

17:00  P2019  Adipocyte gene expression and DNA methylation patterns differ significantly between lean and obese pigs.
M. J. Jacobsen1, J. H. Havgaard2, C. M. Junker Mentzel1, P. M. Sorensen1, S. Pundhir3, C. Anthon1, P. Karlskov-Mortensen1, C. S. Braun1, S. Cirera1, J. Gorodkin1, C. B. Jorgensen1, R. Barres1, and M. Fredholm1, 1Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark, 2BRIC, University of Copenhagen, Denmark, 3The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Denmark
Workshop: Pig Genetics & Genomics
14:00 - 17:30

Chairs: Kyle M Schachtschneider, Wageningen University; Ramona N. Pena, University of Lleida

Sponsor: Zoetis

Grand Ballroom B

14:00  P6034  Associations between cis-expression quantitative trait loci (cis-eQTL) markers and host response to porcine reproductive and respiratory syndrome virus (PRRSV) infection.
H. Bao1, A. Kommadath1, I. Choi2, J. M. Reecy1, J. E. Koltes1, E. Fritz-Waters1, C. J. Eisley1, R. R. R. Rowland1, C. K. Tuggle1, J. C. M. Dekkers4, L. L. Guan1, P. Stothard1, G. Plastow1, and J. K. Lunney1, 1University of Alberta, Edmonton, AB, Canada, 2USDA ARS BARC APDL, Beltsville, MD, 3Iowa State University, Ames, 4University of Arkansas, Fayetteville, AR, 5Kansas State University, Manhattan, KS, 6Department of Animal Science, Iowa State University, Ames, 7Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 8Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada

14:30  P6009  Focus on atherosclerosis and the pig as a model to identify genes affecting cholesterol and other plasma lipid levels.
P. Karlskov-Mortensen*, S. D. Frederiksen, S. D. Pant, S. Cirera, C. B. Jørgensen, T. Mark, and M. Fredholm, Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark

14:45  P7006  Generation of a porcine model of obesity and complications by Leptin knockout.
T. Tan1, Y. Xing1, X. Hu2, and N. Li1, 1The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China, 2China Agricultural University, Beijing, China

15:00  P7004  Screen of transgenic integration sites and construction of site-specific transgenic pig by CRISPR-Cas9.
L. Ma1, X. Hu1, Y. Xing2, and N. Li1, 1China Agricultural University, Beijing, China, 2The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China

15:15  P1016  The Pig’s other genome: a reference gene catalogue of the gut microbiome as a new resource for deep studies of the interplay between the host and its microbiome.
L. Xiao1, J. Estellé2, P. Kühlerich1, Y. Ramayo-Caldas3, Z. Xia1, Q. Feng1, A. Ø. Pedersen2, N. J. Kjeldsen1, E. Maguin1, J. Döré4, N. Pons4–5, E. le Chatelier4–5, L. Madsen3, J. Wang3, S. D. Ehrlich3, K. Kristiansen3, and C. Rogel-Gaillard6, 1BGI-Shenzhen, Shenzhen, China, 2Gemini Biosciences, Seattle, WA, USA, 3CNRS, Génopole, Saclay, France, 4GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, 5Department of Biology, University of Copenhagen, Copenhagen, Denmark, 6Department of Animal Science, Iowa State University, Ames, IA, USA, 7Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 8Department of Animal Sciences, Iowa State University, Ames, IA, USA, 9Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy

15:30  Break

15:45  P3012  Deconstructing the pig genome-metabolome functional interactions.
L. Fontanesi1, S. Bovo1, G. Schiavo1, G. Mazzoni1, A. Ribani1, V. J. Utzeri1, S. Dall’Olio1, F. Bertolini2, S. L. Pant3, S. Cirera1, C. S. Bruun4, T. Mark1, and M. Fredholm, Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 5Department of Animal Science, Iowa State University, Ames, IA, USA, 6Department of Animal Science, Iowa State University, Manhattan, KS, 7Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 8Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada

16:15  P5012  Integrative analysis of metabolomic, proteomic and genomics data to reveal functional pathways and candidate genes for drip loss in pigs.
J. Welzenbach1, C. Grosse-Brinkhaus1, C. Neuhoff1, C. Loof1, K. Schellander2, and E. Tholen1, 1Institute of Animal Science, University of Bonn, Bonn, Germany, 2Institute of Animal Science, University of Bonn, Bonn, Germany

16:30  P3029  Identification of regulatory genes involved in Longissimus dorsi transcriptomic differences between pig genotypes.
M. Ayuso1, J. Garrayo1, A. Fernández1, Y. Núñez1, R. Benítez2, B. Isabel1, A. I. Fernández3, A. I. Rey1, A. González-Bulnes4, 1University of Bonn, Bonn, Germany, 2Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, 3University of California, Davis, CA, USA, 4University of Alberta, Edmonton, AB, Canada

16:45  P5057  Use of genomics to simultaneously improve feed efficiency and meat quality in grow-finish pigs.
C. Zhang1, R. A. Kemp2, N. J. Boddicker3, J. C. M. Dekkers1, Z. Wang2, and G. Plastow1, 1University of Alberta, Edmonton, AB, Canada, 2Genesus Inc, Lethbridge, AB, Canada, 3Department of Animal Science, Iowa State University, Ames, IA, USA, 4Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada

17:00  Panel Discussion
Workshop: Havemeyer Workshop on Gene Expression and Annotation in Horse  
14:00 - 17:30

Chairs: Ernest Bailey, University of Kentucky;  
Rebecca Bellone, University of California-Davis

Sponsor: Havemeyer  
Seminar Theater

14:00 Welcoming Remarks: Dr. Ernest Bailey.
14:05 Lessons from other Species: Dr. Huaijun Zhou.
14:25 Recap: Functional Annotation in the Horse: Dr. Jessica Petersen.
14:35 Discussion: Community Based Workshop Initiative for Functional Annotation of the Horse Genome.

Workshop: Bovine Species Genomics Working Group  
14:00-17:30

Chair: Hans Lenstra, Utrecht University

14:00 Informal discussion of the genomes of other bovine species other than the well-studied Bos taurus: zebu, banteng, gaur, gayal, yak, bison, wisent and water buffalo.

ORAL SESSIONS & WORKSHOPS — Tuesday, July 26

Workshop: Applied Genetics of Companion Animals  
8:30 - 12:00

Chair: Leslie Lyons, University of Missouri-Columbia

Sponsor: Neogen

Canyon C

8:30 Welcoming Remarks.
8:35 Dog CT Duty Lab Report, P. Dovec.
8:50 Dog CT Analysis Lab Report, L. van de Goor.
9:05 Discussion - Secondary canine STR Panel.
9:35 Discussion.
10:00 Break.
10:30 Cat CT Duty Lab Report, M. Longeri.
10:45 Cat CT Analysis Lab Report, L. Lyons.
11:00 SNP Panels for Domestic Cat Parentage.
11:15 P5002 You say variation, they say mutation, we say confusion - Genetic communication, why it needs standardisation!.  
G. Sofronidis*, Orivet Genetic Pet Care, Melbourne, Australia
11:30 Discussion - Trait reporting & SNPs Panels for Cats & Dogs.
11:55 Motions and Votes.
Workshop: Applied Sheep & Goat Genetics  
8:30 - 12:00  
Chair: Gesine Luehken, Justus-Liebig University  
Canyon B

8:30  P5017  Identifying genetic regions to spring ewes to lamb out of season.  
  C. J. Posbergh*, M. L. Thonney, and H. J. Huson, Cornell University, Ithaca, NY

8:45  P5039  A landscape genomic approach to unravel the genomic mechanism of adaptation in indigenous goats of South Africa.  
  K. Mdladla*1,2, E. F. Dzomba2, and F. C. Muchadeyi1, 1Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa, 2University of KwaZulu-Natal, Pietermaritzburg, South Africa

9:00  P5051  Genetic investigation of sheep families demonstrating the entropion eye condition.  
  T. Hadfield* and N. E. Cockett, Utah State University, Logan

9:15  P7000  Growth performance and meat characteristics of Awassi sheep that holds the Callipyge gene.  
  K. I. Jawasreh, A. H. Al-Amareen*, and A. Y. Abdullah, Jordan University of Science and Technology, Irbid, Jordan

9:30  S0115  SNP parentage testing in sheep – a comparison of technologies.  
  S. M. Clarke*, K. G. Dodds, R. Brauning, T. van Stijn, R. A. Anderson, and J. C. McEwan, AgResearch, Mosgiel, New Zealand

10:00  Break.

10:45  P6050  Extended scrapie incubation time in goats singly heterozygous for PRNP S146 or K222: An update after 7 years.  
  S. White*1,2, J. O. Reynolds2, D. F. Waldron1, D. A. Schneider2,3, and K. I. O'Rourke2, 1USDA-ARS Animal Disease Research, Pullman, WA, 2Washington State University, Pullman, 3Texas A&M AgriLife Research, San Angelo

11:00  P7001  Heritable gene disruption in goats with CRISPR/Cas9 results in expected phenotypes.  
  X. Wang* and Y. Chen, Northwest A&F University, Yangling, China

11:15  Results of comparison tests 2015-16.

11:45  Plans for next comparison tests.

11:55  Elections.

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Workshop: Comparative & Functional Genomics  
8:30 - 12:00  
Chair: Klaus Wimmers, Leibniz Institute for Farm Animal Biology (FBN)  
Grand Ballroom A

8:30  Welcoming Remarks.

8:31  P3010  Effect of rumen content exchange on gene expression in rumen epithelium of lactating cows.  
  J. Vilkki*, D. Fischer1, I. Tapio1, and K. J. Shingfield2, 1Natural Resources Institute Finland, Jokioinen, Finland, 2Aberystwyth University, Aberystwyth, United Kingdom

8:45  P3044  Characterization of exosomal immune-related microRNAs incolostrum and milk from average, low and high immune responder cows.  
  H. Atalla1,2, B. Mallard2,3, and N. A. Karrow2, 1Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Department of Pathobiology, University of Guelph, Guelph, ON, Canada

9:00  P3028  The suppression of mir-16 maturation induced by 54-bp insertion activates a novel feedback regulatory via the insulin signaling pathway.  
  X. Jia*, J. Xu1, Q. Nie2, X. Zhang2, and S. J. Lamont3, 1South China Agricultural University, Guangzhou, China, 2Iowa State University, Ames, 3College of Animal Science, South China Agricultural University, Guangzhou, China

9:15  P3026  RNA silencing – targeted transcriptome of porcine alveolar macrophages upon infection with porcine respiratory and reproductive syndrome viruses (PRRSV) of different virulence.  
  S. Pollet1, P. Renson1, F. Jaffrezic1, G. Marot1, M. Moroldo1, J. Lecardonnel1, O. Bourry2, and E. Giuffra1, 1GABI, INRA, AgroParisTech, Université Paris Saclay, 78350 Jouy en Josas, France, 2ANSES, Unité Virologie Immunologie Porcines, 22440 Ploufragan, France, 3EA 2694 Biostatistiques, Université de Lille, Inria Lille Nord Europe, MODAL, 59650 Villeneuve d’Ascq, France
9:30  P3006  Integrated network multi-omics approach highlights muscle late fetal maturation process.  
V. Voillet1, M. San Cristobal1, L. Lefaucheur2, and L. Liaubet1, 1INRA UMR 1388 GenPhySE, Castanet-Tolosan, France  
2INRA, Saint-Gilles, France

9:45  P8005  Genes responding to recent selection in Berkshire and Duroc pigs.  
K. D. Song1, D. Shin2, and H.K. Lee2, 1The Animal Molecular Genetics and Breeding Center, Chonbuk National University, Jeonju, The Republic of Korea, 2Department of Animal Biotechnology, Chonbuk National University, Jeonju, The Republic of Korea

10:00  Business meeting.

10:15  Break.

10:30  P3051  Comparative aspects of functional annotation of genomes in the FAANG project.  
Christopher K. Tuggle and the FAANG Consortium, Iowa State University, Ames

11:00  P1037  Predicting regulatory SNPs within enhancers and promoters in cattle.  
Q. Nguyen, R. L. Tellam, J. Kijas, W. Barendse, and B. P. Dalrymple*, CSIRO Agriculture, Brisbane, Australia

11:15  P1042  Combining RNA sequencing technologies to annotate the bovine genome.  
D. E. Hagen1, D. R. Unni, and C. G. Elsk, University of Missouri, Columbia

11:30  P8002  A genomic landscape of mitochondrial DNA insertions in the nuclear pig genome.  
G. Schiavo1, O. I. Hoffmann1, A. Ribani1, V. J. Utzeri1, M. C. Ghionda1, S. Bovo1, and L. Fontanesi1, 1Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 2Agricultural Biotechnology Center, Godollo, Hungary

11:45  P8001  3D nuclear positioning of IGF2 alleles and trans interactions with imprinted genes.  
Y. Lahbib-Mansais1, M. Marti Marimon1, V. Voillet1, F. Mompart1, J. Riquet1, S. Foissac1, D. Robelin1, H. Acloque1, Y. Billon2, N. Villa-Vialaneix3, L. Liaubet1, and M. Bouissou Matet Yerle1, 1INRA UMR 1388 GenPhySE, Castanet-Tolosan, France, 2INRA UE 1372 GenESI, Surgères, France, 3INRA UR0875 MIAT, Castanet-Tolosan, France

Workshop: Genetics & Genomics of Aquaculture Species  
8:30 - 12:00

Chair: Björn Höyheim, Norwegian University of Life Sciences  
Sponsor: Illumina  
Canyon A

8:30  Welcoming Remarks.

8:31  P4030  Diversity and linkage disequilibrium in farmed Tasmanian Atlantic Salmon.  
J. Kijas1, P. D. Kube2, B. Evans3, N. Botwright4, H. King5, C. Primmer6, and K. Verbyla7, 1CSIRO Agriculture, Brisbane, Australia, 2CSIRO, Hobart, Australia, 3SALTAS, Hobart, Australia, 4CSIRO, Brisbane, Australia, 5CSIRO Agriculture, Hobart, Australia, 6University of Turku, Turku, Finland, 7Data 61, Canberra, Australia

8:45  P4035  Exploiting genomic data of Spanish Atlantic salmon to identify genes involved in sex determination and to estimate effective population size.  
M. Saura1, A. Chiotou2, A. I. Fernández3, P. Morán4, M. P. Kent5, and B. Villanueva6, 1INIA, Madrid, Spain, 2Universidad Politécnica de Valencia, Valencia, Spain, 3Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, 4Universidad de Vigo, Vigo, Spain, 5Center for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences (IHA), Norwegian University of Life Sciences (NMBU), As, Norway

9:00  P6044  Genomics assisted introgression of viral resistance in commercial common carp strains.  
R. Tadmor-Levi1, E. Asulin1, G. Halata2, and L. David1, 1The Hebrew University of Jerusalem, Rehovot, Israel, 2Agricultural Research Organization, Beit-Dagan, Israel

9:15  P4065  MicroGBS - High-throughput microsatellite genotyping using Illumina sequencing platforms.  
G. Waldbieser*, USDA, ARS, Warmwater Aquaculture Research Unit, Stoneville, MS

9:30  P4021  Genomic patterns of differentiation in native and introduced populations of the cupped oysters Crassostrea gigas and Crassostrea angulata and in hybrid progenies.  
S. Lapègue1, P. A. Gagnaire2, J. B. Lamy2, F. Cornette2, S. Heartebise2, E. Flahauv2, L. Dégremont1, M. T. Augé1, P. Boudry1, and N. Biern2, 1Ifremer, SG2M-LGPM, Laboratoire de Génétique et Pathologie des Mollusques Marins, La Tremblade, France, 2ISEM - CNRS, UMR5554, SMEL, Sète, France, 3Ifremer, Physiologie Fonctionnelle des Organismes Marins, UMR LEMAR, Brest, France
9:45  P4072  Development of a 55K SNP array for oysters (C. gigas and O. edulis).
A. P. Gutierrez1, F. Turner2, T. P. Bean3, K. Gharbi4, and R. D. Houston5, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 2Edinburgh Genomics, University of Edinburgh, Edinburgh, United Kingdom, 3Center for Environment Fisheries and Aquaculture Science, Cefas Weymouth Laboratory, Weymouth, United Kingdom

10:00 Break.

10:30 S0120  Understanding the biology behind selective improvement of rainbow trout for commercially important traits.
K. Overturf6, USDA-ARS, Hagerman, ID

11:00 P3031  Toward resolving long noncoding RNAs in fish: Identification, mapping and association to disease using strand-specific RNA-seq in rainbow trout fed alternative diets.
J. Abernathy7 and K. Overturf, USDA-ARS, Hagerman, ID

11:15 P4038  Whole genome semiconductor based sequencing of farmed European sea bass (Dicentrarchus labrax) using a DNA pooling approach identifies putative selection signatures in Mediterranean genetic stocks.
C. Geraci8, F. Bertolini9, G. Schiavo8, M. T. Sardina10, V. Chiofalo11, and L. Fontanesi8, 8Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 9Department of Animal Science, Iowa State University, Ames, 10Palermo University, Palermo, Italy, 11Messa University, Messina, Italy

11:30 Business meeting.

11:45 Concluding Remarks.

**Workshop: Livestock Genomics for Developing Countries**
8:30 - 12:00

**Chair: Ntanganedzeni Olivia Mapholi, Agricultural Research Council**
Grand Ballroom B

8:30  S0124  Indigenous stocks as treasure troves for sustainable livestock production in the 21st century: insights from small ruminant genomics.

9:15 P5004  Identification of signatures of selection and assessing the diversity of East African Shorthorn zebu mitochondrial DNA.
H. Bahbahani1*, J. Mwacharo2, and O. Hanotte1, 1Kuwait university, Kuwait, Kuwait, 2International Livestock Research Institute, Addis Ababa, Ethiopia, 3School of Life Sciences, University of Nottingham, Nottingham, United Kingdom

9:30 P4010  Investigation of maternal lineages and genetic diversity of South African goat (Capra hircus) populations using complete Mitochondrial DNA Sequences.
K. T. Ncube6*, Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa

9:45 P1011  Temporal changes for genomic diversity for poultry conservation population based on genome-wide SNP data.
W. Li1*, M. Zhang1, W. Han2, and K. Wu3, 1China Agricultural University, Beijing, China, 2National Chickens Genetic Resources, Yangzhou, China

10:00 Break.

10:30 P4018  Effective population size and inbreeding in South African indigenous chicken populations: Implications for management and conservation of unique genetic resources.
B. Mtileni1*, K. Dzama2, K. Nephawe3, and C. Rhode1, 1Tswane University of Technology, Pretoria, South Africa, 2University of Stellenbosch, Stellenbosch, South Africa, 3Tshwane University of Technology, Pretoria, South Africa, 4University of Stellenbosch, Cape Town, South Africa

10:45 P4026  Discrimination of native chicken breeds using SNP markers selected from the 600K chip data.
11:00 P4022 Genetic diversity of Mexican cattle Lidia breed and its relationships with Spanish populations through bovine SNP 50K beadchip.  
P. G. Eusebi¹, J. Canon², and O. Cortés³, ¹Universitat Autònoma de Barcelona. Faculty of Veterinary, Bellaterra, Spain, ²Universidad Complutense, Madrid, Spain, ³Universidad Complutense de Madrid, Madrid, Spain

11:15 P5062 Comparative genomics reveal common diversity and signature of positive selection in West African taurine cattle populations.  
A. Tijjani¹,², J. Kim¹, H. Kim¹, R. Mrode¹, and O. Hanotte¹,², ¹School of Life Sciences, University of Nottingham, Nottingham, United Kingdom, ²National Biotechnology Development Agency (NABDA), Abuja, Nigeria, ³National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, ³Seoul National University, Seoul, South Korea, ³International Livestock Research Institute, Nairobi, Kenya

11:30 Discussion.
11:45 Concluding Remarks.

