

CONFERENCE INFORMATION SCIENTIFIC PROGRAM

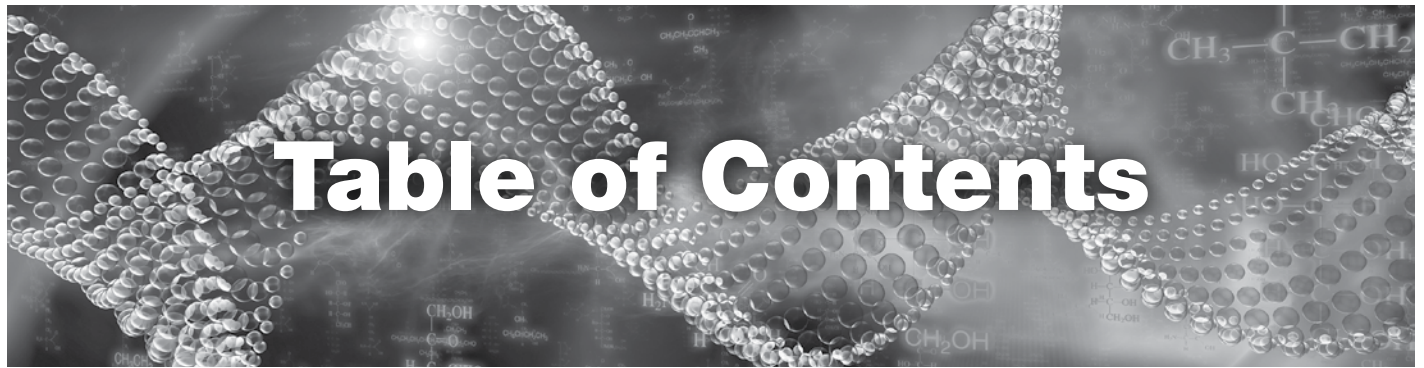


35th International Society for Animal Genetics Conference

7.23.2016 – 7.27.2016
Salt Lake City, Utah



<https://www.asas.org/meetings/isag2016>



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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.



**WELCOME TO THE 35th CONFERENCE OF THE
INTERNATIONAL SOCIETY FOR ANIMAL GENETICS**
Salt Lake City, Utah • July 23 – July 27, 2016

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 Filippo 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

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
Cecelia Penedo
Chris Tuggle
Bruce Whitelaw
Björn Höyheim
Stephen White
Rebecca Bellone, Teruaki Tozaki
Catarina Ginja
Ntanganedzeni Olivia Mapholi
Elisabetta Giuffra
Hans Lenstra
James Kijas

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

Gold Level

Eurofins

LGC Biosearch Technologies

Texas A&M University

Silver Level

Ajinomoto Heartland

American Society of Animal Science

American Society of Animal Science Foundation

Dairy Research Institute/Innovation Center for US Dairy

USAID

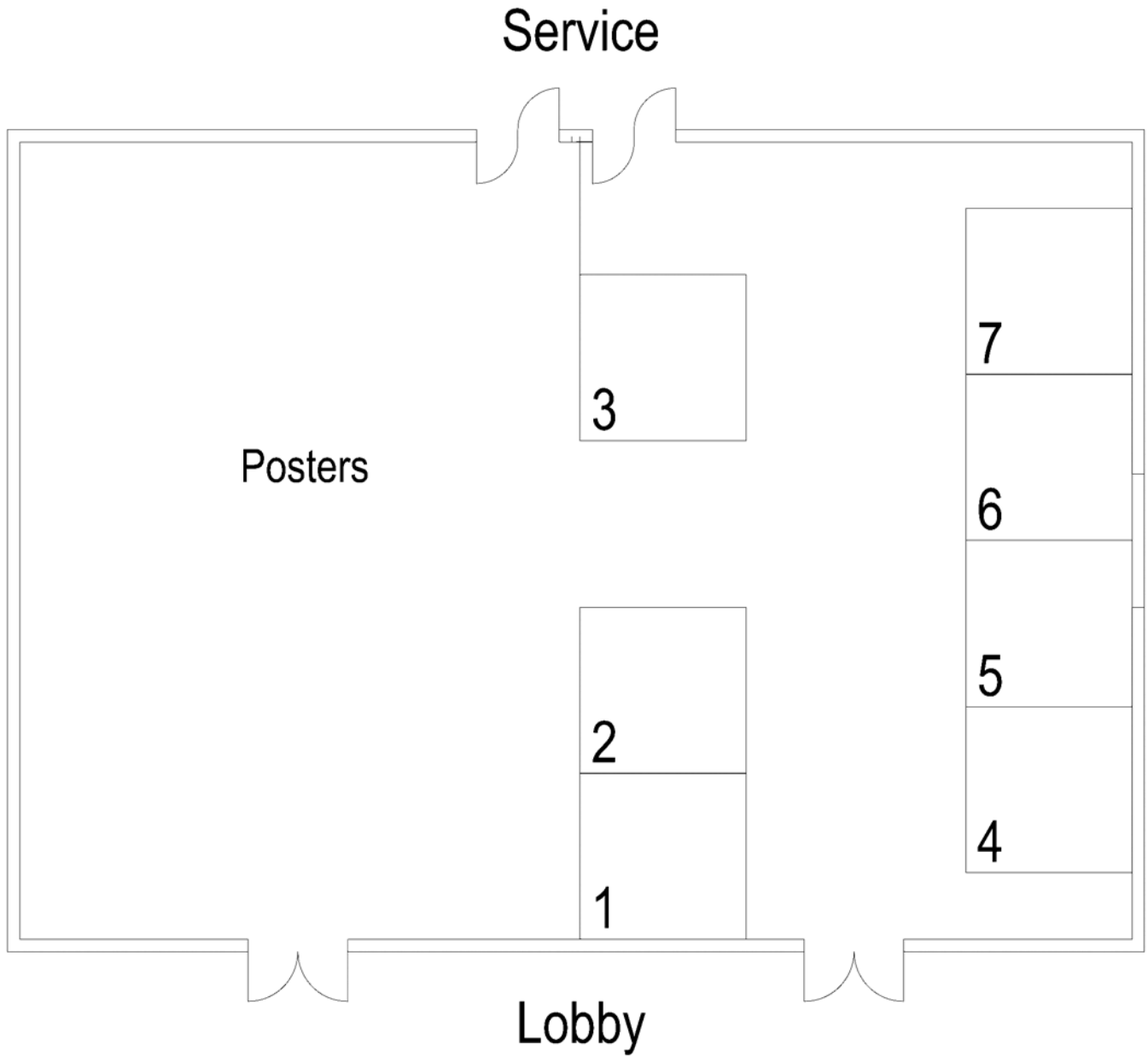
Bronze Level

Cobb-Vantress

PLOS Genetics

Zoetis

Exhibit Floor Plan



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



Scientific Program

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.
Andre Eggen, Illumina
- 8:45 S0100 **Important lessons from complex genomes.**
T. R. Gingeras, Cold Spring Harbor Laboratory, Functional Genomics, Cold Spring Harbor, NY*
- 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. Djebali^{1,2,3}, B. Rodríguez Martín^{2,3}, E. Palumbo^{2,3}, D. D. Pervouchine^{2,3}, A. Breschi^{2,3}, C. Davis⁴, A. Dobin⁴, G. Alonso³, A. Rastrojo⁵, B. Aguado³, T. R. Gingeras⁴, and R. Guigó^{2,3}, 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, A. J. Chamberlain², 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.

ORAL SESSIONS & WORKSHOPS – Sunday, July 24

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 Paul, 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. Penedo², 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. Cole³, S. Davison³, M. Dunn⁴, D. Bannasch⁵, and A. Boyko⁶, 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. Piestrzynska-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. Pirani, 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. Dai¹, J. Wang², B. Tang², and N. Li¹, ¹China Agricultural University, Beijing, ²Beijing Genprotein Biotechnology Company, Beijing, China*
- 16:15 P7002 **Skin-specific transgenic expression of ovine β -catenin in mice.**
*J. Wang*¹, K. Cui², D. Han², Z. Yang², and X. Deng³, ¹College of Animal Science and Technology, China Agricultural University, Beijing, China, ²China Agricultural University, Beijing, China, ³Key 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. McDanel**, L. A. Kuehn, and J. W. Keele, 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. Neuhoff¹, C. Große-Brinkhaus², M. J. Pröll¹, M. J. Uddin³, S. Aqter 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. Xu², Y. Zhang², A. Black Pyrkosz³, M. E. Delany⁴, D. Frishman², and H. H. Cheng³, 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/Resistance to Bovine Tuberculosis.**
K. E. Killick¹, K. E. McLoughlin¹, N. C. Nalpas², L. Burkitt-Gray¹, I. W. Richardson³, H. L. Wiencko⁴, D. A. Magee¹, J. A. Browne¹, B. Villarreal-Ramos⁵, H. M. Vordermeier⁵, D. P. Berry⁶, D. G. Bradley³, E. Gormley⁷, S. V. Gordon⁷, and D. E. MacHugh¹, ¹School of Agriculture and Food Science, University College Dublin, Ireland, ²Proteome Center, University of Tübingen, 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. White^{1,2}, M. V. Gonzalez^{2,3}, J. O. Reynolds², J. B. Taylor⁴, and D. P. Knowles^{1,2}, 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. Sargolzaei³, J. J. van der Poel¹, B. J. Ducro¹, 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
- 16:45 P6041 **Microarray analysis of genomic aberrations of horse sarcoids.**
K. Pawlina¹, A. Gurgul¹, J. Klukowska-Rötzler², C. Koch², K. Mählmann³, 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 colonic polyps revealed by studies on the porcine model of human familial adenomatous polyposis.**
T. Flisikowska¹, M. Stachowiak², C. Wander¹, A. Wagner¹, C. Wurmser³, A. Perkowska², F. Bruening¹, S. Bauersachs⁴, A. Kind¹, R. Fries³, M. Switonski², D. Saur², 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 Muenchen, Freising, Germany, ⁴Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland, ⁵Klinikum Rechts der Isar II, Technische Universität München, Munich, Germany

- 17:15 P6017 **A high density genome-wide scan for genetic risk factors of insect bite hypersensitivity (IBH): A Horsegene Project Initiative.**
B. D. Velie¹, M. Shrestha¹, L. Francois², A. Schurink³, A. Stinckens², S. Blott⁴, B. J. Ducro³, S. Mikko¹, R. Thomas⁵, M. Sundquist⁶, S. Eriksson¹, N. Buys², and G. Lindgren¹, ¹Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, 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, ⁶Östra Greda Research Group, Borgholm, Sweden
- 17:19 P6021 **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*
- 17:23 P6040 **Allele specific expression analysis of the porcine blood transcriptome reveals extensive cis-regulation in immunity-related genes.**
T. Maroille¹, G. Lemonnier¹, D. Esquerré², M. J. Mercat³, C. Rogel-Gaillard⁴, and J. Estellé¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²INRA, UMRI388 GenPhySe, GeT-PlaGe Genomic Facility, Castanet-Tolosan, France, ³IFIP-BIOPORC, Le Rheu, France, ⁴GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France
- 17:27 P6047 **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. Wagter-Lesperance^{}, H. Atalla, M. Emam, N. Gallo, D. Hodgins, M. McLean, L. Read, and B. Mallard, Department of Pathobiology, University of Guelph, Guelph, ON, Canada*

**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. Wiedemar¹, J. Dietrich¹, V. Jagannathan¹, M. Drögemüller¹, T. Druet⁴, A. Galichet⁵, M. C. Penedo⁶, E. Müller², P. Roosje⁷, M. Welle⁸, and T. Leeb¹, 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. Schubert³, S. Ghosh⁴, T. A. Stout⁵, B. P. Chowdhary⁶, 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, ⁵Utrecht University, Utrecht, Netherlands, ⁶Qatar University, Doha, Qatar
- 14:45 S0122 **Improving the structural and functional annotation of the equine reference genome.**
J. N. MacLeod¹, M. S. Hestand², L. Orlando³, and T. S. Kalbfleisch⁴, ¹University of Kentucky, Lexington, KY, ²KU Leuven, Leuven, Belgium, ³Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark, ⁴University of Louisville, KY
- 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. 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
- 16:15 P2021 **Age-related methylation patterns of equine blood leukocytes.**
T. Zqbek^{}, 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. Finno¹, J. L. Petersen², R. Bellone³, and J. N. MacLeod⁴, 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

- 14:00 **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.**
T. Zerjal¹, G. Monneret^{1,2}, M. Moroldo³, J. L. Coville¹, M. Tixier-Boichard¹, A. Rau¹, G. Nuel², and F. Jaffrezic⁴, ¹INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, ²UPMC, LPMA, Paris, France, ³INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, ⁴GABI, INRA, AgroParisTech, Université Paris Saclay, 78350 Jouy en Josas, France
- 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. Lawal¹, D. Wragg², P. Silva³, K. Vanmechelen⁴, A. Vereijken⁵, D. D. Wu⁶, R. M. Al-Atiyat⁷, and O. Hanotte⁸, 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 Applied Sciences, 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. Nassar^{*1,2}, 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. Chen^{*1}, X. Du¹, C. Zhang², 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. Kern^{*1}, P. Saelao¹, Y. Wang¹, M. Halstead¹, J. Chitwood¹, T. Kim¹, P. J. Ross¹, I. Korf¹, M. E. Delany¹, H. Cheng², 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. Halstead^{*}, C. Kern, P. Saelao, Y. Wang, H. Zhou, and P. J. Ross, University of California-Davis
- 11:30 P3052 **Characterization of circular RNAs in relation to embryonic muscle development in chicken.**
H. Ouyang¹, Q. Nie^{*2}, 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. Khoo^{*1,2}, 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: Affematrix
Canyon C

