ISAG 2021
VIRTUAL CONFERENCE

INTERNATIONAL SOCIETY
FOR ANIMAL GENETICS

JULY 26–30, 2021

CONFERENCE PROGRAM

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Committees

ISAG Executive Committee

Clare Gill, Texas A&M University, USA (President)

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Chris Tuggle, Iowa State University, USA

Hans Lenstra, Utrecht University, Netherlands (ex officio)

ISAG 2021 Workshop Chairs

Note: Due to the virtual nature of the 2021 conference, the workshop chairs also served as the scientific committee.

Animal epigenetics
Kyle Schachtschneider, University of Illinois at Urbana-Champaign

Animal forensic genetics
Guillermo Giovambattista, Universidad Nacional De La Plata

Applied genetics and genomics in other species of economic importance
Leanne Van de Goor, Dr. van Haeringen Laboratorium B.V.

Applied genetics of companion animals
Leslie Lyons, University of Missouri, and Jiansheng Qiu, Neogen GeneSeek

Avian genetics and genomics
Klaus Wimmers, FBN-Dummerstorf

Cattle molecular markers and parentage testing
Jiansheng Qiu, Neogen GeneSeek

Companion animal genetics and genomics
Heather Huson, Cornell University, and Jeffrey Schoenbeck, Roslin Institute (University of Edinburgh)

Comparative and functional genomics
Fiona McCarthy, The University of Arizona

Comparative MHC genetics: populations and polymorphism
John Hammond, The Pirbright Institute

Domestic animal sequencing and annotation
George Liu, USDA

Equine genetics and Thoroughbred parentage testing
Marcela Martinez, Laboratorio De Genetica AplicadaSociedad Rural Argentina

Genetics and genomics of aquaculture species
Francesca Bertolini, Iowa State University, and Maria Saura, INIA

Genetics of immune response and disease resistance
Huaijun Zhou, University of California, Davis

Genome edited animals
Wang Xiaolong, Northwest A&F University

Horse genetics and genomics
Ted Kalbfleisch, University of Kentucky

ISAG-FAO genetic diversity
Juha Kantanen, Natural Resources Institute Finland, and Catarina Ginja, CIBIO-InBIO, Universidade do Porto, Portugal

Livestock genomics for developing countries
Abdulfatai Tijjani, International Livestock Research Institute

Microbiomes
Claire Rogel-Gaillard, GABI, INRA, AgroParisTech, Université Paris-Saclay

Pig genetics and genomics
Amanda Warr, The Roslin Institute, and Andreia Amaral, University of Lisbon

Ruminant genetics and genomics
Laercio Porto-Neto, CSIRO Agriculture

Small Ruminant Genetics and Genomics
Meng-Hua Li, China Agricultural University, and Rebecca Simon, Justus Liebig University Giessen

Schedule of Events

Monday, July 26

Time (CDT)	
1:00 AM – 3:55 AM	Comparative MHC Genetics: Populations and Polymorphisms Workshop
7:45 AM – 8:45 AM	**Plenary Session I:** Combining quantitative genetics and population genomics to improve beef sustainability (J. E. Decker)
9:00 AM –12:00 PM	Small Ruminant Genetics and Genomics Workshop
1:00 PM – 3:30 PM	Ruminant Genetics and Genomics Workshop

Tuesday, July 27

1:00 AM – 4:00 AM	Avian Genetics and Genomics Workshop
9:00 AM –12:00 PM	Cattle Molecular Markers and Parentage Testing Workshop
9:00 AM –12:00 PM	Horse Genetics and Genomics Workshop
1:00 PM – 4:00 PM	Animal Epigenetics Workshop
5:00 PM – 6:00 PM	**Plenary Session II:** Harnessing the power of genomics and AI to breed new species for aquaculture (M. Wellenreuther)

Wednesday, July 28

12:30 AM – 4:00 AM	Pig Genetics and Genomics Workshop
7:00 AM – 8:00 AM	**Plenary Session III:** Diversification and sustainability of aquaculture production: What can (and cannot) we do as geneticists? (F. Bertolini)
8:00 AM – 10:00 AM	Livestock Genomics for Developing Countries Workshop
9:00 AM –12:00 PM	Applied Genetics of Companion Animals Committee Workshop
1:00 PM – 4:15 PM	Domestic Animal Sequencing and Annotation Workshop
5:00 PM – 8:00 PM	Animal Forensic Genetics Workshop

Thursday, July 29

1:00 AM – 4:00 AM	Microbiomes Workshop
5:00 AM – 8:00 AM	ISAG-FAO Advisory Group on Animal Genetic Diversity Workshop
9:00 AM –12:00 PM	Applied Genetics/ Genomics in Other Species of Economic Interest Workshop
9:00 AM –12:00 PM	Comparative and Functional Genomics Workshop
1:00 PM – 3:00 PM	Agricultural Genome To Phenome Initiative (AG2PI): Introduction and Community Building and Listening Workshop
3:00 PM – 5:00 PM	Companion Animal Genetics and Genomics Workshop
7:00 PM – 8:00 PM	**Plenary Session IV:** Applying functional knowledge to accelerate animal genetic improvement (A. J. Chamberlain)

Friday, July 30

7:00 AM – 8:00 AM	General Business Meeting
9:00 AM –12:00 PM	Equine Genetics and Thoroughbred Parentage Testing Workshop
9:00 AM –12:15 PM	Genetics/Genomics of Aquaculture Species Workshop
1:00 PM – 4:00 PM	Genetics of Immune Response Workshop

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POSTER SCHEDULE

Poster presentations arranged by section (all posters available for on-demand viewing):

Section	Poster numbers	Oral numbers	Workshop day
Animal Epigenetics	P100–P109	W149–W157	Tuesday
Animal Forensic Genetics	P110–P112	W192–W198	Wednesday
Applied Genetics and Genomics in Other Species of Economic Importance	P113–P118	W216–W218	Thursday
Applied Genetics of Companion Animals	P119–P121	W175–W180	Wednesday
Avian Genetics and Genomics	P122–P150	W128–W137	Tuesday
Cattle Molecular Markers and Parentage Testing	P151–P159	W138–W140	Tuesday
Companion Animal Genetics and Genomics	P160–P181	W225–W231	Thursday
Comparative and Functional Genomics	P182–P200	W219–W223	Thursday
Comparative MHC Genetics: Populations and Polymorphism	P201–P210	W100–W108	Monday
Domestic Animal Sequencing and Annotation	P211–P223	W181–W191	Wednesday
Equine Genetics and Thoroughbred Parentage Testing	P224–P228	W233–W235	Friday
Genetics and Genomics of Aquaculture Species	P229–P239	W236–W246	Friday
Genetics of Immune Response and Disease Resistance	P240–P263	W247–W260	Friday
Horse Genetics and Genomics	P264–P285	W141–W148	Tuesday
ISAG-FAO Genetic Diversity	P286–P291	W207–W215	Thursday
Livestock Genomics for Developing Countries	P292–P300	W169–W174	Wednesday
Microbiomes	P301–P312	W199–W206	Thursday
Pig Genetics and Genomics	P313–P344	W159–W167	Wednesday
Ruminant Genetics and Genomics	P345–P405	W121–W127	Monday
Small Ruminant Genetics and Genomics	P406–P421	W110–W120	Monday

Meeting time zones:

			Key meeting times in Central daylight time (UTC −5 h)						
Location	**Time zone**	**UTC offset**	1:00 AM	7:00 AM	9:00 AM	12:00 PM	4:00 PM	7:00 PM	9:00 PM
Vancouver	PDT	UTC −7	*11:00 PM*	5:00 AM	7:00 AM	10:00 AM	2:00 PM	5:00 PM	7:00 PM
Salt Lake City	MDT	UTC −6	12:00 AM	6:00 AM	8:00 AM	11:00 PM	3:00 PM	6:00 PM	8:00 PM
		UTC	6:00 AM	12:00 PM	2:00 PM	5:00 PM	9:00 PM	**12:00 AM**	**2:00 AM**
Dublin, London	IST, BST	UTC +1	7:00 AM	1:00 PM	3:00 PM	6:00 PM	10:00 PM	**1:00 AM**	**3:00 AM**
Western Europe	CEST	UTC +2	8:00 AM	2:00 PM	4:00 PM	7:00 PM	11:00 PM	**2:00 AM**	**4:00 AM**
Minsk	MSK	UTC +3	9:00 AM	3:00 PM	5:00 PM	8:00 PM	**12:00 AM**	**3:00 AM**	**5:00 AM**
Perth	AWST	UTC +8	2:00 PM	8:00 PM	10:00 PM	**1:00 AM**	**5:00 AM**	**8:00 AM**	**10:00 AM**
Beijing	CST	UTC +8	2:00 PM	8:00 PM	10:00 PM	**1:00 AM**	**5:00 AM**	**8:00 AM**	**10:00 AM**
Seoul, Tokyo	KST, JST	UTC +9	3:00 PM	9:00 PM	11:00 PM	**2:00 AM**	**6:00 AM**	**9:00 AM**	**11:00 AM**
Sydney	AEST	UTC +10	4:00 PM	10:00 PM	**12:00 AM**	**3:00 AM**	**7:00 AM**	**10:00 AM**	**12:00 PM**
Wellington	NZST	UTC +12	6:00 PM	**12:00 AM**	**2:00 AM**	**5:00 AM**	**9:00 AM**	**12:00 PM**	**2:00 PM**

*Times shown in italics indicate the previous day and times shown in bold indicate the following day relative to the meeting day and time in CDT.

Monday, July 26

Comparative MHC Genetics: Populations and Polymorphism Workshop

Chair: **John Hammond, The Pirbright Institute**
1:00 AM – 3:55 AM CDT
6:00 AM – 8:55 AM UTC

1:00 AM **Welcoming remarks**

1:05 AM W100 **Characterization of the functional and transcriptional variation of cattle MHC class I alleles.**
J. C. Schwartz*[1], G. Maccari[1],[2], D. Heimeier[1], and J. A. Hammond[1], [1]*The Pirbright Institute, Guildford, UK*, [2]*Anthony Nolan Research Institute, London, UK*.

1:20 AM W101 **Association of bovine leukemia virus-induced lymphoma with BoLA-DRB3 polymorphisms at the DNA, amino acid, and binding pocket property levels.**
C.-W. Lo*[1], S.-N. Takeshima[2],[3], K. Okada[4], E. Saitou[5], T. Fujita[6], Y. Matsumoto[1], S. Wada[7], H. Inoko[8], and Y. Aida[1],[2], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Viral Infectious Diseases Unit, RIKEN, Saitama, Japan*, [3]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*, [4]*Iwate University, Iwate, Japan*, [5]*Hyogo Prefectural Awaji Meat Inspection Center, Hyogo, Japan*, [6]*Livestock Research Institute of Oita Prefectural Agriculture, Forestry and Fisheries, Research Center, Oita, Japan*, [7]*Photonics Control Technology Team, RIKEN Center for Advanced Photonics, Saitama, Japan*, [8]*Genome Analysis Division, GenoDive Pharma Inc., Kanagawa, Japan*.

1:35 AM W102 **Application of MHC sequencing to vaccine development: Proteome-wide analysis of zoonotic bacterium *Coxiella burnetii* for conserved T-cell epitopes presented by multiple host species.**
L. M. Wright Piel[1], C. J. Durfee[1], and S. N. White*[1,2], [1]*USDA-ARS Animal Disease Research, Pullman, WA, USA*, [2]*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA*, [3]*Center for Reproductive Biology, Washington State University, Pullman, WA, USA*.

1:50 AM W103 **Development of a comprehensive high-resolution typing method for SLA-3, an MHC classical class I gene of pigs, using genomic DNA PCR and direct sequencing.**
S. Youk*[1], M. T. Le[1], M. Kang[1], B. Ahn[1], M. Choi[1], C. Ho[2], and C. Park[1], [1]*Konkuk University, Seoul, Republic of Korea*, [2]*Gift of Hope Organ and Tissue Donor Network, Itasca, IL, USA*.

2:05 AM W104 **Molecular characterization of swine leukocyte antigen (SLA) gene diversity in European farmed pigs.**
S. E. Hammer*[1], T. Duckova[1], S. Groiss[1], M. Stadler[1], M. Jensen-Wearn[2], W. T. Golde[3], U. Gimsa[4], and A. Saalmueller[1], [1]*University of Veterinary Medicine Vienna, Vienna, Austria*, [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [3]*Moredun Research Institute, Edinburgh, Scotland, UK*, [4]*Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany*.

2:20 AM **Break**

2:30 AM W105 **Expression of genes related with immunomodulation and immunogenicity of equine mesenchymal stem cells: Influence of major histocompatibility complex.**
A. Cequier*[1], S. Fuente[1,2], A. Vitoria[1,2], A. Romero[1,2], F. Vázquez[1,2], C. Rodellar[1], and L. Barrachina[1,2], [1]*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza), Instituto Agroalimentario de Aragón (IA, Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

2:45 AM W106 **Sequencing of LEI0258 marker reveals populations' specific alleles and new repeat motif patterns.**
P. Manjula*[1], T. Kalhari[2], S. Cho[1], M. Kim[2], E. Cho[3], and J. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Republic of Korea*, [3]*Department of Bio big Data, Chungnam National University, Daejeon, Republic of Korea*.

3:00 AM W107 **Evaluation of polymorphisms in BLB-2 gene in Korean Ogye chicken using NGS data.**
T. Kalhari*[1], P. Manjula[2], S. Cho[2], M. Kim[1], E. Cho[3], and J. Lee[1,2], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*, [3]*Department of Bio-big data, Chungnam National University, Daejeon, Korea*.

3:15 AM W108 **The IPD-MHC Database: Novel tools for the study of the major histocompatibility complex.**
G. Maccari*[1,2], J. Robinson[2,3], J. A. Hammond[1], and S. G. E. Marsh[2,3], [1]*The Pirbright Institute, Pirbright, Woking, Surrey, UK*, [2]*Anthony Nolan Research Institute, Royal Free Campus, London, UK*, [3]*UCL Cancer Institute, Royal Free Campus, London, UK*.

3:40 AM **Workshop business meeting**

Plenary Session I

Chairs: Tosso Leeb, University of Bern, Institute of Genetics, and Christine Baes, University of Bern/University of Guelph

7:45 AM – 8:45 AM CDT

12:45 PM – 1:45 PM UTC

7:45 AM W109 **Combining quantitative genetics and population genomics to improve beef sustainability.**
J. E. Decker*[1,2,3], T. N. Rowan[1,2,4,5], S. M. Nilson[1], H. J. Durbin[1,2], C. U. Braz[1], R. D. Schnabel[1,2,3], and C. M. Seabury[6], [1]*Division of Animal Sciences, University of Missouri, Columbia, MO, USA*, [2]*Genetics Area Program, University of Missouri, Columbia, MO, USA*, [3]*Institute for Data Science and Informatics, University of Missouri, Columbia, MO, USA*, [4]*Department of Animal Science, University of Tennessee, Knoxville, Knoxville, TN, USA*, [5]*College of Veterinary Medicine, Large Animal Clinical Science, University of Tennessee, Knoxville, TN, USA*, [6]*Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA*.

Small Ruminant Genetics and Genomics Workshop

Chairs: Meng-Hua Li, China Agricultural University, and Rebecca Simon, Justus Liebig University Giessen

9:00 AM – 12:00 PM CDT

2:00 PM – 5:00 PM UTC

9:00 AM W110 **Invited Workshop Presentation: High-quality assembly of Tibetan sheep genome helps reveal high-altitude hypoxia adaptation's genetic mechanism.**
X. Li*[1,2] and M.-H. Li[3,1], [1]*CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences (CAS), Beijing, China*, [2]*University of Chinese Academy of Sciences (UCAS), Beijing, China*, [3]*College of Animal Science and Technology, China Agricultural University, Beijing, China*.

9:30 AM W111 **Invited Workshop Presentation: The genome landscape of worldwide sheep reveals genetic mechanism of multiple morphological and agronomic traits.**
M.-H. Li*, *College of Animal Science and Technology, China Agricultural University, Beijing, China*.

10:00 AM W112 **Comparative transcriptome analysis between suckling lambs with different levels of perirenal adipose tissue in the carcass.**
M. Alonso-García[1], A. Suárez-Vega[1], J. Mateo[2], H. Marina[1], R. Pelayo[1], C. Esteban-Blanco[1], J. J. Arranz[1], and B. Gutiérrez-Gil*[1], [1]*Departamento de Producción Animal, Facultad de Veterinária, Universidad de León, Campus de Vegazana, León, León, Spain*, [2]*Departamento de Higiene y Tecnología de los Alimentos, Facultad de Veterinária, Universidad de León, Campus de Vegazana, León, León, Spain*.

10:10 AM W113 **Exploring differentially expressed genes in hypothalamic transcriptome in different sexual behavior phenotypes in rams using RNA-seq.**
K. Lakhssassi*[1,2], I. Ureña[3], B. Marín[4], M. P. Sarto[1], B. Lahoz[1], J. L. Alabart[1], J. Folch[1], M. Serrano[3], and J. H. Calvo[1,5], [1]*Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA)-IA, Zaragoza, Spain*, [2]*Institut National de la Recherche Agronomique, Rabat, Morocco*, [3]*Instituto Nacional de Investigación y Tecnología Agrária y Alimentaria (INIA), Madrid, Spain*, [4]*Universidad de Zaragoza, Zaragoza, Spain*, [5]*Fundación Agencia Aragonesa para la Investigación y el Desarrollo (ARAID), Zaragoza, Spain*.

10:20 AM W114 **Unveiling genomic regions that underlie footrot resistance in Portuguese Merino sheep.**
D. Gaspar*[1,2], A. Usié[1,3], C. Leão[3,4], C. Matos[5], L. Padre[3], C. Dias[3], C. Ginja[2], and A. M. Ramos[1,3], [1]*CEBAL – Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Beja, Portugal*, [2]*CIBIO/InBIO – Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, Porto, Portugal*, [3]*MED-Mediterranean Institute for Agriculture, Environment and Development, University of Évora, Évora, Portugal*, [4]*INIAV (Instituto Nacional de Investigação Agrária e Veterinária), Santarém, Portugal*, [5]*ACOS – Agricultores do Sul, Beja, Portugal*.

10:30 AM **Break**

10:45 AM W115 **Identification of a novel loss-of-function variant in the ovine *TMCO6* gene associated with motor neuron disease of North Country Cheviot sheep.**
A. Letko*[1], I. M. Häfliger[1], E. Corr[2], F. Brulisauer[2], S. Scholes[2], and C. Drögemüller[1], [1]*Institute of Genetics, Bern, Switzerland*, [2]*SRUC Consulting Veterinary Services, Penicuik, Midlothian, UK*.

10:55 AM W116 **A homozygous frameshift variant in *MFSD2A* associated with congenital brain hypoplasia in a Kerry Hill sheep family.**
G. Lühken*[1], A. Letko[2], M. Häfliger[2], M. J. Schmidt[3], C. Herden[4], L. Herkommer[4], J. Müller[4], and C. Drögemüller[2], [1]*Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Germany*, [2]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [3]*Clinic for Small Animals, Neurosurgery, Neuroradiology and Clinical Neurology, Justus Liebig University, Giessen, Germany*, [4]*Institue of Veterinary Pathology, Justus Liebig University, Giessen, Germany*.

11:05 AM W117 **Identification of novel SNPs associated with litter size in Rasa Aragonesa sheep breed.**
K. Lakhssassi[1,2], J. Grimplet[1], M. P. Sarto[1], B. Lahoz[1], J. L. Alabart[1], J. Folch[1], M. Serrano[3], and J. H. Calvo*[1,4], [1]*Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA) – IA, Zaragoza, Spain*, [2]*Institut National de la Recherche Agronomique (INRA), Rabat, Morocco*, [3]*Instituto Nacional de Investigación y Tecnología Agrária y Alimentaria (INIA), Madrid, Spain*, [4]*Fundación Agencia Aragonesa para la Investigación y el Desarrollo (ARAID), Zaragoza, Spain*.

11:15 AM W118 **Machine learning algorithm to predict coagulating milk factor through milk traits in 2 sheep breeds.**
H. Marina*, B. Gutiérrez-Gil, R. Pelayo, A. Suárez-Vega, C. Esteban-Blanco, and J. Arranz, *Departamento de Producción Animal, Facultad de Veterinária, Universidad de León, Campus de Vegazana, León, Spain*.

11:25 AM W119 **Identification of selection signatures on the X chromosome in East Adriatic sheep.**
M. Shihabi[1], B. Lukic[2], I. Drzaic[1], M. Ferencakovic[1], V. Brajkovic[1], L. Vostry[3], V. Cubric-Curik[1], and I. Curik*[1], [1]*University of Zagreb, Faculty of Agriculture, Zagreb, Croatia*, [2]*J.J. Strossmayer University of Osijek, Faculty of Agrobiotechnical Sciences, Osijek, Croatia*, [3]*Czech University of Life Sciences, Prague, Czech Republic*.

11:35 AM W120 **Study on fiber characteristics of different Inner Mongolia Cashmere goats.**
Z. Chongyan, X. Yuchun, G. Juntao, S. Xin, Z. Cun, Q. Qing, D. Dongliang, W. Zhixin, L. Jinquan, and L. Zhihong*, *Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China*.

11:45 AM **Election of new committee**

Ruminant Genetics and Genomics Workshop

Chair: **Laercio R. Porto Neto, CSIRO Agriculture & Food**

1:00 PM – 3:30 PM CDT
6:00 PM – 8:30 PM UTC

1:00 PM W121 **A comprehensive catalog of regulatory variants in the cattle transcriptome: A case study for the FarmGTEx Project.**
G. E. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD, USA*.

1:20 PM W122 **Comparison of sequencing and assembly strategies for the cattle pangenome effort.**
A. Leonard*[1], Z.-H. Fang[1], B. Rosen[2], D. Bickhart[2], T. Smith[2], and H. Pausch[1], [1]*ETH Zürich, Zürich, Switzerland*, [2]*ARS, USDA, Beltsville, MD, USA*.

1:35 PM W123 **Dissection of the scurs phenotype to refine the mapping of scurs.**
G. Wang* and C. Gill, *Texas A&M University, College Station, TX, USA*.

1:50 PM **Break**

2:00 PM W124 **Genomic breeding values from low-coverage Nanopore sequencing.**
H. J. Lamb, B. J. Hayes, L. T. Nguyen, and E. M. Ross*, *The Queensland Alliance for Agriculture and Food Innovation, St Lucia, Queensland, Australia*.