ORAL SESSIONS & WORKSHOPS — Wednesday, July 27

Plenary Session: Genetic Diversity and Adaptation  
8:30 - 10:00
Chairs: Ntanganedzeni Olivia Mapholi, Agricultural Research Council; Leslie Lyons, University of Missouri-Columbia  
Sponsor: ISAG  
Grand Ballroom A/B

8:30 S0111 Genomics of South American wild cats: Insights into evolutionary history and adaptation.  
E. Eizirik¹, Laboratory of Genomics and Molecular Biology, Faculdade de Biociências, PUCRS, Porto Alegre, Brazil

9:15 S0112 Applications of genomics to address adaptation of livestock to stressful environments to prevent food insecurity in the developing world.  
M. F. Rothschild¹, Department of Animal Science, Iowa State University, Ames

Plenary Session: Steve Bishop Memorial Session on Animal Disease Genetics  
10:30 - 12:00
Chairs: Alan L. Archibald, The Roslin Institute and R(D)SVS; University of Edinburgh; Joan K. Lunney, USDA ARS BARC APDL  
Sponsor: ISAG  
Grand Ballroom A/B

10:30 S0113 Unraveling the contribution of host genetics to infectious disease.  
A. B. Doeschl-Wilson¹, The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom

11:15 S0114 Genetic basis of resistance to infectious disease in aquaculture species.  
R. D. Houston¹, The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom
POSTER PRESENTATIONS — Sunday, July 24

Genetic Markers and Selection I
7:30 - 8:30
Alpine Ballroom

P5065  1 Comparison of SNP and haplotype models for genome-wide association studies for feed efficiency traits in crossbred beef cattle.
K. R. Schweer1, S. D. Kachman1, L. A. Kuehn1, and M. L. Spangler1, 1University of Nebraska-Lincoln, 2USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

P5053  2 Test duration for feed and water intake in beef cattle using an Insentec system.
C. M. Ahlberg1, C. R. Krebs4, C. J. Richards1, S. E. Place1, U. Desilva1, D. L. VanOverbeke1, R. Mateescu1, J. A. Reed1, K. Allwardt1, A. Taylor1, and M. Rolf1, 1Oklahoma State University, Stillwater; 2University of Florida, Gainesville

P5054  3 Characterization of a region within bovine chromosome 6 associated with gray coat color in a Nellore-Angus cross.
K. Scienski1, P. W. Holland1, J. O. Sanders1, D. G. Riley1, and C. A. Gill1, 1Texas A&M University, College Station, 2Department of Animal Science, Texas A&M University, College Station

P5055  4 Association between g.98535683A>G:BTaU7 marker the CAST gene and meat characteristics of Nellore cattle (Bos indicus) and their crosses with Bos taurus.
L. A. L. Chardulo1, R. A. Curi1, H. N. Oliveira2, J. A. I. V. Silva1, G. L. Pereira2, C. E. Enríquez-Valencia2, J. M. Malheiros3, and E. C. Nadalim1, 1Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu-SP, Brazil; 2Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista, Jaboticabal-SP, Brazil; 3State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil

P5056  5 Genome-wide association study for stayability measures in Nellore-Angus crossbred cows.
B. N. Engle*, A. D. Herring, J. E. Sawyer, D. G. Riley, J. O. Sanders, and C. A. Gill, Department of Animal Science, Texas A&M University, College Station

P5057  6 Use of genomics to simultaneously improve feed efficiency and meat quality in grow-finish pigs.
C. Zhang1, R. A. Kemp2, N. J. Boddicker3, J. C. M. Dekkers3, Z. Wang4, and G. Plastow4, 1University of Alberta, Edmonton, AB, Canada, 2Genesus Inc, Lethbridge, AB, Canada, 3Department of Animal Science, Iowa State University, Ames, 4Livestock Genetec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada

P5058  7 The Ovar-DRB1 *0404 haplotype is associated with growth and lifetime prolificacy ewe traits.
M. U. Cinar1, M. R. Mousel2, J. O. Reynolds1, L. M. Hermann-Hoesing1, J. B. Taylor4, D. P. Knowles3, and S. N. White1,5,6, 1Washington State University College of Veterinary Medicine, Pullman, 2USDA, ARS, Animal Disease Research Unit, Pullman, 3USDA, ARS, Animal Disease Research Unit, Pullman, 4USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID, 5USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID, 6Washington State University, Pullman, 6Center for Reproductive Biology, Washington State University, Pullman

P5059  8 Ovine MYADM-like repeat gene association with lifetime cumulative ewe production and wool traits.
M. U. Cinar1, M. R. Mousel1, M. V. Gonzales1, J. O. Reynolds1, J. B. Taylor1, D. P. Knowles3, and S. N. White1, 1Washington State University College of Veterinary Medicine, Pullman, 2USDA, ARS, Animal Disease Research Unit, Pullman, 3USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID, 4Washington State University, Pullman, 5Center for Reproductive Biology, Washington State University, Pullman

P5060  9 The effect of selection over years on breed composition in tropical composite cattle.
L. R. Porto-Neto1, S. Harburg2, R. Bunch1, R. E. Lyons3, S. A. Lehnert1, and A. Reverter4, 1CSIRO Agriculture, Brisbane, Australia, 2North Australian Pastoral Company, Brisbane, Australia, 3University of Queensland, Gatton, Australia

P5061  10 Association study between SNPs of the genes within bovine QTLs and meat quality of Hanwoo.
D. Yoon* and E. Ko, Department of Animal Science, Kyungpook National University, Sangju, South Korea

P5062  11 Comparative genomics reveal common diversity and signature of positive selection in West African taurine cattle populations.
A. Tijjani1,2, J. Kim1, H. Kim1, R. Mrode4, and O. Hanotte1,2,3, 1School of Life Sciences, University of Nottingham, Nottingham, United Kingdom, 2National Biotechnology Development Agency (NABDA), Abuja, Nigeria, 3National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 4Seoul National University, Seoul, South Korea, 5International Livestock Research Institute, Nairobi, Kenya

P5063  12 The effect of the IG2F gene on pork and fat quality traits in two populations of the South African Landrace and Large White pig breeds.
P. D. Soma*, Agricultural Research Council, Animal Production Institute, Pretoria, South Africa
Accuracy of genome-wide predictions of heterosis in beef cattle using 50K genotypes.
E. C. Akanno¹, L. Chen², C. Li³, M. K. Abou-Ismaïl⁴, J. Basarab⁵, and G. Plastow⁶, ¹Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, ²Animal and Poultry Production, Damanhour University, Damanhour, Egypt, ³Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada

Genetics and disease I
8:30 - 12:00
Alpine Ballroom

Whole genome sequencing of canine family trios to identify rare alleles for Mendelian diseases.
S. Mäkeläinen*, G. Andersson, and T. F. Bergström, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

Effectively managing bovine genetic disease risk via genotyping the Irish national herd.
M. C. McClure¹, M. Mullen², S. M. Waters³, F. Kearney⁴, J. McClure⁴, P. Flynn⁴, and R. Weld⁵, ¹Irish Cattle Breeding Federation, Bandon, Ireland, ²Athlone Institute of Technology, Athlone, Ireland, ³Teagasc Grange, Meath, Ireland, ⁴Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, ⁵Weatherbys Ireland, Naas, Ireland

Evaluating the metagenome of nasal samples from cattle with bovine respiratory disease complex (BRDC).
T. G. McDaniel¹, L. A. Kuehn, and J. W. Keele, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

The use of Kosher phenotyping for mapping QTL affecting susceptibility to bovine respiratory disease.
E. Lipkin¹, M. G. Strillacci², H. Eitam³, M. Yishay¹, F. Schiavini³, M. Soller¹, A. Bagnato³, and A. Shabtay⁴*, ¹Hebrew University of Jerusalem, Jerusalem, Israel, ²Università degli Studi di Milano, Milano, Italy, ³Department of Ruminant Sciences, Agricultural Research Organization (ARO), Bet-Dagan, Ramat Yishai, Israel, ⁴Department of Ruminant Sciences, Agricultural Research Organization (ARO), Newe Ya’ar Research Center, Ramat Yishai, 30095, Israel

Estimation of heritability for fracture in the Thoroughbred racehorse.
T. Tozaki¹, T. Miyake², M. Kikutchi¹, H. Kakoi¹, K. I. Hirota¹, and S. I. Nagata¹, ¹Laboratory of Racing Chemistry, Utsunomiya, Japan, ²Comparative Agricultural Sciences, Kyoto University, Kyoto, Japan

Diversity of Toll-Like Receptor genes in the indigenous Czech cattle breeds.
K. Novák¹, V. Czerneković¹, A. E. Kalashnikov¹, and V. Müllövš¹, ¹Institute of Animal Science, Prague, Czech Republic, ²L.K. Ernst Research Institute of Animal Husbandry, Dubrovice, Russian Federation

The cytokines expression in the milk somatic cells of goats infected with small ruminant lentivirus.
J. Jaraczak¹, E. Kościuczuk², J. Kaba³, D. Sloniewska³, and E. Bagnicka¹, ¹Institute of Genetics and Animal Breeding, Jastrzębiec, Poland, ²Robert H. Lurie Comprehensive Cancer Center of Northwestern University, Chicago, IL, ³Warsaw University of Life Sciences, Faculty of Veterinary Medicine, Warsaw, Poland, ²Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzębiec, Poland

Cell-type dependent immune response post porcine reproductive and respiratory syndrome virus infection.
M. J. Proll¹, C. Neuhoff¹, C. Grosse-Brinkhaus¹, M. A. Müller², C. Drosten³, M. J. Uddin¹, D. Tesfaye¹, E. Tholen¹, and K. Schellander¹, ¹Institute of animal science, University of Bonn, Bonn, Germany, ²Institute of Virology University of Bonn Medical Centre, Bonn, Germany, ³School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia, ²Institute of Animal Science, University of Bonn, Bonn, Germany

Genomic basis of Lipomatous Myopathy in Piedmontese beef cattle.
S. Peletto¹, M. T. Capuccchio¹, M. G. Strillacci¹, C. Boin¹, E. Biasibetti¹, P. Modesto¹, F. Schiavini¹, P. L. Acutis¹, and A. Bagnato¹*, ¹Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d’Aosta, Torino, Italy, ²Università degli Studi di Torino, Torino, Italy, ³Università degli Studi di Milano, Milano, Italy

Focus on atherosclerosis and the pig as a model to identify genes affecting cholesterol and other plasma lipid levels.
P. Karlsvik-Mortensen¹, S. D. Frederiksen, S. D. Pant, S. Cirera, C. B. Jørgensen, C. S. Bruun, T. Mark, and M. Fredholm, Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark

Identification of novel genetic variants in the equine collagenous lectin genes through targeted, next generation re-sequencing.
R. S. Fraser¹, A. Meyer², L. G. Arroyo³, J. D. Hammermueller¹, and B. N. Lillie¹, ¹Department of Pathobiology, University of Guelph, Guelph, ON, Canada, ²Ontario Institute for Cancer Research, Toronto, ON, Canada, ³Department of Clinical Studies, University of Guelph, Guelph, ON, Canada
Bioinformatics, Statistical Genetics, and Genomic Technologies I
7:30 - 8:30
Alpine Ballroom

P1000 25  Genomic imputation of a multigenerational Nellore-Angus mapping population.
C. A. Gill*, Texas A&M University, College Station

P1001 26  SNP calling in transcriptome of Holstein cows and their contribution in genetic variance of residual feed intake.
M. H. Banabazi*, A. Nejati Javaremi*, I. G. Inumori*, M. Ghaderi-Zefreh*, and S. R. Mirael Ashtani*1, 2University of Tehran, Karaj, Iran (Islamic Republic of), 3University of Tehran, Karaj, Iran (Islamic Republic of), 4Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY, 5University of Yassou, Yassou, Iran

P1002 27  Evolution of hypothalamus-pituitary growth axis among fish, amphibian, birds and mammals.
M. Moaeen-ud-Din*, PMAS-Arid Agriculture University, Rawalpindi, Pakistan

P1003 28  MiRNAs expression profiling of Myostatin transgenic and wild type littermate mice by Solexa deep sequencing.
R. Javed*, Huazhong Agricultural University, Wuhan, China

P1004 29  Genotyping in thousands by sequencing (GT-seq): A low cost, high-throughput, targeted SNP genotyping method.
N. Campbell*, S. Harmon, and S. R. Narum, Columbia River Inter-Tribal Fish Commission, Hagerman, ID

P1005 30  Genome-wide association study identifies a QTL for fat percentage in rib-eye area on BTA10 in Japanese Black cattle.
A. Inoue*, T. Nakajima1, A. Nakajima1, Y. Uemoto2, M. Fukushima3, E. Yoshida4, E. Iwamoto4, 1Takamatsu University, Takamatsu, Japan, 2National Livestock Breeding Center, Nishigo, Japan, 3Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, Asago, Japan, 4Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, Kasa, Japan, 5Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, 6Food Resources Education & Research Center, Kobe University, Kasa, Hyogo, Japan

P1006 31  Identification of polymorphisms associated with oleic acid percentage by pool-based genome wide association study in Japanese Black cattle.
F. Kawaguchi*, A. Nakajima1, Y. Matsumoto1, Y. Uemoto2, M. Fukushima3, E. Yoshida4, E. Iwamoto4, T. Akiyama1, N. Kohama1, E. Kobayashi1, K. Oyama1, T. Honda1, H. Mannen1, and S. Sasazaki1, 1Graduate School of Agricultural Science, Kobe University, Kobe, Japan, 2National Livestock Breeding Center, Nishigo, Japan, 3Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, Asago, Japan, 4Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, Kasa, Japan, 5Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, 6Food Resources Education & Research Center, Kobe University, Kasa, Hyogo, Japan

P1007 32  Genetic and protein study of alpaca fibre.
Y. T. Wong*, Deakin University, Geelong, Australia

P1008 33  Genetic diversity and origin of mtDNA haplogroup P observed in Japanese Shorthorn.
A. Noda*, S. Sasazaki1, H. Mannen1, 1Kobe university, Kobe, Japan, 2Graduate School of Agricultural Science, Kobe University, Kobe, Japan

Genetic Diversity and Polymorphisms I
7:30 - 8:30
Alpine Ballroom

P4000 34  Specific polymorphisms in mitochondrial region D-loop of the Tunisian domestic goat.
Y. M. Ressaissi1, ISA-Chott Mariem, TUNIS, Tunisia

P4001 35  Molecular analysis of genetic variability in Egyptian buffalo using microsatellite DNA markers.
S. Abou Bakr1, 2, M. Atia1, A. A. Nigm1, S. Abdelghany2, and N. Abdallah4, 1Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt, 2animal Production dept. faculty of agriculture Cairo University, giza, Egypt, 3animal production dept. faculty of agriculture Cairo University, giza, Egypt, 4Genetic dept. faculty of agriculture Cairo University, Giza, Egypt

P4002 36  Genetic polymorphisms of caprine stearoyl-coA desaturase (SCD) gene and their relationship with blood cholesterol and triglyceride of goats for meat in southern Thailand.
C. Supakorn*, Walailak University, Tha sala, Thailand
P4003 37 Variations of Adipocyte Fatty-Acid Binding Protein (A-FABP) gene in Chinese sheep.  
W. Yan*, L. Xu, J. Hu, and Y. Luo, Gansu Key Laboratory of Herbivorous Animal Biotechnology, Gansu Agricultural University, Lanzhou, China

P4004 38 Polymorphism information content as a measure of the usefulness of microsatellites for genetic analysis.  
L. H. McClean*, The University of the West Indies, Cave Hill Campus, Bridgetown, Barbados

P4005 39 Associations of SNPs in hormone-sensitive lipase-like gene 5' terminal-sequences with fatty acid content in longissimus muscle of Chinese Simmental steers.  
X. Fang*, R. Yang, H. Xiao, P. Jiang, Y. Yang, and Z. Zhao, College of Animal Science, Jilin University, Changchun, China

P4006 40 Equine Major Histocompatibility Complex Class II region: Long-read sequencing and annotation of nine Bacterial Artificial Chromosome clones.  
A. Viluma*, S. Mikko, T. F. Bergström, and G. Andersson, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

P4007 41 High genetic diversity and distribution of Bubu-DQA alleles in swamp buffaloes (Bubalus bubalis carabensis): Identification of new Bubu-DQA loci and haplotypes.  
S. K. Mishra*, Gautam Buddha University, Gr. Noida, India; National Bureau of Animal Genetics Resource, Karnal, India

P4008 42 Genome-wide copy number variation in the bovine genome detected using low coverage sequence of popular beef breeds.  
B. N. Keel*, W. M. Snelling, and J. W. Keele, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

P4009 43 Diversity of West African dwarf goat in southwestern Nigeria based on allozyme markers.  
O. K. Awobajo*, Tai Solarin University of Education, Ijebu-Ode, Nigeria

P4010 44 Investigation of maternal lineages and genetic diversity of South African goat (Capra hircus) populations using complete Mitochondrial DNA Sequences.  
K. T. Ncube*, Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa

P4011 45 Analysis of cytochrome b gene variations shows that Amami rabbit (Pentalagus furnessi) and European rabbit (Oryctolagus cuniculus) have close genetic structure.  
R. Ashidate1, T. Kurakishi2, and Y. Mizoguchi3, 1School of Agriculture, Meiji university, Kawasaki, Japan, 2Amami Laboratory, The Institute of Medical Science, The University of Tokyo, Kagoshima, Japan, 3School of Agriculture, Meiji University, Kawasaki, Japan

P4013 47 Applicability of using bovine, ovine and caprine SNP chips for alpaca and dromedary genomic studies.  
F. Bertolini1, A. Elbeltagy1,2, F. A. Ponce de Leon1, G. A. Gutiérrez2, and M. F. Rothschild1, 1Department of Animal Science, Iowa State University, Ames, 2Department of Animal Science, University of Minnesota, St. Paul, 3Department of Animal Production, Universidad Nacional Agraria La Molina, Lima, Peru

**Functional Genomics I**  
7:30 - 8:30  
Alpine Ballroom

P3000 48 Variation of goat interferon regulatory factor 3 gene and its implication in goat evolution.  
M. Okpeku1,2, A. Esmaeilzadeh1,3, A. C. Adeola1, L. Shu1, Y. Zhang1, Y. Wang2, T. M. Sanni4, I. G. Imumorin5, S. O. Peters6, J. Zhang7, Y. Dong2,3, and W. Wang2, 1Department of Animal Science, Niger Delta University, Wilberforce Island, Nigeria, 2State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences (CAS), Kunming, China, 3Department of Animal Science, Shahid Bahonar University of Kerman, Kerman, Iran (Islamic Republic of), 4Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Nigeria, 5Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY, 6Department of Animal Science, berry College, mount Berry, GA, 7School of Science and Information Engineering, Yunnan Agricultural University, Kunming, China, 4Laboratory of Applied Genomics and Synthetic Biology, College of Life Science, Kunming University of Science and Technology, Kunming, China

P3001 49 Transcriptomic signature of high dietary selenium supplementation In sheep: A nutrigenomic insight using a custom microarray platform and gene set enrichment analysis.  
R. Elgendy1, M. Giantin1, F. Castellani2, L. Grotta2, F. Palazzo1, M. Dacasto1, and G. Martino2, 1University of Padova, Padova, Italy, 2University of Teramo, Teramo, Italy, 3Parco Tecnologico Padano, Lodi, Italy

P3002 50 Functional annotation of the equine genome.  
C. J. Finno1, J. L. Petersen1, R. Bellone1, and J. N. MacLeod1, 1University of California-Davis, 2University of Nebraska-Lincoln, 1University of Kentucky, Lexington
The extent of cis-regulation of gene expression and its influence on complex trait variation in cattle.  
Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia; Dairy Futures Cooperative Research Centre, Bundoora, Australia; University of Melbourne, Parkville, Australia; La Trobe University, Bundoora, Australia; Department of Economic Development, Jobs, Transport and Resources, Ellinbank, Australia; NSW Department of Primary Industries, Menangle, Australia.