- 8:30 **Introductory Remarks.**
- 8:31 P4020 **Diversity analysis of transcribed MHC class II β loci in Japanese quail.**
S. Asaji¹, S. Suzuki², T. Ishige³, K. Hosomichi⁴, T. Shiina², H. Hara¹, T. Hirano¹, and K. Hanzawa^{*1}, 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. Le^{*}, H. J. Lee, J. Lee, and C. Park, Konkuk University, Seoul, The Republic of Korea
- 9:00 P5034 **Differential proportion of ancestral MHC haplotypes in Brangus breed.**
D. Goszczyński^{*1}, C. Corbi¹, H. Morales¹, D. Posik¹, E. Villegas Castagnasso¹, S. Munilla², P. Peral García¹, A. Rogberg^{1,2}, R. J. C. Cantet^{2,3}, and G. Giovambattista¹, ¹IGEVEV – Instituto de Genética Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, ²Departamento de Producción, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina, ³INPA – Unidad Ejecutora UBA-CONICET de Investigaciones en Producción Animal, Buenos Aires, Argentina
- 9:15 P4052 **The Swine Leukocyte Antigen (SLA) Nomenclature System of the International Society for Animal Genetics (ISAG) and the International Union of Immunological Societies (IUIS): Update 2016.**
S. Ho^{*1}, 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, Université 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, Austria

- 9:30 P5058 **The Ovar-DRB1 *0404 haplotype is associated with growth and lifetime prolificacy ewe traits.**
M. U. Cinar^{1,2}, M. R. Mouse³, J. O. Reynolds³, L. M. Hermann-Hoesing¹, J. B. Taylor⁴, D. P. Knowles^{3,5}, and S. N. White^{3,5,6}
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
- 9:45 P6054 **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. Lin², and C. J. McInnes², ¹Moredun Research Institute, Edinburgh, United Kingdom, ²Moredun Research Institute, Penicuik, United Kingdom
- 10:00 **Break.**
- 10:30 S0117 **Development of the IPD-MHC Database.**
J. Robinson¹, G. Maccari², R. E. Bontrop³, S. Ho⁴, U. Grimholt⁵, J. Kaufman⁶, L. Guethlein⁷, K. Ballingall⁸, S. G. Marsh¹, and J. A. Hammond², ¹Anthony Nolan Research Institute and UCL Cancer Institute, London, United Kingdom, ²The Pirbright Institute, Guildford, United Kingdom, ³Biomedical Primate Research Centre, Rijswijk, Netherlands, ⁴Gift of Life Michigan, Ann Arbor, MI, ⁵Norwegian Veterinary Institute, Oslo, Norway, ⁶University of Cambridge, United Kingdom, ⁷Stanford University, CA, ⁸Moredun Research Institute, Edinburgh, United Kingdom
- 11:00 P8003 **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
- 11:15 P6052 **Evaluating the accuracy of imputation in the highly polymorphic MHC region of genome.**
M. Emam¹, M. Sargolzaei², S. Tabatabaei¹, S. L. Cartwright³, F. S. Schenkel⁴, F. Miglior⁴, J. P. Chesnais², and B. Mallard⁴
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
- 11:30 P4071 **Extensive functional class I MHC diversity in sheep.**
K. Ballingall¹, S. Goh², J. M. Pemberton³, and K. Dicks³, ¹Moredun Research Institute, Edinburgh, United Kingdom, ²Royal Veterinary College, Hatfield, United Kingdom, ³The University of Edinburgh, United Kingdom
- 11:40 **Discussion: IPD-MHC and dealing with next generation sequence data.**
- 11:55 **Committee Business Meeting.**

Workshop: Equine Genetics & Thoroughbred Parentage Testing

8:30 - 12:00

Chair: Cecilia Penedo, University of California-Davis

Sponsor: ASAS Foundation
 Canyon A

- 8:30 **Welcoming Remarks.**
- 8:35 **Horse Comparison Test (Standing Committee).**
- 9:30 **ISBC Directives and Lab Performance (Cecilia Penedo).**
- 10:00 **Break.**
- 10:30 P4046 **Development and evaluation of a set of 100 SNP markers for DNA typing in the domestic horse.**
H. Holl¹, J. Vanhnasy², R. Everts², D. Cook¹, S. Brooks¹, M. Carpenter¹, C. Bustamante¹, and C. Lafayette¹, 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. Xu*¹, *R. Haas*², *J. Sun*³, *Y. Zhou*¹, *D. Bickhart*¹, *J. Li*⁴, *J. Song*⁵, *T. Sonstegard*⁶, *C. P. VanTassell*¹, *H. Lewin*⁷, and *G. E. Liu*^{*1},
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, 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. Shabtay*¹, *M. Soller*², *J. Sölkner*³, *G. Mészáros*³, *T. Sonstegard*⁴, *E. O. Ünal*⁵, *H. J. Huson*⁶, *Y. T. Utsunomiya*⁷, and *E. Lipkin*^{*2}, ¹Department of Ruminant Sciences, Agricultural Research Organization (ARO), Neve 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
- 9:45 P4029 **Launching SheepGenomesDB: 100 million variants from nearly 500 sheep genomes.**
J. Kijas^{*1}, *R. Brauning*², *S. M. Clarke*², *A. McCulloch*³, *N. E. Cockett*⁴, *G. Saunders*⁵, *M. Naval Sanchez*¹, *S. McWilliam*¹, and *H. Daetwyler*⁶, 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.**
- 10:45 P4041 **Pooled whole-genome sequencing reveals molecular signatures of natural adaptive selection in Djallonke sheep of Ghana.**
M. Yaro^{*1}, *K. A. Munyard*¹, *E. Morgan*¹, *R. J. Allcock*², *M. J. Stear*³, and *D. M. Groth*¹, 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. Elbeltagy^{*1,2}, *D. S. Fleming*¹, *F. Bertolini*¹, *A. G. Van Goor*¹, *C. M. Ashwell*³, *C. J. Schmidt*⁴, *S. J. Lamont*¹, and *M. F. Rothschild*¹, 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.**
H. Blackburn^{*1}, *D. A. Faria*², *C. Wilson*³, and *S. R. Paiva*⁴, ¹National Animal Germplasm Program ARS-USDA, Ft. Collins, CO, ²National Animal Germplasm Program, Fort Collins, CO, ³National Animal Germplasm Program - ARS- USDA, Fort Collins, CO, ⁴EMBRAPA-LABEX US - Secretariat International Affairs, Brasilia, Brazil
- 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. Ginja^{*1}, *C. Penedo*², *O. Cortés*³, *I. Martín-Burriel*⁴, *A. Egito*⁵, *L. T. D. Gama*⁶, *J. V. Delgado Bermejo*⁷, *B. Consortium*⁷, and *A. Martínez-Martínez*⁷, 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 Veterinária, Universidade Técnica de Lisboa, Lisboa, Portugal, ⁷Departamento de Genética, Universidad de Córdoba, Córdoba, 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. Murali¹, R. A. Harris¹, A. C. English¹, X. Qin¹, E. Skinner¹, S. Richards¹, J. Rogers¹, Y. Han¹, V. Vee¹, M. Wang¹, Q. Meng¹, M. P. Heaton², T. P. L. Smith², B. P. Dalrymple³, J. Kijas³, N. E. Cockett⁴, E. A. Boerwinkle⁵, 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
- 8:45 P3040 **Large-scale gene co-expression network as a source of functional annotation for bovine genes.**
H. Beiki¹, J. M. Reecy², 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. Chamberlain^{1,2}, M. Khansefid^{1,2,3}, C. J. Vander Jagt^{1,2}, B. J. Hayes^{1,2,4}, L. C. Maret⁵, Y. Chen⁶, S. Bolormaa¹, C. A. Millen^{2,3}, T. T. Nguyen¹, and M. E. Goddard^{1,3}, 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. Bunch¹, 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. Nguyen¹, A. McCulloch³, N. E. Cockett⁴, W. Zamani⁵, F. Pompanon⁶, P. Taberlet⁶, S. McWilliam¹, H. Daetwyler⁷, and J. Kijas¹, 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. Skuce^{2,3}, M. Bermingham¹, J. A. Woolliams¹, and L. J. Glass¹, 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. 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*
- 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. Hubin⁴, A. Stinckens¹, C. Saegerman², T. Druet², B. Losson², E. Claerebout³, 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. 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, ⁶Tierzuchtforschung e.V. München, Grub, Germany

- 11:30 P6024 **Holstein Friesian lethal haplotype 5 is caused by a 138kbp deletion on chromosome 9.**
C. Wehrhahn¹, E. Schütz¹, M. Wanjek², R. Bortfeld², J. Beck³, and B. Brenig¹, ¹Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, ²Institute for Livestock Reproduction GmbH, Schönow, Germany, ³Chronix Biomedical GmbH, Göttingen, Germany
- 11:45 P6026 **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 S0116 **Genomic evaluations in dairy cattle, beef cattle and sheep in Ireland.**
D. P. Berry¹, F. Kearney², R. Evans², E. Wall³, and A. Cromie⁴, ¹Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ²Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, ³Sheep Ireland, Bandon, Ireland, ⁴Irish Cattle Breeding Federation, Bandon, Ireland
- 16:30 P6001 **Effectively managing bovine genetic disease risk via genotyping the Irish national herd.**
M. C. McClure¹, M. Mullen², S. M. Waters³, F. Kearney⁴, J. McClure¹, P. Flynn⁵, 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 P6027 **Study of the mutant MDR1 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*
- 14:15 P4037 **Around the tail of the Khmer cat.**
A. Cristalli¹, S. P. Marelli², P. Valiati², F. Genova², and M. Longeri², ¹DVM, PhD, Arezzo, Italy, ²Università degli Studi di Milano, Milan, Italy
- 14:30 P5031 **Runs of homozygosity highlight candidate genes and biological pathways related to athletic performance in Alaskan sled dogs.**
H. J. Huson, A. Valenti, and A. Boyko, 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 **Discussions - new projects.**
- 17:15 **Selection of 2016 - 2019 committee members.**
- 17:25 **Concluding Remarks.**

**Workshop: Domestic Animal Epigenetics
14:00 - 17:30**

Chair: Hasan Khatib, University of Wisconsin-Madison

**Sponsor: Eurofins
Grand Ballroom A**

- 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. Zhang⁵*, *M. Buckley³*, *I. C. McMillen⁶*, *S. J. Clark²*, and *R. L. Tellam¹*, 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
- 14:45 P2002 **The conserved functional role of non-CpG methylation in mammalian and avian brain.**
K. M. Schachtschneider^{1,2}, *M. F. Derks^{1,3,4}*, *O. Madsen¹*, *V. N. Laine³*, *L. B. Schook²*, *M. A. Groenen¹*, *K. J. Verhoeven⁵*, 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
- 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. Carson²*, *J. M. Reecy¹*, and *J. E. Koltes^{*1,3}*, 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. Estrella^{1,2}, *K. L. Kind^{1,3}*, *M. Ghanipour-Samami^{1,2}*, *A. Javadmanesh^{1,2}*, *C. T. Roberts^{1,4}*, and *S. Hiendleder^{*1,2}*, 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. Jacobsen^{*1}*, *J. H. Havgaard¹*, *C. M. Junker Mentzel¹*, *P. M. Sørensen¹*, *S. Pundhir²*, *C. Anthon¹*, *P. Karlskov-Mortensen¹*, *C. S. Bruun¹*, *S. Cirera¹*, *J. Gorodkin¹*, *C. B. Jørgensen¹*, *R. Barrès³*, 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. Reecy³, J. E. Koltes⁴, E. Fritz-Waters³, C. J. Easley³, R. R. Rowland⁵, C. K. Tuggle³, J. C. M. Dekkers⁶, L. L. Guan⁷, P. Stothard⁸, G. Plastow⁸, and J. K. Lunney^{9,2}, 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, C. S. Bruun, 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. Li², 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. Estelle², P. Kiilerich³, Y. Ramayo-Caldas², Z. Xia¹, Q. Feng¹, A. Ø. Pedersen⁴, N. J. Kjeldsen⁴, E. Maguin⁵, J. Doré^{5,6}, N. Pons^{5,6}, E. le Chatelier^{5,6}, L. Madsen^{1,3,7}, J. Wang¹, S. D. Ehrlich^{6,8}, K. Kristiansen^{1,3}, and C. Rogel-Gaillard⁹, ¹BGI-Shenzhen, Shenzhen, China, ²GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ³Department of Biology, University of Copenhagen, Copenhagen, Denmark, ⁴Danish Pig Research Centre, Nutrition and Reproduction, Copenhagen, Denmark, ⁵MICALIS Institute, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ⁶MGP MetaGénoPolis, INRA, Université Paris-Saclay, Jouy-en-Josas, France, ⁷National Institute of Nutrition and Seafood 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
- 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. Bertolini^{1,2}, F. Fanelli³, M. Mezzullo³, G. Galimberti⁴, D. G. Calò⁴, P. Trevisi¹, P. L. Martelli⁵, R. Casadio⁵, 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
- 16:15 P5012 **Integrative analysis of metabolomic, proteomic and genomic data to reveal functional pathways and candidate genes for drip loss in pigs.**
J. Welzenbach¹, C. Grosse-Brinkhaus¹, C. Neuhoff¹, C. Looft², K. Schellander², and E. Tholen², 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. Garrayo², A. Fernández³, Y. Núñez³, R. Benítez³, B. Isabel¹, A. I. Fernández⁴, A. I. Rey¹, A. Gonzalez-Bulnes³, J. F. Medrano⁵, A. Cánovas⁶, C. López-Bote¹, and C. Ovilo³, 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, CA, ⁶University of Guelph, Ontario, ON, 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. Boddicker², J. C. M. Dekkers³, Z. Wang¹, and G. Plastow⁴, ¹University of Alberta, Edmonton, AB, Canada, ²Genesis Inc, Lethbridge, AB, Canada, ³Department of Animal Science, Iowa State University, Ames, ⁴Livestock Gentec, Department 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. Dovc.
8:50 Dog CT Analysis Lab Report, L. van de Goor.
9:05 Discussion - Secondary canine STR Panel.
9:20 Evaluation of single nucleotide polymorphism (SNP) markers for canine parentage analysis. Abstract 14879 - J. Qiu.
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. Waldron³, D. A. Schneider^{1,2}, 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.**