2:15 PM W125 **Can SNPs associated with variation in the level of stress biomarkers be used for the selection of stress-resilient dairy cows?**
M. M. Passamonti*[1], M. Milanesi[4], J. Ramirez Diaz[1], A. Stella[2], M. Barbato[1], M. Premi[1], R. Negrini[1], A. Cecchinato[3], E. Trevisi[1], J. L. Williams[1], and P. Ajmone Marsan[1], [1]*Universitá Cattolica del Sacro Cuore, Piacenza, Italy*, [2]*Consiglio Nazionale della Ricerca, Milan, Italy*, [3]*Universitá di Padova, Padua, Italy*, [4]*Università della Tuscia, Viterbo, Italy*.

2:30 PM W126 **The distinct morphological phenotypes of domestic sheep are shaped by introgressions from their sibling wild species.**
H. Cheng*, J. Wen, Z. Zhang, and Y. Jiang, *Northwest A&F University, Yangling, Shaanxi, China*.

2:45 PM W127 **Genome-wide local ancestry and direct evidence for cytonuclear disequilibria in hybrid African cattle populations (*Bos taurus/indicus*).**
J. A. Ward*[1], G. P. McHugo[1], M. J. Dover[1], T. J. Hall[1], S. I. Ng'ang'a[2,3], T. S. Sonstegard[4], D. G. Bradley[5], L. A. F. Frantz[2,3], M. Salter-Townshend[6], and D. E. MacHugh[1,7], [1]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilian University, Munich, Germany*, [3]*School of Biological and Chemical Sciences, Queen Mary University of London, London, UK*, [4]*Acceligen, Eagan, MN, USA*, [5]*Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland*, [6]*UCD School of Mathematics and Statistics, University College Dublin, Dublin, Ireland*, [7]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland*.

3:00 PM **Workshop business meeting**

Tuesday, July 27

Avian Genetics and Genomics Workshop

Chair: **Klaus Wimmers, FBN-Dummerstorf**
1:00 AM – 4:00 AM CDT
6:00 AM – 9:00 AM UTC

1:00 AM **Introduction**

1:05 AM W128 **Genetic diversity and population structure of Myanmar native chickens using double digest restriction-site associated DNA sequencing (ddRAD-seq).**
S. L. Y. Mon*[1], M. Lwin[2], A. A. Maw[3], L. L. Htun[3], S. Bawm[3], K. Kawabe[4], Y. Nagano[5,1], A. J. Nagano[6], Y. Wada[5,1], S. Okamoto[1], and T. Shimogiri[1], [1]*The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, Japan*, [2]*Livestock Breeding and Veterinary Department, Yangon, Myanmar*, [3]*University of Veterinary Science, Nay Pyi Taw, Myanmar*, [4]*Education Center, Kagoshima University, Kagoshima, Japan*, [5]*Faculty of Agriculture, Saga University, Saga, Japan*, [6]*Faculty of Agriculture, Ryukoku University, Otsu, Shiga, Japan*.

1:20 AM W129 **Taxonomy classification of Nigerian local turkey using 12S mitochondrial rRNA gene.**
D. I. Ibiwoye*[1,2], F. E. Sola-Ojo[1], D. O. Aremu[1], I. A. Abubakar[1], N. B. Afolabi-Balogun[3], C. A. Adeniyi[4], and A. O. Oni[3], [1]*University of Ilorin, Ilorin, Kwara, Nigeria*, [2]*Huazhong Agricultural University, Wuhan, China*, [3]*Fountain University, Osogbo, Osun, Nigeria*, [4]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*.

1:35 AM W130 **Transcriptomic analysis of the *Musculus complexus* in naked neck broiler chickens.**
A. C. Mott*, C. Blaschka, A. Mott, A. R. Sharifi, and J. Tetens, *Georg-August University, Göttingen, Lower Saxony, Germany*.

1:50 AM W131 **Study on differentially expressed genes in granular layer and theca layer of laying Silky Fowl and White Leghorn.**
Y. Tai*[1], X. Yang[1], D. Han[2], and X. Deng[1], [1]*China Agricultural University, Lab of Animal Genetic Resource and Molecular Breeding, Beijing, China*, [2]*College of Veterinary Medicine, China Agricultural University, Beijing, China*.

2:05 AM W132 **Hypothalamic and ovarian transcriptome profiling reveals potential candidate genes in low and high egg production of White Muscovy ducks (*Cairina moschata*).**
S. Bello*, H. Xu, and Q. Nie, *South China Agricultural University, Guangzhou, Guangdong, China*.

2:20 AM **Break**

2:30 AM W133 **Nextflow IsoSeq (nf-isoseq) pipeline provides a first insight into the chicken transcript landscape.**
S. Guizard*, J. Smith, R. Kuo, K. Miedzinska, J. Smith, M. Davey, and M. Watson, *The Roslin Institute, Edinburgh, Scotland, UK*.

2:45 AM W134 **A new chromosome-level turkey genome.**
C. P. Barros*[1], M. F. L. Derks[1], J. Mohr[2], B. J. Wood[2,3], M. C. A. M. Bink[4], and M. A. M. Groenen[1], [1]*Wageningen University and Research, Wageningen, the Netherlands*, [2]*Hybrid Turkeys, Kitchener, ON, Canada*, [3]*School of Veterinary Science, University of Queensland, Gatton, QLD, Australia*, [4]*Hendrix Genetics Research, Technology and Services, Boxmeer, the Netherlands*.

3:00 AM W135 **Bridge 60k SNP panel for the chicken genome-wide study.**
D. Seo*[1,2], S. Cho[1], D. Lee[1], M. Kim[1], P. Manjula[1], J. Shin[1], D. Lim[3], H. Choo[4], J. Cha[4], K. Kim[4], I.-S. Jeon[4], K.-T. Lee[3], B. Park[4], S. H. Lee[1,2], J. H. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, South Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, South Korea*, [3]*Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju, South Korea*, [4]*Poultry Research Institute, National Institute of Animal Science, RDA, Pyeongchang, South Korea*.

3:15 AM W136 **Genomic signatures of selection for egg production rate using whole-genome sequence in Hinaidori chickens.**
T. Goto*[1], S. Fukuda[2], K. Rikimaru[2], R. A. Lawal[3], J. Pool[4], and O. Hanotte[5,6], [1]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan*, [2]*Akita Prefectural Livestock Experiment Station, Akita, Japan*, [3]*The Jackson Laboratory, Bar Harbor, ME, USA*, [4]*University of Wisconsin-Madison, Madison, WI, USA*, [5]*University of Nottingham, Nottingham, UK*, [6]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*.

3:30 AM W137 **Dissecting the polygenic genetic architecture of growth using genotyping by low-coverage sequencing in a deep intercross of the Virginia body weight lines: Novel loci revealed by increased power and improved genome coverage.**
T. Rönneburg*[1], Y. Zan[2,1], C. Honaker[3], P. Siegel[3], and Ö. Carlborg[1], [1]*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*, [2]*Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Science, Umeå, Sweden*, [3]*Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA*.

3:45 AM **Workshop business meeting**

Cattle Molecular Markers and Parentage Testing Workshop

Chair: **Jiansheng Qiu, Neogen**
9:00 AM – 12:00 PM CDT
2:00 PM – 5:00 PM UTC

9:00 AM **Welcoming remarks**

9:05 AM **Cattle STR/SNP Comparison Test 2020–2021.**

9:10 AM S100 **Presentation by Cattle CT Duty Lab.**
Emiliano Lasagna.

9:25 AM S101 **Presentation of Cattle STR results.**
Emiliano Lasagna.

9:40 AM S102 **Presentation of Cattle SNP results.**
Jiansheng Qiu.

9:55 AM S103 **Evaluation of the Cattle CT results by the chair.**
Jiansheng Qiu.

10:10 AM **Next Comparison Test (2022–2023).**

10:30 AM **Break**

10:40 AM W138 **Impact of genomic breed composition on production traits in crossbred dairy cattle.**
M. Jaafar*[1], B. Heins[2], C. Dechow[3], and H. Huson[1], [1]*Cornell University, Ithaca, NY, USA*, [2]*University of Minnesota, Morris, MN, USA*, [3]*Penn State University, University Park, PA, USA*.

11:00 AM W139 **A high-throughput Applied Biosystems Axiom Bovine Genotyping array with 100,000 markers optimized for dairy evaluation.**
A. Pirani*, D. Oliver, C. Bertani, and M. Patil, *Thermo Fisher Scientific Inc., Santa Clara, CA, USA*.

11:20 AM W140 **Investigating the accuracy of imputing variants on chromosome X in admixed dairy cattle using the ARS-UCD1.2 assembly of the bovine genome.**
Y. Wang*[1,2], K. Tiplady[1,2], T. J. J. Johnson[2], C. Harland[2], M. Keehan[1,2], T. J. Lopdell[2], R. G. Sherlock[2], A. Wallace[2], B. Harris[2], M. D. Littlejohn[2], R. Spelman[2], D. Garrick[1], and C. Couldrey[2], [1]*AL Rae Centre for Genetics and Breeding, School of Agriculture, Massey University, Hamilton, Waikato, New Zealand*, [2]*Research and Development, Livestock Improvement Corporation, Hamilton, Waikato, New Zealand*.

11:40 AM **Election of committee**

11:50 AM **Any other business**

Horse Genetics and Genomics Workshop

IMPORTANT: The Horse Genetics and Genomics Workshop will require that participants watch the full abstract video presentations in advance. The live session will include a brief introduction and overview from each author followed by breakout sessions in individual Zoom rooms.

Chair: **Theodore Kalbfleisch, University of Kentucky**
9:00 AM – 12:00 PM CDT
2:00 PM – 5:00 PM UTC

Main Room

W141 **Will selection for elasticity maintain the allele causing fragile foals?**
M. Ablondi*[1,2], M. Johnsson[2], S. Eriksson[2], A. Sabbioni[1], Å. Viklund[2], and S. Mikko[2], [1]*Department of Veterinary, Università degli Studi di Parma Science, Parma, Italy*, [2]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

W142 **Quantitative trait loci associated with alternative gaits in Colombian Paso horses.**
M. Novoa-Bravo*[1,3], F. Serra-Bragança[2], R. Naboulsi[3], M. Sole[3], M. Rhodin[4], and G. Lindgren[3], [1]*Genética Animal de Colombia SAS, Bogotá, Colombia*, [2]*Department of Clinical Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands*, [3]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*, [4]*Department of Anatomy, Physiology and Biochemistry, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

W143 **Genetic structure of maternal lines in Przewalski horses based on mtDNA variation.**
A. D. Musial*[1], K. Ropka-Molik[1], M. Stefaniuk-Szmukier[2], G. Mycka[2], A. Fornal[1], and N. Yasynetska[3], [1]*National Research Institute of Animal Production, Balice, Poland*, [2]*University of Agriculture, Krakow, Poland*, [3]*Biosphere Reserve, Askania-Nova, Ukraine*.

W144 **Epigenetic characterization of horse centromeric domains in different tissues and individuals.**
E. Cappelletti*[1], F. M. Piras[1], R. Hijaz[1], L. Sola[1], J. L. Petersen[2], R. R. Bellone[3,4], C. J. Finno[3], T. S. Kalbfleisch[5], E. Bailey[5], S. G. Nergadze[1], and E. Giulotto[1], [1]*Department of Biology and Biotechnology, University of Pavia, Pavia, Italy*, [2]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA*, [3]*University of California-Davis, School of Veterinary Medicine, Department of Population Health and Reproduction, Davis, CA, USA*, [4]*University of California-Davis, School of Veterinary Medicine, Veterinary Genetics Laboratory, Davis, CA, USA*, [5]*University of Kentucky, Gluck Equine Research Center, Lexington, KY, USA*.

Breakout Session 1

Breakout Session 2

W145 **Genomic improvement of the horse X chromosome and characterization of the pseudoautosomal boundary.**
M. Jevit*[1], B. Davis[1], C. Casanteda[1], D. Miller[2], and T. Raudsepp[1], [1]*Department of Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [2]*Cornell University, Ithaca, NY, USA*.

W146 **Integration of long-read sequencing technology improves transcriptome annotation of the equine genome.**
S. Peng*[1], T. S. Kalbfleisch[2], R. Bellone[1,3], J. L. Petersen[4], and C. J. Finno[1], [1]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [2]*Department of Veterinary Science, Gluck Equine Research Center, University of Kentucky, Lexington, KY, USA*, [3]*Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [4]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA*.

W147 **Transcriptome analysis of 8 priority tissues in 2 Thoroughbred stallions for the Functional Annotation of Animal Genomes project.**
A. Barber*[1], S. Peng[2], A. Fuller[1], E. Giulotto[3], T. Kalbfleisch[4], C. Finno[2], R. Belone[2], and J. Petersen[1], [1]*University of Nebraska–Lincoln*, *Lincoln, NE, USA*, [2]*University of California-Davis*, *Davis, CA, USA*, [3]*University of Pavia*, *Pavia, Italy*, [4]*University of Kentucky*, *Lexington, KY, USA*.

W148 **Rare and common variant discovery by whole-genome sequencing of 101 Thoroughbred racehorses.**
T. Tozaki*, A. Ohnuma, M. Kikuchi, T. Ishige, H. Kakoi, K.-I. Hirora, and S.-I. Nagata, *Laboratory of Racing Chemistry*, *Utsunomiya, Tochigi, Japan*.

Breakout Session 3

Breakout Session 4

Animal Epigenetics Workshop

Chair: Kyle Schachtschneider, University of Illinois at Urbana-Champaign

1:00 PM – 4:00 PM CDT
6:00 PM – 9:00 PM UTC

1:00 PM **Welcome**

1:05 PM W149 **Micrococcal nuclease sequencing of pig sperm suggests a relationship between nucleosome retention and both semen quality and early embryo development.**
M. Gòdia[1], S. S. Hammoud[2], M. Naval-Sánchez[3], I. Ponte[4], J. E. Rodriguez-Gil[4], A. Sánchez[4,1], and A. Clop*[1,5], [1]*Centre for Research in Agricultural Genomics CRAG*, *Cerdanyola del Valles, Catalonia, Spain*, [2]*University of Michigan*, *Ann Arbor, MI, USA*, [3]*CSIRO*, *St Lucia, Brisbane, Australia*, [4]*Universitat Autonoma de Barcelona*, *Cerdanyola del Valles, Catalonia, Spain*, [5]*CSIC*, *Barcelona, Catalonia, Spain*.

1:20 PM W150 **ISO-seq data reveals allele-specific isoform expression.**
S. Bardoloi*, L. Nguyen, B. Engle, B. Hayes, and E. Ross, *University of Queensland*, *Brisbane, Queensland, Australia*.

1:35 PM W151 **A comprehensive RNA editome reveals RNA editing sites affecting the function of HSPA12B in myogenesis via altering binding ability for miRNA-181b.**
A. A. Adetula*[1,2], X. Fan[1], Y. Zhang[1], Y. Yao[1], J. Yan[1], M. Chen[1], Y. Tang[1], Y. Liu[1], G. Yi[1], K. Li[1,2], and Z. Tang[1,2], [1]*Genome Analysis Laboratory of the Ministry of Agriculture, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences*, *Shenzhen, China*, [2]*Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

1:50 PM W152 **Livestock methylomics: Systematic evaluation of DNA methylation profiling assays for industry.**
A. Caulton*[1,2], R. Brauning[1], K. G. Dodds[1], A. Hagani[3], J. Zoller[4], C. Couldrey[5], S. Horvath[3], and S. M. Clarke[1], [1]*AgResearch, Invermay Agricultural Centre*, *Mosgiel, New Zealand*, [2]*University of Otago*, *Dunedin, New Zealand*, [3]*Department of Human Genetics, David Geffen School of Medicine, University of California Los Angeles*, *Los Angeles, CA, USA*, [4]*Department of Biostatistics, Fielding School of Public Health, University of California Los Angeles*, *Los Angeles, CA, USA*, [5]*Livestock Improvement Corporation*, *Hamilton, New Zealand*, [6]*University of Idaho*, *Moscow, ID, USA*.

2:05 PM W153 **Genetic and epigenetic regulation of immune response and resistance to infectious diseases in domestic ruminants.**
I. Onjoko*, *Farming Experts Network*, *Abeokuta, Ogun, Nigeria*.

2:20 PM **Break**

2:40 PM W154 **Identifications of epigenetic regulation mechanism according to the growth of pig in abdominal fat tissue through multi-omics integration analysis.**
D.-Y. Kim* and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University*, *Anseong, Gyeonggi-do, Republic of Korea*.

2:55 PM W155 **Epigenetic marks in the promoter of *GNAS* and *EBF3* are associated with meat tenderness in *Bos indicus*.**
M. M. de Souza[1,2], S. C. M. Niciura[1], M. I. P. Rocha[1,3], W. J. S. Diniz[1,4], J. J. Bruscadin[1,3], J. Afondo[1], P. S. N. de Oliveira[1], G. B. Mourão[5], A. Zerlotini[6], L. L. Coutinho[5], J. E. Koltes[2], and L. C. A. Regitano*[1], [1]*Embrapa Pecuária Sudeste, Empresa Brasileira de Pesquisa Agropecuária, São Carlos, São Paulo, Brazil*, [2]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [3]*Department of Genetics and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [4]*Department of Animal Sciences, North Dakota State University, Fargo, ND, USA*, [5]*Department of Animal Science, Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil*, [6]*Embrapa Informática Agropecuária, Empresa Brasileira de Pesquisa Agropecuária, Campinas, São Paulo, Brazil*.

3:10 PM W156 **Characterization of the adipose tissue DNA methylation framework between male and female suckling lambs.**
A. Suárez-Vega, C. Esteban-Blanco, H. Marina, R. Pelayo, M. Alonso-Garcia, C. Hervas-Rivero, B. Gutierrez-Gil, and J.-J. Arranz*, *Universidad de León, León, Spain*.

3:25 PM W157 **Maternal methionine supplementation alters alternative splicing and DNA methylation in bovine skeletal muscle.**
L. Liu* and F. Peñagaricano, *University of Wisconsin-Madison, Madison, WI, USA*.

3:40 PM **Workshop business meeting**

Plenary Session II

Chairs: **Brenda Murdoch, University of Idaho, and Guosong Wang, Texas A&M University**

5:00 PM – 6:00 PM CDT

10:00 PM – 11:00 PM UTC

5:00 PM W158 **Harnessing the power of genomics and AI to breed new species for aquaculture.**
M. Wellenreuther*[1,2], [1]*The New Zealand Institute for Plant and Food Research Ltd., Nelson, New Zealand*, [2]*School of Biological Sciences, University of Auckland, Auckland, New Zealand*.

Wednesday, July 28

Pig Genetics and Genomics Workshop

Chair: **Amanda Warr, Roslin Institute**
12:30 AM – 4:00 AM CDT
5:30 AM – 9:00 AM UTC

12:30 AM **Committee business and new elections**

12:45 AM W159 **Pig genome functional annotation enhances biological interpretations of complex traits and comparative epigenomics.**
Z. Pan*[1], Y. Yao[2], H. Yin[3], Z. Cai[4], Y. Wang[1], L. Bai[3], C. Kern[1], M. Halstead[1], K. Chanthavixay[1], N. Trakooljul[5], K. Wimmers[5], G. Sahana[4], G. Su[4], M. Sandø Lund[4], M. Fredholm[6], P. Karlskov-Mortensen[6], C. W. Ernst[7], P. Ross[1], C. K. Tuggle[8], L. Fang[2], and H. Zhou[1], [1]*Department of Animal Science, University of California, Davis, Davis, CA, USA*, [2]*MRC Human Genetics Unit at the Institute of Genetics and Molecular Medicine, The University of Edinburgh, Edinburgh, UK*, [3]*Agricultural Genome Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China*, [4]*Center for Quantitative Genetics and Genomics, Faculty of Technical Sciences, Aarhus University, Tjele, Denmark*, [5]*Leibniz-Institute for Farm Animal Biology, Dummerstorf, Germany*, [6]*Animal Genetics, Bioinformatics and Breeding, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark*, [7]*Department of Animal Science, Michigan State University, East Lansing, MI, USA*, [8]*Department of Animal Science, Iowa State University, Ames, IA, USA*.

1:05 AM W160 **Alteration of expression of miRNA and mRNA transcripts in fetal muscle tissue in the context of sex, mother and variable fetal weight.**
S. Ponsuksili*[1], A. Ali[1], F. Hadlich[1], E. Murani[1], and K. Wimmers[1,2], [1]*Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*.

1:25 AM W161 **Time serial ovarian transcriptome analysis for entire porcine estrous cycle reveals changes of steroid metabolism and corpus luteum development.**
Y. Park*, Y.-B. Park, S.-W. Lim, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.

1:45 AM W162 **Identifying muscle transcriptional regulatory elements in the pig genome.**
D. Crespo-Piazuelo*[1], O. González-Rodríguez[1], M. Mongellaz[2], H. Acloque[2], M.-J. Mercat[3], M. C. A. M. Bink[4], A. E. Huisman[5], Y. Ramayo-Caldas[1], J. P. Sánchez[1], and M. Ballester[1], [1]*Animal Breeding and Genetics Program, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain*, [2]*Institut national de recherche pour l'agriculture, l'alimentation et l'environnement (INRAE), Génétique animale et biologie intégrative (GABI), Jouy-en-Josas, France*, [3]*IFIP-Institut du porc and Alliance R&D, Le Rheu, France*, [4]*Hendrix Genetics Research Technology and Services B.V, Boxmeer, the Netherlands*, [5]*Hypor B.V, Boxmeer, the Netherlands*.

2:05 AM **Break**

2:20 AM W163 **Characterization of circulating microRNA profile in Iberian pigs with and without heat stress.**
M. Muñoz*[1], A. Fernández-Rodríguez[2], F. García[1], A. García-Cabrero[1], C. Caraballo[1,3], G. Gómez[4], G. Matos[4], C. Óvilo[1], and J. García-Casco[1,3], [1]*Animal Breeding Department, INIA (CSIC), Madrid, Spain*, [2]*Unit of Viral Infection and Immunity, National Center for Microbiology, Institute of Health Carlos III, Majadahonda (Madrid), Spain*, [3]*Centro de Investigación en cerdo Ibérico INIA-Zafra (INIA, CSIC), Zafra (Badajoz), Spain*, [4]*Sánchez Romero Carvajal—Jabugo, SRC, Huelva, Spain*.

2:40 AM W164 **Historical biogeography of Philippine native pigs and the perplexing mitochondrial DNA variation in Philippine wild pigs.**
J. Layos*[1,2], C. Godinez[1,3], L. Liao[4], Y. Yamamoto[1], and M. Nishibori[1], [1]*Laboratory of Animal Genetics, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*, [2]*College of Agriculture and Forestry, Capiz State University, Burias Campus, Mambusao, Capiz, Philippines*, [3]*Department of Animal Science, Visayas State University, Visca, Baybay City, Leyte, Philippines*, [4]*Laboratory of Aquatic Ecology, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*.