Differential expression of microRNAs in synovial fluid as biomarkers of osteochondrosis in equine hock joints.  
GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; Veterinary Clinic of Grosbois, Boissy St Léger, France; Université Paris-Est, Ecole Nationale Vétérinaire d’Alfort, Maisons-Alfort, France.

Genome-wide transcriptomic analysis of liver in sex-linked Dwarf and wild type chickens.  
INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France; UPMC, LPMA, Paris, France; INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy en Josas, France; GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy en Josas, France.

Integrated network multi-omics approach highlights muscle late fetal maturation process.  
INRA UMR 1388 GenPhySE, Castanet-Tolosan, France; INRA, Saint-Gilles, France.

Time course of the response to ACTH in pig: Biological and transcriptomic study.  
INRA UMR 1388 GenPhySE, Castanet-Tolosan, France; INRA UMR 1331 ToxAlim, Toulouse, France; INRA UE 1372 GenESI, Surgères, France; INRA UR 0875 MIAT, Castanet-Tolosan, France.

Transcriptome profiling of reproductive tissues characterizes genetic basis of the prolificacy traits in sheep (Ovis aries).  
Natural Resources Institute Finland (Luke), Jokioinen, Finland; Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland; Green Technology, Natural Resources Institute Finland (Luke), Jokioinen, Finland; Pro Agria Rural Advisory Centre, Tampere, Finland; Institute of Zoology, Chinese Academy of Sciences (CAS), Beijing, China.

Polymorphisms of NELL1 and RNCK1 in relation to porcine growth, carcass and meat quality traits.  
Institute of Animal Science, University of Bonn, Bonn, Germany; Institute of Animal Science, University of Bonn, Bonn, Germany; School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia; Faculty of Agriculture, Melikgazi Kayseri, Turkey.

Genome Editing and Transgenic Animals  
7:30 - 8:30  
Alpine Ballroom
P7005  63  Characterization of RNA editing on porcine NR3C1, COG3 and ACSM2B genes.

P7006  64  Generation of a porcine model of obesity and complications by Leptin knockout.
T. Tan*, Y. Xing, X. Hu, and N. Li, The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China, *China Agricultural University, Beijing, China

P7007  65  Targeted IGF1 promoter modification in mice using small intestine-specific regulatory element binding sites.
Y. Zheng*, R. Zhang, Z. Yu, and N. Li, China Agricultural University, Beijing, China

P7008  66  Characterization of CD163 modification pig for PRRSV resistance.
J. Chen*, N. Li, Y. Zhao, X. Hu, and Y. Xing, China Agricultural University, Beijing, China

P7009  67  Precancerous molecular features committing development of colonic polyps revealed by studies on the porcine model of human familial adenomatous polyposis.
T. Flisikowska, M. Stachowiak*, C. Wander, A. Wagner, C. Wurmser, A. Perkowska, F. Brüning, S. Bauersachs, A. Kind, R. Fries, M. Switonski, K. Flisikowska, and A. Schnieke, Technische Universität München, Freising, Germany, *Department of Genetics and Animal Breeding, Poznan University of Life Sciences, Poznań, Poland, Chair of Livestock Biotechnology, Technische Universität München, Freising, Germany, Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland, Klinikum Rechts der Isar II, Technische Universität München, Munich, Germany

P7010  68  Generation of a novel glycosylated anti-CD20 monoclonal antibody in milk of transgenic cattle.
R. Zhang*, Y. Dai, J. Wang, B. Tang, and N. Li, China Agricultural University, Beijing, China, *Beijing Genprotein Biotechnology Company, Beijing, China

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**Genetic Markers and Selection II**

**13:00 - 14:00**

Alpine Ballroom

P5000  1  Confirmation of genome-wide associations for clinical mastitis in German Holstein cattle.
H. Abdel-Shafy*1,2, R. H. Bortfeldt3, M. Reißmann1, and G. A. Brockmann4, Department for Crop and Animal Sciences, Humboldt-Universität zu Berlin, Berlin, Germany, *Department of Animal Production, Faculty of Agriculture, Cairo University, Cairo, Egypt, ‘Akreth Daniel Thaer-Institut for Agricultural and Horticultural Sciences, Faculty of Life Sciences, Humboldt-Universität zu Berlin, Berlin, Germany

P5001  2  Molecular exploration of genetic resistance in riverine buffalo.
M. Javed* and A. Nadeem, University of Veterinary & Animal Sciences, Lahore, Pakistan

P5002  3  You say variation, they say mutation, we say confusion - Genetic communication, why it needs standardisation!.
G. Sofronidis*, Orivet Genetic Pet Care, Melbourne, Australia

P5003  4  Genome-wide association for calving interval in buffaloes.
G. M. de Camargo*1, R. R. Aspilcueta Borquís2, D. J. A. Santos1, D. F. Cardoso1, N. Hurtado-Lugo2, and H. Tonhati2, *Universidade Tecnológica Federal do Paraná, Brazil, Dois Vizinhos, Brazil, *State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, Sao Paulo State University, Jaboticabal, Brazil, Fundação de Amparo à Pesquisa do Estado de São Paulo -FAPESP(Bolsista), Sao Paulo, Brazil

P5004  5  Identification of signatures of selection and assessing the diversity of East African Shorthorn zebu mitochondrial DNA.
H. Bahbahani*3, J. Mwacharo2, and O. Hanotte1, *Kuwait university, Kuwait, Kuwait, *International Livestock Research Institute, Addis Ababa, Ethiopia, School of Life Sciences, University of Nottingham, United Kingdom

P5005  6  Hitchhiking effects influence allele frequencies and exclusion probabilities of microsatellites used for parentage control in Holstein Friesian cattle.
B. Brenig and E. Schütz, Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany

P5006  7  Genome-wide linkage analysis of fatty acid composition in the F2 intercross between Landrace and Korean native pigs.
Y. Ramayo-Calda*, G. Renand, M. Ballester, R. Saintilan, and D. Rocha, GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, 2GABI, INRA, AgroParisTech, Université Paris-Saclay, 78352, Jouy en Josas, France, 3Département de Génétique i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain, 4INRA UMR 1313 GABI, Jouy-en-Josas, France

P5008  An initial exploration on the genetic variability of a selection sweep region on OAR6 by exploiting massive genome sequencing of dairy and meat breeds.
P. K. Chitneedi*, B. Gutiérrez-Gil, C. Esteban-Blanco, and J. J. Arranz, 1University of León, León, Spain, 2Supercomputing Center of Castilla y León, León, Spain

P5009  A genome-wide association analysis for carcass and meat quality traits in Duroc pigs.
R. González, P. G. Eusebi, R. Quintanilla, T. Figueiredo, A. Manunza, J. L. Noguera, A. Clop, and M. Amills*, 1Center for Research in Agricultural Genomics, Bellaterra, Spain, 2Universitat Autònoma de Barcelona. Faculty of Veterinary, Bellaterra, Spain, 3IRTA, Caldes de Montbui, Spain, 4IRTA, Lleida, Spain, 5Center for Research in Agricultural Genomics (CRAG), Cerdanyola del Valles (Barcelona), Spain

P5010  Optimization of a genomic breeding program for a moderately sized dairy cattle population.
J. I. Weller*, A. Reiner-Benaim, and E. Ezra, 1ARO, The Volcani Center, Bet Dagan, Israel, 2Israel Cattle breeders Association, Caesarea, Israel, 3Israel Cattle Breeders Association, Caesarea, Israel

P5011  Fine mapping the QTL for growth traits in outbred chicken advanced intercross lines by improved ddGBS.
Y. Wang, X. Cao, X. Gu, and X. Hu, China Agricultural University, Beijing, China

P5012  Integrative analysis of metabolomic, proteomic and genomic data to reveal functional pathways and candidate genes for drip loss in pigs.
J. Welzenbach*, C. Grosse-Brinkhaus, C. Neuhoff, C. Looff, K. Schellander, and E. Tholen, 1Institute of Animal Science, University of Bonn, Bonn, Germany, 2Institute of Animal Science, University of Bonn, Bonn, Germany

Genetics and Disease II
13:00 - 14:00
Alpine Ballroom

P6011  Transcriptome profiling of the peripheral blood mononuclear cells following PRRSV vaccination in Pietrain pig.

P6012  Use of targeted next generation re-sequencing in the identification of polymorphisms in the bovine collagenous lectin gene family.
R. S. Fraser*, J. D. Hamermueller, J. S. Lumsden, M. A. Hayes, and B. N. Lillie, Department of Pathobiology, University of Guelph, Guelph, ON, Canada

P6013  Identifying driver mutations for Marek’s disease lymphomas in chicken using integrated genomic screens.
A. Steep, H. Xu, Y. Zhang, A. Black Pykorsz, M. E. Delany, D. Frishman, and H. H. Cheng, 1Michigan State University, East Lansing, 2Technische Universität München, Freising, Germany, 3USDA, ARS, ADOL, East Lansing, MI, 4University of California-Davis

P6014  Mapping and exome sequencing of a weak calf syndrome with premature birth.
T. Hirano*, A. Okazaki, S. Sasaki, Y. Suzuki, H. Harada, Y. Sugimoto, and K. Hanzawa, 1Tokyo University of Agriculture, Atsugi, Japan, 2National Livestock Breeding Center, Fukushima, Japan, 3Graduate School of Frontier Sciences, University of Tokyo, Kashiwa, Japan, 4Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Fukushima, Japan

P6015  An Intrinsic MBTPS2 Variant Results in a Splicing Defect in Horses with Brindle Coat Texture.
L. Mugniano, D. Waluk, R. Towers, N. Wiedemar, J. Dietrich, V. Jagannathan, M. Drogmüller, T. Druet, A. Galicher, M. C. Penedo, E. Müller, P. Roosje, M. Welle, and T. Leeb*, 1Institute of Genetics, University of Bern, Bern, Switzerland, 2Department of Dermatology, University Hospital of Bern, Bern, Switzerland, 3Institute of Medical Genetics, Cardiff University, Cardiff, United Kingdom, 4University of Liège, Liège, Belgium, 5Department of Dermatology, University Hospital of Bern, Bern, Switzerland, 6Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, 7Division of Clinical Dermatology, Department of Clinical Veterinary Medicine, University of Bern, Bern, Switzerland, 8Institute of Animal Pathology, University of Bern, Bern, Switzerland
P6016 19 Epistatic interactions of more than two loci are involved in the rat-tail phenotype in cattle.
C. Kühn1, R. Weikard1, J. Knaust1, and F. Hadlich1, 1Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany

P6017 20 A high density genome-wide scan for genetic risk factors of insect bite hypersensitivity (IBH): A Horsegene Project Initiative.
B. D. Velče1*, M. Shrestha1, L. Francois1, A. Schurink1, A. Stinchens2, S. Blott4, B. J. Ducro4, S. Mikko1, R. Thomas5, M. Sandquis1, S. Eriksson1, N. Bays1, and G. Lindgren1, 1Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Upsala, Sweden, 2KU Leuven, Leuven, Belgium, 3Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 4University of Nottingham, Nottingham, United Kingdom, 5Exmoor Pony Society, NA, United Kingdom

P6018 21 Revealing the importance of SLA-DRB1 to post-weaning piglet survivability by a case-control analysis and subsequent validation using in silico epitope binding analysis and molecular structural modeling.
M. T. Lee*, H. J. Lee, J. Lee, and C. Park, Konkuk University, Seoul, The Republic of Korea

P6019 22 Host genetics of resistance to bovine tuberculosis infection in dairy cows.
S. Wilkinson1, S. C. Bishop1, A. R. Allen2, S. H. McBride2, R. A. Skuce2, M. Bermingham1, J. A. Woolliams1, and L. J. Glass1, 1The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom, 2Agri-Food and Biosciences Institute Stormont, Belfast BT4 3SD, United Kingdom, 3Queen’s University Belfast, Belfast BT9 7BL, United Kingdom

P6020 23 Deficiency of Trim63 leads to hypertrophic cardiomyopathy in pig.
Y. Hu1*, Y. Xing2, X. Hu3, and N. Li3, 1The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China, 2The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China, 3China Agricultural University, Beijing, China

P6021 24 The potential of serum IL-10 as a diagnostic biomarker of resilience in the domestic chicken to infection from Eimeria Spp.
K. Boulton*, Z. Wu, A. Psifidi, and D. Hume, The Roslin Institute, Edinburgh, United Kingdom

Bioinformatics, Statistical Genetics, and Genomic Technologies II
13:00 - 14:00
Alpine Ballroom

P1009 25 Sheep reference genome sequence updates: Texel improvements and Rambouillet progress.
Y. Liu1, S. C. Murali1, R. A. Harris1, A. C. English1, X. Qin1, E. Skinner1, S. Richards1, J. Rogers1, Y. Han1, V. Vee1, M. Wang1, Q. Meng2, M. P. Heaton2, T. P. L. Smith2, B. P. Dalrymple1, J. Kijas1, N. E. Cockett3, E. A. Boerwinkle4, D. M. Muzny1, R. A. Gibbs1, and K. C. Worley1*, 1Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, 2USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 3CSIRO Agriculture, Brisbane, Australia, 4Utah State University, Logan, 5University of Texas Health Science Center at Houston, TX

P1010 26 Genotype by environment interaction and genetic heterogeneity of environmental variance of body weight at harvest in Genetically Improved Farmed Tilapia (GIFT) (Oreochromis niloticus) reared in three different countries.
S. Agha1,2, W. Mekkawy1, N. Ibanez-Escriche1, J. Kumar3, A. Mandal4, C. E. Lind3, J. Benzie3, and A. B. Doeschl-Wilson3, 1The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom, 2Animal Production Department, Faculty of Agriculture, Ain Shams University, Cairo, Egypt, 3WorldFish, Penang, Malaysia, 4Rajiv Gandhi Center for Aquaculture, Tamil Nadu, India

P1011 27 Temporal changes for genomic diversity for poultry conservation population based on genome-wide SNP data.
W. Li1*, M. Zhang1, W. Han2, and K. Wu1, 1China Agricultural University, Beijing, China, 2National Chickens Genetic Resources, Yangzhou, China

P1012 28 Liver transcriptome from pre versus post-pubertal Brahman heifers.
L. T. Nguyen1,2, A. Reverter-Gomez1, A. Canovas1, B. Venus1, A. Islas-Trejo1, S. A. Lehner1, J. F. Medrano1, S. S. Moore1, and M. R. Fortes1, 1The University of Queensland, School of Chemistry and Molecular Biosciences, St Lucia, Australia, 2Vietnam National University of Agriculture, Hanoi, Viet Nam, 3CSIRO Food Futures Flagship, Brisbane, Australia, 4University of California-Davis, 5The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia, 6University of California-Davis, 7CSIRO Agriculture, Brisbane, Australia
H. Ozaki¹, T. Tamura², K. Fukazawa¹, Y. Uemoto³, M. Nishio⁴, E. Kobayashi⁴, T. Matsushashi⁴, S. Maruyama⁵, T. Honda⁶, K. Oyama⁶, S. Sasazaki⁷, and H. Mannen⁷, ¹Kobe University, Kobe, Japan, ²National Livestock Breeding Center, Nishigo, Japan, ³NAO Institute of Livestock and Grassland Science, Tsukuba, Japan, ⁴Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, ⁵Gifu Prefectural Livestock Research Institute, Kiyomi, Takayama, Gifu 506-0101, Japan., ⁶Gifu, Japan, ⁷Food Resources Education & Research Center, Kobe University, Kasai, Hyogo, Japan, ⁷Graduate School of Agricultural Science, Kobe University, Kobe, Japan

Genetic association between a missense mutation in the positional candidate gene GRIP1 and backfat thickness traits in pigs.
J. B. Lee¹, H. S. Kim¹, H. B. Park¹, C. K. Yoo¹, I. C. Cho¹, and H. T. Lim¹, ¹KoZRI, Chonbuk National University, Iksan, The Republic of Korea. ²Division of Applied Life Science (BK21 program), Gyeongsang National University, Jinju, The Republic of Korea, ³NIAS, Rural Development Administration, Jeju, The Republic of Korea, ⁴Division of Applied Life Science (BK21 program), Gyeongsang National University, Jinju, The Republic of Korea

The Caprinae Genome database: multispecies goats/sheep genome and incorporation of RNA-seq data and re-sequencing data to study comparative genomics and genome assistant breeding.
R. SU, Inner Mongolia Agricultural University China, Hohhot, China

The Pig’s other genome: a reference genome of the gut microbiome as a new resource for deep studies of the interplay between the host and its microbiome.
L. Xiao¹, J. Estellé¹, P. Kümmerli¹, Y. Ramayo-Calduy¹, Z. Xia¹, Q. Feng¹, A. O. Pedersen¹, N. J. Kjeldsen¹, E. Maguin¹, J. Doré², N. Pons³, E. le Chatelier³, L. Madsen², J. Wang³, S. D. Ehrlich³, K. Kristiansen², and C. Rogel-Gaillard³, ¹BGI-Shenzhen, Shenzhen, China. ²GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France. ³Department of Biology, University of Copenhagen, Copenhagen, Denmark. ⁴ Danish Pig Research Centre, Nutrition and Reproduction, Copenhagen, Denmark, ⁵MICALIS Institute, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ⁶MGP MetaGeNoPolis, INRA, Université Paris-Saclay, Jouy-en-Josas, France, ⁷National Institute of Nutrition and Food Research (NIFES), Bergen, Norway, ⁸King’s College London, Centre for Host-Microbiome Interactions, Dental Institute Central Office, Guy’s Hospital, London, United Kingdom, ⁹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France

Genome-wide association study using F2 population to reanalyse white feather gene.
G. Hua¹, X. Zhang², and X. Deng³, ¹Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing, China. ²Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing, China. ³Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing, China