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*¹*, 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 in colostrum and milk from average, low and high immune responder cows.**
H. Atalla^{1,2}*, B. Mallard^{1,2}, 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
- 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^{1,2}*, H. Xu¹, Q. Nie¹, X. Zhang³, and S. J. Lamont⁴, 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
- 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. Renson², F. Jaffrezic¹, G. Marot³, M. Moroldo¹, J. Lecardonnel¹, O. Bourry², and E. Giuffra*¹, 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. Hagen, D. R. Unni, and C. G. Elsik, University of Missouri, Columbia*
- 11:30 P8002 **A genomic landscape of mitochondrial DNA insertions in the nuclear pig genome.**
G. Schiavo¹, O. I. Hoffmann², 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. Mompert¹, 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. Chtioui^{1,2}, A. I. Fernández³, P. Morán⁴, M. P. Kent⁵, and B. Villanueva¹, 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), Ås, Norway
- 9:00 P6044 **Genomics assisted introgression of viral resistance in commercial common carp strains.**
R. Tadmor-Levi¹, E. Asulin¹, G. Hulata², 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. Lamy¹, F. Cornette¹, S. Heurtebise¹, E. Flahaur¹, L. Dégremont¹, M. T. Augé², P. Boudry³, and N. Bierne², ¹Ifremer, SG2M-LGPMM, 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. Gharbi², and R. D. Houston¹, 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. Overturf^{}, 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. Abernathy^{} 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. Geraci¹, F. Bertolini², G. Schiavo¹, M. T. Sardina³, V. Chiofalo⁴, and L. Fontanesi¹, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ²Department of Animal Science, Iowa State University, Ames, ³Palermo University, Palermo, Italy, ⁴Messina 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.**
Joram M Mwacharo¹, Ahmed R Elbeltagy², Eui-Soo Kim³, Aynalem Haile⁴, Barbara Rischkowsky⁵, International Sheep Genomics Consortium, ADAPMap, and Max F Rothschild³, ¹International Centre for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia, ²Department of Animal Biotech. Animal Production Research Institute, Cairo, Egypt, ³Department of Animal Science, Iowa State University, Ames, ⁴International Centre for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia, ⁵International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia
- 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. Hanotte³, 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. Ncube^{}, 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. Wu¹, 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. Mtsheni¹, K. Dzama², K. Nephawe³, and C. Rhode⁴, 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.**
N. R. Choi^{}, D. Seo, S. Jin, P. Manjula, S. H. Lee, and J. H. Lee, Chungnam National University, Daejeon, The Republic of Korea*

- 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. Tijjani^{1,2}, J. Kim³, H. Kim⁴, R. Mrode⁵, and O. Hanotte^{1,5}, 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
- 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. Eizirik, 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. Rothschild, 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-Wilson, The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom*
- 11:15 S0114 **Genetic basis of resistance to infectious disease in aquaculture species.**
R. D. Houston, 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. Kuehn², 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. Krehbiel¹, C. J. Richards¹, S. E. Place¹, U. Desilva¹, D. L. VanOverbeke¹, R. Mateescu², 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. Sanders², 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. Enriquez-Valencia³, J. M. Malheiros⁴, and E. C. Nadalini⁵, 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, ⁴Faculdade de Ciências Agrárias e Veterinárias - Universidade Estadual Paulista, Jaboticabal - SP, Brazil, ⁵Faculdade de Medicina Veterinária e Zootecnia - Universidade Estadual Paulista, Botucatu - SP, 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. Boddicker², J. C. M. Dekkers³, Z. Wang¹, and G. Plastow⁴, ¹University of Alberta, Edmonton, AB, Canada, ²Genesis Inc, Lethbridge, AB, Canada, ³Department of Animal Science, Iowa State University, Ames, ⁴Livestock Gentec, 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. Cinar^{*1,2}, M. R. Mouse³, J. O. Reynolds³, L. M. Hermann-Hoesing¹, J. B. Taylor⁴, D. P. Knowles^{3,5}, and S. N. White^{3,5,6}, ¹Washington State University College of Veterinary Medicine, Pullman, ²Erciyes University Faculty of Agriculture, Kayseri, Turkey, ³USDA, ARS, Animal Disease Research Unit, Pullman, ⁴USDA, ARS, Rangeland Sheep Production Efficiency Research, Dubois, ID, ⁵Washington 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. Cinar^{*1}, M. R. Mouse², M. V. Gonzales¹, J. O. Reynolds², J. B. Taylor³, D. P. Knowles^{2,4}, and S. N. White⁵, 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-Neto^{*1}, S. Harburg², R. Bunch¹, R. E. Lyons³, S. A. Lehnert¹, and A. Reverter¹, 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. Tijjani^{*1,2}, J. Kim³, H. Kim⁴, R. Mrode⁵, and O. Hanotte^{1,5}, 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 IGF2 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*

- P5064 13 **Accuracy of genome-wide predictions of heterosis in beef cattle using 50K genotypes.**
E. C. Akanno¹, L. Chen¹, C. Li¹, M. K. Abo-Ismael^{1,2}, J. Basarab³, and G. Plastow¹, 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

- P6000 14 **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*
- P6001 15 **Effectively managing bovine genetic disease risk via genotyping the Irish national herd.**
M. C. McClure¹, M. Mullen², S. M. Waters³, F. Kearney⁴, J. McClure¹, P. Flynn⁵, 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
- P6002 16 **Evaluating the metagenome of nasal samples from cattle with bovine respiratory disease complex (BRDC).**
T. G. McDanel, L. A. Kuehn, and J. W. Keele, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*
- P6003 17 **The use of Kosher phenotyping for mapping QTL affecting susceptibility to bovine respiratory disease.**
E. Lipkin¹, M. G. Strillacci², H. Eitam³, M. Yishay³, F. Schiavini², M. Soller¹, A. Bagnato², 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), Neve Ya'ar Research Center, Ramat Yishay, 30095, Israel
- P6004 18 **Estimation of heritability for fracture in the Thoroughbred racehorse.**
T. Tozaki¹, T. Miyake², M. Kikuchi¹, H. Kakoi¹, K. I. Hirota¹, and S. I. Nagata¹, ¹Laboratory of Racing Chemistry, Utsunomiya, Japan, ²Comparative Agricultural Sciences, Kyoto University, Kyoto, Japan
- P6005 19 **Diversity of Toll-Like Receptor genes in the indigenous Czech cattle breeds.**
K. Novák¹, V. Czerneková¹, A. E. Kalashnikov², and V. Mátlová¹, ¹Institute of Animal Science, Prague, Czech Republic, ²L.K. Ernst Research Institute of Animal Husbandry, Dubrovitsy, Russian Federation
- P6006 20 **The cytokines expression in the milk somatic cells of goats infected with small ruminant lentivirus.**
J. Jarczak¹, E. Kościuczuk², J. Kaba³, D. Słoniewska⁴, and E. Bagnicka⁴, ¹Institute of Genetics and Animal Breeding, Jastrzebiec, Poland, ²Robert H. Lurie Comprehensive Cancer Center of Northwestern University, Chicago, IL, ³Warsaw University of Life Sciences, Faculty of Veterinary Medicine, Warsaw, Poland, ⁴Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland
- P6007 21 **Cell-type dependent immune response post porcine reproductive and respiratory syndrome virus infection.**
M. J. Pröll¹, C. Neuhoff¹, C. Grosse-Brinkhaus¹, M. A. Müller², C. Drosten², M. J. Uddin³, D. Tesfaye¹, E. Tholen⁴, and K. Schellander⁴, 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, ⁴Institute of Animal Science, University of Bonn, Bonn, Germany
- P6008 22 **Genomic basis of Lipomatous Myopathy in Piedmontese beef cattle.**
S. Peletto¹, M. T. Capucchio², M. G. Strillacci³, C. Boin¹, E. Biasibetti², P. Modesto¹, F. Schiavini³, P. L. Acutis¹, and A. Bagnato³, 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
- P6009 23 **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, 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*
- P6010 24 **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. Banabazi¹, A. Nejati Javaremi², I. G. Imumorin³, M. Ghaderi-Zefrehei⁴, and S. R. Miraei Ashtani², ¹University of Tehran, Karaj, Iran (Islamic Republic of), ²University of tehran, Karaj, Iran (Islamic Republic of), ³Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY, ⁴University of Yasouj, Yasouj, Iran
- P1002 27 **Evolution of hypothalamus-pituitary growth axis among fish, amphibian, birds and mammals.**
*M. Moaen-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. Inoue¹, T. Nakajima¹, A. Nakajima¹, Y. Uemoto², M. Fukushima³, E. Yoshida⁴, E. Iwamoto⁴, T. Akiyama³, N. Kohama³, E. Kobayashi⁵, K. Oyama⁶, T. Honda⁶, 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, Kasai, Japan, ⁵Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, ⁶Food Resources Education & Research Center, Kobe University, Kasai, Hyogo, Japan
- P1006 31 **Identification of polymorphisms associated with oleic acid percentage by pool-based genome wide association study in Japanese Black cattle.**
F. Kawaguchi¹, A. Nakajima¹, Y. Matsumoto¹, Y. Uemoto², M. Fukushima³, E. Yoshida⁴, E. Iwamoto⁴, T. Akiyama³, N. Kohama³, E. Kobayashi⁵, T. Honda⁶, K. Oyama⁶, 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, Kasai, Japan, ⁵Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan, ⁶Food Resources Education & Research Center, Kobe University, Kasai, 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. Noda¹, S. Sasazaki², and H. Mannen², 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. Ressaissi**, ISA-Chott Mariem, TUNIS, Tunisia
- P4001 35 **Molecular analysis of genetic variability in Egyptian buffalo using microsatellite DNA markers.**
S. Abou Bakr¹, M. Attia², A. A. Nigm³, S. Abdelghany³, 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 carabanesis*): 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. Ashidate**¹, T. Kuraishi², and Y. Mizoguchi³, ¹*School of Agriculture, Meiji university, Kawasaki, Japan*, ²*Amami Laboratory, The Institute of Medical Science, The University of Tokyo, Kagoshima, Japan*, ³*School of Agriculture, Meiji University, Kawasaki, Japan*
- P4013 47 **Applicability of using bovine, ovine and caprine SNP chips for alpaca and dromedary genomic studies.**
*F. Bertolini**¹, A. Elbeltagy^{1,2}, F. A. Ponce de Leon³, G. A. Gutiérrez⁴, and M. F. Rothschild¹, ¹*Department of Animal Science, Iowa State University, Ames*, ²*Animal Production Research Institute, Cairo, Egypt*, ³*Department of Animal Science, University of Minnesota, St. Paul*, ⁴*Department 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. Okpeku**^{1,2}, A. Esmailzadeh^{2,3}, A. C. Adeola², L. Shu², Y. Zhang², Y. Wang², T. M. Sanni⁴, I. G. Imumorin⁵, S. O. Peters⁶, J. Zhang⁷, Y. Dong^{2,8}, and W. Wang², ¹*Department of Animal Science, Niger Delta University, Wilberforce Island, Nigeria*, ²*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences (CAS), Kunming, China*, ³*Department of Animal Science, Shahid Bahonar University of Kerman, Kerman, Iran (Islamic Republic of)*, ⁴*Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Nigeria*, ⁵*Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY*, ⁶*Department of Animal Science, Berry College, Mount Berry, GA*, ⁷*School of Science and Information Engineering, Yunnan Agricultural University, Kunming, China*, ⁸*Laboratory 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. Elgendy**¹, M. Giantin¹, F. Castellani², L. Grotta², F. Palazzo³, M. Dacasto¹, and G. Martino², ¹*University of Padova, Padova, Italy*, ²*University of Teramo, Teramo, Italy*, ³*Parco Tecnologico Padano, Lodi, Italy*
- P3002 50 **Functional annotation of the equine genome.**
*C. J. Finno**¹, J. L. Petersen², R. Bellone¹, and J. N. MacLeod³, ¹*University of California-Davis*, ²*University of Nebraska-Lincoln*, ³*University of Kentucky, Lexington*