3:00 AM W165 **The genomic inbreeding trends in Italian heavy pig breeds over the last 25 years.**
G. Schiavo*[1], S. Bovo[1], A. Ribani[1], S. Tinarelli[1,2], V. Utzeri[1], M. Cappelloni[2], M. Gallo[2], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Associazione Nazionale Allevatori Suini (ANAS), Rome, Italy*.

3:20 AM W166 **The common warthog (*Phacochoerus africans*) reference genome and sequence variation.**
L. Eory[1], P. Wiener[1], H. A. Finlayson[1], K. Gharbi[2], S. Girling[3], C. Palgrave[1], E. Okoth[4], T. Burdon[1], M. Watson[1], and A. L. Archibald*[1], [1]*The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK*, [2]*Edinburgh Genomics, University of Edinburgh, Edinburgh, UK*, [3]*The Royal Zoological Society of Scotland, Edinburgh, UK*, [4]*International Livestock Research Institute, Nairobi, Kenya*.

3:40 AM W167 **A pan-genome of commercial pig breeds.**
M. Derks*[1,3], B. Harlizius[2], M. van Son[2], M. Lopes[1], E. Grindflek[2], E. Knol[1], E. Sell-Kubiak[4], and A. Gjuvsland[2], [1]*Topigs Norsvin Research Center, Beuningen, the Netherlands*, [2]*Norsvin SA, Hamar, Norway*, [3]*Wageningen University and Research, Wageningen, the Netherlands*, [4]*Poznan University if Life Sciences, Poznan, Poland*.

Plenary Session III

Chair: **Sabine Hammer, University of Veterinary Medicine Vienna**
7:00 AM – 8:00 AM CDT
12:00 PM – 1:00 PM UTC

7:00 AM W168 **Diversification and sustainability of aquaculture production: What can (and cannot) we do as geneticists?**
F. Bertolini*, *Technical University of Denmark, National Institute of Aquatic Resources, Lyngby, Denmark*.

Livestock Genomics for Developing Countries Workshop

Chair: **Abdulfatai Tijjani, CGIAR**
8:00 AM – 10:00 AM CDT
1:00 PM – 3:00 PM UTC

8:00 AM W169 **Genetic basis of thermo-tolerance in African indigenous chickens.**
A. A. Gheyas*[1], M. Rachman[2], A. Vallejo-Trujillo[2], O. Bamidele[3,4], A. Kebede[3,5], T. Dessie[3], J. Smith[1], and O. Hanotte[2,3], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Midlothian, Scotland, UK*, [2]*School of Life Sciences, University of Nottingham, Nottingham, UK*, [3]*LiveGene – CTLGH, International Livestock Research Institute, Addis Ababa, Ethiopia*, [4]*Kings University, Ode Omu, Nigeria*, [5]*Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia*.

8:15 AM W170 **Whole-genome sequence analysis to detect potential candidate genes for reproduction in South African beef cattle.**
K. Nxumalo*[1,2], M. B. Malima[1], J. Grobler[2], M. Makgahlela[1,3], J. Kantanen[4], C. Ginja[5], D. R. Kugonza[6], N. Mohamed[7], R. P. M. A. Crooijmans[8], and A. A. Zwane[1], [1]*Animal Breeding and Genetics, Agricultural Research Council-Animal Production, Pretoria, South Africa*, [2]*Department of Genetics, University of the Free State, Bloemfontein, Free State, Bloemfontein, South Africa*, [3]*Department of Animal, Wildlife and Grassland Sciences, University of Free State, Bloemfontein, Bloemfontein, South Africa*, [4]*Animal Production Research, Agricultural Research Centre (MTT), Jokioinen, Finland*, [5]*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*, [6]*Department of Agricultural Production, School of Agricultural Sciences, College of Agricultural and Environmental Sciences, Makerere University, Kampala, Uganda*, [7]*Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt*, [8]*Animal Breeding and Genomics Group, Wageningen University and Research, Wageningen, the Netherlands*.

8:30 AM	W171	**Population structure, inbreeding and admixture for indigenous goats within a pilot community-based breeding program in Pella, North West, South Africa.** T. Mtshali*[1,3], F. Muchadeyi[2], O. Mapholi[3], E. Dzomba[4], and K. Hadebe[2], [1]*Agricultural Research Council, Vegetable and Ornamental Plants, Pretoria, South Africa*, [2]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, South Africa*, [3]*University of South Africa, Florida, Johannesburg, South Africa*, [4]*University of KwaZulu-Natal, Scottsville, Pietermaritzburg, South Africa*.
8:45 AM	W172	**Genetics of base coat color variations and coat color patterns of the South African Nguni cattle investigated using high-density SNP genotypes.** L. Kunene*[1], F. Muchadeyi[2], K. Hadebe[2], G. Mészáros[3], J. Sölkner[3], and E. Dzomba[1], [1]*University of KwaZulu-Natal, Scottsville, South Africa*, [2]*Agricultural Research Council, Onderstepoort, South Africa*, [3]*University of Natural Resources and Life Sciences, Vienna, Austria*.
9:00 AM		**Break**
9:15 AM	W173	**Correlation between resilience and tolerance in Angus females exposed to *Rhipicephalus* (*Boophilus*) *microplus*.** C. D. S. Arce*[1], F. R. Araújo Neto[2], A. M. Maiorano[1], L. G. Albuquerque[1], and H. N. Oliveira[1], [1]*Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, Sao Paulo, Brazil*, [2]*Instituto Federal Goiano, Rio Verde, Goias, Brazil*.
9:30 AM	W174	**Signature of stress-related characteristics according to changes in pig breeding condition through transcriptome analysis.** S.-W. Lim*, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.
9:45 AM		**Business meeting and election of committee**

Applied Genetics of Companion Animals Workshop

Chair: Leslie Lyons, University of Missouri–Columbia, College of Veterinary Medicine

9:00 AM – 12:00 PM CDT

2:00 PM – 5:00 PM UTC

9:00 AM		**Welcome and agenda**
9:10 AM	S104	**Dog STR and SNP Comparison Test and Discussion: Duty Lab Presentation.** Hubert Bauer.
9:30 AM	S105	**Dog STR and SNP Comparison Test and Discussion: Duty Lab Presentation: Committee Chair Presentation (SNP Data, STR Data, issues).** Leslie Lyons.
9:50 AM	S106	**Group presentation of abstracts W175, W176, and W177.** A. Burrell, K.R. Gujjula, and H. Suren.
9:51 AM	W175	**Supplementation of the AgriSeq Canine SNP Parentage and ID panel with additional ISAG and sex determination markers.** A. Burrell*, K. Gujjula, H. Suren, and R. Conrad, *Thermo Fisher Scientific, Austin, TX, USA*.
9:56 AM	W176	**Development of a highly informative SNP panel for parentage assessment in dogs.** K. R. Gujjula*, H. Suren, A. Burrell, and S. Chadaram, *Thermo Fisher Scientific, Austin, TX, USA*.
10:01 AM	W177	**AgriSum Toolkit Plugin 2.0: Enabling multi-species panel analysis for AgriSeq.** H. Suren*[1], S. Daly[2], and K. R. Gujjula[1], [1]*Thermo Fisher Scientific, Austin, TX, USA*, [2]*Thermo Fisher Scientific, Lissieu, France*.
10:05 AM		**Discussion: Proposal – Record assay on ISAG certificate**

10:13 AM		**Discussion: Proposal – How to share data between laboratories**
10:20 AM		**Break**
10:30 AM	S107	**Cat STR and SNP Comparison Test and Discussion: Duty Lab Presentation.** Robert Grahn.
10:50 AM	S108	**Cat STR and SNP Comparison Test and Discussion: Duty Lab Presentation: Committee Chair Presentation (SNP Data, STR Data, issues. Call for SNP back-up panel data).** Leslie Lyons.
11:10 AM	W178	**Whole-genome sequencing analysis of a cat family with radial hemimelia.** N. Bilgen*[1], M. Y. Akkurt[1], B. Çinar Kul[1], R. M. Buckley[2], L. A. Lyons[2], and Ö. S. Çildir[1], [1]*Faculty of Veterinary Medicine, Department of Genetics, Ankara University, Ankara, Turkey*, [2]*Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*.
11:20 AM		**New Business: Proposal – New workshop "Standards of Genetic Testing"**
11:21 AM	W179	**Breed, trait, locus, and allele nomenclature standardization for the domestic cat.** L. A. Lyons*, *College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*.
11:25 AM	W180	**Online Mendelian Inheritance in Animals (OMIA): Standardized vocabularies for breeds and traits.** I. Tammen[1], N. Vasilevsky[2], C. A. Park[3], Z. Hu[3], M. Haendel[4], and F. W. Nicholas*[1], [1]*Sydney School of Veterinary Science, University of Sydney, Sydney, NSW, Australia*, [2]*Oregon Clinical and Translational Research Institute, Department of Medical Informatics and Clinical Epidemiology, Oregon Health and Science University, Portland, OR, USA*, [3]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [4]*Center for Health AI, University of Colorado Anschutz Medical Campus, Aurora, CO, USA*.
11:35 AM		**Discussion**
11:45 AM		**Committee and duty laboratory elections**
11:59 AM		**Adjourn**

Domestic Animal Sequencing and Annotation Workshop

Chair: **George Liu, USDA**
1:00 PM – 4:15 PM CDT
6:00 PM – 9:15 PM UTC

1:00 PM	W181	**Bovine genome annotation using integration of multi-omics data.** H. Beiki[1], C. Gill[2], H. Jiang[3], W. Liu[5], Z. Jiang[4], S. McKay[6], B. M. Murdoch[7], J. Koltes[1], M. Rijnkels[2], T. P. L. Smith[8], P. Ross[9], H. Zhou[9], and J. Reecy*[1], [1]*Iowa State University, Ames, IA, USA*, [2]*Texas A&M University, College Station, TX, USA*, [3]*Virginia Tech University, Blacksburg, VA, USA*, [4]*Washington State University, Pullman, WA, USA*, [5]*Penn State University, State College, PA, USA*, [6]*University of Vermont, Burlington, VT, USA*, [7]*University of Idaho, Moscow, ID, USA*, [8]*US Meat Animal Research Center, Clay Center, NE, USA*, [9]*University of California–Davis, Davis, CA USA*.
1:15 PM	W182	**BovReg: A high-resolution functional annotation of the cattle genome using novel breeds/crosses.** G. Costa Monteiro Moreira*[1], S. Dupont[1], D. Becker[2], M. Salavati[3], R. Clark[4], E. L. Clark[3], G. Plastow[5], C. Kühn[2,6], C. Charlier[1], and on behalf of the BovReg Consortium[6], [1]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège,Belgium*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [3]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [4]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

1:30 PM W183 **Annotation of transcription start sites in the bovine genome reveals novel breed-specific complexity.**

M. Salavati*[1], R. Clark[2], D. Becker[3], C. Kühn[3,4], G. Plastow[5], G. Costa Monteiro Moreira[6], C. Charlier[6],[7], E. L. Clark[1], and on behalf of the BovReg Consortium[4], [1]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [2]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [3]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [4]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium*, [7]*Faculty of Veterinary Medicine, University of Liège, Liège, Belgium*.

1:45 PM W184 **The Ovine Functional Annotation of Animal Genomes project.**

B. M. Murdoch*[1,6], K. M. Davenport[1], M. Salavati[2], E. Clark[2], A. Archibald[2], A. T. Massa[3], M. R. Mousel[4,5], M. K. Herndon[3], S. N. White[3,4,6], K. C. Worley[7], S. Bhattarai[8], S. D. McKay[8], B. Dalrymple[9], J. Kijas[10], A. Caulton[11], S. Clarke[11], R. Brauning[11], T. Hadfield[12], T. P. L. Smith[13], and N. E. Cockett[12], [1]*Department of Animal, Veterinary, and Food Science, University of Idaho, Moscow, ID, USA*, [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, UK*, [3]*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA*, [4]*USDA, ARS, Animal Disease Research Unit, Pullman, WA, USA*, [5]*Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA*, [6]*Center for Reproductive Biology, Washington State University, Pullman, WA, USA*, [7]*Baylor College of Medicine-Human Genome Sequencing Center, Houston, TX, USA*, [8]*University of Vermont, Burlington, VT, USA*, [9]*University of Western Australia, Crawley, Western Australia, Australia*, [10]*CSIRO Agricultural Flagship, St. Lucia, Brisbane, Australia*, [11]*AgResearch, Hamilton, New Zealand*, [12]*Utah State University, Logan, UT, USA*, [13]*USDA, ARS, US Meat Animal Research Center (USMARC), Clay Center, NE, USA*.

2:00 PM W185 **AQUA-FAANG: Genome functional annotation of the 6 major European farmed fish species.**

D. J. Macqueen*[1], S. Lien[2], and the AQUA-FAANG Consortium[3], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, UK*, [2]*Centre for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway*, [3]*AQUA-FAANG Consortium, Europe*.

2:15 PM W186 **The Farm Animal Genotype-Tissue expression (FarmGTEx) consortium.**

L. Fang*, *The University of Edinburgh, Edinburgh, UK*.

2:30 PM **Break**

2:45 PM W187 **The Bovine Pangenome Consortium.**

B. D. Rosen*[1], D. M. Bickhart[2], T. P. L. Smith[3], D. Boichard[4], G. A. Brockmann[5], A. J. Chamberlain[6], C. Couldrey[7], H. D. Daetwyler[6], A. Djikeng[8], C. Drögemüller[9], S. Elzaki[5], R. K. Gandham[10], D. Hagen[11], O. Hanotte[12], M. P. Heaton[3], Y. Jiang[13], Z. Jiang[14], D. Larkin[15], G. Liu[1], W. Y. Low[16], P. Ajmone Marsan[17], B. M. Murdoch[18], F. C. Muchadeyi[19], J. Mwacharo[20], H. L. Neibergs[14], H. Pausch[21], S. Demyda-Peyrás[22], J. Prendergast[23], P. J. Ross[24], R. D. Schnabel[25], J. Sölkner[26], A. Soudre[27], A. Tijjani[12], J. L. Williams[17], and Bovine Pangenome Consortium[28], [1]*USDA ARS AGIL, Beltsville, MD, USA*, [2]*USDA ARS DFRC, Madison, WI, USA*, [3]*USDA ARS MARC, Clay Center, NE, USA*, [4]*INRAE Animal Genetics and Integrative Biology, Jouy-en-Josas, France*, [5]*Humboldt-Universität zu Berlin, Berlin, Germany*, [6]*Agriculture Victoria, Melbourne, Victoria, AU*, [7]*LIC, Hamilton, New Zealand*, [8]*Centre for Tropical Livestock Genetics and Health, Midlothian, Scotland, UK*, [9]*University of Bern, Bern, Switzerland*, [10]*National Institute of Animal Biotechnology, Hyderabad, India*, [11]*Oklahoma State University, Stillwater, OK, USA*, [12]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [13]*Northwest A&F University, Yangling, China*, [14]*Washington State University, Pullman, WA, USA*, [15]*Royal Veterinary College, University of London, London, UK*, [16]*The University of Adelaide, Adelaide, South Australia, Australia*, [17]*Università Cattolica del Sacro Cuore, Piacenza, Italy*, [18]*University of Idaho, Moscow, ID, USA*, [19]*Agricultural Research Council, South Africa, Pretoria, South Africa*, [20]*Scotland's Rural College, Midlothian, Scotland, UK*, [21]*ETH Zürich, Zürich, Switzerland*, [22]*Universidad de Córdoba, Córdoba, Spain*, [23]*The Roslin Institute, Midlothian, Scotland, UK*, [24]*STgenetics, Navasota, TX, USA*, [25]*University of Missouri, Columbia, MO, USA*, [26]*University of Natural Resources and Life Sciences, Vienna, Austria*, [27]*Université Norbert ZONGO, Koudougou, Burkina Faso*, [28]*Bovine Pangenome Consortium*.

3:00 PM W188 **An improved, high-quality ovine reference genome to facilitate functional annotation of gene regulatory elements.**

K. M. Davenport*[1], D. M. Bickhart[2], K. C. Worley[3], S. C. Murali[3], N. E. Cockett[4], M. P. Heaton[5], T. P. L. Smith[5], B. M. Murdoch[1], and B. D. Rosen[6], [1]*Department of Animal, Veterinary, and Food Sciences, University of Idaho, Moscow, ID, USA*, [2]*US Dairy Forage Research Center, USDA-ARS, Madison, WI, USA*, [3]*Baylor College of Medicine, Houston, TX, USA*, [4]*Utah State University, Logan, UT, USA*, [5]*US Meat Animal Research Center, USDA-ARS, Clay Center, NE, USA*, [6]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA*.

3:15 PM W189 **Annotation of full-length transcripts including alternative splicing from 19 chicken tissues using Oxford Nanopore long-read sequencing.**
D. Guan*[1], M. M. Halstead[1], A. D. Islas-Trejo[1], D. E. Goszczynski[1], H. H. Cheng[2], P. Ross[1], and H. Zhou[1], [1]*Department of Animal Science, University of California-Davis, Davis, CA, USA*, [2]*Avian Disease and Oncology Laboratory, USDA-ARS, East Lansing, MI, USA*.

3:30 PM W190 **Uncovering abundant missing genes in the chicken reference genome solves the avian gene depletion puzzle.**
M. Li*[1], N. Xu[1], P. Bian[1], X. Hu[2], Y. Jiang[1], and N. Yang[3], [1]*Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China*, [2]*State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, China*, [3]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture and Rural Affairs, China Agricultural University, Beijing, China*.

3:45 PM W191 **Chromatin accessibility and regulatory vocabulary in indicine cattle.**
P. Alexandre*[1], M. Naval-Sánchez[1,2], M. Menzies[1], L. Nguyen[3], L. Porto-Neto[1], M. Fortes[4], and A. Reverter[1], [1]*CSIRO Agriculture and Food, St. Lucia, QLD, Australia*, [2]*Institute for Molecular Bioscience, The University of Queensland, Brisbane, QLD, Australia*, [3]*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD, Australia*, [4]*School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, QLD, Australia*.

4:00 PM **Workshop business meeting**

Animal Forensic Genetics Workshop

Chair: Guillermo Giovambattista, Universidad Nacional De La Plata
5:00 PM – 8:00 PM CDT
10:00 PM – 1:00 AM UTC

5:00 PM W192 **Invited Workshop Presentation: Allelic ladder design and production for short tandem repeat (STR) genotyping.**
M. E. D'Amato*, *Forensic DNA Laboratory, Dept. Biotechnology, Faculty of Natural Sciences, University of the Western Cape, Bellville, South Africa*.

5:30 PM W193 **SNP marker combination for discrimination of Korean native chickens using a machine learning model.**
S. Cho*[1], D. Seo[1,2], M. Kim[2], E. Cho[3], P. Manjula[1], T. Kalhari[2], and J. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Republic of Korea*, [3]*Department of Bio-big data, Chungnam National University, Daejeon, Republic of Korea*.

5:45 PM W194 **Development of 14-short tandem repeat (STR) panel for forensic DNA analysis of red fox.**
A. E. Hrebianchuk*[1], N. S. Parfionava[1], V. N. Lukashkova[1], S. A. Kotava[1], and I. S. Tsybovsky[2], [1]*Scientific and Practical Centre of the State Forensic Examination Committee of the Republic of Belarus, Minsk, Republic of Belarus*, [2]*Republican unitary service enterprise "BelJurZabespechenne", Minsk, Republic of Belarus*.

6:00 PM W195 **Genetic profiling of horses in forensic cases.**
A. Fornal*, K. Kowalska, T. Zabek, A. Piestrzynska-Kajtoch, and K. Ropka-Molik, *National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland*.

6:15 PM W196 **Design of a low-density panel of SNPs to detect fraud in cured goat cheese.**
A. M. Martínez*[1], A. Canales[1,2], M. Macri[1,2], and J. V. Delgado[1], [1]*University of Cordoba, Cordoba, Spain*, [2]*Animal Breeding Consulting S.L, Cordoba, Spain*, [3]*Instituto Canario de Investigaciones Agrarias, Tenerife, Spain*.

6:30 PM **Break**

6:45 PM W197 **Genomic DNA extraction from canine feces for genotyping and identification with targeted GBS application.**
Q. Hoang, K. Kice, C. Carrasco, S. Chadaram*, and R. Conrad, *Thermo Fisher Scientific, Austin, TX, USA*.

7:00 PM W198 **A *Bos indicus* epigenetic clock predicts age from tail hair.**
L. T. Nguyen*, M. Forutan, B. J. Hayes, and E. M. Ross, *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Queensland, Australia*.

7:15 PM	S109	**Results of the 2020–2021 Forensic Genetics Comparison Test.** Guillermo Giovambattista.
7:30 PM		**Election of committee members**
7:45 PM		**Other business**

Thursday, July 29

Microbiomes Workshop

Chair: **Claire Rogel-Gaillard, GABI, INRA, AgroParisTech, Université Paris-Saclay**
Co-chairs: **Oscar González-Recio, INIA, and Jordi Estelle-Fabrellas, INRAE**
1:00 AM – 4:00 AM CDT
6:00 AM – 9:00 AM UTC

1:00 AM **Welcome**

1:05 AM W199 **Response to selection on fecal microbiota composition in Large White piglets.**
C. Larzul*[1], M. Borey[2], Y. Billon[3], M.-N. Rossignol[2], G. Lemonnier[2], J. Estelle[2], and C. Rogel-Gaillard[2], [1]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*INRAE, GenESI, Surgères, France*.

1:20 AM W200 **The impact of host genetics, independently of environmental factors, on porcine gut microbiota composition.**
A. Heras-Molina*[1], J. Estellé[2], A. López-García[1], J. L. Pensantez-Pacheco[1,3], S. Astiz[1], C. Garcia-Contreras[1], M. Vazquez-Gomez[4,5], B. Isabel[4], A. Gonzalez-Bulnes[6], and C. Ovilo[1], [1]*INIA (CSIC), Madrid, Spain*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*School of Veterinary Medicine and Zootechnics, Faculty of Agricultural Sciences, University of Cuenca, Cuenca, Ecuador*, [4]*Faculty of Veterinary Medicine, UCM, Ciudad Universitaria, Madrid, Spain*, [5]*Nutrition and Obesities: Systemic Approaches Research Unit (NutriOmics), INSERM, Sorbonne Université, Paris, France*, [6]*Departamento de Producción y Sanidad Animal, Facultad de Veterinaria, Universidad Cardenal Herrera-CEU, CEU Universities, Valencia, Spain*.