Global and local admixture analyses of Baladi cattle.
A. Shabtay¹, M. Soller¹, J. Sölkner¹, G. Mészáros¹, T. Sonstegard¹, E. O. Ünal¹, H. J. Huson², Y. T. Utsunomiya³, and E. Lipkin⁴, ¹Department of Ruminant Sciences, Agricultural Research Organization (ARO), Newe Ya’ar Research Center, Ramat Yishay, 30095, Israel, ²Hebrew University of Jerusalem, Jerusalem, Israel, ³University of Natural Resources and Life Sciences, Vienna, Austria, ⁴Recombinetics, Inc., St. Paul, MN, ⁵Namik Kemal University, Agriculture Faculty, Department of Animal Sci., Tekirdag, Turkey, ⁶Cornell University, Ithaca, NY, ⁷UNESP Univ Estadual Paulista, Jaboticabal, Brazil

Molecular phylogeny and domestication pattern of river buffalo through mitochondrial D-loop DNA analysis.
M. T. Zahoor¹, ¹University of Veterinary & Animal Sciences, Lahore, Pakistan

Paternal genetic characterization of wild boars and domestic pigs in Japan, based on SRY and TSPY gene haplotypes.
Y. Sato¹, K. Sato, and Y. Mizoguchi, School of Agriculture, Meiji University, Kawasaki, Japan

Distribution of Y chromosomal haplotypes in Japanese native horse populations.
H. Kakoi¹, T. Tozaki¹, M. Kikuchi¹, K. I. Hirota¹, S. I. Nagata¹, and M. Takasai¹, ¹Laboratory of Racing Chemistry, Utsunomiya, Japan, ²Faculty of Applied Biological Sciences, Gifu University, Gifu, Japan

Effective population size and inbreeding in South African indigenous chicken populations: Implications for management and conservation of unique genetic resources.
B. Mitleni¹, K. Dzama¹, K. Nephawe¹, and C. Rhode¹, ¹Tswane University of Technology, Pretoria, South Africa, ²University of Stellenbosch, Stellenbosch, South Africa, ³Tshwane University of Technology, Pretoria, South Africa, ⁴University of Stellenbosch, Cape Town, South Africa
P4019  39  Statistical analysis of alleles in 4,703 Thoroughbred racing horses using fifteen microsatellite DNA markers.
S. W. Kang*, Korea Racing Authority, Gwacheon-Si, The Republic of Korea

P4020  40  Diversity analysis of transcribed MHC class IIB loci in Japanese quail.
S. Asaji1, S. Suzuki1, T. Ishige1, K. Hosomichi1, T. Shinya2, H. Haru1, T. Hirano1, and K. Hanawa1, 1Tokyo University of Agriculture, Atsugi, Japan, 2Tokai University School of Medicine, Isehara, Japan, 3Tokyo University of Agriculture, Setagaya, Japan, 4Kanazawa University, Kanazawa, Japan

P4021  41  Genomic patterns of differentiation in native and introduced populations of the cupped oysters Crassostrea gigas and Crassostrea angulata and in hybrid progenies.
S. Lapegue1, P. A. Gagnaire1, J. B. Lamy1, F. Cornette1, S. Heartebise1, E. Flahauw1, L. Dégremont1, M. T. Augé2, P. Boudry2, and N. Bierne3, 1Ifremer, SG2M-LGPM, Laboratoire de Génétique et Pathologie des Mollusques Marins, La Tremblade, France, 2ISEM - CNRS, UMR5554, SMEL, Sète, France, 3Ifremer, Physiologie Fonctionnelle des Organismes Marins, UMR LEMAR, Brest, France

P4022  42  Genetic diversity of Mexican cattle Lidia breed and its relationships with Spanish populations through bovine SNP 50K beadchip.
P. G. Eusebi1, J. Canon2, and O. Cortés3, 1Universitat Autònoma de Barcelona. Faculty of Veterinary, Bellaterra, Spain, 2Universidad Complutense, Madrid, Spain, 3Universidad Complutense de Madrid, Madrid, Spain

P4023  43  Cloned horses: mtDNA heteroplasmy makes difficult the differentiation protocol.
M. Costa, B. Elguero, C. Ratti, and M. Martinez*, Laboratorio de Genética Aplicada, Sociedad Rural Argentina, Buenos Aires, Argentina

P4024  44  Identification of TLR polymorphisms of the main cattle breeds in Russia.
K. Novák1, M. I. Dunin2, and A. E. Kalashnikov2, 1Institute of Animal Science, Prague, Czech Republic, 2All Russian Research Institute of Animal Breeding, Lesnye Polyany, Russian Federation, 3L.K. Ernst Research Institute of Animal Husbandry, Dubrovitsy, Russian Federation

P4025  45  Random forest based approaches identify breed-informative SNPs matching selection signature regions in the pig genome.
G. Schiavo1, F. Bertolini1,2, G. Galimberti3, D. G. Cali4, D. Matassino5, V. Russo1, S. Dall’Olio1, L. Nanni Costa1, and L. Fontanini1, 1Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 2Department of Animal Science, Iowa State University, Ames, 3Department of Statistical Sciences “Paolo Fortunati”, University of Bologna, Bologna, Italy, 4ConSDABI, Benevento, Italy

P4026  46  Discrimination of native chicken breeds using SNP markers selected from the 600K chip data.

P4027  47  Systematic profiling of short tandem repeats in the cattle genome.
L. Xu1, R. Haas2, J. Sun1, Y. Zhou1, D. Bickhart1, J. Li1, J. Song2, T. Sonstegard2, C. P. VanTassell1, H. Levin2, and G. E. Liu1, 1Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, 2University of Wisconsin–Platteville, 3South China Agricultural University, Guangzhou, China, 4Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China, 5University of Maryland, Animal Science and Avian, College Park, MD, 6Recombinetics, Inc., St Paul, MN, 7University of California-Davis, Department of Evolution and Ecology

**Functional Genomics II**
13:00 - 14:00
Alpine Ballroom

P3010  48  Effect of rumen content exchange on gene expression in rumen epithelium of lactating cows.
J. Vilkki1, D. Fischer2, I. Tapio3, and K. J. Shingfield2, 1Natural Resources Institute Finland, Jokioinen, Finland, 2Aberystwyth University, Aberystwyth, United Kingdom

P3011  49  Towards robust blood biomarkers for residual feed intake in pigs.
M. Schroyen1, K. M. Feye1, Y. T. Nguyen1, A. Rakhshandeh1, N. K. Gabler1, D. Nettleton1, J. C. M. Dekkers2, and C. K. Tuggle1, 1Department of Animal Science, Iowa State University, Ames, 2Department of Biomedical Sciences, Iowa State University, Ames, 3Department of Statistics, Iowa State University, Ames, 4Department of Animal and Food Sciences, Texas Tech University, Lubbock, 5Iowa State University, Ames
Deconstructing the pig genome-metabolome functional interactions.
L. Fontanesi1, S. Bovo1, G. Schiavo1, G. Mazzoni1, A. Ribani1, V. J. Utzeri1, S. Dall’Olio1, F. Bertolini2, F. Fanelli3, M. Mezzullo1, G. Galimberti1, D. G. Calò1, P. Trevisi1, P. L. Martelli1, R. Casadio1, U. Pagotto3, and P. Bosi1, 1Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 2Department of Animal Science, Iowa State University, Ames, 3Department of Surgical and Medical Sciences, Endocrinology Unit, University of Bologna, Bologna, Italy, 4Department of Statistical Sciences “Paolo Fortunati”, University of Bologna, Bologna, Italy, 5Biocomputing Group, University of Bologna, Bologna, Italy

Characterization of endometrium protein expression during mid-late gestation in Meishan and Duroc sows with iTRAQ analysis.
K. Wang1 and M. Fang, China Agricultural University, Beijing, China

The study on the genetic mechanism of varied Atrogin-1 expression in different chicken lines.
J. Li1,2, Y. Hu3, H. Lan3, L. Li3, X. Hu4, and N. Li5, 1Beijing Institute of genomics, Chinese Academy of Science, Beijing, China, 2China Agricultural University, Beijing, China, 3The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China

Analysis of G protein-coupled receptor gene expression during bovine intramuscular adipogenesis.
T. Kiwabara1 and Y. Mizoguchi, School of Agriculture, Meiji University, Kawasaki, Japan

Breed and feeding factors influencing adipose tissue lipogenic and lipolytic gene expression in growing Iberian and Duroc pigs.
R. Benitez1, A. Fernandez2, B. Isabel2, Y. Nuñez1, E. Alves1, E. De Mercado1, E. Gómez-Izquierdo1, J. M. García-Casco1, M. C. Rodriguez1, C. López-Bote2, L. Silió2, and C. Ovilo2, INIA, Madrid, Spain, 3UCM, Madrid, Spain, 4INSTITUTO TECNOLÓGICO AGRARIO, Segovia, Spain, 5INSTITUTO TECNOLÓGICO AGRARIO, Segovia, Spain, 6INIA, Zafra, Spain

Functional analysis and association studies of bovine MYOT gene with meat quality.
C. M. Adoligue1, L. Zan2, and S. Farougou1, 1University of Abomey-Calavi, Abomey-Calavi, Benin, 2Northwest A&FUniversity, Yangling, China

Gene expression analysis in backfat and identification of eQTL regions for fatness and fatty acid composition candidate genes in pigs.
M. Revilla1,2, M. Ballester1, A. Puig-Oliveras1,2, A. Castelló2, A. I. Fernández2, and J. M. Folch1,2, 1Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Spain, 2Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Spain, 3Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain, 4Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain

Screening and characterization of copy number variation in South African Nguni cattle using next generation sequencing data.
M. D. Wang1,2, K. Dzama2, J. Rees3, C. Hefer1, and F. C. Muchadeyi1, 1ARC Biotechnology Platform, Pretoria, South Africa, 2University of Stellenbosch, Stellenbosch, South Africa, 3Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa

Epigenetics and Epigenomics I
13:00 - 14:00
Alpine Ballroom

DNA methylation and hydroxymethylation in early rabbit embryo: Consequence of in vitro culture.
M. N. Bedhane1 and J. Salvaing2, 1Jigjiga university, Jigjiga, Ethiopia, 2INRA, Paris, France

CD4 promoter hyper methylation is associated with lower gene expression in clinical mastitis cows and vice versa in the healthy controls.
T. Usman1,2, Y. Yu1, and Y. Wang1, 1Abdul Wali Khan University Mardan, Mardan, Pakistan, 2Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 3College of Animal Science and Technology, China Agricultural University, Beijing, China

The conserved functional role of non-CpG methylation in mammalian and avian brain.
K. M. Schachtenschneider1,2, M. F. Derks3,4, O. Madsen1, V. N. Laine1, L. B. Schook2, M. A. Groenen2, K. J. Verhoeven2, and K. van Oers3, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Department of Animal Sciences, University of Illinois at Urbana-Champaign, 3Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands, 4Bioinformatics Group, Wageningen University, Wageningen, Netherlands, 5Department of Terrestrial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands
P2003 61  Altered hippocampal DNA methylation, gene transcription, and RNA editing in response to early life environmental insults in two independent studies of cognitive development.
K. M. Schachtschneider*1,2, L. A. Rund2, O. Madsen1, R. W. Johnson2, M. A. Groenen1, and L. B. Schook2, 1Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, 2Department of Animal Sciences, University of Illinois at Urbana-Champaign

P2004 62  Association of bta-miR-24-3p with serum antibody response to mycoplasma spp. In beef cattle.

P2005 63  Identifying DNA methylation differences that contribute to an age-dependent increase in bovine innate immunity using reduced representation bisulfite sequencing and the dermal fibroblast model.
F. Korkmaz* and D. E. Kerr, University of Vermont, Burlington

P2006 64  Transgenerational effects of modifications of the embryonic environment in quail.
T. Zerjal1, S. Leroux2, D. Gourichon3, C. Leterrier4, Y. Labrune2, V. Cosatham1, J. L. Coville1, M. Morisson2, F. Minvielle1, and F. Ptel1, 1INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, 2UMR INRA / INPT ENSAT / INPT ENSAT - GenPhysE, 31326 Castanet Tolosan, France, 3UE1295 Pôle d’Expérimentation Avicole de Tours, 37380 Nouzilly, France, 4INRA, UMR85 Physiologie de la Reproduction et des Comportements, 37280 Nouzilly, France, 5INRA - URA, 37380 Nouzilly, France

P2007 65  Sulforaphane enhances proliferation of porcine satellite cells through suppression of TGF-beta signaling pathway.
R. Zhang1, C. Neuhoff1, H. Fan2, J. Welzenbach2, Q. Yang1, M. J. Uddin1, M. U. Cinar4, D. Tesfaye1, E. Tholen1, C. Looft1, and K. Schellander1, 1Institute of animal science, University of Bonn, Bonn, Germany, 2Department of Basic Medical Science and Center for Cancer Research, Purdue University West Lafayette, West Lafayette, IN, 3School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia, 4Faculty of Agriculture, Department of Animal Science, Erciyes University, Kayseri, Turkey, 5Institute of Animal Science, University of Bonn, Bonn, Germany

P2008 66  Lipopolysaccharide-induced Gene Expression of CD14 in TRIF pathway is Epigenetically regulated by Sulforaphane in Porcine Pulmonary Alveolar Macrophages.
Q. Yang1, M. J. Pröll1, D. S. Wondim1, R. Zhang1, D. Tesfaye1, H. Fan2, M. U. Cinar1, C. Grosse-Brinkhaus1, E. Tholen1, C. Looft1, and K. Schellander1, 1Institute of animal science, University of Bonn, Bonn, Germany, 2Department of Basic Medical Science and Center for Cancer Research, Purdue University West Lafayette, West Lafayette, IN, 3School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia, 4Faculty of Agriculture, Department of Veterinary Science, Bangladesh Agricultural University, Mymensingh, Bangladesh, 5School of Veterinary Science, The University of Queensland, Gatton campus, Gatton, Australia

P2009 67  Initial analysis of sperm DNA methylome in Holstein bulls using whole genome bisulfite sequencing.
G. E. Liu*, Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD

P2010 68  Discovery of tissue-specific and gene-expression associated CpG methylations in the swine genome.
M. K. Choi1, J. Lee, J. Lee, M. T. Le, and C. Park, Konkuk University, Seoul, The Republic of Korea

POSTER PRESENTATIONS — Monday, July 25

Genetic Markers and Selection III
7:30 - 8:30
Alpine Ballroom

P5013 1  Evaluation of gene interactions affecting carcass yield and marbling in beef cattle.
J. L. Duncombe1, S. M. Schmutz1, K. M. Maddern1, and F. C. Buchanan2*, 1University of Saskatchewan, Saskatoon, SK, Canada, 2Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada

P5014 2  Porcine beta-casein: a new selection marker?.
M. Suteu* and A. Vlaic, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania

P5015 3  A genome-wide association study for quantitative trait loci of speed index in the racing line of Quarter Horses.
R. A. Curi1, G. L. Pereira1, J. A. I. V. Silva1, L. A. L. Chardulo1, and H. N. Oliveira2, 1Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu-SP, Brazil, 2Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista, Jaboticabal-SP, Brazil
F. Bertolini* and M. F. Rothschild, Department of Animal Science, Iowa State University, Ames

P5017 5 Identifying genetic regions to spring ewes to lamb out of season.
C. J. Posbergh*, M. L. Thonney, and H. J. Huson, Cornell University, Ithaca, NY

P5018 6 Genome wide association studies for dry-cured ham quality traits in Italian Large White and Italian Duroc pigs.
L. Fontanesi1*, G. Schiavo1, G. Galimberti2, S. Bovo1, F. Bertolini13, M. Gallo2, V. Russo1, and L. Buttazzoni5, 1Department of Agricultural and Food Sciences, University of Bologna, Italy, 2Department of Statistical Sciences “Paolo Fortunati”, University of Bologna, Italy, 3Department of Animal Science, Iowa State University, Ames, 4ANAS, Roma, Italy, 5Consiglio per la Ricerca in Agricoltura e l’Analisi dell’Economia Agraria, Roma, Italy

P5019 7 Identification of QTLs for the fatty acid composition in chicken.
S. Jin*, H. B. Park2, D. Seo1, N. R. Choi1, C. K. Yoo1, S. Jung1, C. Jo1, P. Manjula1, S. H. Lee1, and J. H. Lee1, 1Chungnam National University, Daejeon, The Republic of Korea, 2NIAS, Rural Development Administration, Jeju, The Republic of Korea, 3Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, The Republic of Korea

P5020 8 Gene networks driving meat quality and palatability of beef.
R. Mateescu1*, J. W. Buchanan2, D. J. Garrick3, and J. M. Reecy4, 1University of Florida, Gainesville, 2University of California-Davis, 3Iowa State University, Ames

P5021 9 Indel polymorphism in 3'-UTR of RXFP2 does not segregate with horns status in sheep breeds with a variable and/or sex-limited horns status.
G. Lühken1*, S. Krebs2, S. Rothammer3, J. D. Küpper4, B. Mioč5, I. Russ6, and I. Medugorac3, 1Department of Animal Breeding and Genetics, Justus Liebig University, Gießen, Germany, 2Laboratory for Functional Genome Analysis, Gene Center, Ludwig Maximilians University, Munich, Germany, 3Chair of Animal Genetics and Husbandry, Ludwig Maximilians University, Munich, Germany, 4Department of Animal Breeding and Genetics, Justus Liebig University of Gießen, Gießen, Germany, 5Department of Animal Science and Technology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia, 6Tierzüchtungsforschung e.V. München, Grub, Germany

P5022 10 Identification of genetic markers associated with feeding efficiency in fattening Holstein calves, using targeted sequence capture.
M. Cohen-Zinder1*, E. Lipkin2, A. Shabtay1, A. Brosh1, and A. Asher1, 1Department of Ruminant Sciences, Agricultural Research Organization (ARO), Newe Ya’ar Research Center, Ramat Yishay, 30095, Israel, 2Department of Genetics, Hebrew University of Jerusalem, Jerusalem, Israel

P5023 11 Searching imputed sequence for mutations influencing fatty acid composition of beef fat.
S. P. Miller1*, D. Lu1, R. Brauning1, S. M. Hickey1, D. Hyndman1, N. Cullen3, and S. M. Clarke2, 1AgResearch Limited, Mosgiel, New Zealand, 2AgResearch, Mosgiel, New Zealand, 3AgResearch Limited, Hamilton, New Zealand

P5024 12 Investigating the molecular regulation and control of spawning performance in domesticated Penaeus monodon broodstock.
J. Goodall1*, N. Botwright1, N. Wade2, D. Merritt1, G. Coman1, and M. Sellars2, 1The University of Queensland, St Lucia, Australia, 2CSIRO, Integrated Sustainable Aquaculture Production, St Lucia, Australia

P5025 13 Production of chickens with high body weights, low amounts of abdominal fat, and a high thigh meat yield using DNA microsatellite marker-assisted selection.
K. Tatsuda*, Hyogo Prefectural Institute of Agriculture, Forestry and Fisheries, KASAI, Japan

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**Genetics and Disease III**

*7:30 - 8:30*

Alpine Ballroom

P6022 14 Transcriptomic study of bovine macrophages infected in vitro with Streptococcus agalactiae.
A. M. Lewandowska-Sabat1*, S. C. Furre Hansen1, P. Boysen1, A. K. Siorset2, T. R. Solberg2, O. Østerås2, B. Heringstad1,5, and I. Olsaker1, 1Section for Genetics, NMBU School of Veterinary Medicine, Norwegian University of Life Sciences, Oslo, Norway, 2Section for Microbiology, Immunology and Parasitology, NMBU School of Veterinary Medicine, Norwegian University of Life Sciences, Oslo, Norway, 3Geno Breeding and A.I. Association, Hamar, Norway, 4Norwegian Cattle Health Services and TINE Extension Services, Ås, Norway, 5Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway
P6023  15  Novel miRNA involved in host response to avian pathogenic *Escherichia coli* identified by deep sequencing and integration analysis.