- P3003 51 **The extent of cis-regulation of gene expression and its influence on complex trait variation in cattle.**
*A. J. Chamberlain^{*1,2}, M. Khansefid^{1,2,3}, C. J. Vander Jagt^{1,2}, B. J. Hayes^{1,2,4}, L. C. Marett⁵, Y. Chen⁶, S. Bolormaa¹, C. A. Millen^{2,3}, T. T. Nguyen¹, and M. E. Goddard^{1,3}.* 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
- P3004 52 **Differential expression of microRNAs in synovial fluid as biomarkers of osteochondrosis in equine hock joints.**
*E. Barrey^{*1}, J. Rivière¹, C. Morgenthaler¹, F. Rossignol², C. Mespoulhès-Rivière³, and C. Robert¹.* ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²Veterinary Clinic of Grosbois, Boissy St Léger, France, ³Université Paris-Est, Ecole Nationale Vétérinaire d'Alfort, Maisons-Alfort, France
- P3005 53 **Genome-wide transcriptomic analysis of liver in sex-linked Dwarf and wild type chickens.**
*T. Zerjal^{*1}, G. Monneret^{1,2}, M. Moroldo³, J. L. Coville¹, M. Tixier-Boichard¹, A. Rau¹, G. Nuel², and F. Jaffrezic⁴.* ¹INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, ²UPMC, LPMA, Paris, France, ³INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, ⁴GABI, INRA, AgroParisTech, Université Paris Saclay, 78350 Jouy en Josas, France
- P3006 54 **Integrated network multi-omics approach highlights muscle late fetal maturation process.**
*V. Voillet^{*1}, M. San Cristobal¹, L. M. Lefaucheur², and L. Liaubet¹.* ¹INRA UMR 1388 GenPhySE, Castanet-Tolosan, France, ²INRA, Saint-Gilles, France
- P3007 55 **Time course of the response to ACTH in pig: Biological and transcriptomic study.**
*V. Sautron^{*1}, E. Terenina¹, L. Gress¹, Y. Lippi², Y. Billon³, N. Villa-Vialaneix⁴, and P. Mormede¹.* ¹INRA UMR 1388 GenPhySE, Castanet-Tolosan, France, ²INRA UMR 1331 ToxAlim, Toulouse, France, ³INRA UE 1372 GenESI, Surgères, France, ⁴INRA UR 0875 MIAT, Castanet-Tolosan, France
- P3008 56 **Transcriptome profiling of reproductive tissues characterizes genetic basis of the prolificacy traits in sheep (*Ovis aries*).**
*K. Pokharel^{*1,2}, T. M. Hamama³, M. Honkatukia³, J. Peippo³, J. Rautiainen⁴, A. Seppälä³, M. H. Li⁵, and J. Kantanen^{1,2}.* ¹Natural Resources Institute Finland (Luke), Jokioinen, Finland, ²Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland, ³Green Technology, Natural Resources Institute Finland (Luke), Jokioinen, Finland, ⁴Pro Agraria Rural Advisory Centre, Tampere, Finland, ⁵Institute of Zoology, Chinese Academy of Sciences (CAS), Beijing, China
- P3009 57 **Polymorphisms of NELL1 and RNCK1 in relation to porcine growth, carcass and meat quality traits.**
R. Zhang¹, C. Große-Brinkhaus², H. Heidt¹, M. J. Uddin³, M. U. Cinar⁴, D. Tesfaye¹, E. Tholen², K. Schellander², and C. Neuhoﬀ¹. 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, ⁴Faculty of Agriculture, Melikgazi Kayseri, Turkey

Genome Editing and Transgenic Animals

7:30 - 8:30

Alpine Ballroom

- P7000 58 **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
- P7001 59 **Heritable gene disruption in goats with CRISPR/Cas9 results in expected phenotypes.**
X. Wang^{} and Y. Chen,* Northwest A&F University, Yangling, China
- P7002 60 **Skin-specific transgenic expression of ovine β -catenin in mice.**
*J. Wang^{*1}, K. Cui², D. Han², Z. Yang², and X. Deng³.* ¹College of Animal Science and Technology, China Agricultural University, Beijing, China, ²China Agricultural University, Beijing, China, ³Key Laboratory of Animal Genetic Improvement, Beijing & Animal Genetic Resources and Molecular Breeding Laboratory, China Agricultural University, Beijing, China, Beijing, China
- P7003 61 **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
- P7004 62 **Screen of transgenic integration sites and construction of site-specific transgenic pig by CRISPR-Cas9.**
*L. Ma^{*1}, X. Hu¹, Y. Xing², and N. Li¹.* ¹China Agricultural University, Beijing, China, ²The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China

- P7005 63 **Characterization of RNA editing on porcine NR3C1, COG3 and ACSM2B genes.**
A. I. Fernandez¹, R. Benítez², Y. Nuñez², C. Garcia-Contreras², J. M. Folch³, and Á. M. Martínez-Montes², ¹Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, ²INIA, Madrid, Spain, ³Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Spain
- P7006 64 **Generation of a porcine model of obesity and complications by Leptin knockout.**
T. Tan¹, Y. Xing¹, X. Hu², and N. Li², ¹The State Key Laboratory for Agro-biotechnology, China Agricultural University, Beijing, China, ²China 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. Flisikowska¹, M. Stachowiak², C. Wanderl¹, A. Wagner¹, C. Wurmser³, A. Perkowska², F. Bruening¹, S. Bauersachs⁴, A. Kindl¹, R. Fries³, M. Switonski², D. Saur⁵, 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
- P7010 68 **Generation of a novel glycosylated anti-CD20 monoclonal antibody in milk of transgenic cattle.**
R. Zhang¹, Y. Dai¹, J. Wang², B. Tang², and N. Li¹, ¹China Agricultural University, Beijing, China, ²Beijing Genprotein Biotechnology Company, Beijing, China

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. Bortfeldt¹, M. Reißmann¹, and G. A. Brockmann³, ¹Department for Crop and Animal Sciences, Humboldt-Universität zu Berlin, Berlin, Germany, ²Department of Animal Production, Faculty of Agriculture, Cairo University, Cairo, Egypt, ³Albrecht 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 Camargo¹, R. R. Aspilueta Borquis², D. J. A. Santos³, D. F. Cardoso⁴, N. Hurtado-Lugo², and H. Tonhati², ¹Universidade Tecnológica Federal do Paraná, Brazil, Dois Vizinhos, Brazil, ²State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, ³Sao Paulo State University, Jaboticabal, Brazil, ⁴Fundação 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. Bahbahani¹, J. Mwacharo², and O. Hanotte³, ¹Kuwait university, Kuwait, Kuwait, ²International Livestock Research Institute, Addis Ababa, Ethiopia, ³School 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.**
I. C. Cho¹, S. H. Han², and H. B. Park¹, ¹NIAS, Jeju, The Republic of Korea, ²Educational Science Research Institute, Jeju National University, Jeju, The Republic of Korea

- P5007 8 **Systems biology approach provides novel insights into gene networks controlling tenderness and meat quality traits across French beef breeds.**
Y. Ramayo-Caldas¹, G. Renand², M. Ballester³, R. Saintilan⁴, and D. Rocha¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²GABI, INRA, AgroParisTech, Université Paris-Saclay, 78352, Jouy en Josas, France, ³Departament de Genètica 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 9 **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. Chiineedi¹, B. Gutiérrez-Gil¹, C. Esteban-Blanco², and J. J. Arranz¹, ¹University of León, León, Spain, ²Supercomputing Center of Castilla y León, Leon, Spain
- P5009 10 **A genome-wide association analysis for carcass and meat quality traits in Duroc pigs.**
R. Gonzalez¹, P. G. Eusebi², R. Quintanilla³, T. Figueiredo¹, A. Manunza¹, J. L. Noguera⁴, A. Clop⁵, and M. Amills¹, 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 11 **Optimization of a genomic breeding program for a moderately sized dairy cattle population.**
J. I. Weller¹, A. Reiner-Benaim², and E. Ezra³, ¹ARO, The Volcani Center, Bet Dagan, Israel, ²Israel Cattle breeders Association, Caesarea, Israel, ³Israel Cattle Breeders Association, Caesaria, Israel
- P5011 12 **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 13 **Integrative analysis of metabolomic, proteomic and genomic data to reveal functional pathways and candidate genes for drip loss in pigs.**
J. Welzenbach¹, C. Grosse-Brinkhaus¹, C. Neuhoff¹, C. Looft², K. Schellander², and E. Tholen², 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 14 **Transcriptome profiling of the peripheral blood mononuclear cells following PRRSV vaccination in Pietrain pig.**
A. Islam¹, C. Neuhoff¹, C. Große-Brinkhaus¹, M. J. Pröll¹, M. J. Uddin², S. Aqter Rony¹, D. Tesfaye¹, E. Tholen¹, M. Hölker¹, and K. Schellander¹, ¹Institute of Animal Science, University of Bonn, Bonn, Germany, ²School of Veterinary Science, The University of Queensland, Gatton campus, Australia
- P6012 15 **Use of targeted next generation re-sequencing in the identification of polymorphisms in the bovine collagenous lectin gene family.**
R. S. Fraser^{}, J. D. Hammermueller, J. S. Lumsden, M. A. Hayes, and B. N. Lillie, Department of Pathobiology, University of Guelph, Guelph, ON, Canada*
- P6013 16 **Identifying driver mutations for Marek's disease lymphomas in chicken using integrated genomic screens.**
A. Steep¹, H. Xu², Y. Zhang², A. Black Pyrkosz³, M. E. Delany⁴, D. Frishman², and H. H. Cheng³, ¹Michigan State University, East Lansing, ²Technische Universität München, Freising, Germany, ³USDA, ARS, ADOL, East Lansing, MI, ⁴University of California-Davis
- P6014 17 **Mapping and exome sequencing of a weak calf syndrome with premature birth.**
T. Hirano¹, A. Okazaki¹, S. Sasaki², Y. Suzuki³, H. Hara¹, Y. Sugimoto⁴, and K. Hanzawa¹, 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 18 **An Intronic MBTPS2 Variant Results in a Splicing Defect in Horses with Brindle Coat Texture.**
L. Murgiano¹, D. Waluk², R. Towers³, N. Wiedemar¹, J. Dietrich¹, V. Jagannathan¹, M. Drögemüller¹, T. Druet⁴, A. Galichet⁵, M. C. Penedo⁶, E. Müller², P. Roosje⁷, M. Welle⁸, and T. Leeb¹, 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. Kühn^{*1}, R. Weikard¹, J. Knaust², and F. Hadlich², 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. Velie^{*1}, M. Shrestha¹, L. Francois², A. Schurink³, A. Stinckens², S. Blott⁴, B. J. Ducro³, S. Mikko¹, R. Thomas⁵, M. Sundquist⁶, S. Eriksson¹, N. Buys², and G. Lindgren¹, ¹Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, 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, ⁶Östra Greda Research Group, Borgholm, Sweden
- 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. Le^{*}, 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. Wilkinson^{*1}, S. C. Bishop¹, A. R. Allen², S. H. McBride², R. A. Skuce^{2,3}, M. Bermingham¹, J. A. Woolliams¹, and L. J. Glass¹, 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
- P6020 23 **Deficiency of Trim63 leads to hypertrophic cardiomyopathy in pig.**
Y. Hu^{*1}, 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. Meng¹, M. P. Heaton², T. P. L. Smith², B. P. Dalrymple³, J. Kijas³, N. E. Cockett⁴, E. A. Boerwinkle⁵, D. M. Muzny¹, R. A. Gibbs¹, and K. C. Worley^{*1}, 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. Agha^{*1,2}, W. Mekkawy^{2,3}, N. Ibanez-Escriche¹, J. Kumar⁴, A. Mandal¹, C. E. Lind³, J. Benzie³, and A. B. Doeschl-Wilson¹, 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. Li^{*1}, 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. Nguyen^{*1,2}, A. Reverter-Gomez³, A. Canovas⁴, B. Venus⁵, A. Islas-Trejo⁶, S. A. Lehnert⁷, J. F. Medrano⁶, S. S. Moore⁵, 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

- P1013 29 **Identification of SNP associated with fertility trait using pool-based genome-wide association study in Japanese Black cattle.**
H. Ozaki¹, T. Tamura¹, K. Fukazawa¹, Y. Uemoto², M. Nishio³, E. Kobayashi⁴, T. Matsuhashi⁵, S. Maruyama⁵, T. Honda⁶, K. Oyama⁶, S. Sasazaki⁷, and H. Mannen⁷, ¹Kobe University, Kobe, Japan, ²National Livestock Breeding Center, Nishigo, Japan, ³NARO 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., Gifu, Japan, ⁶Food Resources Education & Research Center, Kobe University, Kasai, Hyogo, Japan, ⁷Graduate School of Agricultural Science, Kobe University, Kobe, Japan
- P1014 30 **Genetic association between a missense mutation in the positional candidate gene GRIP1 and backfat thickness traits in pigs.**
J. B. Lee¹, H. S. Kim², H. B. Park³, C. K. Yoo⁴, I. C. Cho³, and H. T. Lim², 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
- P1015 31 **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*
- P1016 32 **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. Kiilerich³, Y. Ramayo-Caldas², Z. Xia¹, Q. Feng¹, A. Ø. Pedersen⁴, N. J. Kjeldsen⁴, E. Maguin⁵, J. Doré^{5,6}, N. Pons^{5,6}, E. le Chatelier^{5,6}, L. Madsen^{1,3,7}, J. Wang¹, S. D. Ehrlich^{6,8}, K. Kristiansen^{1,3}, and C. Rogel-Gaillard⁹, ¹BGI-Shenzhen, Shenzhen, China, ²GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ³Department of Biology, University of Copenhagen, Copenhagen, Denmark, ⁴Danish Pig Research Centre, Nutrition and Reproduction, Copenhagen, Denmark, ⁵MICALIS Institute, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ⁶MGP MetaGénoPolis, INRA, Université Paris-Saclay, Jouy-en-Josas, France, ⁷National Institute of Nutrition and Seafood 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
- P1017 33 **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