1:35 AM W201 **Rumen eukaryotes are the main risk factors for larger methane emissions in dairy cattle.**
A. Saborío-Montero*[1,2], M. Gutiérrez-Rivas[1], R. Atxaerandio[3], A. García-Rodríguez[3], I. Goiri[3], J. López-Paredes[4], J. A. Jiménez-Montero[4], and O. González-Recio[1,5], [1]*Departamento de Mejora Genética Animal, Instituto Nacional de Tecnología Agraria y Alimentaria, Madrid, Spain*, [2]*Centro de Investigación en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San Pedro, San José, Costa Rica*, [3]*Department of Animal Production NEIKER - Basque Institute for Agricultural Research and Development, Basque Research and Technology Alliance (BRTA), Campus Agroalimentario de Arkaute s/n, Vitoria, País Vasco, Spain*, [4]*Departamento técnico de Confederación de Asociaciones de Frisona Española (CONAFE), Valdemoro, Madrid, Spain*, [5]*Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, Madrid, Spain*.

1:50 AM W202 **Cecal microbiota composition of experimental laying hens infected with infectious bronchitis virus differs according to genetics and vaccination.**
M. Borey*[1], B. Bed Hom[1,2], N. Bruneau[1], J. Estellé[1], F. Larsen[3], F. Blanc[1], M.-H. Pinard-van der Laan[1], T. Dalgaard[3], and F. Calenge[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, UMR GABI, Jouy-en-Josas, France*, [2]*Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France*, [3]*Department of Animal Science, Aarhus University, Tjele, Denmark*.

2:05 AM W203 **Could the gut microbiome modulate environmental variance and animal resilience?**
C. Casto-Rebollo*[1], M. Argente[2], M. García[2], A. Blasco[1], and N. Ibáñez-Escriche[1], [1]*Institute for Animal Science and Technology, Universitat Politècnica de València, València, Spain*, [2]*Departamento de Tecnología Agroalimentaria, Universidad Miguel Hernández de Elche, Orihuela, Spain*.

2:20 AM **Break**

2:40 AM W204 **The difference of lipid metabolism based on intestinal microbiome and transcriptome between Dorper and Tan sheep.**
Y. Ma*, X. Yang, G. Hua, and X. Deng, *National Key Laboratory of Animal Genetics, Breeding and Reproduction, China Agricultural University, Beijing, China*.

2:55 AM W205 **The potential of using rumen microbial profiles for the prediction of enteric methane emissions traits for commercial livestock breeding.**
T. Bilton*[1], M. Bastiaanse[1], M. Hess[1], J. Budel[2], G. Noronha[2], H. Henry[1], S. Hickey[3], G. Pile[1], P. Janssen[4], J. McEwan[1], and S. Rowe[1], [1]*AgResearch, Mosgiel, New Zealand*, [2]*Universidade Federal do Pará (UFPa), Belém Do Pará, Brazil*, [3]*AgResearch, Ruakura, New Zealand*, [4]*AgResearch, Palmerston North, New Zealand*.

3:10 AM W206 **Mapping the livestock microbiome.**
M. Watson*, L. Glendinning, A. Warr, and J. Mattock, *The Roslin Institute, University of Edinburgh, Midlothian, Edinburgh, UK*.

3:40 AM **Business meeting**

ISAG-FAO Genetic Diversity Workshop

Chairs: **Juha Kantanen, Natural Resources Institute Finland, and Catarina Ginja, CIBIO-InBIO, Universidade do Porto, Portugal**
5:00 AM – 8:15 AM CDT
10:00 AM – 1:15 PM UTC

5:00 AM **Updated FAO guidelines for characterization of animal genetic resources.**
Catarina Ginja.

5:30 AM W207 **Donkey worldwide diversity based on control-region data and entire mitochondrial genomes.**
D. Bigi[1], N. Rambaldi Migliore[2], M. Milanesi[3,4], P. Zambonelli[1], R. Negrini[3], A. Verini-Supplizi[5], L. Liotta[6], F. Chegdani[7], S. Agha[8], A. Torroni[2], P. Ajmone-Marsan[3,9], A. Achilli[2], and L. Colli*[3,10], [1]*Dipartimento di Scienze e Tecnologie Agro-Alimentari (DISTAL), Alma Mater Studiorum University of Bologna, Bologna, BO, Italy*, [2]*Dipartimento di Biologia e Biotecnologie "Lazzaro Spallanzani," University of Pavia, Pavia, PV, Italy*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti (DIANA), Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [4]*Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo, VT, Italy*, [5]*Dipartimento di Medicina Veterinaria, University of Perugia, Perugia, PG, Italy*, [6]*Dipartimento di Scienze Veterinarie, University of Messina, Messina, ME, Italy*, [7]*Department of Biology, Faculty of Sciences Aïn Chock, University HAssan II, Casablanca, Morocco*, [8]*Animal Production Department, Faculty of Agriculture, Ain Shams University, Cairo, Egypt*, [9]*PRONUTRIGEN Centro Ricerca Nutrigenomica e proteomica, Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [10]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del S. Cuore, Piacenza, PC, Italy*.

5:45 AM W208 **Estimation of inbreeding load and purging in animal conservation programs.**
N. Pérez-Pereira*[1], E. López-Cortegano[1,3], A. García-Dorado[2], and A. Caballero[1], [1]*Centro de Investigación Mariña, Universidade de Vigo, Vigo, Spain*, [2]*Universidad Complutense de Madrid, Madrid, Spain*, [3]*Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, UK*.

6:00 AM W209 **Functional and population genomics of admixed trypanotolerant African cattle breeds.**
G. P. McHugo*[1], J. A. Ward[1], T. J. Hall[1], G. M. O'Gorman[2], E. W. Hill[1], and D. E. MacHugh[1,3], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*National Office of Animal Health Ltd, Enfield, UK*, [3]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*.

6:15 AM W210 **Microbiota characterization of traditional cattle breeds.**
R. Gonzalez-Prendes[1], R. Gomez Exposito[2], T. Reilas[3], M. Makgahlela[4], J. Kananen[3], C. Ginja[5], D. Kugonza[6], N. Ghanem[7], H. Smidt[2], and R. Crooijmans*[1], [1]*Animal Breeding and Genomics Group, Wageningen University and Research, Wageningen, the Netherlands*, [2]*Micriobiology group, Wageningen University and Research, Wageningen, Wageningen, the Netherlands*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*, [4]*Agricultural Research Council-Animal Production Institute, Pretoria, South Africa*, [5]*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*, [6]*Department of Agricultural Production, School of Agricultural Sciences, College of Agricultural and Environmental Sciences, Makerere University, Kampala, Uganda*, [7]*Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt*.

6:30 AM W211 **Towards a comprehensive horse Y-chromosomal tree: Signatures from local breeds and ancient DNA.**
E. Bozlak*[1,2], L. Radovic[1,2], D. Rigler[2], T. Kunieda[3], R. Juras[4], G. Cothran[4], and B. Wallner[2], [1]*Vienna Graduate School of Population Genetics*, *Vienna, Austria*, [2]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna*, *Vienna, Austria*, [3]*Faculty of Veterinary Medicine, Okayama University of Science*, *Imabari, Japan*, [4]*Department of Integrative Biosciences, College of Veterinary and Biomedical Sciences, Texas A&M University*, *College Station, TX, USA*.

6:45 AM **Break**

7:00 AM W212 **Researching on the fine-structure and admixture of the worldwide chicken population reveal connections between populations and important events in breeding history.**
Y. Guo*[1,3], J.-H. Ou[5], Y. Zan[5], Y. Wang[1], H. Li[4], C. Zhu[4], K. Chen[4], X. Zhou[3], X. Hu[1,2], and Ö. Carlborg[5], [1]*State Key Laboratory for Agro-Biotechnology, China Agricultural University*, *Beijing, China*, [2]*National Engineering Laboratory for Animal Breeding, China Agricultural University*, *Beijing, China*, [3]*Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University*, *Beijing, China*, [4]*Jiangsu Institute of Poultry Science*, *Jiangsu Yangzhou, China*, [5]*Department of Medical Biochemistry and Microbiology, Uppsala University*, *Uppsala, Sweden*.

7:15 AM W213 **Demographic history and genetic diversity of wild African harlequin quail (*Coturnix delegorguei*) populations of Kenya.**
S. Ogada[1], N. Otecko[2], G. Kennedy[1], J. Musina[3], B. Agwanda[3], V. Obanda[4], J. Lichoti[5], M.-S. Peng[2], Y.-P. Zhang[2], and S. Ommeh*[1], [1]*Institute For Biotechnology Research (IBR), Jomo Kenyatta University of Agriculture and Technology (JKUAT)*, *Nairobi, Kenya*, [2]*State Key Laboratory of Genetic Resources and Evolution, Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Germplasm Bank of Wild Species, Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, China*, [3]*Department of Zoology, National Museums of Kenya*, *Nairobi, Kenya*, [4]*Department of Veterinary Services, Kenya Wildlife Service*, *Nairobi, Kenya*, [5]*State Department of Livestock, Ministry of Agriculture, Livestock, Fisheries and Irrigation*, *Nairobi, Kenya*.

7:30 AM W214 **Genetic relationships among Canarian, African, and European goats using SNPs.**
M. Macri*[1,2], A. Martínez[2], M. G. Luigi[3], J. Capote[4], A. Canales[1,2], M. Amills[3], J. V. Delgado[2], and M. R. Fresno[4], [1]*Animal Breeding Consulting, S.L*, *Cordoba, Cordoba, Spain*, [2]*Department of Genetics, University of Córdoba*, *Cordoba, Cordoba, Spain*, [3]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, University of Barcelona*, *Bellaterra, Barcelona, Spain*, [4]*ICIA, Canary Islands Institute for Agricultural Research*, *San Cristóbal de La Laguna, Santa Cruz de Tenerife, Spain*.

7:45 AM W215 **The eastward dispersal of domestic goats and their introgression, population stratification, and genetic adaptation in East Asia.**
Y. Cai*, W. Fu, Z. Zheng, X. Liu, Y. Jiang, and X. Wang, *Northwest A&F University*, *Yangling, Shaanxi, China*.

8:00 AM **Workshop committee business meeting**

Applied Genetics and Genomics in Other Species of Economic Importance Workshop

Chair: **Leanne van de Goor, VHLGenetics**
9:00 AM – 12:00 PM CDT
2:00 PM – 5:00 PM UTC

9:00 AM **Welcoming remarks**

9:05 AM S110 **Pig CT Discussion.**
Felipe Avila.

9:20 AM S111 **Dromedary CT Discussion.**
Marcela Martinez.

9:35 AM S112 **Alpaca/Llama CT Discussion.**
Felipe Avila.

9:50 AM	S113	**Goat CT Discussion.** Clementine Rodellar.
10:05 AM	S114	**Sheep CT Discussion.** Agata Piestrzynska-Kajtoch.
10:30 AM		**Break**
11:00 AM	S115	**Pigeon CT Discussion.** Angelika Podbielska.
11:15 AM	S116	**Mutation frequency Pigeon STR marker PIGN26.** Leanne van de Goor.
11:30 AM		**Workshop business meeting: Selection of new Duty Labs for 2020-2021 Comparison tests, election of committee, and any other business**
11:45 AM	W216	**Evaluation of population structure alpacas maintained in Poland and identification of alpaca-llama hybrids based on microsatellite markers.** A. Podbielska*[1], K. Piórkowska[1], and T. Szmatola[1,2], [1]*Department of Animal Molecular Biology, National Research Institute of Animal Production*, *Balice, Poland*, [2]*Center for Experimental and Innovative Medicine, University of Agriculture in Krakow*, *Kraków, Poland*.
11:50 AM	W217	**Rate of rejection of first-degree relationships for assigning parent-offspring relationships and estimation of genotyping errors with a high-density array in pigs.** L. Gomez-Raya*[1], E. Gomez Izquierdo[2], E. de Mercado[1], and W. M. Rauw[1], [1]*INIA-CSIC*, *Madrid, Spain*, [2]*ITACyL*, *Hontalbilla, Spain*.
11:55 AM	W218	**Molecular characterization and occurrence of variation within the promoter region of *CASK* gene in racing pigeons.** M. Stefaniuk-Szmukier*[1], K. Piórkowska[2], K. Ropka-Molik[2], and A. Dybus[3], [1]*University of Agriculture in Kraków*, *Krakow, Poland*, [2]*National Research Institute of Animal Production*, *Balice, Poland*, [3]*West Pomeranian University of Technology*, *Szczecin, Poland*.

Comparative and Functional Genomics Workshop

Chair: **Fiona McCarthy, University of Arizona**
9:00 AM – 11:45 AM CDT
2:00 PM – 4:45 PM UTC

9:00 AM	W219	**Invited Workshop Presentation: The Functional Annotation of Animal Genomes Project: Progress and challenges for our continued global effort.** P. W. Harrison*, *EMBL-European Bioinformatics Institute*, *Cambridge, UK*.
9:30 AM	S117	**Panel 1: FAANG progress to date, gaps, challenges, and the path forward.** Peter Harrison, Christine Elsik, Emily Clark.
10:00 AM	W220	**Insights into translation through transfer RNA sequencing and ribosome profiling.** A. Goldkamp* and D. Hagen, *Oklahoma State University*, *Stillwater, OK, USA*.
10:15 AM	W221	**Reference transcriptomes of porcine peripheral blood immune cells created through bulk and single-cell RNA sequencing.** J. Herrera-Uribe[1], J. E. Wiarda[2,5], S. K. Sivasankaran[2,6], L. Daharsh[1], H. Liu[1], K. A. Byrne[2], T. P. L. Smith[3], J. K. Lunney[4], C. L. Loving[2], and C. K. Tuggle*[1], [1]*Iowa State University*, *Ames, IA, USA*, [2]*USDA-ARS-NADC*, *Ames, IA, USA*, [3]*USDA-ARS-MARC*, *Clay Center, NE, USA*, [4]*USDA-ARS-BARC*, *Beltsville, MD, USA*, [5]*Immunobiology Program Iowa State University*, *Ames, IA, USA*, [6]*Genome Informatics Facility Iowa State University*, *Ames, IA, USA*.

10:30 AM S118 **Panel 2: Organizing and coordinating FAANG at a global level.**
Lingzhao Fang.

11:00 AM W222 **Detailed molecular and epigenetic characterization of pig IPECJ-2 and chicken SL-29 cell lines.**
J. de Vos*[1], R. Crooijmans[1], M. Derks[1], S. Kloet[2], M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genetics Group, Wageningen University and Research, Wageningen, the Netherlands*, [2]*Leids Universitair Medisch Centrum, Leiden, the Netherlands*.

11:15 AM W223 **Genome-wide analysis of transcription start sites across *Bos indicus* tissues.**
M. Forutan*, E. Ross, L. Nguyen, and B. Hayes, *Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD, Australia*.

11:30 AM **Business meeting**

Agricultural Genome To Phenome Initiative (AG2PI)

Chair: **Christopher Tuggle, Iowa State University**
1:00 PM – 3:00 PM CDT
6:00 PM – 8:00 PM UTC

1:00 PM W224 **Agricultural Genome to Phenome Initiative: Introduction and community building and listening workshop.**
C. K. Tuggle*[1], J. Clarke[2], J. C. M. Dekkers[1], C. Lawrence-Dill[1], E. Lyons[3], B. Murdoch[4], P. S. Schnable[1], and D. Ertl[5], [1]*Iowa State University, Ames, IA, USA*, [2]*University of Nebraska–Lincoln, Lincoln, NE, USA*, [3]*University of Arizona, Tucson, AZ, USA*, [4]*University of Idaho, Moscow, ID, USA*, [5]*Iowa Corn Growers Association, Johnston, IA, USA*.

1:30 PM **Short survey to gather community opinion**

1:40 PM **Structured brainstorming and small group discussion**

2:30 PM **Wrap-up and session summaries**

Companion Animal Genetics and Genomics Workshop

Chair: **Heather Jay Huson, Cornell University**
3:00 PM – 5:00 PM CDT
8:00 PM – 10:00 PM UTC

3:00 PM W225 **ROS_Cfam_1.0: A high-quality, *de novo* assembly of a male Labrador retriever.**
L. Eory, W. Zhang, D. Ozdemir, E. Clark, A. Archibald, and J. Schoenebeck*, *The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian, UK*.

3:15 PM W226 **Genome-wide association studies identify novel quantitative trait loci for canine health traits.**
H. J. Huson*[1], D. M. Holle[2], A. Walker[1], N. Anclade[1], and K. M. Evans[2], [1]*Department of Animal Science, Cornell University, Ithaca, NY, USA*, [2]*The Seeing Eye Inc., Morristown, NJ, USA*.

3:30 PM W227 ***ABHD5* frameshift deletion in golden retrievers with ichthyosis.**
S. Kiener*[1,2], D. J. Wiener[3], K. Hopke[4], A. B. Diesel[4], V. Jagannathan[1], E. A. Mauldin[5], M. L. Casal[5], and T. Leeb[1,2], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Dermfocus, University of Bern, Bern, Switzerland*, [3]*Department of Veterinary Pathobiology, Texas A&M College of Veterinary Medicine and Biomedical Sciences, College Station, TX, USA*, [4]*Department of Small Animal Clinical Sciences, Texas A&M College of Veterinary Medicine and Biomedical Sciences, College Station, TX, USA*, [5]*University of Pennsylvania, School of Veterinary Medicine, Philadelphia, PA, USA*.

3:45 PM W228 **A genome-wide association study of hypertrophic cardiomyopathy susceptibility in cats.**
J. Raffle*, J. N. Matos, D. J. Connolly, V. L. Fuentes, and A. Psifidi, *Royal Veterinary College, London, UK*.

4:00 PM W229 **Canine Y chromosome features uncovered by long-read sequencing assembly and male dog phylogeny inferred from Y haplotype.**
W. Zhang*, L. Eory, E. Clark, A. Archibald, and J. Schoenebeck, *Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK*.

4:15 PM W230 **More than a moggy: A population genetics analysis of the United Kingdom's non-pedigree cats.**
J. Irving McGrath*[1], W. Zhang[1], R. Hollar[2], A. Collings[3], R. Powell[4], R. Foale[5], N. Thurley[5], R. Campbell[5], R. Mellanby[1], D. Gunn Moore[1], J. Brockman[2], and J. Schoenebeck[2], [1]*Royal (Dick) School of Veterinary Studies and Roslin Institute, University of Edinburgh, Easter Bush Veterinary Campus, Midlothian, UK*, [2]*Hill's Pet Nutrition Centre, Topeka, KS, USA*, [3]*Idexx Laboratories, Wetherby, UK*, [4]*DragonVet Consulting Ltd., Hertfordshire, UK*, [5]*Dick White Referrals, Station Farm, Six Mile Bottom, Cambs., UK*.

4:30 PM W231 **New variant in *ADAMTS2* segregates with recessively inherited Ehlers-Danlos syndrome in a cat family.**
R. Simon*[1], S. Kiener[2,3], N. Thom[4], L. Schäfer[4], M. Roy[1], E. K. Schlohsarczyk[5], C. Herden[5], T. Leeb[2,3], and G. Lühken[1], [1]*Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Germany*, [2]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [3]*Dermfocus, University of Bern, Bern, Switzerland*, [4]*Clinic for Small Animals, Justus Liebig University, Giessen, Germany*, [5]*Institute of Veterinary Pathology, Justus Liebig University, Giessen, Germany*.

4:45 PM **Business meeting**

Plenary Session IV

Chair: **Chris Tuggle, Iowa State University**
7:00 PM – 8:00 PM CDT
12:00 AM – 1:00 AM UTC (Friday, July 30)

7:00 PM W232 **Applying functional knowledge to accelerate animal genetic improvement.**
A. J. Chamberlain*[1], R. Xiang[1,2], I. M. MacLeod[1], M. Khansefid[1], C. P. Prowse-Wilkins[2], M. E. Goddard[1,2], and H. D. Daetwyler[1,3], [1]*Agriculture Victoria, Agribio, Centre for AgriBiosciences, Bundoora, Victoria, Australia*, [2]*Faculty of Veterinary and Agricultural Science, The University of Melbourne, Parkville, Victoria, Australia*, [3]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.

Friday, July 30

7:00 AM – 9:00 AM		**General business meeting**

Equine Genetics and Thoroughbred Parentage Testing Workshop

Chair: Marcela Martinez, Laboratorio De Genetica Aplicada Sociedad Rural Argentina

9:00 AM – 12:00 PM CDT

2:00 PM – 5:00 PM UTC

9:00 AM		**Welcoming remarks**
9:10 AM	S119	**Horse STR Comparison Test.** Rebecca Bellone.
9:25 AM	S120	**Donkey STR Comparison Test.** Peter Dovc.
9:40 AM	S121	**Horse SNP Comparison Test.** Rebecca Bellone.
9:55 AM		**Introduction to Horse SNP Panel discussion and related author presentations**
10:00 AM	W233	**Comparative analysis of single nucleotide polymorphisms and microsatellite markers for parentage verification and sire/dam allocation within equine Thoroughbred breed.** P. Flynn*[1,2], R. Morrin-O'Donnell[1], R. Weld[1], J. Carlsson[2], P. Siddavatam[3], and K. Reddy[3], [1]*Weatherbys Scientific, Naas, Ireland*, [2]*University College Dublin, School of Biology and Environmental Science, Belfield, Dublin, Ireland*, [3]*Thermo Fisher Scientific, Austin, TX, USA*.
10:15 AM	S122	**Availability of whole genome sequencing database for selecting SNP marker in Thoroughbreds.** Teruaki Tozaki.
10:25 AM		**Break**
10:40 AM	W234	**Evaluation of the ISAG equine parentage testing SNP panel across multiple breeds.** R. Bellone*[1,2], B. Till[1], A. Kallenberg[1], F. Avila[1], and R. Grahn[1], [1]*Veterinary Genetics Laboratory, University of California–Davis, Davis, CA, USA*, [2]*Department of Population Health and Reproduction, University of California–Davis, Davis, CA, USA*.
10:55 AM		**Presentation results of Horse Survey and decisions on the Horse Core Panel**
11:25 AM	W235	**Pioneer 100 Horse Health Project: A deep phenotypic and multiomic resource.** C. Donnelly*[1], N. Cohen[2], G. Mulcahy[3], J. Manfredi[4], S. Valberg[5], E. Oberhaus[6], J. Morgan[7], E. Graham-Williams[8], K. Knickelbein[8], R. Bellone[1,9], N. Price[10,11], and C. Finno[1], [1]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [2]*Large Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [3]*School of Veterinary Medicine, University College Dublin, Dublin, Ireland*, [4]*Department of Pathobiology and Diagnostic Investigation, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA*, [5]*Department of Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA*, [6]*School of Animal Sciences, Louisiana State University, Baton Rouge, LA, USA*, [7]*Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [8]*Veterinary Medical Teaching Hospital, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [9]*Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California-Davis, Davis, CA, USA*, [10]*Institute for Systems Biology, Seattle, WA, USA*, [11]*Onegevity Health, New York, NY, USA*.
11:40 AM		**Duty labs election**
11:45 AM		**Election of new committee members and other business**
11:55 AM		**Adjourn**

Genetics and Genomics of Aquaculture Species Workshop

Chair: **Francesca Bertolini, Technical University of Denmark**
9:00 AM – 12:15 PM CDT
2:00 PM – 5:15 PM UTC

9:00 AM W236 **Invited Workshop Presentation: Monitoring of fish and pathogens around aquaculture facilities through analysis of environmental DNA (eDNA) using an environmental sample processor.**
M. W. Jacobsen*[1], B. K. Hansen[1], A. Krolicka[2], D. Strand[2], T. Vrålstad[3], T. Baussant[3], and E. E. Nielsen[1], [1]*Danish Technical University, Section for Marine Living Resources, Silkeborg, Denmark*, [2]*Norwegian Research Centre AS (NORCE), Stavanger, Norway*, [3]*Norwegian Veterinary Institute, Oslo, Norway*.