X. Jia*, Q. Nie, H. Lin, E. E. Sandford, X. Zhang, L. K. Nolan, 1 Iowa State University, Ames, 2 South China Agricultural University, Guangzhou, China, 3 College of Animal Science, South China Agricultural University, Guangzhou, China, 4 Department of Animal Science, Iowa State University, Ames

P6024  16  Holstein Friesian lethal haplotype 5 is caused by a 138kbp deletion on chromosome 9.

C. Wehrhahn*, E. Schütz, M. Wanjek, B. Bortfeld, J. Beck, and B. Brenig, 1 Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, 2 Institute for Livestock Reproduction GmbH, Schönow, Germany, 3 ChroniBiomedical GmbH, Göttingen, Germany

P6025  17  Network-based integration of gene expression and genome-wide association data to prioritize genomic variants associated with susceptibility/resistance to bovine tuberculosis.

K. E. Killick, K. E. McLoughlin, N. C. Nalpas, L. Burkitt-Gray, I. W. Richardson, H. L. Wiencko, D. A. Magee, J. A. Browne, B. Villarreal-Ramos, H. M. Vordermeier, D. P. Berry, D. G. Bradley, E. Gormley, S. V. Gordon, and D. E. MacHugh, 1 School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, 2 Proteome Center, University of Tübingen, Tübingen, Germany, 3 Department of Genetics, Trinity College Dublin, Dublin, Ireland, 4 Equinome Ltd., NovaUCD, Dublin, Ireland, 5 Animal and Plant Health Agency, Weybridge, Surrey, United Kingdom, 6 Teagasc, Moorepark, Co. Cork, Ireland, 7 School of Veterinary Medicine, University College Dublin, Dublin, Ireland

P6026  18  Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with high-altitude pulmonary hypertension.

M. P. Heaton*, T. P. L. Smith, J. K. Carnahan, V. Basnayake, J. Qiu, B. Simpson, and T. S. Kalbfleisch, 1 USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 2 GeneSeek, a Neogen Company, Lincoln, NE, 3 University of Louisville, KY

P6027  19  Study of the mutant MDRI allele in four Collie breeds in Italy.

S. P. Marelli, G. Minozzi*, M. Longeri, R. Rizzi, G. Gandini, and M. Polli, Università degli Studi di Milano, Milan, Italy

P6028  20  A frameshift mutation in MOCOS is associated with familial renal syndrome in Tyrolean Grey cattle.

L. Murgiano*, V. Jagannathan, C. Piffer, C. Drögemüller, and A. Gentile, 1 Giga, Liege, Belgium, 2 Institute of Genetics, Bern, Switzerland, 3 Institute of Genetics, University of Bern, Bern, Switzerland, 4 Azienda Sanitaria Alto Adige, Bozen, Italy, 5 Institute of Genetics, Vettsuisse Faculty, University of Bern, Bern, Switzerland, 6 Department of Veterinary Medical Sciences, Bologna, Italy

P6029  21  Congenital cataract formation in Holstein Friesian cattle.

A. K. Hollmann*, J. E. Wemheuer, J. Beck, B. Brenig*, and E. Schütz, 1 Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, 2 ChroniBiomedical GmbH, Göttingen, Germany

P6030  22  Three diverse mutations underlying canine xanthine urolithiasis.

N. M. Tate*, K. M. Minor, J. R. Mickelson, K. Peterson, J. P. Lulich, and E. Furrow, University of Minnesota, Saint Paul

P6031  23  Confirmation of genome wide analysis of transcriptional responses to porcine reproductive and respiratory syndrome virus (PRRSV) infection in a pregnant gilt model.

L. Hong*, J. W. Wilkinson, A. Ladinig, H. Bao, P. Stothard, J. K. Lunney, G. Plastow, and J. C. S. Harding, 1 USDA ARS BARC APDL, Beltsville, MD, 2 University of Alberta, Edmonton, AB, Canada, 3 University of Veterinary Medicine, Vienna, Austria, 4 Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 5 University of Saskatchewan, Saskatoon, SK, Canada

P6032  24  Identification and characterization of a novel pathogen causing bovine abortion.

B. T. Welly, M. R. Miller, J. L. Stott, M. T. Blanchard, A. Islas-Trejo, S. M. O’Rourke, A. E. Young, J. F. Medrano, and A. L. Van Eenennaam*, University of California-Davis

Bioinformatics, Statistical Genetics, and Genomic Technologies III

7:30 - 8:30

Alpine Ballroom

P1018  25  Comparison of high-density SNP chip versus Rad sequencing in cattle and related species.

L. Pérez-Pardal*, I. K. Saglam, V. Costa, S. Chen, M. R. Miller, and A. Beja-Pereira, 1 Cibio, Porto, Portugal, 2 University of California-Davis, 3 School of Life Sciences, Yunnan University, Kunming, China
Genetic introgression through selection in domestic chickens: Insight from whole genome sequence analysis.
1School of Life Sciences, University of Nottingham, University Park, Nottingham, United Kingdom, 2Institut National de la Recherche Agronomique (INRA), UMR 1338 GenPhySE, 31326, Castanet Tolosan, France, 3Department of Animal Science, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka, 4Open University of Diversity, Hasselt, Belgium, 5Hendrix Genetics, Boxmeer, Netherlands, 6State Key Laboratory of Genetic Resources and Evolution, Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Science, Kunming, China, 7King Saud University, Riyadh, Saudi Arabia, 8School of Life Sciences, University of Nottingham, Nottingham, United Kingdom

Identification of polymorphisms modifying gene expression regulation in cattle.
G. Guillocheau and D. Rocha.
1GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy-en-Josas, France, 2GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France

A next generation semiconductor based target re-sequencing DNA pool-seq approach for the identification of SNPs and association studies: application to bitter taste receptor genes in different pig populations.
1Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, 2Department of Animal Science, Iowa State University, Ames

Bridging SNP genotyping platforms to high-throughput computing for agricultural genomic applications: A perspective from a commercial service provider.
GeneSeek, a Neogen Company, Lincoln, NE

RNA editing in swine is associated with PRE-1 retrotransposons.
1Genetics Program, Michigan State University, East Lansing, 2Department of Fisheries and Wildlife, Michigan State University, East Lansing, 3Department of Animal Science, Michigan State University, East Lansing

Inferring genotypes of functional variants in crossbred beef cattle.
USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

A method for the identification of unfavorable haplotypes contained within runs of homozygosity that impact fitness traits and its application to different swine nucleus lines.
J. T. Howard, F. Tiezzi, Y. Huang, K. A. Gray, and C. Maltecca.
1North Carolina State University, Raleigh, 2Smithfield Premium Genetics, Rose Hill, NC

Additive and heterotic effects estimation from a F2 Duroc x Pietrain crossbreed using 60K realized breed composition and heterozygosis.
1IGEVET (CONICET La Plata - Fac. Cs. Veterinarias U. Nacional de La Plata), La Plata, Argentina, 2Department of Animal Science, Agronomical School, Buenos Aires University, Buenos Aires, Argentina, 3Department of Animal Science, Michigan State University, East Lansing, 4Departamento de Produccion, Facultad de Agronomia, Universidad de Buenos Aires, Buenos Aires, Argentina, 5Michigan State University, East Lansing, 6INP A – Unidad Ejecutora UBA-CONICET de Investigaciones en Produccion Animal, Buenos Aires, Argentina

Genetic Diversity and Polymorphisms III
7:30 - 8:30
Alpine Ballroom

Hematopoietic chimerism in Italian horses.
C. Grassi, M. Bonuglia, M. Dobosz, and V. CHIOFALO.
1UNIRELAB, Settimo Milanese, Italy, 2University of Perugia, Perugia, Italy, 3UNIRELAB s.r.l., Settimo Milanese, Italy

Launching SheepGenomesDB: 100 million variants from nearly 500 sheep genomes.
1CSIRO Agriculture, Brisbane, Australia, 2AgResearch, Mosgiel, New Zealand, 3AgResearch Limited, Mosgiel, New Zealand, 4Utah State University, Logan, UT, 5CEMRI-EBF, Hinxton, United Kingdom, 6Department of Economic Development, Jobs, Transport and Resources, Bundroo, Australia

Diversity and linkage disequilibrium in farmed Tasmanian Atlantic Salmon.
1CSIRO Agriculture, Brisbane, Australia, 2CSIRO, Hobart, Australia, 3SALTAS, Hobart, Australia, 4CSIRO, Brisbane, Australia, 5CSIRO Agriculture, Hobart, Australia, 6University of Turku, Turku, Finland, 7Data 61, Canberra, Australia
P4031 37 Ancient DNA analysis of the \textit{MC1R} gene in wild boar specimens from Mesolithic Ertebølle sites. J. Tetens\textsuperscript{1}, D. Ellinghaus\textsuperscript{1}, M. Nusua\textsuperscript{2}, G. Thaller\textsuperscript{1}, A. Nebel\textsuperscript{1}, and B. Krause-Kyora\textsuperscript{1}, \textsuperscript{1}Institute of Animal Breeding and Husbandry, Kiel University, Kiel, Germany, \textsuperscript{2}Institute of Clinical Molecular Biology, Kiel University, University Hospital Schleswig-Holstein, Kiel, Germany

P4032 38 Polymorphism of 10 microsatellite DNA used for parentage control in pigeons in Poland. A. Radko\textsuperscript{1}, A. Szumiec\textsuperscript{1}, and T. Borkowski, \textsuperscript{1}National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland, \textsuperscript{2}Veterinary Laboratory, Coba Diagnostic, Sosnowice, Poland

P4033 39 Characterization and diversity analysis of European local pig breeds and production systems under Treasure project framework. A. I. Fernández\textsuperscript{1}, L. Fontanesi\textsuperscript{2}, R. Bozzi\textsuperscript{1}, J. Estellé\textsuperscript{1}, C. Ovilo\textsuperscript{3}, R. M. Nieto\textsuperscript{3}, J. M. Garcia-Casco\textsuperscript{3}, C. Pugliese\textsuperscript{3}, J. M. Gil\textsuperscript{4}, B. Lebret\textsuperscript{3}, M. A. Oliver\textsuperscript{5}, and M. Canek-Potokar\textsuperscript{6}, \textsuperscript{1}Department of Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, \textsuperscript{2}Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, \textsuperscript{3}University of Florence, Florence, Italy, \textsuperscript{4}GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, \textsuperscript{5}INIA, Madrid, Spain, \textsuperscript{6}Consejo Superior De Investigaciones Científicas, Armilla, Spain, \textsuperscript{7}INIA, Zafra, Spain, \textsuperscript{8}Department of Agrifood Production and Environmental Sciences, University of Firenze, Firenze, Italy, \textsuperscript{9}CREDA-UPC-IRTA, Castelldefels, Barcelona, Spain, \textsuperscript{10}INRA, Saint Gilles, France, \textsuperscript{11}IRTA, Monells, Spain, \textsuperscript{12}KIS-Agricultural Institute of Slovenia, Ljubljana, Slovenia

P4034 40 Milk protein polymorphisms in African indigenous cattle: opportunity for sustainable breeding program. I. Houaga, \textsuperscript{1}JOMO KENYATTA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY, JUJA-KENYA, Kenya; University of Abomey-Calavi, Benin

P4035 41 Exploiting genomic data of Spanish Atlantic salmon to identify genes involved in sex determination and to estimate effective population size. M. Saura\textsuperscript{1}, A. Chitoui\textsuperscript{2,3}, A. I. Fernandez\textsuperscript{1}, P. Morán\textsuperscript{1}, M. P. Kent\textsuperscript{1}, and B. Villanueva\textsuperscript{1}, \textsuperscript{1}INIA, Madrid, Spain, \textsuperscript{2}Universidad Politécnica de Valencia, Valencia, Spain, \textsuperscript{3}Department of Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, \textsuperscript{4}University of Vigo, Vigo, Spain, \textsuperscript{5}Center for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences (IIA), Norwegian University of Life Sciences (NMBU), Ås, Norway

P4036 42 Estimation of linkage disequilibrium and effective population size in Korean native chicken. D. Seo\textsuperscript{1}, P. Sudrajad, D. Lee, N. R. Choi, S. Jin, S. H. Lee, and J. H. Lee, Chungnam National University, Daejeon, The Republic of Korea

P4037 43 Around the tail of the Khmer cat. A. Cristalli\textsuperscript{1}, S. P. Marelli\textsuperscript{2}, F. Valiati\textsuperscript{2}, F. Genova\textsuperscript{2}, and M. Longeri\textsuperscript{2}, \textsuperscript{1}DVM, PhD, Arezzo, Italy, \textsuperscript{2}Università degli Studi di Milano, Milan, Italy

P4038 44 Whole genome semiconductor based sequencing of farmed European sea bass (Dicentrarchus labrax) using a DNA pooling approach identifies putative selection signatures in Mediterranean genetic stocks. C. Geracci\textsuperscript{1}, F. Bertolini\textsuperscript{2}, G. Schiavo\textsuperscript{3}, M. T. Sardina\textsuperscript{4}, V. Chiofalo\textsuperscript{4}, and L. Fontanesi, \textsuperscript{1}Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, \textsuperscript{2}Department of Animal Science, Iowa State University, Ames, \textsuperscript{3}Palermo University, Palermo, Italy, \textsuperscript{4}Messina University, Messina, Italy

P4039 45 Design of a polymorphic microsatellites set for domestic turkey (Meleagris Gallopavo) genetics characterization. A. Canales\textsuperscript{1}, A. M. Martinez\textsuperscript{1,2}, V. Landi\textsuperscript{1,2}, P. Cervantes\textsuperscript{3}, J. V. Delgado\textsuperscript{4}, and M. E. Camacho\textsuperscript{5}, \textsuperscript{1}University of Cordoba, Cordoba, Spain, \textsuperscript{2}Animal Breeding Consulting SL, Cordoba, Spain, \textsuperscript{3}Universidad Veracruzana, Veracruz, Mexico, \textsuperscript{4}Departamento de Genética, Universidad de Córdoba, Córdoba, Spain, \textsuperscript{5}IFAPA Centro Alameda del Obispo, Córdoba, Spain

P4040 46 Computer analysis of genetic parentage: Application in equine diversity maintenance in Brazil. A. Atomiyama\textsuperscript{1}, M. S. Lauretto\textsuperscript{1}, F. Nakano\textsuperscript{1}, J. M. Stern\textsuperscript{1}, D. Levy\textsuperscript{1}, S. P. Bydlowski\textsuperscript{1}, and C. R. Bydlowski, \textsuperscript{1}LinkGen Biotecnologia, Sao Paulo, Brazil, \textsuperscript{2}Universidade Sao Paulo (USP) - Zona Leste, Sao Paulo, Brazil, \textsuperscript{3}Instituto Butantan, Sao Paulo, Brazil, \textsuperscript{4}Instituto de Matemática e Estatística da USP, Sao Paulo, Brazil, \textsuperscript{5}Faculdade de Medicina da USP, Sao Paulo, Brazil

P4041 47 Pooled whole-genome sequencing reveals molecular signatures of natural adaptive selection in Djallonke sheep of Ghana. M. Yaro\textsuperscript{1}, K. A. Munyard\textsuperscript{1}, E. Morgan\textsuperscript{1}, R. J. Alcock\textsuperscript{2}, M. J. Stear\textsuperscript{3}, and D. M. Groth\textsuperscript{1}, \textsuperscript{1}Curtin University, Perth, Australia, \textsuperscript{2}University of Western Australia, Perth, Australia, \textsuperscript{3}University of Glasgow, Glasgow, United Kingdom
P3020 48 The potential relationship between comb color and egg production revealed by GWAS in Blue-shelled chicken.
X. Dong*, J. Li, Y. Zhang, X. Deng, and C. Wu, Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing, China

P3021 49 Effects of dietary on the expression of lipid metabolism signaling genes in the longissimus dorsi muscle of Polish Holstein bulls.
K. Rutkowska*, D. Reczynska, M. Lukaszewicz, E. Bugnicka, and J. Oprzadek, Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland

P3022 50 Hepatic genes and pathways related to haematological and biochemical traits promoting resilience.
S. Ponsuktil*, N. Trakooljul, E. Murani, and K. Wimmers, Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany

P3023 51 Dietary supplementation with Vitamin E or Grape pomace influences antioxidant and lipid metabolism candidate gene expression in broiler muscle.
Y. Núñez*, A. Fernández*, R. Benítez, I. Arija*, A. Viveros*, A. Brenes*, and C. Ovilo*, 1INIA, Madrid, Spain, 2Facultad de Veterinaria, UCM, Madrid, Spain, 3Instituto de ciencia y tecnología de alimentos y nutrición, CSIC, Madrid, Spain

P3024 52 Transcriptome analysis of longissimus thoracis et lumborum from pigs divergent in residual feed intake.
J. Horodyńska*, M. Oster, K. Wimmers, A. M. Mullen, P. G. Lawlor, and R. M. Hamill, 1Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2Teagasc Food Research Centre, Dublin, Ireland, 3Teagasc Pig Production Development, AGRIC, Cork, Ireland

P3025 53 RNA depletion for highly abundant transcripts in bovine mammary gland improves the sensitivity of RNAseq analysis.
R. Weikard* and C. Kühn, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany

P3026 54 RNA silencing – targeted transcriptome of porcine alveolar macrophages upon infection with porcine respiratory and reproductive syndrome viruses (PRRSV) of different virulence.
S. Poller*, P. Renson*, F. Jaffrezic*, G. Marot*, M. Moroldo*, J. Lecardonnel*, O. Borry*, and E. Giuffra*, 1GABI, INRA, AgroParisTech, Université Paris Saclay, 78350 Jouy en Josas, France, 2ANSES, Unité Virologie Immunologie Porcines, 22440 Ploufragan, France, 3EA 2694 Biostatistiques, Université de Lille, Inria Lille Nord Europe, MODAL, 59650 Villeneuve d’Ascq, France

P3027 55 Bioactivity of colostrum and milk exosomes containing microRNA from cows genetically selected as high, average, and low immune responders based on their estimated breeding values.
M. Ross*, H. Atalla*, and B. Mallard*, 1Department of Pathobiology, University of Guelph, Guelph, ON, Canada, 2Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