Genetic Diversity and Polymorphisms II

13:00 - 14:00

Alpine Ballroom

- P4014 34 **Global and local admixture analyses of Baladi cattle.**
A. Shabtay¹, M. Soller², J. Sölkner³, G. Mészáros³, T. Sonstegard⁴, 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, Jaboticabal, Brazil
- P4015 35 **Molecular phylogeny and domestication pattern of river buffalo through mitochondrial D-loop DNA analysis.**
M. Y. Zahoor, University of Veterinary & Animal Sciences, Lahore, Pakistan*
- P4016 36 **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*
- P4017 37 **Distribution of Y chromosomal haplotypes in Japanese native horse populations.**
H. Kakoi¹, T. Tozaki¹, M. Kikuchi¹, K. I. Hirota¹, S. I. Nagata¹, and M. Takasu², ¹Laboratory of Racing Chemistry, Utsunomiya, Japan, ²Faculty of Applied Biological Sciences, Gifu University, Gifu, Japan
- P4018 38 **Effective population size and inbreeding in South African indigenous chicken populations: Implications for management and conservation of unique genetic resources.**
B. Mtsheni¹, K. Dzama², K. Nephawe³, and C. Rhode⁴, 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 II β loci in Japanese quail.**
*S. Asaji¹, S. Suzuki², T. Ishige³, K. Hosomichi⁴, T. Shiina², H. Hara¹, T. Hirano¹, and K. Hanzawa**, 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. Lapègue**, *P. A. Gagnaire², J. B. Lamy¹, F. Cornette¹, S. Heurtebise¹, E. Flahauw¹, L. Dégremont¹, M. T. Augé², P. Boudry³, and N. Bierne²*, ¹Ifremer, SG2M-LGPMM, 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. Kalashnikov³, 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. Bertolini^{1,2}, G. Galimberti³, D. G. Calò³, D. Matassino⁴, V. Russo¹, S. Dall'Olio¹, L. Nanni Costa¹, and L. Fontanesi**, 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.**
N. R. Choi, D. Seo, S. Jin, P. Manjula, S. H. Lee, and J. H. Lee*, Chungnam National University, Daejeon, The Republic of Korea
- P4027 47 **Systematic profiling of short tandem repeats in the cattle genome.**
*L. Xu¹, R. Haas², J. Sun³, Y. Zhou¹, D. Bickhart¹, J. Li⁴, J. Song⁵, T. Sonstegard⁶, C. P. VanTassell¹, H. Lewin⁷, and G. E. Liu**, 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, 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. Vilkki**, *D. Fischer¹, I. Tapio¹, 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. Schroyen**, *K. M. Feye², Y. T. Nguyen³, A. Rakhshandeh⁴, N. K. Gabler¹, D. Nettleton³, J. C. M. Dekkers¹, and C. K. Tuggle³*, 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

- P3012 50 **Deconstructing the pig genome-metabolome functional interactions.**
*L. Fontanesi^{*1}, S. Bovo¹, G. Schiavo¹, G. Mazzoni¹, A. Ribani¹, V. J. Utzeri¹, S. Dall'Olio¹, F. Bertolini^{1,2}, F. Fanelli³, M. Mezzullo³, G. Galimberti⁴, D. G. Calò⁴, P. Trevisi¹, P. L. Martelli⁵, R. Casadio⁵, 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*
- P3013 51 **Characterization of endometrium protein expression during mid-late gestation in Meishan and Duroc sows with iTRAQ analysis.**
K. Wang^{} and M. Fang, China Agricultural University, Beijing, China*
- P3014 52 **The study on the genetic mechanism of varied Atrogin-1 expression in different chicken lines.**
*J. Li^{*1,2}, Y. Hu³, H. Lan³, L. Li³, X. Hu², and N. Li², 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*
- P3015 53 **Analysis of G protein-coupled receptor gene expression during bovine intramuscular adipogenesis.**
T. Kuwabara^{} and Y. Mizoguchi, School of Agriculture, Meiji University, Kawasaki, Japan*
- P3016 54 **Breed and feeding factors influencing adipose tissue lipogenic and lipolytic gene expression in growing Iberian and Duroc pigs.**
R. Benítez¹, A. Fernandez¹, B. Isabel², Y. Nuñez¹, E. Alves¹, E. De Mercado³, E. Gómez-Izquierdo⁴, J. M. García-Casco⁵, M. C. Rodríguez¹, C. López-Bote², L. Silió¹, and C. Ovilo¹, ¹INIA, Madrid, Spain, ²UCM, Madrid, Spain, ³INSTITUTO TECNOLÓGICO AGRARIO, Segovia, Spain, ⁴INSTITUTO TECNOLÓGICO AGRARIO, Segovia, Spain, ⁵INIA, Zafra, Spain
- P3017 55 **Functional analysis and association studies of bovine MYOT gene with meat quality.**
*C. M. Adoligbe^{*1}, L. Zan², and S. Farougou¹, ¹University of Abomey-Calavi, Abomey-Calavi, Benin, ²Northwest A&F University, Yangling, China*
- P3018 56 **Gene expression analysis in backfat and identification of eQTL regions for fatness and fatty acid composition candidate genes in pigs.**
*M. Revilla^{*1,2}, M. Ballester³, A. Puig-Oliveras^{1,2}, A. Castelló², A. I. Fernández⁴, and J. M. Folch^{1,2}, 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*
- P3019 57 **Screening and characterization of copy number variation in South African Nguni cattle using next generation sequencing data.**
*M. D. Wang^{*1,2}, K. Dzama², J. Rees³, C. Hefer¹, and F. C. Muchadeyi³, 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

- P2000 58 **DNA methylation and hydroxymethylation in early rabbit embryo: Consequence of in vitro culture.**
*M. N. Bedhane^{*1} and J. Salvaing², ¹Jigjiga university, Jigjiga, Ethiopia, ²INRA, Paris, France*
- P2001 59 **CD4 promoter hyper methylation is associated with lower gene expression in clinical mastitis cows and vice versa in the healthy controls.**
*T. Usman^{*1,2}, Y. Yu³, and Y. Wang³, 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*
- P2002 60 **The conserved functional role of non-CpG methylation in mammalian and avian brain.**
*K. M. Schachtschneider^{*1,2}, M. F. Derks^{1,3,4}, O. Madsen¹, V. N. Laine³, L. B. Schook², M. A. Groenen¹, K. J. Verhoeven⁵, 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.**
E. Casas¹, G. Cai¹, L. A. Kuehn², K. B. Register¹, J. D. Neill¹, and T. G. McDanel², ¹USDA, ARS, National Animal Disease Center, Ames, IA, ²USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE
- 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. Coustham⁵, J. L. Coville¹, M. Morisson², F. Minvielle¹, and F. Pitel², ¹INRA, AgroParisTech, Université Paris-Saclay, GABI, 78350 Jouy en Josas, France, ²UMR INRA / INPT ENSAT / INPT ENVT - 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. Welzenbach¹, Q. Yang¹, M. J. Uddin³, M. U. Cinar⁴, D. Tesfaye¹, E. Tholen⁵, C. Looft⁵, and K. Schellander⁵, 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. Cinar³, C. Grosse-Brinkhaus¹, E. Tholen⁴, C. Looft⁴, A. Islam⁵, M. Hölker¹, K. Schellander⁴, M. J. Uddin⁶, and C. Neuhoff¹, 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, ³Faculty of Agriculture, Melikgazi Kayseri, Turkey, ⁴Institute of Animal Science, University of Bonn, Bonn, Germany, ⁵Department of Medicine, Faculty of Veterinary Science, Bangladesh Agricultural University, Mymensingh, Bangladesh, ⁶School 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. Choi, 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. Madder¹, 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. Pereira², 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

- P5016 4 **Golden milk: Increasing beta-carotene content in developing countries: first step.**
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. Bertolini^{1,3}, M. Gallo⁴, 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. Jin¹, H. B. Park², D. Seo¹, N. R. Choi¹, C. K. Yoo³, S. Jung¹, C. Jo⁴, 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, ³Division of Applied Life Science (BK21 program), Gyeongsang National University, Jinju, The Republic of Korea, ⁴Department 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. Reecy³, 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. Rothhammer³, 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, ⁶Tierzuchforschung 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, R. Agmon¹, A. Asher¹, A. Brosh¹, and A. Shabtay¹, ¹Department of Ruminant Sciences, Agricultural Research Organization (ARO), Neve 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. Brauning², S. M. Hickey³, 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. Goodall^{1,2}, N. Botwright², N. Wade², D. Merritt¹, G. Coman², 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*

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 Hansen², P. Boysen², A. K. Storset², T. R. Solberg³, O. Østerås⁴, B. Heringstad^{3,5}, 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^{*1,2}, Q. Nie², H. Lin², E. E. Sandford¹, X. Zhang³, L. K. Nolan¹, and S. J. Lamont⁴, ¹Iowa State University, Ames, ²South China Agricultural University, Guangzhou, China, ³College of Animal Science, South China Agricultural University, Guangzhou, China, ⁴Department 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^{*1}, E. Schütz¹, M. Wanjek², R. Bortfeld², J. Beck³, and B. Brenig¹, ¹Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, ²Institute for Livestock Reproduction GmbH, Schönow, Germany, ³Chronix Biomedical 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. Killick¹, K. E. McLoughlin¹, N. C. Nalpas², L. Burkitt-Gray¹, I. W. Richardson³, H. L. Wiencko⁴, D. A. Magee¹, J. A. Browne¹, B. Villarreal-Ramos⁵, H. M. Vordermeier⁵, D. P. Berry⁶, D. G. Bradley³, E. Gormley⁷, S. V. Gordon⁷, and D. E. MacHugh^{*1}, ¹School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, ²Proteome Center, University of Tübingen, Tübingen, Germany, ³Department of Genetics, Trinity College Dublin, 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, 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^{*1}, 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*
- P6027 19 **Study of the mutant MDR1 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^{*1,2}, V. Jagannathan³, C. Piffer⁴, C. Drögemüller⁵, and A. Gentile⁶, ¹GIGA, Liege, Belgium, ²Institute of Genetics, Bern, Switzerland, ³Institute of Genetics, University of Bern, Bern, Switzerland, ⁴Azienda Sanitaria Alto Adige, Bozen, Italy, ⁵Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, ⁶Department of Veterinary Medical Sciences, Bologna, Italy*
- P6029 21 **Congenital cataract formation in Holstein Friesian cattle.**
*A. K. Hollmann^{*1}, W. E. Wemheuer¹, J. Beck², B. Brenig¹, and E. Schütz¹, ¹Institute of Veterinary Medicine, Georg-August-University, Göttingen, Germany, ²Chronix Biomedical 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^{*1}, J. W. Wilkinson², A. Ladinig³, H. Bao², P. Stothard⁴, J. K. Lunney¹, G. Plastow⁴, and J. C. S. Harding⁵, ¹USDA ARS BARC APDL, Beltsville, MD, ²University of Alberta, Edmonton, AB, Canada, ³University of Veterinary Medicine, Vienna, Austria, ⁴Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, ⁵University of Saskatchewan, Saskatoon, SK, Canada*
- P6032 24 **Identification and characterization of a novel pathogen causing bovine abortion.**
B. T. Welby, 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-Pardal¹, I. K. Saglam², V. Costa¹, S. Chen³, M. R. Miller², and A. Beja-Pereira¹, ¹Cibio, Porto, Portugal, ²University of California-Davis, ³School of Life Sciences, Yunnan University, Kunming, China

- P1019 26 **Genetic introgression through selection in domestic chickens: Insight from whole genome sequence analysis.**
R. A. Lawal¹, D. Wragg², P. Silva³, K. Vanmechelen⁴, A. Vereijken⁵, D. D. Wu⁶, R. M. Al-Atiyat⁷, and O. Hanotte⁸, 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 Univeristy 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
- P1020 27 **Identification of polymorphisms modifying gene expression regulation in cattle.**
G. Guillocheau¹ and D. Rocha², ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy-en-Josas, France, ²GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France
- P1021 28 **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.**
A. Ribani¹, F. Bertolini^{1,2}, G. Schiavo¹, E. Scotti¹, V. J. Utzeri¹, S. Dall'Olio¹, P. Trevisi¹, P. Bosi¹, and L. Fontanesi¹, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ²Department of Animal Science, Iowa State University, Ames
- P1022 29 **Bridging SNP genotyping platforms to high-throughput computing for agricultural genomic applications: A perspective from a commercial service provider.**
X. L. Wu, J. Qiu, J. Walker, B. Simpson, and S. Bauck*, GeneSeek, a Neogen Company, Lincoln, NE
- P1023 30 **RNA editing in swine is associated with PRE-1 retrotransposons.**
S. A. Funkhouser¹, J. P. Steibel^{2,3}, R. O. Bates³, N. E. Raney³, and C. W. Ernst³, 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
- P1024 31 **Inferring genotypes of functional variants in crossbred beef cattle.**
W. M. Snelling, L. A. Kuehn, and A. K. Lindholm-Perry*, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE
- P1025 32 **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. Howard¹, F. Tiezzi¹, Y. Huang², K. A. Gray², and C. Maltecca¹, ¹North Carolina State University, Raleigh, ²Smithfield Premium Genetics, Rose Hill, NC
- P1026 33 **Additive and heterotic effects estimation from a F2 Duroc x Pietrain crossbreed using 60K realized breed composition and heterozygosity.**
A. Rogberg-Muñoz^{1,2}, N. S. Forneris², J. P. Steibel³, S. Munilla⁴, C. W. Ernst⁵, R. O. Bates³, G. Giovambattista¹, and R. J. C. Cantet^{2,6}, 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, ⁶INPA – Unidad Ejecutora UBA-CONICET de Investigaciones en Produccion Animal, Buenos Aires, Argentina