9:30 AM W237 **Pikeperch *Sander lucioperca* genome data: Basis for smart farming in aquaculture.**
T. Goldammer*[1,2], M. Verleih[1], R. M. Brunner[1], A. Rebl[1], J. A. Nguinkal[1], L. de los Ríos-Pérez[1], N. Schäfer[1], M. Stüeken[3], F. Swirplies[3], and D. Wittenburg[1], [1]*Fish Genetics Unit, Institute of Genome Biology and Statistics in Genomics Unit, Institute of Genetics and Biometry, Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Molecular Biology and Fish Genetics, Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany*, [3]*Research Centre for Agriculture and Fisheries, State Research Center of Agriculture and Fisheries M-V, Rostock, Germany*.

9:45 AM W238 **A blue mussel chromosome-scale assembly and genomic resources for aquaculture, marine ecology, and evolution.**
T. Hori*[1,2], [1]*PEI Marine Sciences Organization, Charlottetown, PE, Canada*, [2]*Atlantic Aqua Farms, Charlottetown, PE, Canada*.

10:00 AM W239 **An application of the MedFish SNP array: Determining population structure and genetic variability of gilthead seabream (*Sparus aurata*) and European seabass (*Dicentrarchus labrax*).**
M. Saura*[1], A. Fernández[1], J. Fernández[1], R. Peiro-Pastor[1], C. Peñaloza[2], L. Bargelloni[3], T. Manousaki[4], C. Tsigenopoulos[4], and B. Villanueva[1], [1]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA, CSIC), Madrid, Spain*, [2]*The Roslin Institute, University of Edinburgh, Midlothian, Scotland, UK*, [3]*University of Padova, Padova, Italy*, [4]*Hellenic Centre for Marine Research (HCMR), Heraklion, Crete, Greece*.

10:15 AM W240 **Signatures of selection and genomic diversity of muskellunge (*Esox masquinongy*) from 2 populations in North America.**
J. Chinchilla-Vargas*[1], J. R. Meerbeek[2], M. F. Rothschild[1], and F. Bertolini[3], [1]*Iowa State University, Ames, IA, USA*, [2]*Iowa Department of Natural Resources, Spirit Lake Fish Hatchery, Spirit Lake, IA, USA*, [3]*National Institute of Aquatic Resources, Technical University of Denmark, Lyngby, Denmark*.

10:30 AM W241 **Influence of estimated breeding value for growth trait on spawning quality in gilthead seabream (*Sparus aurata*).**
C. Pérez-García*[1], Á. Lorenzo-Felipe[1], S. Ferosekhan[1], S. Leon-Bernabeu[1,2], M. Izquierdo[1], R. Ginés[1], J. M. Afonso[1], H. S. Shin[1], and M. J. Zamorano[1], [1]*Universidad de Las Palmas de Gran Canaria (ULPGC), Instituto Universitario de Acuicultura Sostenible y Ecosistemas Marinos (IU-ECOAQUA), Grupo de Investigación en Acuicultura (GIA), Telde, Spain*, [2]*Quanaria, Prolongación Bentejui, San Bartolomé de Tirajana, Las Palmas, Spain*.

10:45 AM **Break**

11:00 AM W242 **Resistance of common carp to Cyprinid herpes virus-3: Individual survival is more affected by different genomic loci than family percent survival.**
M. Amir[1], J. Lighten[2], and L. David*[1], [1]*The Hebrew University of Jerusalem, Rehovot, Israel*, [2]*University of Exeter, Devon, UK*.

11:15 AM W243 **Omics study for viral hemorrhagic septicemia virus (VHSV) resistance in *Paralichthys olivaceus*.**
J. Shin*[1], S. H. Lee[1], W. J. Kim[2], J.-W. Park[3], D.-I. Lee[3], H. S. Jung[3], and J. Kim[3], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*, [2]*East Sea Fisheries Research Institute, National Institute of Fisheries Science, Gangneung, Korea*, [3]*Fish Genetics and Breeding Research Center, National Institute of Fisheries Science, Geoje, Korea*.

11:30 AM W244 **Genome editing to produce monosex and sterile fish for aquaculture.**
X. Lauth*[1], T. Umazume[1], S. Herbert[1], V. Williams[2], and J. Buchanan[1], [1]*Center for Aquaculture Technologies, San Diego, CA, USA*, [2]*The JEM Project, San Diego, CA, USA*.

11:45 AM W245 **Thermal stress generates oxidative damage in liver and gills of red cusk-eel (*Genypterus chilensis*) juvenile.**
P. Dettleff*[1,2], R. Zuloaga[2], P. Gonzalez[2], M. Fuentes[2], J. Aedo[2], J. M. Estrada[3], A. Molina[2], and J. A. Valdes[2], [1]*Nucleus of Applied Research in Veterinary and Agronomic Sciences, Universidad de Las Americas, Santiago, Chile*, [2]*Laboratory of Molecular Biotechnology, Faculty of Life Sciences, Andres Bello University, Santiago, Chile*, [3]*Marine research center of Quintay, Andres Bello University, Quintay, Chile*.

12:00 PM W246 **Reproductive performance of the sea urchin *Tripneustes gratilla* in first- and second-generation cultured cohorts.**
M. Brink-Hull*[1,2], C. Rhode[1], M. D. Cyrus[2,3], B. M. Macey[2,3], J. du Plessis[1], K. L. Hull[1], and R. Roodt-Wilding[1], [1]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [2]*University of Cape Town, Cape Town, Western Cape, South Africa*, [3]*Department of Forestry, Fisheries and the Environment, Cape Town, Western Cape, South Africa*.

Genetics of Immune Response and Disease Resistance Workshop

Chair: **Graham Plastow, Livestock Gentec, Dept of AFNS**
1:00 PM – 4:00 PM CDT
6:00 PM – 9:00 PM UTC

1:00 PM W247 **Invited Workshop Presentation: Genome-wide association study of disease resilience traits from a natural polymicrobial disease challenge model in pigs identifies the importance of the MHC.**
J. Cheng[1], R. Fernando[1], H. Cheng[2], S. D. Kachman[3], K.-S. Lim[1], J. C. S. Harding[4], M. K. Dyck[5], F. Fortin[6], G. S. Plastow[5], PigGen Canada[7], and J. C. M. Dekkers*[1], [1]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [2]*Department of Animal Science, University of California, Davis, CA, USA*, [3]*Department of Statistics, University of Nebraska–Lincoln, Lincoln, NE, USA*, [4]*Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada*, [5]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*, [6]*Centre de Développement du Porc du Québec Inc, Québec City, QC, Canada*, [7]*PigGen Canada Research Consortium, Guelph, ON, Canada*.

1:30 PM W248 **Exploration of glucocorticoid and inflammatory responses in porcine PBMC to reveal mechanisms underlying the enhanced endotoxin sensitivity of $GR_{Ala610Val}$ pigs.**
E. Murani*, Z. Li, F. Hadlich, N. Trakooljul, S. Ponsuksili, and K. Wimmers, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

1:40 PM W249 **Genome-wide association study of thyroid hormone suppression following challenge with porcine reproductive and respiratory syndrome virus.**
A. Van Goor[1], A. Pasternak[2], M. Walugembe[3], N. Chehab[1], G. Hamonic[4], J. Dekkers[3], J. Harding*[4], and J. Lunney[1], [1]*USDA ARS BARC Animal Parasitic Diseases Laboratory, Beltsville, MD, USA*, [2]*Department of Animal Science, Purdue Univ, West Lafayette, IN, USA*, [3]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [4]*Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada*.

1:50 PM W250 **Molecular characterization of the serum amyloid A (SAA) mutation R90S in chicken hepatocellular carcinoma (LMH) cells.**
C. Falker-Gieske*[1], N. Paul[1], J. Gilthorpe[2], K. Gustmann[1], and J. Tetens[1], [1]*Department of Animal Sciences, Georg-August-University, Göttingen, Germany*, [2]*Department of Integrative Medical Biology, Umeå University, Umeå, Sweden*.

2:00 PM W251 **Ovine mastitis: Does early life nutrition influence immunity response in later life?**
C. Hervás-Rivero, R. Pelayo, B. Gutiérrez-Gil, C. Esteban-Blanco, H. Marina, J. Arranz, and A. Suárez-Vega*, *Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, Castilla y León, Spain*.

2:10 PM W252 **The natural cytotoxicity receptor genes in the family Felidae.**
J. Bubenikova[1,2], J. Futas[1,2], J. Oppelt[2], M. Plasil[2], R. Vodicka[3], and P. Horin*[1,2], [1]*Department of Animal Genetics, University of Veterinary Sciences, Brno, Czech Republic*, [2]*Ceitec VETUNI, University of Veterinary Sciences, Brno, Czech Republic*, [3]*Zoo Prague, Prague, Czech Republic*.

2:20 PM W253 **Systemic transcriptomic response of sheep and cattle to acute and chronic *Fasciola hepatica* infection.**
D. A. Niedziela*[1], A. Naranjo-Lucena[1], V. Molina-Hernández[2], J. A. Browne[3], Á. Martínez-Moreno[4], J. Pérez[2], D. E. MacHugh[3,5], and G. Mulcahy[1,5], [1]*UCD School of Veterinary Medicine, University College Dublin, Dublin, Ireland*, [2]*Department of Anatomy and Comparative Pathology and Toxicology, Faculty of Veterinary Medicine, University of Córdoba, Córdoba, Spain*, [3]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, Dublin, Ireland*, [4]*Parasitology section, Department of Animal Health, Faculty of Veterinary Medicine, University of Córdoba, Córdoba, Spain*, [5]*UCD Conway Institute of Biomolecular and Biomedical Research, Dublin, Ireland*.

2:30 PM **Break**

2:40 PM W254 **Bimodal haplotype distribution in bovine antibacterial toll-like receptors.**
K. Samaké*[1] and K. Novák[2], [1]*Charles University, Prague, Czech Republic*, [2]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*.

2:50 PM W255 **Variation in circulatory serum biomarkers in dairy heifers exposed to endotoxin indicate disparity in induced physiological responses.**
A. Sharma*, T. Sullivan, K. Lamers, and N. Karrow, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada*.

3:00 PM W256 **Transcriptomic analysis of host resistance to tick infestation with *Rhipicephalus microplus* in leukocytes of Brangus cattle.**
E. Mantilla Valdivieso*[1], E. Ross[1], A. Raza[1], B. Hayes[1], N. Jonsson[2], P. James[1], and A. Tabor[1], [1]*Queensland Alliance for Agriculture and Food Innovation, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Queensland, Australia*, [2]*Institute of Biodiversity Animal Health and Comparative Medicine, Institute of Biodiversity Animal Health and Comparative Medicine, Glasgow, UK*.

3:10 PM S123 **NEIKER joint presentation of abstracts W257, W258, and W259.**
M. Canive, M. Alonso-Hearn, and G. Badia-Bringué.

3:30 PM W257 **Identification of loci associated with susceptibility to paratuberculosis in Holstein cattle using combinations of diagnostic tests and imputed whole-genome sequence data.**
M. Canive*[1], G. Badia-Bringué[1], O. González-Recio[2],[3], A. Fernandez[2], P. Vázquez[1], J. Garrido[1], R. Juste[1], and M. Alonso-Hearn[1], [1]*Department of Animal Health, NEIKER-Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, CSIC, Madrid, Spain*, [3]*Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, Madrid, Spain*.

3:32 PM W258 **The host genetic underlying pathological outcomes to *Mycobacterium avium* subsp. *paratuberculosis* infection is governed by distinct genetic variants.**
M. Alonso-Hearn*[1], M. Canive[1], G. Badia-Bringué[1], O. González-Recio[2,3], A. Fernández[2,3], P. Vázquez[1], J. Garrido[1], and R. Juste[1], [1]*NEIKER-Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, CSIC, Madrid, Spain*, [3]*Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, Madrid, Spain*.

3:34 PM W259 **Alternative splicing modulates the immune response in peripheral blood and gut tissues of Holstein cattle naturally infected with *Mycobacterium avium* subsp. *paratuberculosis*.**
G. Badia-Bringué*[1], M. Canive[1], J. Lavín[2], R. Casais[3], C. Blanco-Vázquez[3], and M. Alonso-Hearn[1], [1]*Department of Animal Health, NEIKER-Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Department of Applied Mathematics, NEIKER- Basque Institute for Agricultural Research and Development, Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [3]*SERIDA, Servicio Regional de Investigación y Desarrollo Agroalimentario, Center of Animal Biotechnology, Deva, Asturias, Spain*.

3:35 PM W260 **Identification and validation of loci associated with facial eczema tolerance in New Zealand sheep.**
K. M. McRae*, S. J. Rowe, P. L. Johnson, and S. M. Clarke, *AgResearch Limited, Mosgiel, New Zealand*.

3:45 PM **Workshop business meeting**

POSTER PRESENTATIONS
Available On Demand

Animal Epigenetics

P100 **Sestrin-3 regulates adipogenesis via the Smad3/miR-124 axis.**
W. Lin, J. Zhao, M. Yan, K. Yang, W. Wei, L. Zhang, and J. Chen*, *College of Animal Science, Nanjing Agricultural University, Nanjing, Jiangsu, China*.

P101 **Livestock methylomics: Systematic evaluation of DNA methylation profiling assays for industry.**
A. Caulton*[1,2], R. Brauning[1], K. G. Dodds[1], A. Hagani[3], J. Zoller[4], C. Couldrey[5], S. Horvath[3], and S. M. Clarke[1], [1]*AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand*, [2]*University of Otago, Dunedin, New Zealand*, [3]*Department of Human Genetics, David Geffen School of Medicine, University of California Los Angeles, Los Angeles, CA, USA*, [4]*Department of Biostatistics, Fielding School of Public Health, University of California Los Angeles, Los Angeles, CA, USA*, [5]*Livestock Improvement Corporation, Hamilton, New Zealand*, [6]*University of Idaho, Moscow, ID, USA*.

P102 **Maternal methionine supplementation alters alternative splicing and DNA methylation in bovine skeletal muscle.**
L. Liu* and F. Peñagaricano, *University of Wisconsin-Madison, Madison, WI, USA*.

P103 **Micrococcal nuclease sequencing of pig sperm suggests a relationship between nucleosome retention and both semen quality and early embryo development.**
M. Gòdia[1], S. S. Hammoud[2], M. Naval-Sánchez[3], I. Ponte[4], J. E. Rodriguez-Gil[4], A. Sánchez[4],[1], and A. Clop*[1,5], [1]*Centre for Research in Agricultural Genomics CRAG, Cerdanyola del Valles, Catalonia, Spain*, [2]*University of Michigan, Ann Arbor, MI, USA*, [3]*CSIRO, St Lucia, Brisbane, Australia*, [4]*Universitat Autonoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain*, [5]*CSIC, Barcelona, Catalonia, Spain*.

P104 **Identifications of epigenetic regulation mechanism according to the growth of pig in abdominal fat tissue through multi-omics integration analysis.**
D.-Y. Kim* and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea*.

P105 **Epigenetic marks in the promoter of *GNAS* and *EBF3* are associated with meat tenderness in *Bos indicus*.**
M. M. de Souza[1,2], S. C. M. Niciura[1], M. I. P. Rocha[1,3], W. J. S. Diniz[1,4], J. J. Bruscadin[1,3], J. Afondo[1], P. S. N. de Oliveira[1], G. B. Mourão[5], A. Zerlotini[6], L. L. Coutinho[5], J. E. Koltes[2], and L. C. A. Regitano*[1], [1]*Embrapa Pecuária Sudeste, Empresa Brasileira de Pesquisa Agropecuária, São Carlos, São Paulo, Brazil*, [2]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [3]*Department of Genetics and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [4]*Department of Animal Sciences, North Dakota State University, Fargo, ND, USA*, [5]*Department of Animal Science, Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil*, [6]*Embrapa Informática Agropecuária, Empresa Brasileira de Pesquisa Agropecuária, Campinas, São Paulo, Brazil*.

P106 **Characterization of the adipose tissue DNA methylation framework between male and female suckling lambs.**
A. Suarez-Vega, C. Esteban-Blanco, H. Marina, R. Pelayo, M. Alonso-Garcia, C. Hervas-Rivero, B. Gutierrez-Gil, and J.-J. Arranz*, *Universidad de León, León, Spain*.

P107 **Pig genome functional annotation enhances biological interpretations of complex traits and comparative epigenomics.**
Z. Pan*[1], Y. Yao[2], H. Yin[3], Z. Cai[4], Y. Wang[1], L. Bai[3], C. Kern[1], M. Halstead[1], K. Chanthavixay[1], N. Trakooljul[5], K. Wimmers[5], G. Sahana[4], G. Su[4], M. Sandø Lund[4], M. Fredholm[6], P. Karlskov-Mortensen[6], C. W. Ernst[7], P. Ross[1], C. K. Tuggle[8], L. Fang[2], and H. Zhou[1], [1]*Department of Animal Science, University of California, Davis, Davis, CA, USA*, [2]*MRC Human Genetics Unit at the Institute of Genetics and Molecular Medicine, The University of Edinburgh, Edinburgh, UK*, [3]*Agricultural Genome Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China*, [4]*Center for Quantitative Genetics and Genomics, Faculty of Technical Sciences, Aarhus University, Tjele, Denmark*, [5]*Leibniz-Institute for Farm Animal Biology, Dummerstorf, Germany*, [6]*Animal Genetics, Bioinformatics and Breeding, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark*, [7]*Department of Animal Science, Michigan State University, East Lansing, MI, USA*, [8]*Department of Animal Science, Iowa State University, Ames, IA, USA*.

P108 **A *Bos indicus* epigenetic clock predicts age from tail hair.**
L. T. Nguyen*, M. Forutan, B. J. Hayes, and E. M. Ross, *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Queensland, Australia*.

P109 **ISO-seq data reveal allele-specific isoform expression.**
S. Bardoloi*, L. Nguyen, B. Engle, B. Hayes, and E. Ross, *University of Queensland*, *Brisbane, Queensland, Australia*.

Animal Forensic Genetics

P110 **SNP marker combination for discrimination of Korean native chickens using a machine learning model.**
S. Cho*[1], D. Seo[1,2], M. Kim[2], E. Cho[3], P. Manjula[1], T. Kalhari[2], and J. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Department of Bio-big data, Chungnam National University*, *Daejeon, Republic of Korea*.

P111 **Development of a 14-short tandem repeat (STR) panel for forensic DNA analysis of red fox.**
A. E. Hrebianchuk*[1], N. S. Parfionava[1], V. N. Lukashkova[1], S. A. Kotava[1], and I. S. Tsybovsky[2], [1]*Scientific and Practical Centre of the State Forensic Examination Committee of the Republic of Belarus*, *Minsk, Republic of Belarus*, [2]*Republican unitary service enterprise "BelJurZabespechenne"*, *Minsk, Republic of Belarus*.

P112 **Genetic profiling of horses in forensic cases.**
A. Fornal*, K. Kowalska, T. Zabek, A. Piestrzynska-Kajtoch, and K. Ropka-Molik, *Department of Animal Molecular Biology, National Research Institute of Animal Production*, *Balice, Poland*.

Applied Genetics and Genomics in Other Species of Economic Importance

P113 **Estimation of inbreeding load and purging in animal conservation programs.**
N. Pérez-Pereira*[1], E. López-Cortegano[1,3], A. García-Dorado[2], and A. Caballero[1], [1]*Centro de Investigación Mariña, Universidade de Vigo*, *Vigo, Spain*, [2]*Universidad Complutense de Madrid*, *Madrid, Spain*, [3]*Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh*, *Edinburgh, UK*.

P114 **Common quail identification by mitochondrial and nuclear DNA analysis.**
L. Borreguero*, M. Hernandez, M. R. Maya, A. Trigo, T. Mayoral, and J. A. Bouzada, *Laboratorio Central de Veterinaria*, *Algete, Madrid, Spain*.

P115 **Evaluation of population structure alpacas maintained in Poland and identification of alpaca-llama hybrids based on microsatellite markers.**
A. Podbielska*[1], K. Piórkowska[1], and T. Szmatola[1,2], [1]*Department of Animal Molecular Biology, National Research Institute of Animal Production*, *Balice, Poland*, [2]*Center for Experimental and Innovative Medicine, University of Agriculture in Krakow*, *Kraków, Poland*.

P116 **Identification of polymorphism in the *MC1R* gene in Polish pastel foxes: Preliminary research.**
G. Smolucha*[1], A. Koseniuk[1], and P. Bielanski[2], [1]*Department of Animal Molecular Biology, National Research Institute of Animal Production*, *Balice, Poland*, [2]*Department of Small Livestock Breeding, National Research Institute of Animal Production*, *Balice, Poland*.

P117 **Genomic structure in a divergent selected mice population for birth weight variability.**
C. Ojeda-Marin*[1], K. Arias[1], L. El-Ouazizi[1], N. Formoso-Rafferty[2], J. P. Gutiérrez[1], and I. Cervantes[1], [1]*Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid*, *Madrid, Spain*, [2]*Departamento de Producción Agraria, E.T.S.I.A.A.B, Universidad Politécnica de Madrid*, *Madrid, Spain*.

P118 **Differential gene expression reveals functional differences between selection strategies and generations in early mass-reared black soldier fly colonies.**
K. L. Hull*, M. P. Greenwood, A. E. Bester-van der Merwe, and C. Rhode, *Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*.

Applied Genetics of Companion Animals

P119 **Development of highly informative SNP panel for parentage assessment in dogs.**
K. R. Gujjula*, H. Suren, A. Burrell, and S. Chadaram, *Thermo Fisher Scientific*, *Austin, TX, USA*.

P120 **Breed, trait, locus, and allele nomenclature standardization for the domestic cat.**
L. A. Lyons*, *College of Veterinary Medicine, University of Missouri*, *Columbia, MO, USA*.