P3028 56 The suppression of miR-16 maturation induced by 54-bp insertion activates a novel feedback regulatory via the insulin signaling pathway.
X. Jia*, X. Xu*, Q. Nie*, X. Zhang*, and S. J. Lamont*, 1South China Agricultural University, Guangzhou, China, 2Iowa State University, Ames, 3College of Animal Science, South China Agricultural University, Guangzhou, China, 4Department of Animal Science, Iowa State University, Ames

P3029 57 Identification of regulatory genes involved in Longissimus dorsi transcriptomic differences between pig genotypes.
M. Ayuso*, J. Garrayo*, A. Fernández*, Y. Núñez*, R. Benítez*, B. Isabel*, A. I. Fernández*, A. I. Rey*, A. Gonzalez-Bulnes*, J. F. Medrano*, A. Cánovas*, C. López-Bote*, and C. Ovilo*, 1UCM, Madrid, Spain, 2UPM, Madrid, Spain, 3INIA, Madrid, Spain, 4Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, 5University of California-Davis, 6University of Guelph, Ontario, ON, Canada

P3030 58 Identification of expression quantitative trait loci for longissimus muscle microRNA expression profiles in the Michigan State University Duroc x Pietrain pig resource population.
K. R. Perry*, D. Velez-Irizarry*, J. P. Steibel*, S. Casiro1, S. A. Funkhouser1, N. E. Raney1, R. O. Bates1, and C. W. Ernst1, 1Department of Animal Science, Michigan State University, East Lansing, 2Department of Fisheries and Wildlife, Michigan State University, East Lansing, 3Genetics Program, Michigan State University, East Lansing

P3031 59 Toward resolving long noncoding RNAs in fish: Identification, mapping and association to disease using strand-specific RNA-seq in rainbow trout fed alternative diets.
J. Abernathy* and K. Overturf, USDA-ARS, Hagerman, ID
P3032  60  Association of skeletal muscle transcripts with fatty acid content in Nellore cattle.
A. S. M. Cesar1, J. M. Reecy1,2, L. C. A. Regitano1, M. D. Poloto1, S. C. S. Andrade1, P. C. Tizioto1, P. S. N. Oliveira1, D. P. D.
Lanna1, R. R. Tullio1, R. T. Nassu1, J. E. Koltes2, E. Fritz-Waters2, and L. L. Coutinho1, 1Animal Biotechnology Laboratory
- ESALQ, University of São Paulo, Piracicaba, Brazil, 2Iowa State University, Ames, 3Embrapa Southeast Livestock, São
Carlos, Brazil, 4University of São Paulo, Piracicaba, Brazil, 5University of São Paulo, São Paulo, Brazil, 6Embrapa Southeast
Livestock, São Carlos, Brazil, 7University of São Paulo / ESALQ, Piracicaba, Brazil, 8University of Arkansas, Fayetteville

P2011  61  Novel analysis of global DNA methylation in the limbic system of the bovine brain.
B. A. Cantrell1, S. D. McKay1, R. L. Weaber2, R. N. Funston3, and H. Lachance1, 1University of Vermont, Burlington, 2Kansas
State University, Manhattan, 3University of Nebraska, West Central Research and Extension Center, North Platte

P2012  62  Investigation of genomic imprinting in chicken embryonic brain and liver through RNA sequencing.
Z. Zhuo1, S. J. Lamont1, and B. Abasht1, 1Department of Animal and Food Sciences, University of Delaware, Newark,
2Department of Animal Science, Iowa State University, Ames

P2013  63  Impact of collection season and storage of semen on methylation activity in swine placental and fetal tissues derived
from summer or winter breedings.
L. A. Rempel1 and J. R. Miles, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

P2014  64  Examining conserved DNA methylation in the bovine 5’ AMPK gene family.
F. Betancourt, S. Friedman, S. Perlee, H. Lachance, and S. D. McKay1, University of Vermont, Burlington

P2015  65  Fto and Irx3 transcription and methylation profiles in adipose tissues of rats fed with high-fat and high-protein diets.
J. Nowacka-Woszuk1, E. Pruszynska-Oszmalek, M. Szydlowski, and I. Szcerbel, Poznan University of Life Sciences, Poznan,
Poland

P2016  66  Combined analysis of DNA methylome and transcriptome reveal novel candidate genes relevant with susceptibility to
bovine Staphylococcus aureus subclinical mastitis.
M. Song*, China Agricultural University, Beijing, China

P2018  68  Maternal Periconceptional Overnutrition alters the Adipose Tissue Epigenome of Offspring.
T. Vuocolo1, D. C. Bauer1, S. McWilliam1, S. Zhang1, M. Buckley1, J. L. Morrison1, J. C. McMillen1, and R. L. Tellam1,1
1CSIRO Agriculture, Brisbane, Australia, 2CSIRO Data61, Sydney, Australia, 3The University of South Australia, Adelaide,
Australia, 4The University of Newcastle, Australia

P5026  1  Genetic analysis of conformation traits in Icelandic horses.
K. Jäderkvist Fegraeus1, M. Shresta1, A. Schurink1, S. Eriksson1, B. J. Ducro1, B. D. Velie1, and G. Lindgren1, 1Department
of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, 2Animal Breeding and
Genomics Centre, Wageningen University, Wageningen, Netherlands

P5027  2  Transcriptome profiling of Arabian horses blood tissue during training regime using Next Generation Sequencing
method.
K. Ropka-Molik1, M. Stefaniuk-Szmukier1, K. Zukowski1, K. Piorkowska1, and A. Gurgul1, 1National Research Institute of
Animal Production, Balice, Poland, 2Department of Horse Breeding, Institute of Animal Science, University of Agriculture in
Cracow, Poland

P5028  3  A genome-wide association study for growth rate in commercial pigs.
J. Horody ska1,2, R. M. Hamill1, H. Reyer1, P. Varley1, and K. Wimmers2, 1Teagasc Food Research Centre, Dublin, Ireland,
2Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 3Hermitage Genetics, Kilkenny,
Ireland

Epigenetics and Epigenomics II
7:30 - 8:30
Alpine Ballroom

Genetic Markers and Selection IV
13:00 - 14:00
Alpine Ballroom
POSTER PRESENTATIONS — Monday, July 25, 2016

P5029 4 The use of Bayesian methods, biological priors and sequence variants to identify genomic regions associated with dairy cow fertility.

P5030 5 Dietary carotenoid levels and stearoyl-coA haplotype exert a complementary action over fat content and composition in pig.
R. N. Pena1*, E. Henríquez-Rodríguez2, A. R. Seradj1, M. Tor1, P. Christou1,2, and J. Estany1, 1University of Lleida - Agrotecnio Center, Lleida, Spain, 2ICREA, Barcelona, Spain

P5031 6 Runs of homozygosity highlight candidate genes and biological pathways related to athletic performance in Alaskan sled dogs.
H. J. Huson1*, A. Valenti, and A. Boyko, Cornell University, Ithaca, NY

P5032 7 A genome-wide association study of young horse test traits in Swedish Warmblood.
S. Eriksson, Å. Viklund, and S. Mikko2, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

P5033 8 A GWAS of test number in pigs.
G. A. Rohrer1* and D. J. Nonneman, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

P5034 9 Differential proportion of ancestral MHc haplotypes in Brangus breed.
D. Goszczyński1*, C. Corbi1, H. Morales1, D. Posik1, E. Villegas Castagnasso1, S. Manilla1, P. Peral Garcia1, A. Rogberg2, R. J. C. Cantet2, and G. Giovambattista1, 1IGEVET – Instituto de Genetica Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, 2Departamento de Produccion, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina, 3INPA – Unidad Ejecutora UBA-CONICET de Investigaciones en Produccion Animal, Buenos Aires, Argentina

P5035 10 Fine mapping of a distal chromosome 4 QTL affecting growth and muscle mass in a chicken advanced intercross line.
S. Lyu1, D. Arends1, M. K. Nassar2,3, and G. A. Brockmann1, 1Albrecht Daniel Thaer-Institut for Agricultural and Horticultural Sciences, Faculty of Life Sciences, Humboldt-Universität zu Berlin, Berlin, Germany, 2Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt

P5036 11 Selection signatures in commercial Duroc pig populations revealed by high density SNP chip.
K. S. Kim1*, Z. Edea1, J. K. Hong2, Y. C. Jung2, E. S. Kim2, and M. F. Rothschild1, 1Chungbuk National University, Cheongju, South Korea, 2National Institute of Animal Science, Cheonan, The Republic of Korea, 3Jung P&C Institute, Yongin, The Republic of Korea, 4Recombetics, Saint Paul, MN, 5Department of Animal Science, Iowa State University, Ames

P5037 12 Targeted-enrichment next generation sequencing in the estimation of QTL variants associated with meat quality on SSC15 in pigs.
K. Piórkowska1, K. Zakowski2, K. Ropka-Molik, and A. Gurgul, National Research Institute of Animal Production, Balice, Poland

P5038 13 Quantitative trait loci for backfat thickness in an F2 population between Landrace and Jeju Black pigs.
S. H. Han1*, Y. K. Kim1, H. S. Oh1, H. B. Park2, and I. C. Cho1, 1Educational Science Research Institute, Jeju National University, Jeju, The Republic of Korea, 2Faculty of Science Education, Jeju National University, Jeju, The Republic of Korea, 3NIAS, Rural Development Administration, Jeju, The Republic of Korea

P5039 14 A landscape genomic approach to unravel the genomic mechanism of adaptation in indigenous goats of South Africa.
K. Mdladla1,2, E. F. Dzomba1, and F. C. Machadey1, 1Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa, 2University of KwaZulu-Natal, Pietermaritzburg, South Africa
**Genetics and Disease IV**  
**13:00 - 14:00**  
**Alpine Ballroom**

**P6033 15**  
Genome association of domestic sheep eosinophils with known parasite resistance QTL.
M. R. Mousel\(^1\), S. N. White\(^1,2\), M. V. Gonzalez\(^3\), J. O. Reynolds\(^2\), and D. P. Knowles\(^1,2\), \(^1\)USDA, ARS, Animal Disease Research Unit, Pullman, WA, \(^2\)Washington State University, Pullman, WA, \(^3\)Center for Applied Genomics, The Children’s Hospital of Philadelphia, Philadelphia, PA, \(^4\)USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID

**P6034 16**  
Associations between cis-expression quantitative trait loci (cis-eQTL) markers and host response to porcine reproductive and respiratory syndrome virus (PRRSV) infection.
H. Bao\(^1\), A. Kommadath\(^1\), I. Choi\(^1\), J. M. Reecy\(^2\), E. Fritz-Waters\(^1\), C. J. Eisle\(^1\), R. R. R. Rowland\(^5\), C. K. Tuggle\(^3\), J. C. M. Dekkers\(^6\), L. L. Guan\(^7\), P. Stothard\(^8\), G. Plastow\(^8\), and J. K. Lunney\(^2\), \(^1\)University of Alberta, Edmonton, AB, Canada, \(^2\)USDA ARS BARC APDL, Beltsville, MD, \(^3\)Iowa State University, Ames, \(^4\)University of Arkansas, Fayetteville, \(^5\)Kansas State University, Manhattan, \(^6\)Department of Animal Science, Iowa State University, Ames, \(^7\)Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, \(^8\)Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada

**P6035 17**  
The expression of genes connected with prion protein metabolism in sheep.
A. Piestrzynska-Kajtoch\(^1\), G. Smolucha\(^1\), M. Oczkowicz\(^1\), A. Fornal\(^2\), and B. Rejduch\(^1\), \(^1\)National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland, \(^2\)National Research Institute of Animal Production, Balice, Poland

**P6036 18**  
A polymorphism of CD163 gene is significantly associated with weight gain of the pigs under persistent PRRSV infection.
B. Lim\(^1\), P. Niu\(^2\), W. I. Kim\(^2\), C. K. Park\(^3\), and K. S. Kim\(^4\), \(^1\)Chungbuk National University, Cheongju, The Republic of Korea, \(^2\)Chunbuk National University, Iksan, The Republic of Korea, \(^3\)Kyungpook National University, Taegu, The Republic of Korea, \(^4\)Chungbuk National University, Cheongju, South Korea

**P6037 19**  
Effects of CAEV infection on expression of acute phase protein genes in goat milk somatic cells.
D. Reczynska\(^1\), J. Jarczak\(^1\), K. Rutkowska\(^1\), M. Czopowicz\(^2\), K. Barlowska\(^1\), J. Oprzadek\(^1\), L. Witkowski\(^1\), D. Słoniewska\(^1\), K. Horbanczuk\(^1\), W. Jarmuz\(^1\), J. Kaba\(^1\), and E. Bagnicka\(^1\), \(^1\)Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland, \(^2\)Warsaw University of Life Sciences, Faculty of Veterinary Medicine, Warsaw, Poland

**P6038 20**  
Tackling the itch: GWAS-based candidate genes for psoroptic mange sensitivity in Belgian Blue cattle.
A. Coussé\(^1\), M. Elansary\(^2\), R. Abo\(^2\), C. Sarre\(^1\), L. Francois\(^1\), X. Hubin\(^1\), A. Stinchens\(^1\), C. Saegerman\(^2\), T. Druet\(^2\), B. Losson\(^2\), E. Claerebout\(^1\), M. Georges\(^1\), and N. Buys\(^1\), \(^1\)KU Leuven, Leuven, Belgium, \(^2\)University of Liège, Belgium

**P6039 21**  
Expression of β-defensin and cathelicidin genes in milk somatic cells derived from mammary glands infected with coagulase-positive or coagulase-negative Staphylococci.
E. Bagnicka\(^*1\), E. Kościuczuk\(^1,2\), P. Lisowski\(^1\), J. Jarczak\(^1\), S. Marczak\(^1\), W. Jarmuz\(^1\), and L. Zwierzchowski\(^1\), \(^1\)Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland, \(^2\)Robert H. Lurie Comprehensive Cancer Center of Northwestern University, Chicago, IL

**P6040 22**  
Allele specific expression analysis of the porcine blood transcriptome reveals extensive cis-regulation in immunity-related genes.
T. Maroilley\(^*1\), G. Lemonnier\(^1\), D. Esquerré\(^1\), M. J. Merca\(^1\), C. Rogel-Gaillard\(^1\), J. Estellé\(^1\), \(^1\)GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, \(^2\)INRA, UMR1388 GenPhySe, GeT-PlaGe Genomic Facility, Castanet-Tolosan, France, \(^3\)IFIP-BIOPORC, Le Rheu, France, \(^4\)GABI, INRA, AgroParisTech, Université© Paris-Saclay, Jouy-en-Josas, France

**P6041 23**  
Microarray analysis of genomic aberrations of horse sarcoids.
K. Pavlina\(^1\), A. Gurgul\(^1\), J. Klukowska-Rötzler\(^2\), C. Koch\(^2\), K. Mählmann\(^2\), and M. Bugno-Poniewierska\(^1\), \(^1\)National Research Institute of Animal Production, Balice, Poland, \(^2\)University of Bern, Switzerland

**P6042 24**  
Transcriptome characteristic of horse sarcoids.
E. Semik\(^1\), A. Gurgul\(^1\), K. Ropka-Molič\(^2\), T. Zabek\(^1\), C. Koch\(^2\), K. Mählmann\(^2\), and M. Bugno-Poniewierska\(^1\), \(^1\)National Research Institute of Animal Production, Balice, Poland, \(^2\)University of Bern, Bern, Switzerland

**P6043 25**  
Evaluation of chromosome rearrangements of an intersex horse applying molecular cytogenetic techniques.
M. Bugno-Poniewierska\(^1\), T. Zabek, A. Gurgul, and K. Pavlina, National Research Institute of Animal Production, Balice, Poland
Bioinformatics, Statistical Genetics, and Genomic Technologies IV  
**13:00 - 14:00**  
Alpine Ballroom

P1027  26  
**Application of analysis tools from Affymetrix on Eureka™ Genotyping Solution to provide accurate and automated animal genotypes.**  
S. Nohzadeh-Malakshah, V. Joshi, and A. Pirani*, Affymetrix Inc., Santa Clara, CA

P1028  27  
**Comparing two strategies for selecting low density SNPs for imputation-mediated, multiple-trait genomic prediction in a U.S. Holstein population.**  
J. He1,2, X. L. Wu1, S. Bauck1, J. Q. Xu2, J. Lee2, G. Morota2, S. D. Kachman2, and M. L. Spangler2, 1Hunan Agricultural University, Changsha, China, 2University of Nebraska-Lincoln, 3GeneSeek, a Neogen Company, Lincoln, NE

P1029  28  
**Pan-microbial detection using Axiom® genotyping solution from Affymetrix.**  
A. Pirani*1, P. Rack1, K. Mcloughlin2, L. Le1, C. Sheppy1, T. Slezak2, and M. Shapero1, 1Affymetrix Inc., Santa Clara, CA, 2LLNL, Livermore, CA

P1030  29  
**Identification of copy number variations in fine wool sheep using Ovine SNP600 BeadChip array.**  
Y. Tian1, X. Huang1, K. Tian2, J. Di2, Y. Bai1, X. Xu2, X. Fu2, W. Wu3, X. Shi2, and B. Zhao1, 1College of Animal Science, Xinjiang Agricultural University, Urumqi, China, 2Xinjiang Academy of Animal Science, Urumqi, China

P1031  30  
**Genetic and genomic testing of cattle from Tissue Sample Units under Australian conditions.**  
R. E. Lyons*1, D. Waine2, E. Collins3, K. Lyons2, L. Frost3, and M. Kelly4, 1University of Queensland, Gatton, Australia, 2University of Queensland, Gatton, Australia, 3AquAgri Genetics, Brisbane, Australia, 4Australian Agricultural Company Limited, Brisbane, Australia

P1032  31  
**Fine mapping of a QTL for number of teats on SSC7.**  
M. S. Lopes1, M. van Son1, N. Duivesteijn1, and B. Hartliuiz1*, 1Topigs Norsvin Research Center, Beuningen, Netherlands, 2Norsvin, Hamar, Norway

P1033  32  
**Relaxation of purifying selection is prevalent among domesticated animals.**  
J. Chen1*, X. Du1, C. Zhang2, and S. Zhao2, 1Huazhong Agricultural University, Wuhan, China, 2Kib, Kunming, China

P1034  33  
**CRISPR-offinder: a CRISPR guide RNA design and off-target searching tool for user-defined protospacer adjacent motif.**  
S. Xie*, Huazhong Agricultural University, Wuhan, China

P1035  34  
**Ensembl: a comprehensive bioinformatics infrastructure for vertebrate genetics.**  
D. R. Zerbino*, B. Aken, L. Clarke, F. Cunningham, A. D. Yates, and P. Flicek, European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridge, United Kingdom

Genetic Diversity and Polymorphisms IV  
**13:00 - 14:00**  
Alpine Ballroom

P4042  35  
**Design of a polymorphic microsatellite set for domestic turkey (Meleagris gallopavo) genetic characterization.**  
A. Canales1, A. M. Martinez1,2, V. Landi1,2, P. Cervantes2, and M. E. Camacho1, 1University of Cordoba, Cordoba, Spain, 2Animal Breeding Consulting SL, Cordoba, Spain, 3Universidad Veracruzana, Veracruz, Mexico, 4Departamento de Genética. Universidad de Córdoba, Cordoba, Spain, 5IFAPA Centro Alameda del Obispo, Cordoba, Spain