Genetic Diversity and Polymorphisms III

7:30 - 8:30

Alpine Ballroom

- P4028 34 **Hematopoietic chimerism in Italian horses.**
C. Grasso¹, M. Bonuglia¹, M. Dobosz², and V. CHIOFALO³, ¹UNIRELAB, Settimo Milanese, Italy, ²University of Perugia, Perugia, Italy, ³UNIRELAB s.r.l., Settimo Milanese, Italy
- P4029 35 **Launching SheepGenomesDB: 100 million variants from nearly 500 sheep genomes.**
J. Kijas¹, R. Brauning², S. M. Clarke², A. McCulloch³, N. E. Cockett⁴, G. Saunders⁵, M. Naval Sanchez¹, 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
- P4030 36 **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

- P4031 37 **Ancient DNA analysis of the *MC1R* gene in wild boar specimens from Mesolithic Ertebølle sites.**
*J. Tetens^{*1}, D. Ellinghaus², M. Nutsua², G. Thaller¹, A. Nebel², and B. Krause-Kyora², ¹Institute of Animal Breeding and Husbandry, Kiel University, Kiel, Germany, ²Institute 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^{*1}, A. Szumiec¹, and T. Borkowski², ¹National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland, ²Veterinary 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^{*1}, L. Fontanesi², R. Bozzi³, J. Estellé⁴, C. Ovilo⁵, R. M. Nieto⁶, J. M. García-Casco⁷, C. Pugliese⁸, J. M. Gil⁹, B. Lebre¹⁰, M. A. Oliver¹¹, and M. Čandek-Potokar¹², ¹Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, ²Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ³University of Florence, Florence, Italy, ⁴GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ⁵INIA, Madrid, Spain, ⁶Consejo Superior De Investigaciones Científicas, Armillá, Spain, ⁷INIA, Zafra, Spain, ⁸Department of Agrifood Production and Environmental Sciences, University of Firenze, Firenze, Italy, ⁹CREDA-UPC-IRTA, Castelldefels, Barcelona, Spain, ¹⁰INRA, Saint Gilles, France, ¹¹IRTA, Monells, Spain, ¹²KIS-Agricultural Institute of Slovenia, Ljubljana, Slovenia*
- P4034 40 **Milk protein polymorphisms in African indigenous cattle: opportunity for sustainable breeding program.**
*I. Houaga^{*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^{*1}, A. Chtioui^{1,2}, A. I. Fernández³, P. Morán⁴, M. P. Kent⁵, and B. Villanueva¹, 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), Ås, Norway*
- P4036 42 **Estimation of linkage disequilibrium and effective population size in Korean native chicken.**
D. Seo^{}, 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. Cristalli¹, S. P. Marelli², P. Valiati², F. Genova², and M. Longeri^{*2}, ¹DVM, PhD, Arezzo, Italy, ²Università 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. Geraci¹, F. Bertolini^{*2}, G. Schiavo¹, M. T. Sardina³, V. Chiofalo⁴, and L. Fontanesi¹, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, ²Department of Animal Science, Iowa State University, Ames, ³Palermo University, Palermo, Italy, ⁴Messina University, Messina, Italy*
- P4039 45 **Design of a polymorphic microsatellites set for domestic turkey (*Meleagris Gallopavo*) genetics characterization.**
*A. Canales¹, A. M. Martínez^{*1,2}, V. Landi^{1,2}, P. Cervantes³, J. V. Delgado⁴, and M. E. Camacho⁵, 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*
- P4040 46 **Computer analysis of genetic parentage: Application in equine diversity maintenance in Brazil.**
*A. Atomiyama^{*1}, M. S. Lauretto², F. Nakano³, J. M. Stern⁴, D. Levy⁵, S. P. Bydlowski⁵, and C. R. Bydlowski¹, ¹LinkGen Biotecnologia, Sao Paulo, Brazil, ²Universidade São Paulo (USP) - Zona Leste, Sao Paulo, Brazil, ³Instituto Butantan, Sao Paulo, Brazil, ⁴Instituto de Matemática e Estatística da USP, Sao Paulo, Brazil, ⁵Faculdade 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^{*1}, K. A. Munyard¹, E. Morgan¹, R. J. Allcock², M. J. Stear³, and D. M. Groth¹, ¹Curtin University, Perth, Australia, ²University of Western Australia, Perth, Australia, ³University of Glasgow, Glasgow, United Kingdom*

Functional Genomics III

7:30 - 8:30

Alpine Ballroom

- 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, 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. Bagnicka, 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. Ponsuksili, 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. Núñez¹, A. Fernández¹, R. Benítez¹, I. Arija², A. Viveros², A. Brenes³, and C. Ovilo¹, 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. Horodyska^{*1,2}, M. Oster¹, K. Wimmers¹, A. M. Mullen², P. G. Lawlor³, and R. M. Hamill², 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. Pollet¹, P. Renson², F. Jaffrezic¹, G. Marot³, M. Moroldo¹, J. Lecardonnel¹, O. Bourry², and E. Giuffra^{*1}, 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^{*1}, H. Atalla^{1,2}, and B. Mallard^{1,2}, 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^{*1,2}, H. Xu¹, Q. Nie¹, X. Zhang³, and S. J. Lamont⁴, 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. Ayuso¹, J. Garrayo², A. Fernández³, Y. Núñez³, R. Benítez³, B. Isabel¹, A. I. Fernández⁴, A. I. Rey¹, A. Gonzalez-Bulnes³, J. F. Medrano⁵, A. Cánovas⁶, C. López-Bote¹, and C. Ovilo^{*3}, 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^{*1}, D. Velez-Irizarry¹, J. P. Steibel^{1,2}, S. Casiro¹, S. A. Funkhouser³, 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. Reecy², L. C. A. Regitano³, M. D. Poletto⁴, S. C. S. Andrade⁵, P. C. Tizioto⁶, P. S. N. Oliveira⁶, D. P. D. Lanna⁷, R. R. Tullio³, R. T. Nassu³, J. E. Koltes⁸, E. Fritz-Waters², and L. L. Coutinho¹, ¹Animal Biotechnology Laboratory - ESALQ, University of São Paulo, Piracicaba, Brazil, ²Iowa State University, Ames, ³Embrapa Southeast Livestock, Sao Carlos, Brazil, ⁴University of São Paulo, Piracicaba, Brazil, ⁵University of São Paulo, São Paulo, Brazil, ⁶Embrapa Southeast Livestock, São Carlos, Brazil, ⁷University of Sao Paulo / ESALQ, Piracicaba, Brazil, ⁸University of Arkansas, Fayetteville

Epigenetics and Epigenomics II

7:30 - 8:30

Alpine Ballroom

- P2011 61 **Novel analysis of global DNA methylation in the limbic system of the bovine brain.**
B. A. Cantrell¹, S. D. McKay¹, R. L. Weaver², 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. Lamont², 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. Rempel^{} 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. McKay^{}, 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-Woszuik^{}, E. Pruszyńska-Oszmalek, M. Szydłowski, and I. Szczerbal, 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. Bauer², S. McWilliam¹, S. Zhang³, M. Buckley², J. L. Morrison³, I. C. McMillen⁴, and R. L. Tellam¹, ¹CSIRO Agriculture, Brisbane, Australia, ²CSIRO Data61, Sydney, Australia, ³The University of South Australia, Adelaide, Australia, ⁴The University of Newcastle, Australia

Genetic Markers and Selection IV

13:00 - 14:00

Alpine Ballroom

- P5026 1 **Genetic analysis of conformation traits in Icelandic horses.**
K. Jäderkvist Fegraeus¹, M. Shrestha¹, A. Schurink², S. Eriksson¹, B. J. Ducro², 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-Szmukier², 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. Horodyska^{1,2}, R. M. Hamill¹, H. Reyer², P. Varley³, and K. Wimmers², ¹Teagasc Food Research Centre, Dublin, Ireland, ²Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, ³Hermitage Genetics, Kilkenny, Ireland

- P5029 4 **The use of Bayesian methods, biological priors and sequence variants to identify genomic regions associated with dairy cow fertility.**
D. C. Purfield¹, I. M. MacLeod², B. J. Hayes², S. Butler³, S. G. Moore⁴, B. Moran⁵, F. Kearney⁶, and D. P. Berry⁷, ¹Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, ²Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, ³Animal & Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland, ⁴University of Missouri, Columbia, ⁵Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland, ⁶Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, ⁷Teagasc, Moorepark, Fermoy, Co. Cork, Ireland
- P5030 5 **Dietary carotenoid levels and stearyl-coA haplotype exert a complementary action over fat content and composition in pig.**
R. N. Pena¹, E. Henríquez-Rodríguez¹, A. R. Seradj¹, M. Tor¹, P. Christou^{1,2}, and J. Estany¹, ¹University of Lleida - Agrotènio 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. Huson^{}, 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. Mikko^{}, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*
- P5033 8 **A GWAS of teat number in pigs.**
G. A. Rohrer^{} 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. Goszczynski¹, C. Corbi¹, H. Morales¹, D. Posik¹, E. Villegas Castagnasso¹, S. Munilla², P. Peral García¹, A. Rogberg^{1,2}, R. J. C. Canter^{2,3}, and G. Giovambattista¹, ¹IGEVEV – Instituto de Genética Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, ²Departamento de Producción, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina, ³INPA – Unidad Ejecutora UBA-CONICET de Investigaciones en Producción 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. Nassar^{1,2}, 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. Jung³, E. S. Kim⁴, and M. F. Rothschild⁵, 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, ⁴Recombinetics, 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. Piórkowska^{}, K. Zukowski, 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. Kim², H. S. Oh², H. B. Park³, and I. C. Cho³, 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. 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

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. Mousel¹, S. N. White^{1,2}, M. V. Gonzalez^{2,3}, J. O. Reynolds², J. B. Taylor⁴, and D. P. Knowles^{1,2}, ¹USDA, ARS, Animal Disease Research Unit, Pullman, WA, ²Washington State University, Pullman, WA, ³Center for Applied Genomics, The Children's Hospital of Philadelphia, Philadelphia, PA, ⁴USDA, 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. Bao¹, A. Kommadath¹, I. Choi², J. M. Reecy³, J. E. Koltes⁴, E. Fritz-Waters³, C. J. Easley³, R. R. Rowland⁵, C. K. Tuggle³, J. C. M. Dekkers⁶, L. L. Guan⁷, P. Stothard⁸, G. Plastow⁸, and J. K. Lunney², ¹University of Alberta, Edmonton, AB, Canada, ²USDA ARS BARC APDL, Beltsville, MD, ³Iowa State University, Ames, ⁴University of Arkansas, Fayetteville, ⁵Kansas State University, Manhattan, 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
- P6035 17 **The expression of genes connected with prion protein metabolism in sheep.**
A. Piestrzynska-Kajtoch¹, G. Smolucha¹, M. Oczkowicz¹, A. Fornal², and B. Rejduch¹, 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
- P6036 18 **A polymorphism of CD163 gene is significantly associated with weight gain of the pigs under persistent PRRSV infection.**
B. Lim¹, P. Niu¹, W. I. Kim², C. K. Park³, and K. S. Kim⁴, ¹Chungbuk National University, Cheongju, The Republic of Korea, ²Chunbuk National University, IKSan, The Republic of Korea, ³Kyungpook National University, Taegu, The Republic of Korea, ⁴Chungbuk National University, Cheongju, South Korea
- P6037 19 **Effects of CAEV infection on expression of acute phase protein genes in goat milk somatic cells.**
D. Reczynska¹, J. Jarczak¹, K. Rutkowska¹, M. Czopowicz², K. Barłowska¹, J. Oprzadek¹, L. Witkowski², D. Słoniewska¹, K. Horbanczuk¹, W. Jarmuz¹, J. Kaba², and E. Bagnicka¹, ¹Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland, ²Warsaw 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. Coussé¹, M. Elansary², R. Abos², C. Sarre³, L. Francois¹, X. Hubin⁴, A. Stinckens¹, C. Saegerman², T. Druet², B. Losson², E. Claerebout³, M. Georges², and N. Buys¹, ¹KU Leuven, Leuven, Belgium, ²University of Liège, Belgium, ³Ghent University, Ghent, Belgium, ⁴AWE asbl, Ciney, 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. Bagnicka¹, E. Kościuczuk^{1,2}, P. Lisowski¹, J. Jarczak¹, S. Marczak¹, W. Jarmuz¹, and L. Zwierzchowski¹, ¹Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland, ²Robert 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. Maroille¹, G. Lemonnier¹, D. Esquerré², M. J. Mercat³, C. Rogel-Gaillard⁴, and J. Estellé¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²INRA, UMRI388 GenPhySe, GeT-PlaGe Genomic Facility, Castanet-Tolosan, France, ³IFIP-BIOPORC, Le Rheu, France, ⁴GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France
- P6041 23 **Microarray analysis of genomic aberrations of horse sarcoids.**
K. Pawlina¹, A. Gurgul¹, J. Klukowska-Rötzler², C. Koch², K. Mählmann³, and M. Bugno-Poniewierska¹, ¹National Research Institute of Animal Production, Balice, Poland, ²University of Bern, Switzerland, ³University of Veterinary Medicine Hannover, Germany
- P6042 24 **Transcriptome characteristic of horse sarcoids.**
E. Semik¹, A. Gurgul¹, K. Ropka-Molik¹, T. Zabek¹, C. Koch², K. Mählmann³, and M. Bugno-Poniewierska¹, ¹National Research Institute of Animal Production, Balice, Poland, ²University of Bern, Bern, Switzerland, ³University of Veterinary Medicine Hannover, Germany
- P6043 25 **Evaluation of chromosome rearrangements of an intersex horse applying molecular cytogenetic techniques.**
M. Bugno-Poniewierska¹, T. Zabek¹, A. Gurgul¹, and K. Pawlina¹, 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. He^{1,2}, X. L. Wu³, S. Bauck³, 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. Pirani¹, 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. Bai², X. Xu², X. Fu², W. Wu², 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. Lyons¹, D. Waine², E. Collis², 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 Son², N. Duijvesteijn¹, and B. Harlizius¹, 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. Zhao¹, 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. Martinez^{1,2}, V. Landi^{1,2}, P. Cervantes³, J. V. Delgado⁴, and M. E. Camacho⁵, 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. Fornal¹, A. Piestrzynska-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
- P4044 37 **Search for polymorphisms through next-generation sequencing of genes involved in reproductive development in Guzerat bulls.**
J. P. Liron¹, A. M. Loaiza Echeverri², M. E. Fernandez¹, M. Drummond², D. Goszczynski¹, D. Cunha Cardoso², P. Peral García¹, M. R. J. M. Henry², G. Giovambattista¹, and D. A. Andrade de Oliveira², ¹IGEVET – Instituto de Genética Veterinaria Ing. Fernando Noel Dulout (UNLP - CONICET La Plata), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Argentina, ²Escola de Veterinaria, Universidad Federal de Minas Gerais, Belo Horizonte, Brazil