P121 **Supplementation of the AgriSeq Canine SNP Parentage and ID Panel with additional ISAG and sex determination markers.**
A. Burrell*, K. Gujjula, H. Suren, and R. Conrad, *Thermo Fisher Scientific*, *Austin, TX, USA*.

Avian Genetics and Genomics

P122 **Genetic diversity and population structure of Myanmar native chickens using double digest restriction-site associated DNA sequencing (ddRAD-seq).**
S. L. Y. Mon*[1], M. Lwin[2], A. A. Maw[3], L. L. Htun[3], S. Bawm[3], K. Kawabe[4], Y. Nagano[5,1], A. J. Nagano[6], Y. Wada[5,1], S. Okamoto[1], and T. Shimogiri[1], [1]*The United Graduate School of Agricultural Sciences, Kagoshima University*, *Kagoshima, Japan*, [2]*Livestock Breeding and Veterinary Department*, *Yangon, Myanmar*, [3]*University of Veterinary Science*, *Nay Pyi Taw, Myanmar*, [4]*Education Center, Kagoshima University*, *Kagoshima, Japan*, [5]*Faculty of Agriculture, Saga University*, *Saga, Japan*, [6]*Faculty of Agriculture, Ryukoku University*, *Otsu, Shiga, Japan*.

P123 **Annotation of full-length transcripts including alternative splicing from 19 chicken tissues using Oxford Nanopore long-read sequencing.**
D. Guan*[1], M. M. Halstead[1], A. D. Islas-Trejo[1], D. E. Goszczynski[1], H. H. Cheng[2], P. Ross[1], and H. Zhou[1], [1]*Department of Animal Science, University of California–Davis*, *Davis, CA, USA*, [2]*Avian Disease and Oncology Laboratory, USDA-ARS*, *East Lansing, MI, USA*.

P124 **Serum creatine kinase as a biomarker to predict wooden breast and white striping on live broilers.**
F. Kong, Z. He, J. Sun, R. Liu*, and J. Wen, *Institute of Animal Sciences, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P125 **Hypothalamic and ovarian transcriptome profiling reveals potential candidate genes in low and high egg production of White Muscovy ducks (*Cairina moschata*).**
S. Bello*, H. Xu, and Q. Nie, *South China Agricultural University*, *Guangzhou, Guangdong, China*.

P126 **Comparison of genomic prediction methods for residual feed intake in broilers.**
Z. He*, S. Li, W. Li, J. Wang, J. Ding, M. Zheng, Q. Li, J. Wen, R. Liu, and G. Zhao, *Institution of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P127 **Phylogenetic characterization of Yoruba ecotype and broiler chicken using 18s rRNA.**
D. I. Ibiwoye[1,2], F. E. Sola-Ojo[1], T. A. Adisa*[1], I. A. Abubakar[1], N. B. Afolabi-Balogun[3], C. A. Adeniyi[4], and A. O. Oni[3], [1]*University of Ilorin*, *Ilorin, Kwara, Nigeria*, [2]*Huazhong Agricultural University*, *Wuhan, China*, [3]*Fountain University*, *Osogbo, Osun, Nigeria*, [4]*Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, Yunnan, China*.

P128 **Cloning, characterization, and expression features of chicken CDS2 splicing variants.**
Y. Y. Xu, S. P. Zhang, Y. J. Guo*, H. Y. Zhang, W. Chen, and Y. Q. Huang, *College of Animal Science and Technology, Henan Agricultural University*, *Zhengzhou, Henan, China*.

P129 **Estimation of genetic diversity in Muscovy duck found in Kwara State, Nigeria, using cytochrome P450 family 2 subfamily U member 1 (*CYP2U1*) mitochondrial gene.**
F. E. Sola-Ojo[1], C. A. Adeola[2], O. A. Yusuf[1], and A. R. Adekoya*[1], [1]*University of Ilorin*, *Ilorin, Kwara State, Nigeria*, [2]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, China*.

P130 **Proteome profile of chicken cecum in the response to *Salmonella enteritidis* inoculation.**
X. Miao, H. Li, L. Liu, L. Liu, Y. Zhao, and X. Li*, *Shandong Agricultural University*, *Tai'an, Shandong, China*.

P131 **Causative variants associated with oculocutaneous albinism genes in Yeonsan Ogye chicken.**
E. Cho*[1], M. Kim[2], P. Manjula[3], S. Cho[3], T. Kalhari[2], D. Seo[2,3], and J. Lee[1,2], [1]*Department of Bio-big data, Chungnam National University, Daejeon, Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Korea*, [3]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*.

P132 **Molecular sexing of Nigerian Guineafowl keets using chromo helicase DNA (CHD) binding gene.**
D. I. Ibiwoye[1,2], F. E. Sola-Ojo[1], I. Abdulkareem[1], I. A. Abubakar*[1], N. B. Afolabi-Balogun[3], C. A. Adeniyi[4], and A. O. Oni[3], [1]*University of Ilorin, Ilorin, Kwara, Nigeria*, [2]*Huazhong Agricultural University, Wuhan, China*, [3]*Fountain University, Osogbo, Osun, Nigeria*, [4]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*.

P133 **Assessment of the effect of genomic selection and detection of selective signatures in broilers.**
X. Tan*[1], R. Liu[1], W. Li[1], M. Zheng[1], D. Zhu[2], D. Liu[2], F. Feng[2], J. Wen[1], and G. Zhao[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*Foshan Gaoming Xinguang Agricultural and Animal Industrials Corporation, Foshan, Guangdong, China*.

P134 **Transcriptomic analysis of the *Musculus complexus* in naked neck broiler chickens.**
A. C. Mott*, C. Blaschka, A. Mott, A. R. Sharifi, and J. Tetens, *Georg-August University, Göttingen, Lower Saxony, Germany*.

P135 **Research on the fine structure and admixture of the worldwide chicken population reveals connections between populations and important events in breeding history.**
Y. Guo*[1,3], J.-H. Ou[5], Y. Zan[5], Y. Wang[1], H. Li[4], C. Zhu[4], K. Chen[4], X. Zhou[3], X. Hu[1,2], and Ö. Carlborg[5], [1]*State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China*, [2]*National Engineering Laboratory for Animal Breeding, China Agricultural University, Beijing, China*, [3]*Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University, Beijing, China*, [4]*Jiangsu Institute of Poultry Science, Jiangsu Yangzhou, China*, [5]*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*.

P136 **Nextflow Iso-seq (nf-isoseq) pipeline provides a first insight into the chicken transcript landscape.**
S. Guizard*, J. Smith, R. Kuo, K. Miedzinska, J. Smith, M. Davey, and M. Watson, *The Roslin Institute, Edinburgh, Scotland, UK*.

P137 **Genomic signatures of selection for egg production rate using whole-genome sequence in Hinaidori chickens.**
T. Goto*[1], S. Fukuda[2], K. Rikimaru[2], R. A. Lawal[3], J. Pool[4], and O. Hanotte[5,6], [1]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan*, [2]*Akita Prefectural Livestock Experiment Station, Akita, Japan*, [3]*The Jackson Laboratory, Bar Harbor, ME, USA*, [4]*University of Wisconsin-Madison, Madison, WI, USA*, [5]*University of Nottingham, Nottingham, UK*, [6]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*.

P138 **Taxonomy classification of Nigerian local turkey using 12S mitochondrial rRNA gene.**
D. I. Ibiwoye[1,2], F. E. Sola-Ojo[1], D. O. Aremu*[1], I. A. Abubakar[1], N. B. Afolabi-Balogun[3], C. A. Adeniyi[4], and A. O. Oni[3], [1]*University of Ilorin, Ilorin, Kwara, Nigeria*, [2]*Huazhong Agricultural University, Wuhan, China*, [3]*Fountain University, Osogbo, Osun, Nigeria*, [4]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*.

P139 **Phylogenetic characterization of male and female exotic chicken using 18S RNA.**
D. I. Ibiwoye[1,2], F. E. Sola-Ojo[1], T. A. Iroko*[1], I. A. Abubakar[1], N. B. Afolabi-Balogun[3], C. A. Adeniyi[4], and A. O. Oni[3], [1]*University of Ilorin, Ilorin, Kwara, Nigeria*, [2]*Huazhong Agricultural University, Wuhan, China*, [3]*Fountain University, Osogbo, Osun, Nigeria*, [4]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*.

P140 **Molecular characterization and occurrence of variation within the promoter region of the *CASK* gene in racing pigeons.**
M. Stefaniuk-Szmukier*[1], K. Piórkowska[2], K. Ropka-Molik[2], and A. Dybus[3], [1]*University of Agriculture in Kraków, Krakow, Poland*, [2]*National Research Institute of Animal Production, Balice, Poland*, [3]*West Pomeranian University of Technology, Szczecin, Poland*.

P141 **Genetic diversity in Muscovy ducks (*Cairina moschata*) found in Baruten local government area of Kwara State, Nigeria.**
F. E. Sola-Ojo[1], C. A. Adeola[2], O. A. Yusuf[1], and O. E. Momoh*[1], [1]*University of Ilorin, Ilorin, Nigeria*, [2]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*.

P142 **Genetic diversity and relationship of Nigerian Muscovy duck populations using mitochondrial cytochrome *b* gene.**
A. O. Yusuf*[1], C. A. Adeola[2], and F. E. Sola-Ojo[1], [1]*University of Ilorin, Ilorin, Nigeria*, [2]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*.

P143 **Bridge 60k SNP panel for the chicken genome-wide study.**
D. Seo*[1,2], S. Cho[1], D. Lee[1], M. Kim[1], P. Manjula[1], J. Shin[1], D. Lim[3], H. Choo[4], J. Cha[4], K. Kim[4], I.-S. Jeon[4], K.-T. Lee[3], B. Park[4], S. H. Lee[1,2], J. H. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, South Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, South Korea*, [3]*Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA*, *Wanju, South Korea*, [4]*Poultry Research Institute, National Institute of Animal Science, RDA*, *Pyeongchang, South Korea*.

P144 **Study on differentially expressed genes in granular layer and theca layer of laying Silky Fowl and White Leghorn.**
Y. Tai*[1], X. Yang[1], D. Han[2], and X. Deng[1], [1]*Lab of Animal Genetic Resource and Molecular Breeding, China Agricultural University*, *Beijing, China*, [2]*College of Veterinary Medicine, China Agricultural University*, *Beijing, China*.

P145 **Genetic markers associated with live body weight and carcass weight of Korean native chicken using 50k SNP panel.**
M. Kim*[1], S. Cho[2], E. Cho[3], D. Seo[1,2], A. Jang[4], K. Kim[5], I. Jeon[5], J. Cha[5], B. Park[5], H. Choo[5], and J. Lee[1,2], [1]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Korea*, [3]*Department of Bio-big data, Chungnam National University*, *Daejeon, Korea*, [4]*Department of Applied Animal Science, Kangwon National University*, *Chuncheon, Korea*, [5]*Poultry Research Institute, National Institute of Animal Science, RDA*, *Pyeongchang, Korea*.

P146 **Genetic markers associated with meat quality traits of Korean native chicken using 50k SNP panel.**
M. Kim[1], S. Cho[2], E. Cho[3], D. Seo[1],[2], A. Jang[4], K. Kim[5], I. Jeon[5], J. Cha[5], B. Park[5], H. Choo[5], and J. Lee*[1,2], [1]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Korea*, [3]*Department of Bio-big data, Chungnam National University*, *Daejeon, Korea*, [4]*Department of Applied Animal Science, Kangwon National University*, *Chuncheon, Korea*, [5]*Poultry Research Institute, National Institute of Animal Science, RDA*, *Pyeongchang, Korea*.

P147 **A new chromosome-level turkey genome.**
C. P. Barros*[1], M. F. L. Derks[1], J. Mohr[2], B. J. Wood[2,3], M. C. A. M. Bink[4], and M. A. M. Groenen[1], [1]*Wageningen University and Research*, *Wageningen, the Netherlands*, [2]*Hybrid Turkeys*, *Kitchener, ON, Canada*, [3]*School of Veterinary Science, University of Queensland*, *Gatton, QLD, Australia*, [4]*Hendrix Genetics Research, Technology and Services*, *Boxmeer, the Netherlands*.

P148 **Effects of exogenous insulin injection on serum biochemical indices and tissue metabolites of different breeds of chicken.**
P. Luo, H. Wang, Z. Wang, Y. Wang, C. Su, H. Zhang, W. Chen, and Y. Huang*, *Henan Agricultural University*, *Zhengzhou, Henan, China*.

P149 **Uncovering abundant missing genes in the chicken reference genome solves the avian gene depletion puzzle.**
M. Li*[1], N. Xu[1], P. Bian[1], X. Hu[2], Y. Jiang[1], and N. Yang[3], [1]*Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University*, *Yangling, China*, [2]*State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University*, *Beijing, China*, [3]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture and Rural Affairs, China Agricultural University*, *Beijing, China*.

P150 **Dissecting the polygenic genetic architecture of growth using genotyping by low-coverage sequencing in a deep intercross of the Virginia body weight lines: Novel loci revealed by increased power and improved genome coverage.**
T. Rönneburg*[1], Y. Zan[2,1], C. Honaker[3], P. Siegel[3], and Ö. Carlborg[1], [1]*Department of Medical Biochemistry and Microbiology, Uppsala University*, *Uppsala, Sweden*, [2]*Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Science*, *Umeå, Sweden*, [3]*Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University*, *Blacksburg, VA, USA*.

Cattle Molecular Markers and Parentage Testing

P151 **Identification of splicing isoforms of bovine *ACSF3* gene and protein structure prediction.**
W. He*, X. Fang, and R. Yang, *College of Animal Science, Jilin University*, *Changchun, Jilin Province, China*.

P152 **Evolution of inbreeding: A gaze into the history of 5 Italian beef cattle breeds.**
G. Rovelli*[1,2], M. Luigi-Sierra[2], D. Guan[2,3], F. Sbarra[4], A. Quaglia[4], M. Amills[2,5], and E. Lasagna[1], [1]*Department of Agricultural, Food and Environmental Sciences (DSA, Perugia*, *Perugia, Italy*, [2]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autonòma de Barcelona*, *Bellaterra, Barcelona, Spain*, [3]*Department of Animal Science, University of California*, *Davis, California, United States of America*, [4]*National Association of Italian Beef-Cattle Breeders (ANABIC)*, *San Martino in Colle, Perugia, Italy*, [5]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*.

P153 **Investigating the accuracy of imputing variants on chromosome X in admixed dairy cattle using the ARS-UCD[1,2] assembly of the bovine genome.**
Y. Wang*[1,2], K. Tiplady[1,2], T. J. J. Johnson[2], C. Harland[2], M. Keehan[1,2], T. J. Lopdell[2], R. G. Sherlock[2], A. Wallace[2], B. Harris[2], M. D. Littlejohn[2], R. Spelman[2], D. Garrick[1], and C. Couldrey[2], [1]*AL Rae Centre for Genetics and Breeding, School of Agriculture, Massey University, Hamilton, Waikato, New Zealand*, [2]*Research and Development, Livestock Improvement Corporation, Hamilton, Waikato, New Zealand*.

P154 **Identification of the β-casein gene genotype in Simmental cattle.**
I. Radkowska[1], D. Rubis[2], and K. Ropka-Molik*[2], [1]*Department of Cattle Breeding, National Research Institute of Animal Production, Balice, Poland*, [2]*Department of Animal Molecular Biology, National Research Institute of Animal Production, Balice, Poland*.

P155 **A high-throughput Applied Biosystems Axiom Bovine Genotyping array with 100,000 markers optimized for dairy evaluation.**
A. Pirani*, D. Oliver, C. Bertani, and M. Patil, *Thermo Fisher Scientific Inc., Santa Clara, CA, USA*.

P156 **Significant role of *PLAGL1* in proliferation and differentiation of bovine myoblasts.**
Y. Wen, J. Xu, X. Li, X. Ding, S. Zhang, P. Yang, Z. Yao, C. Lei, H. Chen, and Y. Huang*, *Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*.

P157 **Effects of copy number variation (CNV) of *CHRDL1* gene on growth traits and proliferation and differentiation of muscle cells in cattle.**
X. Ding, X. Li, Y. Wen, J. Xu, S. Zhang, P. Yang, Z. Yao, C. Lei, H. Chen, and Y. Huang*, *Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*.

P158 **Genetics of base coat color variations and coat color patterns of South African Nguni cattle investigated using high-density SNP genotypes.**
L. Kunene[1], K. Hadebe[2], G. Mészáros[3], J. Sölkner[3], F. Muchadeyi*[2], and E. Dzomba[1], [1]*University of KwaZulu-Natal, Pietermaritzburg, South Africa*, [2]*Agricultural Research Council, Pretoria, South Africa*, [3]*University of Natural Resources and Life Sciences, Boku University, Vienna, Austria*.

P159 **Impact of genomic breed composition on production traits in crossbred dairy cattle.**
M. Jaafar*[1], B. Heins[2], C. Dechow[3], and H. Huson[1], [1]*Cornell University, Ithaca, NY, USA*, [2]*University of Minnesota, Morris, MN, USA*, [3]*Penn State University, University Park, PA, USA*.

Companion Animal Genetics and Genomics

P160 ***PRKG2* splice site variant in Dogo Argentino dogs with dwarfism.**
G. Rudd Garces*[1,2], M. E. Turba[3], V. Jagannathan[1], F. Gentilini[4], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Institute of Veterinary Genetics, La Plata, Argentina*, [3]*Genefast, Forlì, Italy*, [4]*Department of Veterinary Medical Sciences, University of Bologna, Bologna, Italy*.

P161 ***KLF7* gene is a risk factor for congenital deafness in Australian stumpy tail cattle dogs.**
S. Shan*[1], F. Xu[1], S. Sommerlad[2], J. M. Seddon[2], and B. Brenig[1], [1]*Institute of Veterinary Medicine, University of Goettingen, Göttingen, Germany*, [2]*School of Veterinary Science, The University of Queensland, Gatton, QLD, Australia*.

P162 **More than a moggy; A population genetics analysis of the United Kingdom's non-pedigree cats.**
J. Irving McGrath*[1], W. Zhang[1], R. Hollar[2], A. Collings[3], R. Powell[4], R. Foale[5], N. Thurley[5], R. Campbell[5], R. Mellanby[1], D. Gunn Moore[1], J. Brockman[2], and J. Schoenebeck[2], [1]*Royal (Dick) School of Veterinary Studies and Roslin Institute, University of Edinburgh, Easter Bush Veterinary Campus, Midlothian, UK*, [2]*Hill's Pet Nutrition Centre, Topeka, KS, USA*, [3]*Idexx Laboratories, Wetherby, UK*, [4]*DragonVet Consulting Ltd, Hertfordshire, UK*, [5]*Dick White Referrals, Six Mile Bottom, Cambs, UK*.

P163 **Whole-genome sequencing analysis of a cat family with radial hemimelia.**
N. Bilgen*[1], M. Y. Akkurt[1], B. Çinar Kul[1], R. M. Buckley[2], L. A. Lyons[2], and Ö. S. Çildir[1], [1]*Faculty of Veterinary Medicine, Department of Genetics, Ankara University, Ankara, Turkey*, [2]*Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*.

P164 **Assessment of similarity between the canine m.2683G>A variant found in the tRNA-Leu (UUR) gene and the deleterious m.3243A>G variant in the human *TRNL1* gene in carcinogenesis.**
K. Kowal*, A. Tkaczyk-Wlizlo, and B. Slaska, *Institute of Biological Bases of Animal Production, Faculty of Animal Sciences and Bioeconomy, University of Life Sciences in Lublin, Lublin, Poland*.

P166 **Identification of the causative mutation for hair length variation in Sapsarees, a Korean native dog breed, using genome-wide association analysis.**
M. Kang*[1], B. Ahn[1], S. Yook[1], Y. Lee[2], J. Kim[2], and C. Park[1], [1]*Konkuk University*, *Seoul, Republic of Korea*, [2]*Yeungnam University*, *Yeungnam, Republic of Korea*.

P167 **Whole-genome sequence-based analysis of genetic relationships among East Asian dog breeds including Korean native breeds Sapsaree, Donggyeongi, and Jindo.**
B. Ahn*[1], M. Kang[1], J. J. Kim[2], H. Jiang[3], and C. Park[1], [1]*Department of Stem Cell and Regenerative Biotechnology, Konkuk University*, *Seoul, South Korea*, [2]*School of Biotechnology, Yeungnam University*, *Gyeongsan, South Korea*, [3]*College of Animal Science, Jilin University*, *Changchun, China*.

P168 **Recessive deleterious mutations in the *TPO* gene associated with familial thyroid follicular cell carcinoma in Dutch German long-haired pointers.**
Y. Yu*, H. Bovenhuis, Z. Wu, K. Laport, M. Groenen, and R. Crooijmans, *Wageningen University and Research, Animal Breeding and Genomics*, *Wageningen, the Netherlands*.

P169 **Deletion of the *SELENOP* gene leads to CNS atrophy with cerebellar ataxia (CACA) in dogs.**
M. Christen*[1], S. Högler[2], M. Kleiter[3], M. Leschnik[3], C. Weber[4], D. Thaller[5], V. Jagannathan[1], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern*, *Bern, Switzerland*, [2]*Unit of Laboratory Animal Pathology, Department of Pathobiology, University of Veterinary Medicine Vienna*, *Vienna, Austria*, [3]*Department for Companion Animals and Horses, University of Veterinary Medicine Vienna*, *Vienna, Austria*, [4]*Laboklin GmbH & Co. KG, Laboratory for Clinical Diagnostics*, *Bad Kissingen, Germany*, [5]*Institute of Pathology, Department of Pathobiology, University of Veterinary Medicine Vienna*, *Vienna, Austria*.

P170 ***ABHD5* frameshift deletion in golden retrievers with ichthyosis.**
S. Kiener*[1,2], D. J. Wiener[3], K. Hopke[4], A. B. Diesel[4], V. Jagannathan[1], E. A. Mauldin[5], M. L. Casal[5], and T. Leeb[1,2], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern*, *Bern, Switzerland*, [2]*Dermfocus, University of Bern*, *Bern, Switzerland*, [3]*Department of Veterinary Pathobiology, Texas A&M College of Veterinary Medicine and Biomedical Sciences*, *College Station, TX, USA*, [4]*Department of Small Animal Clinical Sciences, Texas A&M College of Veterinary Medicine and Biomedical Sciences*, *College Station, TX, USA*, [5]*University of Pennsylvania, School of Veterinary Medicine*, *Philadelphia, PA, USA*.

P171 **Transcriptomic profile of peripheral whole blood reveals novel potential diagnostic gene biomarkers of degenerative joint disease (osteoarthritis) in German shepherd dogs.**
G. Rudd Garces, P. Peral Garcia, G. Padula, and G. Giovambattista*, *IGEVET – Instituto de Genética Veterinaria "Ing. Noel Dolout" UNLP-CONICET LA PLATA), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata*, *La Plata, Buenos Aires, Argentina*.