P4043  36  
**Construction of the SNP panel for Hucul horse parentage control based on the OpenArray platform.**  
A. Forma1*, A. Piestrzynska-Kajtoch1, and A. Radko1, 1National Research Institute of Animal Production, Balice, Poland, 2National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland

P4044  37  
**Search for polymorphisms through next-generation sequencing of genes involved in reproductive development in Guzerat bulls.**  
J. P. Liron1, A. M. Loaiza Echeverri1, M. E. Fernandez1, M. Drummond2, D. Gosczynski1, D. Cunha Cardoso2, P. Peral Garcia1, M. R. J. M. Henry2, G. Giovambattista1, and D. A. Andrade de Oliveira2, 1IGEVET – Instituto de Genetica Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, 2Escuela de Veterinaria, Universidad Federal de Minas Gerais, Belo Horizonte, Brazil
Genetic characterization of three Korean native cattle breeds using the bovine 640K Affymetrix axiom arrays.
J. Kim1, Y. Kim2, Y. Lee3, and A. Iqbal4, Yeungnam University, Gyeongsan, South Korea, 1Yeungnam University, Gyeongsan, The Republic of Korea, 2Yeungnam University, Gyeongsan, The Republic of Korea

Development and evaluation of a set of 100 SNP markers for DNA typing in the domestic horse.
H. Holl1, J. Vanhansy2, R. Everts1, D. Cook1, S. Brooks2, M. Carpenter1, C. Bustamante3, and C. Lafayette1, 1Etalon Inc., Menlo Park, CA, 2Agema Bioscience, San Diego, CA

Studies on genetic diversity and phylogenetic relationships of Korean Native chicken using the microsatellite marker.
J. H. SEO1,2, J. M. Han3, and H. S. Kong4, 1Genomic Informatics Center, HanKyong National University, Anseong, Gyeonggi-do, The Republic of Korea, 2Major in Genomic Informatics Graduate School of Future Convergence Technology, Anseong, Gyeonggi-do, The Republic of Korea

Comparison of three methods to discover copy number variants in Nellore and Angus cattle.
Y. Xing1 and C. A. Gill2, 1Interdisciplinary Graduate Program in Genetics, Texas A&M University, College Station, 2Department of Animal Science, Texas A&M University, College Station

Molecular and genetic characterization of DGAT1 gene in Sudanese dairy cattle Kenana and Butana.
S. A. M. A. A. Mohammed Ali*, Alneelain University, Khartoum, Sudan

Inference of population structure of purebred dairy and beef cattle using high density genotype data.
M. M. Kelleher1, D. C. Purfield2, F. Kearney3, R. Evans1, and D. P. Berry1, 1Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, 2Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, 3Teagasc, Moorepark, Fermoy, Co. Cork, Ireland

Genetic relationships between Iberian and Criollo horse breeds.
J. L. Vega-Pla1, O. Cortés2, L. T. Gama3, J. Canon4, M. C. Penedo5, M. D. M. Oom6, V. Landí7, J. V. Delgado8, A. M. Martínez9, and B. Consortium9, 1Laboratorio de Investigacion Aplicada. Ministry of Defense, Cordoba, Spain, 2Universidad Complutense de Madrid, Madrid, Spain, 3CIISA – Facultad de Medicina Veterinaria, Universidad de Lisboa, Lisboa, Portugal, 4Universidad Complutense de Madrid, Madrid, Spain, 5Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, 6University of California-Davis, 7University of Illinois at Urbana-Champaign, 8University of Michigan, Ann Arbor, 9USDA ARS BARC APDL, Beltsville, MD, 9University of Veterinary Medicine Vienna, Vienna, Austria

S. Ho1, J. H. Lee2, A. Ando3, C. Rogel-Gaillard4, L. B. Schook5, D. M. Smith6, J. K. Lunney7, and S. E. Hammer8, 1Gift of Life Michigan, Ann Arbor, MI, 2Chungnam National University, Daejeon, The Republic of Korea, 3Tokai University School of Medicine, Isehara, Kanagawa, Japan, 4GABI, INRA, AgroParisTech, Universiti© Paris-Saclay, Jouy-en-Josas, France, 5University of Illinois at Urbana-Champaign, 6University of Michigan, Ann Arbor, 7USDA ARS BARC APDL, Beltsville, MD, 8University of Veterinary Medicine Vienna, Vienna, Austria

Prospects for whole genome sequencing of ancient Finnish cattle.
M. B. Weldenegodguad1,2, C. Der Sarkissian1, A. Bläuer1,4, K. Pokharel1,2, J. P. Tiavitsainen1, L. Orlando2, and J. Kantanen1,2, 1Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland, 2Natural Resources Institute Finland (Luke), Jokioinen, Finland, 3Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark, 4Department of Archaeology, University of Turku, Turku, Finland

Resolving misassembled cattle immune gene clusters with hierarchical, long read sequencing.
D. Bickhart1, J. A. Hammond2, J. C. Schwartz2, D. Harrison2, and T. P. L. Smith2, 1Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, 2The Pirbright Institute, Guildford, United Kingdom, 3The Pirbright Institute, Woking, United Kingdom, 4The Pirbright Institute, Woking, United Kingdom, 5USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

Assessing the genomic status of South African mutton, pelt and dual purpose sheep breeds using genomewide single nucleotide genotypes.
E. F. Dzomba1, M. A. Snyman2, M. Chimonyo3, and F. C. Muchadeyi4, 1University of KwaZulu-Natal, Pietermaritzburg, South Africa, 2Grooteontein Agriculture Development Institute, Middelburg, South Africa, 3Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa

Evaluation of single nucleotide polymorphism (SNP) markers for canine parentage analysis.
J. Qiu1, B. Simpson1, L. Kock1, J. Donner1, C. Cole1, S. Davison1, M. Dunn2, D. Bannush2, and A. Boyko6, 1GeneSeek, a Neogen Company, Lincoln, NE, 2Genoscoper Laboratories, Helsinki, Finland, 3Mars Veterinary, Portland, OR, 4American Kennel Club, Raleigh, NC, 5School of Veterinary Medicine, University of California-Davis, 6Cornell University, Ithaca, NY
P4057 50  Characterization of MITF coding region in llamas.
M. Anello1, M. Silbestro2, F. Veiga2, V. Trasorras2, L. Vidal Rioja1, and F. Di Rocco1, 1Instituto Multidisciplinario de Biología Celular (IMBICE) -CIC-CONICET-UNLP, La Plata, Argentina, 2Facultad de ciencias veterinarias, Universidad de Buenos Aires, Buenos Aires, Argentina

P4058 51  Fecundity genes polymorphism in indigenous sheep of eastern Ethiopia.
H. Nigussie1, M. Agaba2, Y. Mekasha3, and S. Abegaz4, 1Ambo University, Ambo, Ethiopia, 2morris.agaba@nm-aist.ac.tz, Arusha, Tanzania, United Republic of, 3International Livestock Research Institute, Addis Ababa, Ethiopia, 4Ethiopian Institutes of Agricultural Research, Debre Zeit, Ethiopia

Functional Genomics IV
13:00 - 14:00
Alpine Ballroom

P3033 52  A comprehensive porcine blood transcriptome.
H. Liu1, T. P. L. Smith2, D. J. Nonneman3, J. C. M. Dekkers4, and C. K. Tuggle5, 1Bioinformatics and Computational Biology Program, Department of Animal Science, Iowa State University, Ames, 2USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 3Department of Animal Science, Iowa State University, Ames

P3034 53  Analysis of microRNA of ovine preimplantation embryo developed in vitro.
W. Wu1, H. Tulafu, X. Xu, X. Fu, and K. Tian, Xinjiang Academy of Animal Science, Urumqi, China

P3035 54  Analysis of transcriptome profile of ovine preimplantation embryo developed in vitro.
W. Wu1, H. Tulafu, X. Xu, X. Fu, and K. Tian, Xinjiang Academy of Animal Science, Urumqi, China

P3036 55  Differential expression in feed- and energy- absorbing, partitioning, metabolizing and depositing tissues of broilers divergent for feed conversion efficiency.
H. Reyer1, M. Trakooolji1, M. Oster1, E. Magowart2, B. Metzler-Zebeli3, E. Murani1, S. Ponsuksili1, and K. Wimmers4, 1Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2Agri-Food and Biosciences Institute, Hillsborough, United Kingdom, 3University of Veterinary Medicine Vienna, Vienna, Austria

P3038 56  Chromatin accessibility in the liver and circulating immune cells of pigs, goats and chickens.
E. Giuffra1, K. A. Munyard2,3, A. Goubi4, S. Vincent-Naulleau5,6, D. Esquerre7, S. Djebali8, and S. Foissac9, 1GABI, INRA, AgroParisTech, Universite Paris Saclay, 78350 Jouy en Josas, France, 2Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia, 3GenPhySE, INRA 31320, Castanet-Tolosan, France, 4GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France, 5GABI, INRA, AgroParisTech, Universite Paris Saclay, Jouy-en-Josas, France, 6SREIT, iRCM, CEA, Universite Paris Saclay, Jouy-en-Josas, France, 7INRA, UMR1388 GenPhySE, GeF-PlaGe Genomic Facility, Castanet-Tolosan, France, 8GenPhySE, INRA, Castanet-Tolosan, France, 9INRA UMR 1388 GenPhySE, Castanet-Tolosan, France

P3039 57  Elucidating the genetic basis of tick resistance in Nguni cattle.
N. O. Mapholi1, A. A. Maiwashe2, O. Matika1, V. Riggio1, M. D. MacNeil1, C. B. Banga3, J. F. Taylor4, and K. Dzama5, 1ARC-Animal Production Institute, Irene, South Africa, Pretoria, South Africa, 2ARC-Animal Production Institute, Irene, South Africa, 3The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, 4Delta G, Miles City, MT, 5Agricultural Research Council, Irene, South Africa, 6University of Missouri, Columbia, 7University of Stellenbosch, Stellenbosch, South Africa

P3040 58  Large-scale gene co-expression network as a source of functional annotation for bovine genes.
H. Beiki1, J. M. Reece1,2, A. Pakdel1, A. Nejati Javaremi3, and A. Masoudi Nejad4, 1Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran (Islamic Republic of), 2Iowa State University, Ames, 3Isfahan University of Technology, Isfahan, Iran (Islamic Republic of), 4University of Tehran, Tehran, Iran (Islamic Republic of)

P3041 59  A selective region on OAR17 is associated with blackbone trait in Lanping Blackbone sheep.
Y. Zhang1, D. Han1, and X. Deng2, 1China Agricultural University, Beijing, China, 2Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing

P3042 60  Transcriptome profile of genes differentially expressed in the mesenteric adipose tissue of beef cattle with variation in feed intake and gain.
Epigenetics and Epigenomics III  
13:00 - 14:00  
Alpine Ballroom

P2019 61  
Adipocyte gene expression and DNA methylation patterns differ significantly between lean and obese pigs.  
M. J. Jacobsen1, J. H. Havgaard2, C. M. Junker Mentzel1, P. M. Sørensen1, S. Pundhir1, C. Anthor1, P. Karliskov-Mortensen1, C. S. Bruun1, S. Cirera1, J. Gorodkin1, C. B. Jørgensen1, R. Barrès1, and M. Fredholm1, 1Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark, 2BRIC, University of Copenhagen, Copenhagen, Denmark, The Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark

P2020 62  
Genome-wide assessment of inbred chicken lines indicates epigenetics signatures of resistance to Marek’s Disease.  
J. Song*, University of Maryland, Animal Science and Avian, College Park

P2021 63  
Age-related methylation patterns of equine blood leukocytes.  
T. Ząbek1, E. Semík, T. Szmatolka, A. Gurgul, A. Fornal, and M. Bugno-Poniewierska, National Research Institute of Animal Production, Balice, Poland

P2022 64  
Mining functional genomics and epigenetics data with livestock EpiDB.  
E. Fritz-Waters1, M. W. Vaughn1, J. P. Carson1, J. M. Reecy1, and J. E. Koltes1,4, 1Iowa State University, Ames, 2Texas Advance Computing Center, University of Texas, Austin, 3Texas Advanced Computing Center, University of Texas, Austin, 4University of Arkansas, Fayetteville

P2023 65  
Analysis of methylation patterns in bovine spermatozoa.  
M. R. Prause1, B. M. Murdock1, J. E. Sawyer1, J. L. Williams2, S. D. McKay3, and C. A. Gill4, 1Texas A&M University, College Station, 2University of Idaho, Moscow, ID, 3Texas AgriLife Research, College Station, TX, 4Department of Animal Science, Texas A&M University, College Station, 4University of Adelaide, Adelaide, Australia, 5University of Vermont, Burlington

P2024 66  
Profiling of open chromatin in chicken tissues using ATAC-seq.  
M. Halstead*, C. Kern, P. Saelao, Y. Wang1, H. Zhou, and P. J. Ross, University of California-Davis, CA

P2025 67  
Identification of tissue-specific promoters in chickens.  
C. Kern1, P. Saelao1, Y. Wang1, M. Halstead1, J. Chitwood1, T. Kim1, P. J. Ross1, I. Korf1, M. E. Delaney1, H. Cheng2, and H. Zhou1, 1University of California-Davis, 2USDA-ARS Avian Disease and Oncology Laboratory, East Lansing, MI

P2026 68  
Polar overdominance and maternal genome effects in placenta drive heterosis in utero.  
C. A. S. Estrella1,2, K. L. Kind1,3, M. Ghanipoor-Samami1,2, A. Javadmanesh1,2, C. T. Roberts1,4, and S. Hendlleder1,2, 1Robinson Research Institute, The University of Adelaide, Adelaide, Australia, 2JS Davies Epigenetics and Genetics Group, School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia, 3School of Animal and Veterinary Sciences, Roseworthy Campus, Adelaide, Australia, 4Discipline of Obstetrics and Gynaecology, School of Medicine, The University of Adelaide, Adelaide, Australia

POSTER PRESENTATIONS — Tuesday, July 26, 2016

Genetic Markers and Selection V  
7:30 - 8:30  
Alpine Ballroom

P5040 1  
Multiple genes on SSC7 affect the variation of vertebrae numbers in the pigs.  
S. H. Han1, Y. K. Kim2, H. B. Park2, Y. J. Kang3, I. C. Cho4, and H. S. Oh5, 1Educational Science Research Institute, Jeju National University, Jeju, The Republic of Korea, 2Faculy of Science Education, Jeju National University, Jeju, The Republic of Korea, 3NIAS, Rural Development Administration, Jeju, The Republic of Korea, 4Subtropical Livestock Research Institute, National Institute of Animal Science, RDA, Jeju, The Republic of Korea

P5041 2  
Searching for allelic distortion in RNA-seq data from boar’s mature sperm.  
M. Gódia1,2, E. Mayer1,2, J. Nafisi1, J. E. Rodríguez-Gil1, S. Balasch1, A. Sánchez1, and A. Clop1, 1Center for Research in Agricultural Genomics (CRAG), Cerdanyola del Valles (Barcelona), Spain, 2Instituto de Pesquisas Veterinarias Desiderio Finamor, Fundação Estadual de Pesquisa Agropecuaria, Porto Alegre, Brazil, 3Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Universitat Autonoma de Barcelona, Cerdanyola del Valles (Barcelona), Spain, 4Grup GEPORK, Masies de Roda, Spain
Comparative analysis of gene expression during postnatal growth in Czech Fleckvieh Cattle.
J. Kyselova¹, L. Barton¹, D. Burec¹, and J. Simunek¹, ¹Institute of Animal Science, Prague, Czech Republic, ²Institute of Animal Physiology and Genetics AS CR, Prague, Czech Republic

Association analysis between STAT5A and PROP1 genes and milk production in Czech National dairy goat breed: preliminary results.
J. Rychtarova¹, Z. Sztankoova², J. Schmidova², and J. Kyselova¹, ¹Institute of Animal Science, Prague, Czech Republic, ²Institute of animal science, Prague, Czech Republic

Association of acetyl-coenzyme A carboxylase α, lipoprotein lipase and fat acid synthase genes with milk parameters in Czech East Friesian breed.
Z. Sztankoova¹, J. Rychtarova¹, J. Schmidova², J. Kyselova², M. Milerski³, and T. Kott¹, ¹Institute of animal science, Prague, Czech Republic, ²Institute of Animal Science, Prague, Czech Republic

Expression of CYP2C49, CYP7A1, CYP2B22, ACSL5 and APOA4 genes in the liver of Pietrain and Landrace pigs.
M. Oczkowicz¹, K. Ropka-Molik², M. Wojtaszek¹, and J. Warzecha¹, ¹National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland, ²National Research Institute of Animal Production, Balice, Poland

A genome-wide association study for natural antibodies measured in blood of Canadian Holstein cows.
B. de Klerk¹, K. A. Thompson-Crispi², M. Sargolzaei¹, J. J. van der Poel³, B. J. Ducro³, J. A. M. van Arendonk¹, and B. Mallard⁴, ¹Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, ²Trouw Nutrition Agresearch, Guelph, ON, Canada, ³Semex Alliance, Guelph, ON, Canada, ⁴Dept of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada

Male fertility evaluation by a candidate gene approach.
W. Liu¹, Y. Yue¹, T. C. Chang¹, H. A. Adams², and K. B. Krieger³, ¹The Pennsylvania State University, University Park, PA, ²CRI International Center for Biotechnology, Mount Horeb, WI, ³Genes Cooperative, Inc., Shawano, WI

Wide genome involvement in response to long-term selection for antibody response in an experimental population of White Leghorn chickens.
M. Lillie¹, Swedish University of Agricultural Sciences, Uppsala, Sweden

Application of DNA marker-assisted selection using SNPs of reproduction related genes and their genotype combination effects on litter size in black pigs of Jeju island.
J. H. Kang¹, E. A. Lee¹, S. H. Lee¹, Y. C. Ryu¹, Y. I. Oh¹, and K. C. Hong¹, ¹Korea University, Seoul, The Republic of Korea, ²Jeju National University, Jeju, The Republic of Korea

A genome wide scan for signature of positive selection in some Iranian sheep breeds.
Z. Manzari¹, M. Mehrabani Yeghaneh¹, A. Nejati-Javaremi¹, M. Gholizadeh², and M. H. Moradi³, ¹University of Tehran, Tehran, Iran (Islamic Republic of), ²Sari Agricultural Sciences and Natural Resources University, Sari, Iran (Islamic Republic of), ³Arak University, Arak, Iran (Islamic Republic of)

Transcriptome hallmarks of musculoskeletal fatigue in blood of Arabian horses under racing training regime.
M. Stefanik-Szmukier¹, K. Ropka-Molik², K. Zukowskii, and K. Piorkowska¹, ¹Department of Horse Breeding, Institute of Animal Science, University of Agriculture in Cracow, Cracow, Poland, ²National Research Institute of Animal Production, Balice, Poland

Genetic investigation of sheep families demonstrating the entropion eye condition.
T. Hadfield² and N. E. Cockett, Utah State University, Logan