- P4045 38 **Genetic characterization of three Korean native cattle breeds using the bovine 640K Affymetrix axiom arrays.**
*J. Kim^{*1}, Y. Kim², Y. Lee³, and A. Iqbal³, ¹Yeungnam University, Gyeongsan, South Korea, ²Yeungnam University, Gyeongsan, The Republic of Korea, ³Yeungnam Univeristy, Gyeongsan, The Republic of Korea*
- P4046 39 **Development and evaluation of a set of 100 SNP markers for DNA typing in the domestic horse.**
*H. Holl^{*1}, J. Vanhnasy², R. Everts², D. Cook¹, S. Brooks¹, M. Carpenter¹, C. Bustamante¹, and C. Lafayette¹, ¹Etalon Inc., Menlo Park, CA, ²Agena Bioscience, San Diego, CA*
- P4047 40 **Studies on genetic diversity and phylogenetic relationships of Korean Native chicken using the microsatellite marker.**
*J. H. SEO^{*1,2}, J. M. Han¹, and H. S. Kong¹, 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*
- P4048 41 **Comparison of three methods to discover copy number variants in Nellore and Angus cattle.**
*Y. Xing^{*1} 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*
- P4049 42 **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*
- P4050 43 **Inference of population structure of purebred dairy and beef cattle using high density genotype data.**
*M. M. Kelleher^{*1}, D. C. Purfield², F. Kearney¹, R. Evans¹, and D. P. Berry³, 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*
- P4051 44 **Genetic relationships between Iberian and Criollo horse breeds.**
*J. L. Vega-Pla^{*1}, O. Cortés², L. T. Gama³, J. Canon⁴, M. C. Penedo⁵, M. D. M. Oom⁶, V. Landi⁷, J. V. Delgado⁸, A. M. Martinez⁷, and B. Consortium⁹, ¹Laboratorio de Investigacion Aplicada. Ministry of Defense, Cordoba, Spain, ²Universidad Complutense de Madrid, Madrid, Spain, ³CIISA – Faculdade de Medicina Veterinaria. Universidade Tecnica de Lisboa, Lisboa, Portugal, ⁴Universidad Complutense, Madrid, Spain, ⁵Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, ⁶cE3c – Centre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal, ⁷Animal Breeding Consulting SL, Cordoba, Spain, ⁸Departamento de Genética. Universidad de Córdoba, Cordoba, Spain, ⁹<http://biohorse.jimdo.com/investigadores-researchers/>, Cordoba, Spain*
- P4052 45 **The Swine Leukocyte Antigen (SLA) Nomenclature System of the International Society for Animal Genetics (ISAG) and the International Union of Immunological Societies (IUIS): Update 2016.**
*S. Ho^{*1}, 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, Université 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*
- P4053 46 **Prospects for whole genome sequencing of ancient Finnish cattle.**
*M. B. Weldenegodguad^{*1,2}, C. Der Sarkissian³, A. Bläuer^{2,4}, K. Pokharel^{1,2}, J. P. Taavitsainen¹, L. Orlando³, and J. Kantanen^{1,2}, 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*
- P4054 47 **Resolving misassembled cattle immune gene clusters with hierarchical, long read sequencing.**
*D. Bickhart^{*1}, J. A. Hammond², J. C. Schwartz³, D. Harrison⁴, and T. P. L. Smith⁵, ¹Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, ²The Pirbright Institute, Guildford, United Kingdom, ³The Pirbright Institute, Woking, United Kingdom, ⁴The Pirbright Insitute, Woking, United Kingdom, ⁵USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*
- P4055 48 **Assessing the genomic status of South African mutton, pelt and dual purpose sheep breeds using genomewide single nucleotide genotypes.**
*E. F. Dzomba^{*1}, M. A. Snyman², M. Chimonyo¹, and F. C. Muchadeyi³, ¹University of KwaZulu-Natal, Pietermaritzburg, South Africa, ²Grootfontein Agriculture Development Institute, Middelburg, South Africa, ³Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa*
- P4056 49 **Evaluation of single nucleotide polymorphism (SNP) markers for canine parentage analysis.**
*J. Qiu^{*1}, B. Simpson¹, L. Kock¹, J. Donner², C. Cole³, S. Davison³, M. Dunn⁴, D. Bannasch⁵, and A. Boyko⁶, 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*

- P4057 50 **Characterization of MITF coding region in llamas.**
M. Anello¹, M. Silbestro¹, 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. Abegaz¹, 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. Nonneman², J. C. M. Dekkers³, and C. K. Tuggle¹, 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. Wu^{}, 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. Wu^{}, 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, N. Trakooljul¹, M. Oster¹, E. Magowan², B. Metzler-Zebeli³, E. Murani¹, S. Ponsuksili¹, and K. Wimmers^{*1}, 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. Giuffra^{*1}, K. A. Munyard^{2,3}, A. Goubil⁴, S. Vincent-Naulleau^{5,6}, D. Esquerré⁷, S. Djebali⁸, and S. Foissac⁹, ¹GABI, INRA, AgroParisTech, Université 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, Université Paris Saclay, Jouy-en-Josas, France, ⁵GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France, ⁶SREIT, iRCM, CEA, Université Paris Saclay, Jouy-en-Josas, France, ⁷INRA, UMR1388 GenPhySe, GeT-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. Mapholi^{*1}, A. A. Maiwashe², O. Matika³, V. Riggio³, M. D. MacNeil⁴, C. B. Banga⁵, J. F. Taylor⁶, and K. Dzama⁷, 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. 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)*
- P3041 59 **A selective region on OAR17 is associated with backbone 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 gain¹.**
*A. K. Lindholm-Perry^{*1}, H. C. Cunningham², L. A. Kuehn¹, J. W. Keele¹, K. M. Cammack², and H. C. Freetly¹, ¹USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, ²Department of Animal Science, University of Wyoming, Laramie*

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. Jacobsen^{*1}, J. H. Havgaard¹, C. M. Junker Mentzel¹, P. M. Sørensen¹, S. Pundhir², C. Anthon¹, P. Karlskov-Mortensen¹, C. S. Bruun¹, S. Cirera¹, J. Gorodkin¹, C. B. Jørgensen¹, R. Barrès³, 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, ³The 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. Ząbek^{}, E. Semik, T. Szmatoła, 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. Vaughn², J. P. Carson³, J. M. Reecy¹, and J. E. Koltes^{*1,4}, 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. Prause^{*1}, B. M. Murdoch², J. E. Sawyer^{3,4}, J. L. Williams⁵, S. D. McKay⁶, 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, ⁵University of Adelaide, Adelaide, Australia, ⁶University 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. Kern^{*1}, P. Saelao¹, Y. Wang¹, M. Halstead¹, J. Chitwood¹, T. Kim¹, P. J. Ross¹, I. Korf¹, M. E. Delany¹, 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. Estrella^{1,2}, K. L. Kind^{1,3}, M. Ghanipoor-Samami^{1,2}, A. Javadmanesh^{1,2}, C. T. Roberts^{1,4}, and S. Hiendleder^{*1,2}, 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. Han^{*1}, Y. K. Kim², H. B. Park³, Y. J. Kang⁴, I. C. Cho³, and H. S. Oh², 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, 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. Godia^{*1}, F. Mayer^{1,2}, J. Nafissi¹, J. E. Rodríguez-Gil³, S. Balasch⁴, A. Sánchez¹, and A. Clop¹, ¹Center for Research in Agricultural Genomics (CRAG), Cerdanyola del Valles (Barcelona), Spain, ²Instituto de Pesquisas Veterinarias Desiderio Finamor, Fundasao Estadual de Pesquisa Agropecuaria, Porto Alegre, Brazil, ³Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Universitat Autònoma de Barcelona, Cerdanyola del Valles (Barcelona), Spain, ⁴Grup GEPORK, Masies de Roda, Spain*

- P5042 3 **Comparative analysis of gene expression during postnatal growth in Czech Fleckvieh Cattle.**
J. Kyselová¹, L. Barton¹, D. Bures¹, and J. Simunek², ¹Institute of Animal Science, Prague, Czech Republic, ²Institute of Animal Physiology and Genetics AS CR, Prague, Czech Republic
- P5043 4 **Association analysis between STAT5A and PROP1 genes and milk production in Czech National dairy goat breed: preliminary results.**
J. Rychtarová¹, Z. Sztankoová², J. Schmidová², and J. Kyselová¹, ¹Institute of Animal Science, Prague, Czech Republic, ²Institute of animal science, Prague, Czech Republic
- P5044 5 **Association of acetyl-coenzyme A carboxylase á, lipoprotein lipase and fat acid synthase genes with milk parameters in Czech East Friesian breed.**
Z. Sztankoová¹, J. Rychtarová¹, J. Schmidová¹, J. Kyselová², M. Milerski¹, and T. Kott¹, ¹Institute of animal science, Prague, Czech Republic, ²Institute of Animal Science, Prague, Czech Republic
- P5045 6 **Expression of CYP2C49, CYP7A1, CYP2B22, ACSL5 and APOA4 genes in the liver of Pietrain and Landrace pigs.**
M. Oczkowicz¹, K. Ropka-Molik², M. Wojtaszek³, and J. Warzecha³, 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, ³National Research Institute of Animal Production, Cracow, Poland
- P5046 7 **A genome-wide association study for natural antibodies measured in blood of Canadian Holstein cows.**
B. de Klerk¹, K. A. Thompson-Crispi², M. Sargolzaei³, J. J. van der Poel¹, B. J. Ducro¹, 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
- P5047 8 **Male fertility evaluation by a candidate gene approach.**
W. Liu¹, X. 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, ³Genex Cooperative, Inc., Shawano, WI
- P5048 9 **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*
- P5049 10 **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. Ryu², Y. I. Oh³, and K. C. Hong¹, ¹Korea University, Seoul, The Republic of Korea, ²Jeju National University, Jeju, The Republic of Korea, ³Gilgal agricultural association corporation, Jeju, The Republic of Korea
- P5050 11 **A genome wide scan for signature of positive selection in some Iranian sheep breeds.**
Z. Manzar¹, H. 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)
- P5051 12 **Transcriptome hallmarks of musculoskeletal fatigue in blood of Arabian horses under racing training regime.**
M. Stefaniuk-Szmukier¹, K. Ropka-Molik², K. Zukowski², and K. Piórkowska², ¹Department of Horse Breeding, Institute of Animal Science, University of Agriculture in Cracow, Cracow, Poland, ²National Research Institute of Animal Production, Balice, Poland
- P5052 13 **Genetic investigation of sheep families demonstrating the entropion eye condition.**
T. Hadfield^{} and N. E. Cockett, Utah State University, Logan*

Genetics and Disease V

7:30 - 8:30

Alpine Ballroom

- P6044 14 **Genomics assisted introgression of viral resistance in commercial common carp strains.**
R. Tadmor-Levi¹, E. Asulin¹, G. Hulata², and L. David¹, ¹The Hebrew University of Jerusalem, Rehovot, Israel, ²Agricultural Research Organization, Beit-Dagan, Israel
- P6045 15 **Fine mapping a sheep genomic locus involved in viral restriction of ovine lentivirus.**
A. T. Massa¹, M. R. Mouse², M. A. Highland^{1,2}, J. O. Reynolds², D. P. Knowles^{1,2}, J. B. Taylor³, and S. N. White^{1,2}, ¹Washington State University, Pullman, WA, ²USDA, ARS, Animal Disease Research Unit, Pullman, WA, ³USDA, ARS, U.S. Sheep Experiment Station, Dubois, ID
- P6046 16 **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*