P172 **Genome-wide association study identifies a risk locus on CFA18 for congenital laryngeal paralysis in Alaskan sled dogs.**
S. Krishnamoorthy*[1], D. J. F. von Pfeil[2], B. J. Stanley[3], C. Griffitts[4], and H. J. Huson[1], [1]*Department of Animal Science, Cornell University*, *Ithaca, NY, USA*, [2]*Small Animal Surgery Locum, PLLC*, *Dallas, TX, USA*, [3]*Department of Small Animal Clinical Sciences, Michigan State University*, *East Lansing, MI, USA*, [4]*The Travelling Vet LLC*, *CO, USA*.

P173 **Description of breed ancestry and genetic health traits in Arctic sled dog breeds.**
J. Thorsrud* and H. Huson, *Cornell University*, *Ithaca, NY, USA*.

P174 **Genomic DNA extraction from canine feces for genotyping and identification with targeted genotyping by sequencing (GBS) application.**
Q. Hoang, K. Kice, C. Carrasco, S. Chadaram*, and R. Conrad, *Thermo Fisher Scientific*, *Austin, TX, USA*.

P175 **Canine Y chromosome features uncovered by long-read sequencing assembly and male dog phylogeny inferred from Y haplotype.**
W. Zhang*, L. Eory, E. Clark, A. Archibald, and J. Schoenebeck, *Roslin Institute, University of Edinburgh*, *Edinburgh, Scotland, UK*.

P176 **Gene differential expression analysis in spontaneously occurring canine melanoma.**
S. Perga[1], C. Beltramo[1], F. Fruscione[1], I. Martini[1], F. Cavallo[2], F. Riccardo[2], P. Buracco[3], S. Iussich[3], E. Razzuoli[1], K. Varello[1], L. Maniscalco[1], E. Bozzetta[1], A. Ferrari[1], and P. Modesto*[1], [1]*Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, National Reference Center for the Veterinary and Comparative Oncology (CEROVEC)*, *Genoa, Italy*, [2]*Department of Molecular Biotechnology and Health Sciences Molecular Biotechnology Center*, *Turi, Italy*, [3]*Department of Veterinary Science*, *Turin, Italy*.

P177 **A genome-wide association study of hypertrophic cardiomyopathy susceptibility in cats.**
J. Raffle*, J. N. Matos, D. J. Connolly, V. L. Fuentes, and A. Psifidi, *Royal Veterinary College, London, UK*.

P178 **New variant in *ADAMTS2* segregates with recessively inherited Ehlers-Danlos syndrome in a cat family.**
R. Simon*[1], S. Kiener[2,3], N. Thom[4], L. Schäfer[4], M. Roy[1], E. K. Schlohsarczyk[5], C. Herden[5], T. Leeb[2,3], and G. Lühken[1], [1]*Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Germany*, [2]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [3]*Dermfocus, University of Bern, Bern, Switzerland*, [4]*Clinic for Small Animals, Justus Liebig University, Giessen, Germany*, [5]*Institute of Veterinary Pathology, Justus Liebig University, Giessen, Germany*.

P179 **Genome-wide association studies identify novel quantitative trait loci for canine health traits.**
H. J. Huson*[1], D. M. Holle[2], A. Walker[1], N. Anclade[1], and K. M. Evans[2], [1]*Department of Animal Science, Cornell University, Ithaca, NY, USA*, [2]*The Seeing Eye Inc., Morristown, NJ, USA*.

P180 **ROS_Cfam_1.0: A high-quality, *de novo* assembly of a male Labrador retriever.**
L. Eory, W. Zhang, D. Ozdemir, E. Clark, A. Archibald, and J. Schoenebeck*, *The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian, UK*.

P181 **Populational structure analyses of Brazilian Mastiff dog breed.**
F. de Andrade*, R. Nunes, D. Tyska, and J. Cobuci, *Grupo de Pesquisa MegaGen, Departamento de Zootecnia, UFRGS, Porto Alegre, RS, Brazil*.

Comparative and Functional Genomics

P182 **Detailed molecular and epigenetic characterization of pig IPECJ-2 and chicken SL-29 cell lines.**
J. de Vos*[1], R. Crooijmans[1], M. Derks[1], S. Kloet[2], M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genetics Group, Wageningen University and Research, Wageningen, the Netherlands*, [2]*Leids Universitair Medisch Centrum, Leiden, the Netherlands*.

P183 **A comprehensive RNA editome reveals RNA editing sites affecting the function of HSPA12B in myogenesis via altering binding ability for miRNA-181b.**
A. A. Adetula*[1,2], X. Fan[1], Y. Zhang[1], Y. Yao[1], J. Yan[1], M. Chen[1], Y. Tang[1], Y. Liu[1], G. Yi[1], K. Li[1,2], and Z. Tang[1,2], [1]*Genome Analysis Laboratory of the Ministry of Agriculture, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China*, [2]*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

P184 **Update and some new features of the Animal rDNA database.**
J. Sochorová*[1], S. Garcia[2], F. Gálvez[3], R. Symonová[4], and A. Kovarík[1], [1]*Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic*, [2]*Institut Botànic de Barcelona (IBB-CSIC-ICUB), Barcelona, Catalonia, Spain*, [3]*Bioscripts - Centro de Investigación y Desarrollo de Recursos Científicos, Sevilla, Andalusia, Spain*, [4]*Research Institute for Limnology, Mondsee, Mondsee, Austria*.

P185 **Reference transcriptomes of porcine peripheral blood immune cells created through bulk and single-cell RNA sequencing.**
J. Herrera-Uribe[1], J. E. Wiarda[2,5], S. K. Sivasankaran[2,6], L. Daharsh[1], H. Liu[1], K. A. Byrne[2], T. P. L. Smith[3], J. K. Lunney[4], C. L. Loving[2], and C. K. Tuggle*[1], [1]*Iowa State University, Ames, IA, USA*, [2]*USDA-ARS-NADC, Ames, IA, USA*, [3]*USDA-ARS-MARC, Clay Center, NE, USA*, [4]*USDA-ARS-BARC, Beltsville, MD, USA*, [5]*Immunobiology Program Iowa State University, Ames, IA, USA*, [6]*Genome Informatics Facility Iowa State University, Ames, IA, USA*.

P186 **Uncovering *TUG1* lncRNA-chromatin interaction sites in the bovine genome using ChIRP-seq.**
R. Bhushan*[1], D. Becker[1], C. Kühn[1], and R. Weikard[1,2], [1]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Agricultural and Environmental Faculty, University of Rostock, Rostock, Germany*.

P187 **BovReg: A high-resolution functional annotation of the cattle genome using novel breeds/crosses.**
G. Costa Monteiro Moreira*[1], S. Dupont[1], D. Becker[2], M. Salavati[3], R. Clark[4], E. L. Clark[3], G. Plastow[5], C. Kühn[2,6], C. Charlier[1], on behalf of the BovReg Consortium[6], [1]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège,Belgium*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [3]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [4]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

P188 **Seasonal changes in the adipose transcriptomes in semi-domesticated reindeer (*Rangifer tarandus*).**
M. Weldenegodguad*[1,2], K. Pokharel[1], L. Niiranen[3], P. Soppela[4], I. Ammosov[5], M. Honkatukia[6], H. Lindeberg[1], J. Peippo[1,6], T. Reilas[1], N. Mazzullo[4], K. A. Mäkelä[3], T. Nyman[7], A. Tervahauta[2], K.-H. Herzig[8,9], J. Kantanen[1], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland*, [3]*Research Unit of Biomedicine, Faculty of Medicine, University of Oulu, Oulu, Finland*, [4]*Arctic Centre, University of Lapland, Rovaniemi, Finland*, [5]*Board of Agricultural Office of Eveno-Bytantaj Region, Batagay-Alyta, The Sakha Republic (Yakutia), Russia*, [6]*NordGen—Nordic Genetic Resource Center, Ås, Norway*, [7]*Department of Ecosystems in the Barents Region, Norwegian Institute of Bioeconomy Research, Svanvik, Norway*, [8]*Research Unit of Biomedicine, Medical Research Center, Faculty of Medicine, University of Oulu, Oulu, Finland*, [9]*Oulu University Hospital, Oulu, Finland*.

P189 **Genes related to chemotaxis of the immune system underlie ongoing indicine-taurine cattle domestication at copy number variation hotspots.**
V. H. da Silva*[1], L. Correia De Almeida Regitano[2], A. Zerlotini Neto[3], G. Barreto Mourão[1], and L. Lehmann Coutinho[1], [1]*Department of Animal Science, University of São Paulo (USP), Luiz de Queiroz College of Agriculture (ESALQ), Piracicaba, São Paulo, Brazil*, [2]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil*, [3]*Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil*.

P190 **Liver RNA-seq expression analysis in cattle supplemented with rumen-protected choline.**
D. Hernández Maizón[1], P. Alvarez Cecco[1], H. Morales Durand[1], L. H. Olivera[1], M. E. Fernandez[1], P. Peral Garcia*[1], G. Giovambattista[1], and A. Rogberg-Muñoz[1,2], [1]*IGEVET – Instituto de Genética Veterinaria "Ing. Noel Dolout" UNLP-CONICET LA PLATA), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*IMPA - Instituto de Mejoramiento y Producción Animal, Facultad de Agronomía (UBA-CONICET), Ciudad Autónoma de Buenos Aires, Argentina*.

P191 **Influence of fetal weight on liver transcriptome in purebred and crossbred Iberian pig fetuses.**
Y. Núñez*[1], C. García Contreras[1], M. Vázquez Gómez[3], S. Astiz[1], R. Benítez[1], A. Heras Molina[1], B. Isabel[2], A. Rey[2], A. González Bulnes[1], and C. Óvilo[1], [1]*INIA CSIC, Madrid, Spain*, [2]*UCM, Madrid, Spain*, [3]*Sorbonne Université, Paris, France*.

P192 **Expression of taste receptor genes in growing Iberian and Duroc pigs.**
R. Benitez*[1], R. Peiro[1], Y. Nunez[1], F. Garcia[1], E. de Mercado[3], E. Gomez-Izquierdo[3], J. Garcia-Casco[1], and C. Lopez-Bote[2], [1]*INIA-CSIC, Madrid, Spain*, [2]*Faculty of Veterinary Medicine, UCM, Madrid, Spain*, [3]*Pig Test Center ITACYL, Hontalbilla, Segovia, Spain*.

P193 **Investigation of bovine leukemia virus (BLV) proviral DNA integration in cattle genome.**
M. Polat*[1,2], S. Saito[2], K. Hosomichi[3], and Y. Aida[1,2], [1]*The University of Tokyo, Tokyo, Japan*, [2]*RIKEN, Saitama, Japan*, [3]*Kanazawa University, Ishikawa, Japan*.

P194 **Expression profiles of porcine parathyroid glands altered by pre- and postnatal dietary phosphorus supply.**
M. Oster[1], H. Reyer[1], C. Gerlinger[1], N. Trakooljul[1], J. Keiler[2], S. Ponsuksili[1], P. Wolf[3], and K. Wimmers*[1,3], [1]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Institute of Anatomy, Rostock University Medical Center, Rostock, Germany*, [3]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*.

P195 **Insights into translation through transfer RNA sequencing and ribosome profiling.**
A. Goldkamp* and D. Hagen, *Oklahoma State University, Stillwater, OK, USA*.

P196 **FAANGMine genomic data mining warehouse: 2021 update.**
C. Elsik*, A. Walsh, and D. Triant, *University of Missouri, Columbia, MO, USA*.

P197 **Online Mendelian Inheritance in Animals (OMIA): Standardized vocabularies for breeds and traits.**
I. Tammen[1], N. Vasilevsky[2], C. A. Park[3], Z. Hu[3], M. Haendel[4], and F. W. Nicholas*[1], [1]*Sydney School of Veterinary Science, University of Sydney, Sydney, NSW, Australia*, [2]*Oregon Clinical and Translational Research Institute, Department of Medical Informatics and Clinical Epidemiology, Oregon Health and Science University, Portland, OR, USA*, [3]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [4]*Center for Health AI, University of Colorado Anschutz Medical Campus, Aurora, CO, USA*.

P198 **Genome-wide analysis of transcription start sites across *Bos indicus* tissues.**
M. Forutan*, E. Ross, L. Nguyen, and B. Hayes, *Queensland Alliance for Agriculture and Food Innovation, Brisbane QLD, Australia*.

P199 **AgriSum Toolkit plugin 2.0: Enabling multi-species panel analysis for AgriSeq.**
H. Suren*[1], S. Daly[2], and K. R. Gujjula[1], [1]*Thermo Fisher Scientific, Austin, TX, USA*, [2]*Thermo Fisher Scientific, Lissieu, France*.

P200 **Systematic discovery and integration of functional formation in genome-wide analysis of cattle traits.**
R. Xiang*[1,2], E. Breen[2], I. MacLeod[2], A. Chamberlain[2], C. Prowse-Wilkins[1,2], H. Daetwyler[2,3], and M. Goddard[1,2], [1]*Faculty of Veterinary and Agricultural Science, The University of Melbourne, Parkville, Victoria, Australia*, [2]*Agriculture Victoria, AgriBio, Centre for AgriBiosciences, Bundoora, Victoria, Australia*, [3]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.

Comparative MHC Genetics: Populations and Polymorphism

P201 **The Georgian mountain cow breed Khevsurian population exhibits specific single nucleotide polymorphisms across the mitochondrial genome that distinguish it from global cattle populations.**
G. Basiladze[1], L. Tabatadze[1], E. Khmaladze[2], and M. Kotetishvili*[1], [1]*Scientific-Research Center of Agriculture, Tbilisi, Georgia*, [2]*Richard Lugar Center for Public Health Research, National Center for Disease Control and Public Health, Tbilisi, Georgia*.

P202 **Molecular characterization of swine leukocyte antigen (SLA) gene diversity in European farmed pigs.**
S. E. Hammer*[1], T. Duckova[1], S. Groiss[1], M. Stadler[1], M. Jensen-Wearn[2], W. T. Golde[3], U. Gimsa[4], and A. Saalmueller[1], [1]*University of Veterinary Medicine Vienna, Vienna, Austria*, [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [3]*Moredun Research Institute, Edinburgh, Scotland, UK*, [4]*Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany*.

P203 **Development of a comprehensive high-resolution typing method for SLA-3, an MHC classical class I gene of pigs, using genomic DNA PCR and direct sequencing.**
S. Youk*[1], M. T. Le[1], M. Kang[1], B. Ahn[1], M. Choi[1], C. Ho[2], and C. Park[1], [1]*Konkuk University, Seoul, Republic of Korea*, [2]*Gift of Hope Organ and Tissue Donor Network, Itasca, IL, USA*.

P204 **Application of MHC sequencing to vaccine development: Proteome-wide analysis of zoonotic bacterium *Coxiella burnetii* for conserved T-cell epitopes presented by multiple host species.**
L. M. Wright Piel[1], C. J. Durfee[1], and S. N. White*[1,2], [1]*USDA-ARS Animal Disease Research, Pullman, WA, USA*, [2]*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA*, [3]*Center for Reproductive Biology, Washington State University, Pullman, WA, USA*.

P205 **Sequencing of LEI0258 marker reveals populations' specific alleles and new repeat motif patterns.**
P. Manjula*[1], T. Kalhari[2], S. Cho[1], M. Kim[2], E. Cho[3], and J. Lee[1,2], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Republic of Korea*, [3]*Department of Bio-big Data, Chungnam National University, Daejeon, Republic of Korea*.

P206 **Expression of genes related with immunomodulation and immunogenicity of equine mesenchymal stem cells: Influence of major histocompatibility complex.**
A. Cequier*[1], S. Fuente[1,2], A. Vitoria[1,2], A. Romero[1,2], F. Vázquez[1,2], C. Rodellar[1], and L. Barrachina[1,2], [1]*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza), Instituto Agroalimentario de Aragón– IA, Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

P207 **Evaluation of polymorphisms in *BLB2* gene in Korean Ogye chicken using next-generation sequencing data.**
T. Kalhari*[1], P. Manjula[2], S. Cho[2], M. Kim[1], E. Cho[3], and J. Lee[1,2], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*, [3]*Department of Bio-big data, Chungnam National University, Daejeon, Korea*.

P208 **Association of bovine leukemia virus-induced lymphoma with BoLA-DRB3 polymorphisms at the DNA, amino acid, and binding pocket property levels.**
C.-W. Lo*[1], S.-N. Takeshima[2,3], K. Okada[4], E. Saitou[5], T. Fujita[6], Y. Matsumoto[1], S. Wada[7], H. Inoko[8], and Y. Aida[1,2], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Viral Infectious Diseases Unit, RIKEN, Saitama, Japan*, [3]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*, [4]*Iwate University, Iwate, Japan*, [5]*Hyogo Prefectural Awaji Meat Inspection Center, Hyogo, Japan*, [6]*Livestock Research Institute of Oita Prefectural Agriculture, Forestry and Fisheries, Research Center, Oita, Japan*, [7]*Photonics Control Technology Team, RIKEN Center for Advanced Photonics, Saitama, Japan*, [8]*Genome Analysis Division, GenoDive Pharma Inc, Kanagawa, Japan*.

P209 **The IPD-MHC database: Novel tools for the study of the major histocompatibility complex.**
G. Maccari*[1,2], J. Robinson[2,3], J. A. Hammond[1], and S. G. E. Marsh[2,3], [1]*The Pirbright Institute, Pirbright, Woking, Surrey, UK*, [2]*Anthony Nolan Research Institute, Royal Free Campus, London, UK*, [3]*UCL Cancer Institute, Royal Free Campus, London, UK*.

P210 **Characterization of the functional and transcriptional variation of cattle MHC class I alleles.**
J. C. Schwartz*[1], G. Maccari[1,2], D. Heimeier[1], and J. A. Hammond[1], [1]*The Pirbright Institute, Guildford, UK*, [2]*Anthony Nolan Research Institute, London, UK*.

Domestic Animal Sequencing and Annotation

P211 **The importance of annotations (reference genome and parent gene) for the study of circRNAs.**
A. Robic*[1], T. Faraut[1], C. Cerutti[1], J. Demars[1], and C. Kühn[2,3], [1]*GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet-Tolosan, France*, [2]*Institute Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [3]*Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany*.

P212 **A comparison of copy number variant discovery in New Zealand sheep when using different genotyping platforms.**
A. Hess*, H. Baird, R. Brauning, and S. Clarke, *AgResearch Ltd., Mosgiel, Otago, New Zealand*.

P213 **Annotation of transcription start sites in the bovine genome reveals novel breed-specific complexity.**
M. Salavati*[1], R. Clark[2], D. Becker[3], C. Kühn[3,4], G. Plastow[5], G. Costa Monteiro Moreira[6], C. Charlier[6,7], E. L. Clark[1], and on behalf of the BovReg Consortium[4], [1]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [2]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [3]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [4]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium*, [7]*Faculty of Veterinary Medicine, University of Liège, Liège, Belgium*.

P214 **Functional annotation of the bovine genome.**
H. Zhou*[1], X. Xu[1], H. Beiki[8], S. Corum[9], K. M. Davenport[7], X. Han[4], G. Wang[2], H. Wang[4], Y. Xing[2], X. Zhang[4], Y. Zhang[4], C. Kern[5], C. Kern[1], P. Lyu[3], W. Ma[5], J. J. Michal[4], C. A. Gill[2], H. Jiang[3], Z. Jiang[4], W. Liu[5], S. D. McKay[6], J. Medrano[1], B. M. Murdoch[7], J. M. Reecy[8], G. Rincon[9], M. Rijnkels[2], T. P. L. Smith[10], and P. J. Ross[1], [1]*University of California- Davis, Davis, CA, USA*, [2]*Texas A&M AgriLife Research, College Station, TX, USA*, [3]*Virginia Polytechnic Institute and State University, Blacksburg, VA, USA*, [4]*Washington State University, Pullman, WA, USA*, [5]*Pennsylvania State University, State College, PA, USA*, [6]*University of Vermont, Burlington, VT, USA*, [7]*University of Idaho, Moscow, ID, USA*, [8]*Iowa State University, Ames, IA, USA*, [9]*Zoetis Inc., Kalamazoo, MI, USA*, [10]*USDA-ARS-USMARC, Clay Center, NE, USA*.

P215 **Performance of variant pathogenicity prediction methods in veterinary species.**
N. Tate*, K. Mahoney, N. Wanner, S. Durward-Akhurst, N. Gocker, J. Mickelson, S. Friedenberg, M. McCue, and E. Furrow, *University of Minnesota, College of Veterinary Medicine, St. Paul, MN, USA*.

P216 **AQUA-FAANG: Genome functional annotation of the 6 major European farmed fish species.**
D. J. Macqueen*[1], S. Lien[2], and the AQUA-FAANG Consortium[3], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, UK*, [2]*Centre for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway*, [3]*AQUA-FAANG Consortium, Europe*.

P217 **Bovine genome annotation using integration of multi-omics data.**
H. Beiki[1], C. Gill[2], H. Jiang[3], W. Liu[5], Z. Jiang[4], S. McKay[6], B. M. Murdoch[7], J. Koltes[1], M. Rijnkels[2], T. P. L. Smith[8], P. Ross[9], H. Zhou[9], and J. Reecy*[1], [1]*Iowa State University, Ames, IA, USA*, [2]*Texas A&M University, College Station, TX, USA*, [3]*Virginia Tech University, Blacksburg, VA, USA*, [4]*Washington State University, Pullman, WA, USA*, [5]*Penn State University, State College, PA, USA*, [6]*University of Vermont, Burlington, VT, USA*, [7]*University of Idaho, Moscow, ID, USA*, [8]*US Meat Animal Research Center, Clay Center, NE, USA*, [9]*University of California–Davis, Davis, CA USA*.

P218 **The Ovine Functional Annotation of Animal Genomes project.**
B. M. Murdoch*[1,6], K. M. Davenport[1], M. Salavati[2], E. Clark[2], A. Archibald[2], A. T. Massa[3], M. R. Mousel[4,5], M. K. Herndon[3], S. N. White[3,4,6], K. C. Worley[7], S. Bhattarai[8], S. D. McKay[8], B. Dalrymple[9], J. Kijas[10], A. Caulton[11], S. Clarke[11], R. Brauning[11], T. Hadfield[12], T. P. L. Smith[13], and N. E. Cockett[12], [1]*Department of Animal, Veterinary, and Food Science, University of Idaho, Moscow, ID, USA*, [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, UK*, [3]*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA*, [4]*USDA, ARS, Animal Disease Research Unit, Pullman, WA, USA*, [5]*Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA*, [6]*Center for Reproductive Biology, Washington State University, Pullman, WA, USA*, [7]*Baylor College of Medicine-Human Genome Sequencing Center, Houston, TX, USA*, [8]*University of Vermont, Burlington, VT, USA*, [9]*University of Western Australia, Crawley, Western Australia, Australia*, [10]*CSIRO Agricultural Flagship, St. Lucia, Brisbane, Australia*, [11]*AgResearch, Hamilton, New Zealand*, [12]*Utah State University, Logan, UT, USA*, [13]*USDA, ARS, US Meat Animal Research Center (USMARC), Clay Center, NE, USA*.