**Genetics and Disease V**

7:30 - 8:30
Alpine Ballroom

Genomics assisted introgression of viral resistance in commercial common carp strains.
R. Tadmor-Levi¹, E. Asulin¹, G. Halata², and L. David¹, ¹The Hebrew University of Jerusalem, Rehovot, Israel, ²Agricultural Research Organization, Beit-Dagan, Israel

Fine mapping a sheep genomic locus involved in viral restriction of ovine lentivirus.
A. T. Massa¹, M. R. Mousel², M. A. Highland², J. O. Reynolds³, D. P. Knowles³, J. B. Taylor², and S. N. White¹, ¹Washington State University, Pullman, WA, ²USDA, ARS, Animal Disease Research Unit, Pullman, WA, ³USDA, ARS, U.S. Sheep Experiment Station, Dubois, ID

Precision medicine and the 99 lives cat genome sequencing initiative.
L. Lyons¹, Department of Veterinary Medicine & Surgery, College of Veterinary Medicine, University of Missouri-Columbia
Expression of TLR2 Pattern Recognition Receptor on Mononuclear Cells Cultured with Ligands among Cattle Ranked by Estimated Breeding Values for Adaptive Immune Response Traits.
L. Wagner-Lesperance*, H. Atalla, M. Emam, N. Gallo, D. Hodkins, M. McLean, L. Read, and B. Mallard, Department of Pathobiology, University of Guelph, Guelph, ON, Canada

Investigating a single nucleotide polymorphism in DDB2 as a risk factor for squamous cell carcinomas of the nictitans in the Hallinger and Belgian horse breeds.
R. Bellone¹, J. Liu¹, S. Vig¹, T. M. Michaud¹, C. M. Reilly¹, E. Bentley¹, J. L. Petersen¹, and M. Lassaline¹, ¹University of California-Davis, ¹BluePearl, Tampa, FL, ³University of Wisconsin-Madison, ³University of Nebraska-Lincoln

Challenges in the investigation of eight inherited diseases in ruminants – An Australian perspective.
I. Tammen¹, S. A. Woolley¹, E. R. Tsimnadis¹, N. Nowak¹, R. L. Tulloch¹, M. S. Khatkar¹, and B. A. O’Rourke², ¹Faculty of Veterinary Sciences, School of Life and Environmental Sciences, The University of Sydney, Camden, Australia, ²The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, Australia

Extended scrapie incubation time in goats singly heterozygous for PRNP S146 or K222: An update after 7 years.
S. White¹,², J. O. Reynolds², D. F. Waldron¹, D. A. Schneider¹, and K. I. O’Rourke¹, ¹USDA-ARS Animal Disease Research, Pullman, WA, ²Washington State University, Pullman, ³Texas A&M AgriLife Research, San Angelo

Evaluating the accuracy of imputation in the highly polymorphic MHC region of genome.
M. Emam¹, M. Sargolzaei², S. Tabatabaei¹, S. L. Cartwright³, F. S. Schenkel³, F. Miglior³, J. P. Chesnais³, and B. Mallard³, ¹Department of Pathobiology, University of Guelph, Guelph, ON, Canada, ²Semex Alliance, Guelph, ON, Canada, ³Department of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada, ³University of Guelph, Guelph, ON, Canada, ³Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, ³The Semex Alliance, Guelph, ON, Canada, ³Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada

Incidence of SOD1 mutation in a sample of pure breed German Shepherd in Colombia.
M. A. Novoa* and E. Bernal, GENETICA ANIMAL DE COLOMBIA LTDA., Bogota, Colombia

Bioinformatics, Statistical Genetics, and Genomic Technologies V
7:30 - 8:30
Alpine Ballroom

A reduced panel to determine beef cattle breed composition.

Predicting regulatory SNPs within enhancers and promoters in cattle.
Q. Nguyen, R. L. Tellam, J. Kijas, W. Barendse, and B. P. Dalrymple*, CSIRO Agriculture, Brisbane, Australia

BovineMine: A bovine genome data mining warehouse.
C. G. Elsk*, D. R. Unni, A. Tayal, C. M. Diesh, and D. E. Hagen, University of Missouri, Columbia

Bioinformatics resources for animal genomics using CyVerse cyberinfrastructure.
J. E. Koltes¹, J. M. Reecy¹, E. Lyons¹, F. McCarthy¹, M. W. Vaughan¹, J. P. Carson¹, E. Fritz-Waters¹, and J. Williams¹, ¹Iowa State University, Ames, ²University of Arizona, Tucson, AZ, ³Texas Advanced Computing Center, University of Texas, Austin, TX, ³Texas Advanced Computing Center, University of Texas, Austin ³Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

Diet analysis of grasscutter (Thryonomys swinderianus) using next generation sequencing.
C. Adenyo¹,², H. Ando¹, B. B. Kayang¹, E. Inoue¹, and M. Inoue-Murayama¹, ¹University of Ghana, Accra, Ghana, ²Kyoto University, Kyoto, Japan, ³National Institute for Environmental Studies, Tsukuba, Japan, ³Toho University, Funabashi, Japan

Application of artificial neural networks to genome-enabled prediction of growth traits in Brangus heifers.
S. O. Peters¹, M. Sinecen², K. Kizilkaya², and M. Thomas³, ¹Department of Animal Science, Berry College, Mount Berry, GA, ²Adnan Menderes University, Aydin, Turkey, ³Colorado State University, Fort Collins

Combining RNA sequencing technologies to annotate the bovine genome.
D. E. Hagen¹, D. R. Unni, and C. G. Elsk*, University of Missouri, Columbia
P1043 32 Identification of regulatory elements in three domesticated species.

P1044 33 Whole transcriptome termini site sequencing (WTTS-seq): a next generation sequencing method to accurately profile gene expression and alternative polyadenylation with one pipeline.
X. Zhou*, R. Li, J. J. Michal, X. L. Wu, Z. Liu, H. Zhao, Y. Xia, R. M. Harland, and Z. Jiang, 1Washington State University, Pullman, WA, 2The Chinese University of Hong Kong, Hong Kong, China, 3University of California Berkeley

P1045 34 Determination of genome-wide linkage disequilibrium in the South African Bonsmara reference population.
L. M. Bosman, R. R. van der Westhuizen, C. D. Visser, and E. van Marle-Koster, University of Pretoria, Pretoria, South Africa

P1046 35 Deciphering chicken fatness trait with integrative genetics and genomics approaches.
C. K. Kho*, K. K. Cheung, R. Kuo, L. Eory, P. M. Hocking, and D. Burt, 1The Roslin Institute, Royal (Dick) School of Veterinary Medicine, University of Edinburgh, Edinburgh, United Kingdom, 2Department of Veterinary Services, Ministry of Agriculture & Agro-Based Industry Malaysia, Putrajaya, Malaysia

Genetic Diversity and Polymorphisms V
7:30 - 8:30
Alpine Ballroom

P4059 36 Origins and genetic structure of Creole cattle inferred from Y-chromosomal variation.
C. Ginja*, C. Penedo, O. Cortés, J. Martin-Burrel, A. Egió, L. T. D. Gama, J. V. Delgado Bermejo, B. Consortium, and A. Martínez-Martínez, 1CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal, 2Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, 3Univrsidad Complutense de Madrid, Madrid, Spain, 4Labbtorio de Genética Bioquímica, Universidad de Zaragoza, Zaragoza, Spain, 5Embrapa-Laboratório de Genômica e Melhoramento Animal, Campo Grande, Brazil, 6Faculdade de Medicina Veterinária, Universidade Técnica de Lisboa, Lisboa, Portugal, 7Department of Genética, Universidad de Cordoba, Cordoba, Spain

P4060 37 Runs of homozygosity reveal natural selection footprints of some African chicken breeds and village ecotypes.
A. R. Elbeltagy*, D. S. Fleming, F. Bertolini, A. G. Van Goor, C. M. Ashwell, C. J. Schmidt, S. J. Lamont, and M. F. Rothschild, 1Department of Animal Science, Iowa State University, Ames, 2Department of Animal Biotech. Animal Production Research Institute, Cairo, Egypt, 3Department of Poultry Science, North Carolina State University, Raleigh, 4Department of Animal and Food Sciences, University of Delaware, Newark

P4061 38 The ramification of meiotic recombination differences in sheep.
K. M. Davenport and B. M. Murdoch, University of Idaho, Moscow

P4062 39 DNA sequencing and genetic polymorphism discovery in the canine monoamine oxidase A (MAOA) gene.
J. Sacco*, A. Raplin, P. Skonieczny, and M. Ohman, Drake University, Des Moines, IA

P4063 40 Genotyping of ApaLI RFLP at heat shock transcription factor 1 in Creole and Holstein cattle differing in coat type and associations with molecular breeding value and DH traits.
Y. R. Velez*, J. Patino, E. Soto-Moreno, B. Velez, T. S. Sonstegard, and M. Pagán-Morales, 1University of Puerto Rico, Mayagüez, Mayagüez, Puerto Rico, 2University of Puerto Rico, Mayaguez, PR, Puerto Rico, 3USDA, ARS, BFGL, Belville, MD, 4Department of Animal Science, University of Puerto Rico, Mayaguez Campus, Mayaguez, Puerto Rico

P4064 41 Genetic diversity and population structure of wild and semi-domesticated reindeer (Rangifer tarandus) inhabited in Northeastern Siberia based on single nucleotide polymorphism markers.

P4065 42 MicroGBS - High-throughput microsatellite genotyping using Illumina sequencing platforms.
G. Waldhaiser*, USDA, ARS, Warmwater Aquaculture Research Unit, Stoneville, MS

P4066 43 Genetic diversity of pig populations from the US mainland, Pacific islands and China: Autosomal SNP evaluation.

Interaction of STAT1 and PGR specific genotypes affects milk production in slick and normal coat Holsteins.
B. Velez¹, J. Patino¹, Y. R. Velez⁵, T. S. Sonstegard¹, and M. Pagán-Morales⁶, ¹University of Puerto Rico, Mayaguéz, PR, Puerto Rico, ²University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico, ³USDA, ARS, BFGL, Beltsville, MD, ⁴Department of Animal Science, University of Puerto Rico, Mayaguez Campus, Mayaguez, Puerto Rico

Genetic differences in a Colombian Paso horse breed by gait selection.
M. A. Novoa¹, ², and L. F. García³, ¹GENETICA ANIMAL DE COLOMBIA LTDA., Bogota, Colombia, ²UNIVERSIDAD NACIONAL DE COLOMBIA, Bogota, Colombia

SNP discovery and allele frequency estimation in indigenous breeds of South Africa.
A. Zwane¹, A. A. Maitwashe¹, and E. van Marle-Koster⁶, ¹Agricultural Research Council, Pretoria, South Africa, ²ARC-Animal Production Institute, Irene, South Africa, ³University of Pretoria, South Africa

Extensive functional class I MHC diversity in sheep.
K. Ballingall¹, ², S. Goh¹, J. M. Pemberton¹, and K. Dicks¹, ¹Moredun Research Institute, Edinburgh, United Kingdom, ²Royal Veterinary College, Hatfield, United Kingdom

Development of a 55K SNP array for oysters (C. gigas and O. edulis).
A. F. Gutierrez¹, F. Turner², T. P. Bean³, K. Gharbi¹, and R. D. Houston⁴, ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, United Kingdom, ²Edinburgh Genomics, University of Edinburgh, United Kingdom, ³Center for Environment Fisheries and Aquaculture Science, Cefas Weymouth Laboratory, Weymouth, United Kingdom

Functional Genomics V
7:30 - 8:30
Alpine Ballroom

Study of differentially expressed short-RNAs in swine backfat between fat and lean animals and target prediction of genes regulating fat traits.
R. Davoli¹, P. Zambonelli², E. Gaffo³, M. Zappaterra¹, and S. Bortoluzzi¹, ¹Bologna University, Department of Agricultural and Food Sciences (DISTAL), Bologna, Italy, ²Padova University, Department of Molecular Medicine, Padova, Italy

Characterization of exosomal immune-related microRNAs in colostrum and milk from average, low and high immune responder cows.
H. Atalla¹, ², B. Mallard¹, ², and N. A. Karrow¹, ¹Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²Department of Pathobiology, University of Guelph, Guelph, ON, Canada

Identification and expression analysis of Bovine X degenerate Y-Chromosome genes.
F. A. Ponce de Leon¹, Y. Guo¹, B. A. Crooker¹, T. G. McDonnell¹, and T. P. L. Smith¹, ¹Department of Animal Science, University of Minnesota, St. Paul, MN, ²University of Minnesota, Saint Paul, MN, ³USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE

Gene expression In developing goat testes: Sequencing, assembly and identification of caprine spermatogenesis transcriptome.
B. Barcelos¹, ², S. Fuentes-Soriano¹, J. Watts¹, F. Williams¹, F. R. B. Ribeiro¹, W. B. Foxworth¹, L. C. Nuti¹, G. R. Newton¹, and S. K. Lewis¹, ¹Prairie View A&M University, Prairie View, TX, ²School of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Brazil

Reduced cell cycle gene expression in adipose tissue of chickens during juvenile development.
X. Wang¹, ², A. Ropeclewski², N. Cook¹, A. Bohannon-Stewart², and S. Nashashon¹, ¹Tennessee State University, Nashville, ²Pittsburgh Supercomputing Center, Pittsburgh, PA

Gene network analysis identifies rumen epithelial processes perturbed by diet and correlated with methane production and yield.
R. Xiang¹, J. McNally², S. J. Rowe¹, A. Jonker³, C. Pinares-Patino³, J. Bond³, H. V. Oddÿ, P. Vercoe³, J. C. McEwan³, and B. P. Dalrymple³, ¹CSIRO Agriculture, Brisbane, Australia, ²CSIRO Agriculture, Armidale, Australia, ³AgResearch, Mosgiel, New Zealand, ⁴AgResearch, Palmerston North, New Zealand, ⁵CSIRO Agriculture, Canberra, Australia, ⁶NSW Dept Primary Industries, Armidale, Australia, ⁷NSW Department of Primary Industries, Armidale, Australia, ⁸University of Western Australia, Perth, WA, Australia
P3049 56  Gene expression profile of satellite cells differentiation from longissimus dorsi and semimembranosus muscle.
S. De las Heras-Saldana¹, K. Y. Chung², S. H. Lee¹, and C. Gondro³, ¹School of Environmental and Rural Science, University of New England, Armidale, Australia, ²Hanwoo Research Institute, NIAS, RDA, Pyeongchang, The Republic of Korea, ³Chungnam National University, Daejeon, The Republic of Korea, ⁴School of Environmental & Rural Science, University of New England, Armidale, Australia

P3050 57  Functional genomics of high altitude disease in Angus cattle: Leveraging -OMICS and systems biology to better understanding of the function and role of key contributing genes.
A. Canovas¹, R. Cockrum², D. Brown³, S. Riddle³, J. M. Neary⁴, T. N. Holt⁴, J. F. Medrano⁵, R. M. Enns⁶, S. E. Speidel⁴, K. Cammack⁴, K. R. Stenmark⁸, and M. G. Thomas⁷, ¹University of Guelph, Guelph, ON, Canada, ²Virginia Polytechnic Institute and State University, Blacksburg, ³University of Colorado, Denver, ⁴Colorado State University, Fort Collins, ⁵College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, ⁶University of California-Davis, ⁷Department of Animal Science, Colorado State University, Fort Collins, ⁸University of Denver, CO

P3051 58  Comparative aspects of functional annotation of genomes in the FAANG project.
C. K. Tuggle, Iowa State University, Ames

P3052 59  Characterization of circular RNAs in relation to embryonic muscle development in chicken.
H. Ouyang¹, Q. Nie², and X. Zhang¹, ¹College of Animal Science, South China Agricultural University, Guangzhou, China, ²South China Agricultural University, Guangzhou, China

P8000 60  Allelic diversity of productive, reproductive & fertility traits genes of buffalo and cattle.
M. Moaen-ud-Din⁴, PMAS-Arid Agriculture University, Rawalpindi, Pakistan

P8001 61  3D nuclear positioning of IGF2 alleles and trans interactions with imprinted genes.
Y. Lahlhib-Mansais¹, M. Marti Marimon¹, V. Voillet¹, F. Mompart¹, J. Riquet¹, S. Foissac¹, D. Robelins¹, H. Acloque¹, Y. Billon², N. Villa-Vianen³, L. Liabert¹, and M. Boussou-Matet Yerle¹, ¹INRA UMR 1388 GenPhysE, Castanet-Tolosan, France, ²INRA UFI 1372 GenESI, Surgères, France, ³INRA UR0875 MIAT, Castanet-Tolosan, France

P8002 62  A genomic landscape of mitochondrial DNA insertions in the nuclear pig genome.
G. Schiavo¹, O. I. Hoffmann¹, A. Ribanti², V. J. Utzeri², M. C. Ghionda¹, S. Bovo¹, and L. Fontanesi¹, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ²Agricultural Biotechnology Center, Godollo, Hungary

P8003 63  The gene duplication of beta-2 microglobulin in artiodactyla and remains intact only in pigs.
M. T. Le, M. K. Choi, H. Cho, and C. Park³, Konkuk University, Seoul, The Republic of Korea

P8004 64  A comprehensive gene catalogue of the horse Y chromosome.
J. Janécka¹, L. Orlando¹, M. Schuberl¹, S. Ghosh¹, T. A. Stout¹, B. P. Chowdhary³, and T. Raudsepp⁴, ¹Duquesne University, Pittsburgh, PA, ²Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark, ³Natural History Museum of Denmark Copenhagen University, Copenhagen, Denmark, ⁴Texas A&M University, College Station, TX, ⁵Utrecht University, Utrecht, Netherlands, ⁶Qatar University, Doha, Qatar

P8005 65  Genes responding to recent selection in Berkshire and Duroc pigs.
K. D. D. Song¹, D. Shin⁴, and H. K. Lee¹, ¹The Animal Molecular Genetics and Breeding Center, Chonbuk National University, Jeonju, South Korea, ²The Animal Molecular Genetics and Breeding Center, Chonbuk National University, Jeonju, The Republic of Korea, ³Department of Animal Biotechnology, Chonbuk National University, Jeonju, The Republic of Korea

P8006 66  Identification and characterization of Copy Number Variations in cattle.
R. Letai⁶, D. Esquerre², J. Barbier³, C. Grohs¹, S. Fritz⁶, C. Klop², R. Philippe², V. Blanquert², D. Boichard³, D. Rocha³, and M. Boussaha¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²Get-PlaGe, INRA, Castanet-Tolosan, France, ³AGILE, Paris, France, ⁴Sigenae, INRA, Castanet Tolosan, France, ⁵GMA, INRA, Université de Limoges, Limoges, France, ⁶GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France

P8007 67  RefSeq & Gene - NCBI resources to support comparative genomics.
K. D. Pruitt, T. D. Murphy, F. Thibaud-Nissen, and P. A. Kitts, National Institutes of Health, NCBI, Bethesda, MD

P8008 68  The NCBI Eukaryotic Genome Annotation Pipeline.
F. Thibaud-Nissen¹, M. DiCuccio, W. Hlavina, A. Kimchi, P. A. Kitts, T. D. Murphy, K. D. Pruitt, and A. Souvorov, National Institutes of Health, NCBI, Bethesda, MD
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