- P6047 17 **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. Wagter-Lesperance**, H. Atalla, M. Emam, N. Gallo, D. Hodgins, M. McLean, L. Read, and B. Mallard, *Department of Pathobiology, University of Guelph, Guelph, ON, Canada*
- P6048 18 **Investigating a single nucleotide polymorphism in DDB2 as a risk factor for squamous cell carcinomas of the nictitans in the Haffinger and Belgian horse breeds.**
R. Bellone¹, J. Liu¹, S. Vig¹, T. M. Michau², C. M. Reilly¹, E. Bentley³, J. L. Petersen⁴, and M. Lassaline¹, ¹University of California-Davis, ²BluePearl, Tampa, FL, ³University of Wisconsin-Madison, ⁴University of Nebraska-Lincoln
- P6049 19 **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
- P6050 20 **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. Waldron³, D. A. Schneider^{1,2}, and K. I. O'Rourke², ¹USDA-ARS Animal Disease Research, Pullman, WA, ²Washington State University, Pullman, ³Texas A&M AgriLife Research, San Angelo
- P6051 21 **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
- P6052 22 **Evaluating the accuracy of imputation in the highly polymorphic MHC region of genome.**
M. Emam¹, M. Sargolzaei², S. Tabatabaie³, S. L. Cartwright⁴, F. S. Schenkel⁵, F. Miglior⁵, J. P. Chesnais⁶, and B. Mallard⁷, ¹Department of Pathobiology, University of Guelph, Guelph, ON, Canada, ²Semex Alliance, Guelph, ON, Canada, ³Department of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada, ⁴University of Guelph, Guelph, ON, Canada, ⁵Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, ⁶The Semex Alliance, Guelph, ON, Canada, ⁷Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada
- P6053 23 **Domestic animal forensics at the UC Davis Veterinary Genetics Laboratory.**
R. A. Grahn¹, C. D. Lindquist¹, and C. Penedo², ¹University of California-Davis, Veterinary Genetics Laboratory Forensics Unit, ²Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis
- P6054 24 **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. Lin², and C. J. McInnes², ¹Moredun Research Institute, Edinburgh, United Kingdom, ²Moredun Research Institute, Penicuik, United Kingdom

Bioinformatics, Statistical Genetics, and Genomic Technologies V

7:30 - 8:30

Alpine Ballroom

- P1036 25 **A reduced panel to determine beef cattle breed composition.**
L. A. Kuehn, W. M. Snelling, and A. K. Lindholm-Perry*, USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE
- P1037 26 **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
- P1038 27 **BovineMine: A bovine genome data mining warehouse.**
C. G. Elsik, D. R. Unni, A. Tayal, C. M. Diesh, and D. E. Hagen*, University of Missouri, Columbia
- P1039 28 **Bioinformatics resources for animal genomics using CyVerse cyberinfrastructure.**
J. E. Koltes¹, J. M. Reecy¹, E. Lyons², F. McCarthy², M. W. Vaughn³, J. P. Carson⁴, E. Fritz-Waters¹, and J. Williams⁵, ¹Iowa State University, Ames, ²University of Arizona, Tucson, AZ, ³Texas Advance Computing Center, University of Texas, Austin, TX, ⁴Texas Advanced Computing Center, University of Texas, Austin ⁵Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
- P1040 29 **Diet analysis of grasscutter (*Thryonomys swinderianus*) using next generation sequencing.**
C. Adenyo^{1,2}, H. Ando³, B. B. Kayang¹, E. Inoue⁴, and M. Inoue-Murayama², ¹University of Ghana, Accra, Ghana, ²Kyoto University, Kyoto, Japan, ³National Institute for Environmental Studies, Tsukuba, Japan, ⁴Toho University, Funabashi, Japan
- P1041 30 **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
- P1042 31 **Combining RNA sequencing technologies to annotate the bovine genome.**
D. E. Hagen, D. R. Unni, and C. G. Elsik*, University of Missouri, Columbia

- P1043 32 **Identification of regulatory elements in three domesticated species.**
*H. Zhou^{*1}, M. E. Delany¹, H. Cheng², P. J. Ross¹, I. Korf¹, C. Kern¹, P. Saelao¹, Y. Wang¹, T. Kim¹, J. Chitwood¹, M. Halstead¹, J. F. Medrano¹, A. L. Van Eenennaam¹, C. K. Tuggle³, and C. W. Ernst⁴, ¹University of California-Davis, ²USDA-ARS Avian Disease and Oncology Laboratory, East Lansing, ³Iowa State University, Ames, ⁴Michigan State University, East Lansing*
- 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^{*1}, R. Li¹, J. J. Michal¹, X. L. Wu¹, Z. Liu², H. Zhao², Y. Xia², R. M. Harland³, and Z. Jiang¹, 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. Khoo^{*1,2}, A. Gheyas¹, R. Kuo¹, L. Eory¹, P. M. Hocking¹, and D. Burt¹, ¹The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, 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^{*1}, C. Penedo², O. Cortés³, I. Martín-Burriel⁴, A. Egito⁵, L. T. D. Gama⁶, J. V. Delgado Bermejo⁷, B. Consortium⁷, and A. Martínez-Martínez⁷, 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 Veterinária, Universidade Técnica de Lisboa, Lisboa, Portugal, ⁷Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*
- P4060 37 **Runs of homozygosity reveal natural selection footprints of some African chicken breeds and village ecotypes.**
*A. R. Elbeltagy^{*1,2}, 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*
- 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. Ruplin, 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 DHI traits.**
*Y. R. Velez^{*1}, J. Patino², E. Soto-Moreno², B. Velez², T. S. Sonstegard³, and M. Pagán-Morales⁴, ¹University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico, ²University of Puerto Rico, Mayaguez, PR, Puerto Rico, ³USDA, ARS, BFGI, Beltsville, 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.**
*V. R. Kharzinova^{*1}, A. V. Dotsev¹, I. M. Okhlopkov², E. A. Gladyr³, V. I. Fedorov⁴, G. Brem⁵, and N. A. Zinovieva³, ¹L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, ²Science Institute of Biological Problems Cryolithozone, Yakutsk, Russian Federation, ³L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, ⁴Federal Government Budget Scientific Institutions Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russian Federation, ⁵Institute of Animal Breeding and Genetics, VMU, Vienna, Austria*
- P4065 42 **MicroGBS - High-throughput microsatellite genotyping using Illumina sequencing platforms.**
G. Waldbieser^{}, 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.**
*H. Blackburn^{*1}, D. A. Faria², C. Wilson³, and S. R. Paiva⁴, ¹National Animal Germplasm Program ARS-USDA, Ft. Collins, CO, ²National Animal Germplasm Program, Fort Collins, CO, ³National Animal Germplasm Program - ARS- USDA, Fort Collins, CO, ⁴EMBRAPA-LABEX US - Secretariat International Affairs, Brasilia, Brazil*

- P4067 44 **Comparing genetic diversity of pig populations on the US mainland, Pacific Islands and China: Y chromosome evaluation.**
D. A. Faria¹, S. R. Paiva², C. Wilson³, and H. Blackburn⁴, ¹National Animal Germplasm Program, Fort Collins, CO, ²Embrapa - Labex US - Secretariat International Affairs, Brasilia, Brazil, ³National Animal Germplasm Program - ARS- USDA, Fort Collins, CO, ⁴National Animal Germplasm Program ARS-USDA, Ft. Collins, CO
- P4068 45 **Interaction of STAT1 and PGR specific genotypes affects milk production in slick and normal coat Holsteins.**
B. Velez¹, J. Patino¹, Y. R. Velez², T. S. Sonstegard³, and M. Pagán-Morales⁴, ¹University of Puerto Rico, Mayaguez, PR, Puerto Rico, ²University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico, ³USDA, ARS, BFG, Beltsville, MD, ⁴Department of Animal Science, University of Puerto Rico, Mayaguez Campus, Mayaguez, Puerto Rico
- P4069 46 **Genetic differences in a Colombian Paso horse breed by gait selection.**
M. A. Novoa^{1,2} and L. F. Garcia², ¹GENETICA ANIMAL DE COLOMBIA LTDA., Bogota, Colombia, ²UNIVERSIDAD NACIONAL DE COLOMBIA, Bogota, Colombia
- P4070 47 **SNP discovery and allele frequency estimation in indigenous breeds of South Africa.**
A. Zwane¹, A. A. Maiwashe², and E. van Marle-Koster³, ¹Agricultural Research Council, Pretoria, South Africa, ²ARC-Animal Production Institute, Irene, South Africa, ³University of Pretoria, South Africa
- P4071 48 **Extensive functional class I MHC diversity in sheep.**
K. Ballingall¹, S. Goh², J. M. Pemberton³, and K. Dicks³, ¹Moredun Research Institute, Edinburgh, United Kingdom, ²Royal Veterinary College, Hatfield, United Kingdom, ³The University of Edinburgh, United Kingdom
- P4072 49 **Development of a 55K SNP array for oysters (*C. gigas* and *O. edulis*).**
A. P. Gutierrez¹, F. Turner², T. P. Bean³, K. Gharbi², and R. D. Houston¹, 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

- P3043 50 **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. Zambonelli¹, E. Gaffo², M. Zappaterra¹, and S. Bortoluzzi², ¹Bologna University, Department of Agricultural and Food Sciences (DISTAL), Bologna, Italy, ²Padova University, Department of Molecular Medicine, Padova, Italy
- P3044 51 **Characterization of exosomal immune-related microRNAs in colostrum and milk from average, low and high immune responder cows.**
H. Atalla^{1,2}, B. Mallard^{1,2}, 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
- P3045 52 **Identification and expression analysis of Bovine X degenerate Y-Chromosome genes.**
F. A. Ponce de Leon¹, Y. Guo¹, B. A. Crooker², T. G. McDanel³, and T. P. L. Smith³, 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
- P3046 53 **Gene expression In developing goat testes: Sequencing, assembly and identification of caprine spermatogenesis transcriptome.**
B. Barcelos^{1,2}, 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
- P3047 54 **Reduced cell cycle gene expression in adipose tissue of chickens during juvenile development.**
X. Wang¹, A. Ropelewski², N. Cook¹, A. Bohannon-Stewart¹, and S. Nahashon¹, ¹Tennessee State University, Nashville, ²Pittsburgh Supercomputing Center, Pittsburgh, PA
- P3048 55 **Gene network analysis identifies rumen epithelial processes perturbed by diet and correlated with methane production and yield.**
R. Xiang¹, J. McNally², S. J. Rowe³, A. Jonker⁴, C. Pinares-Patino⁵, J. Bond⁶, H. V. Oddy⁷, P. Vercoe⁸, J. C. McEwan³, and B. P. Dalrymple¹, 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. Lee³, and C. Gondro⁴, 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. Holt⁵, J. F. Medrano⁶, A. Islas-Trejo⁶, R. M. Enns⁷, S. E. Speidel⁷, 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 Sciences, 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

Structural and Comparative Genomics

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- P8000 60 **Allelic diversity of productive, reproductive & fertility traits genes of buffalo and cattle.**
M. Moaen-ud-Din^{}, PMAS-Arid Agriculture University, Rawalpindi, Pakistan*
- P8001 61 **3D nuclear positioning of IGF2 alleles and trans interactions with imprinted genes.**
Y. Lahbib-Mansais¹, M. Marti Marimon¹, V. Voillet¹, F. Mompant¹, J. Riquet¹, S. Foissac¹, D. Robelin¹, H. Acloque¹, Y. Billon², N. Villa-Vialaneix³, L. Liaubet¹, and M. Bouissou-Matet Yerle⁴, ¹INRA UMR 1388 GenPhySE, Castanet-Tolosan, France, ²INRA UE 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. Hoffmann², 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
- 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. Park^{}, Konkuk University, Seoul, The Republic of Korea*
- P8004 64 **A comprehensive gene catalogue of the horse Y chromosome.**
J. Janečka¹, L. Orlando², M. Schubert³, S. Ghosh⁴, T. A. Stout⁵, B. P. Chowdhary⁶, 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. Song^{1,2}, D. Shin³, and H. K. Lee³, 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. Letaief¹, D. Esquerré², J. Barbieri², C. Grohs¹, S. Fritz^{1,3}, C. Klopp⁴, R. Philippe⁵, V. Blanquet⁵, D. Boichard⁶, D. Rocha¹, and M. Boussaha¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, ²Get-PlaGe, INRA, Castanet-Tolosan, France, ³ALLICE, 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-Nissen^{}, 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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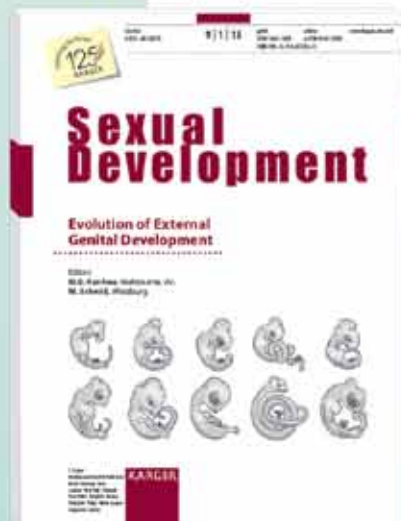
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