P219 **Chromatin accessibility and regulatory vocabulary in indicine cattle.**
P. Alexandre*[1], M. Naval-Sánchez[1,2], M. Menzies[1], L. Nguyen[3], L. Porto-Neto[1], M. Fortes[4], and A. Reverter[1], [1]*CSIRO Agriculture and Food, Queensland, QLD, Australia*, [2]*Institute for Molecular Bioscience, The University of Queensland, Queensland, QLD, Australia*, [3]*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Queensland, QLD, Australia*, [4]*School of Chemistry and Molecular Biosciences, The University of Queensland, Queensland, QLD, Australia*.

P220 **Local farm animal populations as a potential reservoir for SARS-Cov-2 infections.**
M. Zorc, A. Tansek, T. Bevec, and P. Dovc*, *University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Ljubljana, Slovenia*.

P221 **The Farm Animal Genotype-Tissue Expression (FarmGTEx) Consortium.**
L. Fang*, *The University of Edinburgh, Edinburgh, UK*.

P222 **The Bovine Pangenome Consortium.**
B. D. Rosen*[1], D. M. Bickhart[2], T. P. L. Smith[3], D. Boichard[4], G. A. Brockmann[5], A. J. Chamberlain[6], C. Couldrey[7], H. D. Daetwyler[6], A. Djikeng[8], C. Drögemüller[9], S. Elzaki[5], R. K. Gandham[10], D. Hagen[11], O. Hanotte[12], M. P. Heaton[3], Y. Jiang[13], Z. Jiang[14], D. Larkin[15], G. Liu[1], W. Y. Low[16], P. Ajmone Marsan[17], B. M. Murdoch[18], F. C. Muchadeyi[19], J. Mwacharo[20], H. L. Neibergs[14], H. Pausch[21], S. Demyda-Peyrás[22], J. Prendergast[23], P. J. Ross[24], R. D. Schnabel[25], J. Sölkner[26], A. Soudre[27], A. Tijjani[12], J. L. Williams[17], and Bovine Pangenome Consortium[28], [1]*USDA ARS AGIL, Beltsville, MD, USA*, [2]*USDA ARS DFRC, Madison, WI, USA*, [3]*USDA ARS MARC, Clay Center, NE, USA*, [4]*INRAE Animal Genetics and Integrative Biology, Jouy-en-Josas, France*, [5]*Humboldt-Universität zu Berlin, Berlin, Germany*, [6]*Agriculture Victoria, Melbourne, Victoria, AU*, [7]*LIC, Hamilton, New Zealand*, [8]*Centre for Tropical Livestock Genetics and Health, Midlothian, Scotland, UK*, [9]*University of Bern, Bern, Switzerland*, [10]*National Institute of Animal Biotechnology, Hyderabad, India*, [11]*Oklahoma State University, Stillwater, OK, USA*, [12]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [13]*Northwest A&F University, Yangling, China*, [14]*Washington State University, Pullman, WA, USA*, [15]*Royal Veterinary College, University of London, London, UK*, [16]*The University of Adelaide, Adelaide, South Australia, Australia*, [17]*Università Cattolica del Sacro Cuore, Piacenza, Italy*, [18]*University of Idaho, Moscow, ID, USA*, [19]*Agricultural Research Council, South Africa, Pretoria, South Africa*, [20]*Scotland's Rural College, Midlothian, Scotland, UK*, [21]*ETH Zürich, Zürich, Switzerland*, [22]*Universidad de Córdoba, Córdoba, Spain*, [23]*The Roslin Institute, Midlothian, Scotland, UK*, [24]*STgenetics, Navasota, TX, USA*, [25]*University of Missouri, Columbia, MO, USA*, [26]*University of Natural Resources and Life Sciences, Vienna, Austria*, [27]*Université Norbert ZONGO, Koudougou, Burkina Faso*, [28]*Bovine Pangenome Consortium*.

P223 **An improved, high-quality ovine reference genome to facilitate functional annotation of gene regulatory elements.**
K. M. Davenport*[1], D. M. Bickhart[2], K. C. Worley[3], S. C. Murali[3], N. E. Cockett[4], M. P. Heaton[5], T. P. L. Smith[5], B. M. Murdoch[1], and B. D. Rosen[6], [1]*Department of Animal, Veterinary, and Food Sciences, University of Idaho, Moscow, ID, USA*, [2]*US Dairy Forage Research Center, USDA-ARS, Madison, WI, USA*, [3]*Baylor College of Medicine, Houston, TX, USA*, [4]*Utah State University, Logan, UT, USA*, [5]*US Meat Animal Research Center, USDA-ARS, Clay Center, NE, USA*, [6]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA*.

Equine Genetics and Thoroughbred Parentage Testing

P224 **Developmental validation of an equine parentage testing kit producing letter and number alleles with 20 markers.**
S. Zeinali*[1,2], F. Rahiminejhad[1,3], and H. Samiee[3], [1]*Genetek Biopharma GmbH, Berlin, Germany*, [2]*Kawsar Biotechnology Co, Tehran, Iran*, [3]*Kawsar Human Genetic Research Center, Tehran, Iran*.

P225 **Evaluation of SNP markers for parentage testing in the draft horse population.**
T. Ishige*[1], M. Kikuchi[1], H. Kakoi[1], K.-I. Hirora[1], A. Ohnuma[1], T. Tozaki[1], Y. Hirosawa[2], S. Tanaka[2], and S.-I. Nagata[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [2]*National Livestock Breeding Center Tokachi Station, Otofuke, Hokkaido, Japan*.

P226 **Pioneer 100 Horse Health Project: A deep phenotypic and multiomic resource.**
C. Donnelly*[1], N. Cohen[2], G. Mulcahy[3], J. Manfredi[4], S. Valberg[5], E. Oberhaus[6], J. Morgan[7], E. Graham-Williams[8], K. Knickelbein[8], R. Bellone[1,9], N. Price[10,11], and C. Finno[1], [1]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [2]*Large Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [3]*School of Veterinary Medicine, University College Dublin, Dublin, Ireland*, [4]*Department of Pathobiology and Diagnostic Investigation, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA*, [5]*Department of Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA*, [6]*School of Animal Sciences, Louisiana State University, Baton Rouge, LA, USA*, [7]*Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [8]*Veterinary Medical Teaching Hospital, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [9]*Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [10]*Institute for Systems Biology, Seattle, WA, USA*, [11]*Onegevity Health, New York, NY, USA*.

P227 **Comparative analysis of single nucleotide polymorphisms and microsatellite markers for parentage verification and sire/dam allocation within equine Thoroughbred breed.**
P. Flynn*[1],[2], R. Morrin-O'Donnell[1], R. Weld[1], J. Carlsson[2], P. Siddavatam[3], and K. Reddy[3], [1]*Weatherbys Scientific, Naas, Ireland*, [2]*University College Dublin, School of Biology and Environmental Science, Belfield, Dublin, Ireland*, [3]*Thermo Fisher Scientific, Austin, TX, USA*.

P228 **Evaluation of the ISAG equine parentage testing SNP panel across multiple breeds.**
R. Bellone*[1,2], B. Till[1], A. Kallenberg[1], F. Avila[1], and R. Grahn[1], [1]*University of California–Davis, Veterinary Genetics Laboratory, Davis, CA, USA*, [2]*University of California–Davis, Department of Population Health and Reproduction, Davis, CA, USA*.

Genetics and Genomics of Aquaculture Species

P229 **Thermal stress generates oxidative damage in liver and gills of red cusk-eel (*Genypterus chilensis*) juvenile.**
P. Dettleff*[1,2], R. Zuloaga[2], P. Gonzalez[2], M. Fuentes[2], J. Aedo[2], J. M. Estrada[3], A. Molina[2], and J. A. Valdes[2], [1]*Nucleus of Applied Research in Veterinary and Agronomic Sciences, Universidad de Las Americas, Santiago, Chile*, [2]*Laboratory of Molecular Biotechnology, Faculty of Life Sciences, Andres Bello University, Santiago, Chile*, [3]*Marine research center of Quintay, Andres Bello University, Quintay, Chile*.

P230 **Pikeperch *Sander lucioperca* genome data: Basis for smart farming in aquaculture.**
T. Goldammer*[1,2], M. Verleih[1], R. M. Brunner[1], A. Rebl[1], J. A. Nguinkal[1], L. de los Ríos-Pérez[1], N. Schäfer[1], M. Stüeken[3], F. Swirplies[3], and D. Wittenburg[1], [1]*Fish Genetics Unit, Institute of Genome Biology and Statistics in Genomics Unit, Institute of Genetics and Biometry, Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Molecular Biology and Fish Genetics, Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany*, [3]*Research Centre for Agriculture and Fisheries, State Research Center of Agriculture and Fisheries M-V, Rostock, Germany*.

P231 **Signatures of selection and genomic diversity of muskellunge (*Esox masquinongy*) from 2 populations in North America.**
J. Chinchilla-Vargas*[1], J. R. Meerbeek[2], M. F. Rothschild[1], and F. Bertolini[3], [1]*Iowa State University, Ames, IA, USA*, [2]*Iowa Department of Natural Resources, Spirit Lake Fish Hatchery, Spirit Lake, IA, USA*, [3]*National Institute of Aquatic Resources, Technical University of Denmark, Lyngby, Denmark*.

P232 **Optimization of induced ovulation and spawning of Clariid catfish *Heterobranchus bidorsalis* (Geoffroy-Saint-Hilaire, 1809) using synthetic hormone.**
W. Olaniyi*, *Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria*.

P233 **Resistance of common carp to Cyprinid herpes virus-3: Individual survival is more affected by different genomic loci than family percent survival.**
M. Amir[1], J. Lighten[2], and L. David*[1], [1]*The Hebrew University of Jerusalem, Rehovot, Israel*, [2]*University of Exeter, Devon, UK*.

P234 **Reproductive performance of the sea urchin *Tripneustes gratilla* in first- and second-generation cultured cohorts.**
M. Brink-Hull*[1,2], C. Rhode[1], M. D. Cyrus[2,3], B. M. Macey[2,3], J. du Plessis[1], K. L. Hull[1], and R. Roodt-Wilding[1], [1]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [2]*University of Cape Town, Cape Town, Western Cape, South Africa*, [3]*Department of Forestry, Fisheries and the Environment, Cape Town, Western Cape, South Africa*.

P235 **An application of the MedFish SNP array: Determining population structure and genetic variability of gilthead seabream (*Sparus aurata*) and European seabass (*Dicentrarchus labrax*).**
M. Saura*[1], A. Fernández[1], J. Fernández[1], R. Peiro-Pastor[1], C. Peñaloza[2], L. Bargelloni[3], T. Manousaki[4], C. Tsigenopoulos[4], and B. Villanueva[1], [1]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA, CSIC), Madrid, Spain*, [2]*The Roslin Institute, University of Edinburgh, Midlothian, Scotland, UK*, [3]*University of Padova, Padova, Italy*, [4]*Hellenic Centre for Marine Research (HCMR), Heraklion, Crete, Greece*.

P236 **A blue mussel chromosome-scale assembly and genomic resources for aquaculture, marine ecology and evolution.**
T. Hori*[1,2], [1]*PEI Marine Sciences Organization, Charlottetown, PE, Canada*, [2]*Atlantic Aqua Farms, Charlottetown, PE, Canada*.

P237 **Omics study for viral hemorrhagic septicemia virus resistance in *Paralichthys olivaceus*.**
J. Shin*[1], S. H. Lee[1], W. J. Kim[2], J.-W. Park[3], D.-I. Lee[3], H. S. Jung[3], and J. Kim[3], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*, [2]*East Sea Fisheries Research Institute, National Institute of Fisheries Science, Gangneung, Korea*, [3]*Fish Genetics and Breeding Research Center, National Institute of Fisheries Science, Geoje, Korea*.

P238 **Influence of estimated breeding value for growth trait on spawning quality in gilthead seabream (*Sparus aurata*).**
C. Pérez-García*[1], Á. Lorenzo-Felipe[1], S. Ferosekhan[1], S. Leon-Bernabeu[1,2], M. Izquierdo[1], R. Ginés[1], J. M. Afonso[1], H. S. Shin[1], and M. J. Zamorano[1], [1]*Universidad de Las Palmas de Gran Canaria (ULPGC), Instituto Universitario de Acuicultura Sostenible y Ecosistemas Marinos (IU-ECOAQUA), Grupo de Investigación en Acuicultura (GIA), Telde, Spain*, [2]*QUANARIA. C/ Prolongación Bentejui, San Bartolomé de Tirajana, Las Palmas, Spain*.

P239 **Genome editing to produce monosex and sterile fish for aquaculture.**
X. Lauth*[1], T. Umazume[1], S. Herbert[1], V. Williams[2], and J. Buchanan[1], [1]*Center for Aquaculture Technologies*, *San Diego, CA, USA*, [2]*The JEM Project*, *San Diego, CA, USA*.

Genetics of Immune Response and Disease Resistance

P240 **Genetic and epigenetic regulation of immune response and resistance to infectious diseases in domestic ruminants.**
I. Onjoko*, *Farming Experts Network*, *Abeokuta, Ogun, Nigeria*.

P241 **Whole blood transcriptome analysis in sheep affected with caseous lymphadenitis.**
J. Kyselová*[1], J. Marková[2], Z. Sztankóová[1], L. Tichý[1,3], M. Mušková[1], S. Šlosárková[2], and B. Bartošová[2], [1]*Intitute of Animal Science*, *Prague, Czech Republic*, [2]*Veterinary Research Institute*, *Brno, Czech Republic*, [3]*Czech University of Life Sciences*, *Prague, Czech Republic*.

P242 **The host genetic underlying pathological outcomes to *Mycobacterium avium* subsp. *paratuberculosis* infection is governed by distinct genetic variants.**
M. Alonso-Hearn*[1], M. Canive[1], G. Badia-Bringué[1], O. González-Recio[2,3], A. Fernández[2,3], P. Vázquez[1], J. Garrido[1], and R. Juste[1], [1]*NEIKER- Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, CSIC, Madrid, Spain*, [3]*Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid*, *Madrid, Spain*.

P243 **Novel insight into mechanism of lnc-FUT3as regulating *Escherichia coli* F18 bacterial diarrhea in weaned piglets.**
H. Fan*[1], Z. Wu[1], J. Jin[1], X. Xu[1], S. Gao[2], S. Wu[1,3], and W. Bao[1,3], [1]*College of Animal Science and Technology, Yangzhou University*, *Yangzhou, Jiangsu, China*, [2]*College of Veterinary Medicine, Yangzhou University*, *Yangzhou, Jiangsu, China*, [3]*Joint International Research Laboratory of Agriculture and Agri-Product Safety, Yangzhou University*, *Yangzhou, Jiangsu, China*.

P244 **Variation in circulatory serum biomarkers in dairy heifers exposed to endotoxin indicate disparity in induced physiological responses.**
A. Sharma*, T. Sullivan, K. Lamers, and N. Karrow, *Department of Animal Biosciences, University of Guelph*, *Guelph, ON, Canada*.

P245 **Differential expression of cow immune response genes in blood in response to phytochemicals.**
B. Mulakala[2], M. Worku*[1], and H. Ismail[1], [1]*North Carolina A&T State University*, *Greensboro, NC, USA*, [2]*University of Vermont*, *Vermont, VT, USA*.

P246 **Identification of loci associated with susceptibility to paratuberculosis in Holstein cattle using combinations of diagnostic tests and imputed whole-genome sequence data.**
M. Canive*[1], G. Badia-Bringué[1], O. González-Recio[2,3], A. Fernandez[2], P. Vázquez[1], J. Garrido[1], R. Juste[1], and M. Alonso-Hearn[1], [1]*Department of Animal Health, NEIKER-Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, CSIC, Madrid, Spain*, *3Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid*, *Madrid, Spain*.

P247 **Systemic transcriptomic response of sheep and cattle to acute and chronic *Fasciola hepatica* infection.**
D. A. Niedziela*[1], A. Naranjo-Lucena[1], V. Molina-Hernández[2], J. A. Browne[3], Á. Martínez-Moreno[4], J. Pérez[2], D. E. MacHugh[3,5], and G. Mulcahy[1,5], [1]*UCD School of Veterinary Medicine, University College Dublin, Dublin, Ireland*, [2]*Department of Anatomy and Comparative Pathology and Toxicology, Faculty of Veterinary Medicine, University of Córdoba, Córdoba, Spain*, [3]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, Dublin, Ireland*, [4]*Parasitology section, Department of Animal Health, Faculty of Veterinary Medicine, University of Córdoba, Córdoba, Spain*, [5]*UCD Conway Institute of Biomolecular and Biomedical Research*, *Dublin, Ireland*.

P248 **Alternative splicing modulates the immune response in peripheral blood and gut tissues of Holstein cattle naturally infected with *Mycobacterium avium* subsp. *paratuberculosis*.**
G. Badia-Bringué*[1], M. Canive[1], J. Lavín[2], R. Casais[3], C. Blanco-Vázquez[3], and M. Alonso-Hearn[1], [1]*Department of Animal Health, NEIKER-Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [2]*Department of Applied Mathematics, NEIKER-Basque Institute for Agricultural Research and Development, Basque Research and Technology Alliance (BRTA), Derio, Bizkaia, Spain*, [3]*SERIDA, Servicio Regional de Investigación y Desarrollo Agroalimentario, Center of Animal Biotechnology, Deva, Asturias, Spain*.

P249 **Functional and population genomics of admixed trypanotolerant African cattle breeds.**
G. P. McHugo*[1], J. A. Ward[1], T. J. Hall[1], G. M. O'Gorman[2], E. W. Hill[1], and D. E. MacHugh[1,3], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*National Office of Animal Health Ltd, Enfield, UK*, [3]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*.

P250 **Integrative and comparative genomic analyses of mammalian macrophage responses to intracellular mycobacterial pathogens.**
T. J. Hall*[1], G. P. McHugo[1], M. P. Mullen[2], J. A. Ward[1], K. E. Killick[1,7], S. C. Ring[3], D. P. Berry[4], J. A. Browne[1], S. V. Gordon[5,6], and D. E. MacHugh[1,6], [1]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, Belfield, Dublin, Ireland*, [2]*Bioscience Research Institute, Athlone Institute of Technology, Athlone, Westmeath, Ireland*, [3]*Irish Cattle Breeding Federation, Bandon, Cork, Ireland*, [4]*Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Cork, Ireland*, [5]*UCD School of Veterinary Medicine, Belfield, Dublin, Ireland*, [6]*UCD Conway Institute of Biomolecular and Biomedical Research, Belfield, Dublin, Ireland*, [7]*Genuity Science, Loughlinstown, Dublin, Ireland*.

P251 **Molecular characterization of the serum amyloid A (SAA) mutation R90S in chicken hepatocellular carcinoma (LMH) cells.**
C. Falker-Gieske*[1], N. Paul[1], J. Gilthorpe[2], K. Gustmann[1], and J. Tetens[1], [1]*Department of Animal Sciences, Georg-August-University, Göttingen, Germany*, [2]*Department of Integrative Medical Biology, Umeå University, Umeå, Sweden*.

P252 **Whole-genome screening for resilience against porcine reproductive and respiratory syndrome virus outbreaks in breeding sows.**
M. Laplana, R. Ros-Freixedes, J. Estany, L. Fraile, and R. Pena*, *Departament de Ciència Animal, Universitat de Lleida – AGROTECNIO-CERCA Centre, Lleida, Spain*.

P253 **The natural cytotoxicity receptor (NCR) genes in the family Felidae.**
J. Bubenikova[1,2], J. Futas[1,2], J. Oppelt[2], M. Plasil[2], R. Vodicka[3], and P. Horin*[1,2], [1]*Department of Animal Genetics, University of Veterinary Sciences, Brno, Czech Republic*, [2]*Ceitec VETUNI, University of Veterinary Sciences, Brno, Czech Republic*, [3]*Zoo Prague, Prague, Czech Republic*.

P254 ***DEL-1* gene is associated with increased weaning fecal egg counts in Katahdin sheep.**
G. Becker*[1], J. Burke[2], R. Lewis[3], J. Miller[4], J. Morgan[5], D. Notter[6], and B. Murdoch[1], [1]*Department of Animal, Veterinary and Food Sciences, University of Idaho, Moscow, ID, USA*, [2]*USDA, ARS, Dale Bumpers Small Farms Research Center, Booneville, AR, USA*, [3]*Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE, USA*, [4]*Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, Baton Rouge, LA, USA*, [5]*Round Mountain Consulting, Fayetteville, AR, USA*, [6]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA, USA*.

P255 **Genome-wide association study of thyroid hormone suppression following challenge with porcine reproductive and respiratory syndrome virus.**
A. Van Goor[1], A. Pasternak[2], M. Walugembe[3], N. Chehab[1], G. Hamonic[4], J. Dekkers[3], J. Harding*[4], and J. Lunney[1], [1]*USDA ARS BARC Animal Parasitic Diseases Laboratory, Beltsville, MD, USA*, [2]*Department of Animal Science, Purdue Univ, West Lafayette, IN, USA*, [3]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [4]*Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada*.

P256 **Exploration of glucocorticoid and inflammatory responses in porcine PBMC to reveal mechanisms underlying the enhanced endotoxin sensitivity of $\text{GR}_{\text{Ala610Val}}$ pigs.**
E. Murani*, Z. Li, F. Hadlich, N. Trakooljul, S. Ponsuksili, and K. Wimmers, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

P257 **Integrated network based on mRNAs and long noncoding RNAs of porcine reproductive and respiratory syndrome virus-infected multiple tissues revealed the early host responses.**
B. Lim* and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea*.

P258 **Ovine mastitis: Does early life nutrition influence immunity response in later life?**
C. Hervás-Rivero, R. Pelayo, B. Gutiérrez-Gil, C. Esteban-Blanco, H. Marina, J. Arranz, and A. Suárez-Vega*, *Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, Castilla y León, Spain*.

P259 **Association of variants in innate immune genes TLR^4 and TLR^5 with reproductive and milk utility traits in Czech Simmental cattle.**
K. Novák*[1], K. Samaké[2], T. Valcíková[3], and M. Bjelka[4], [1]*Institute of Animal Science, Prague-Uhríneves, Czech Republic*, [2]*Charles University, Prague, Czech Republic*, [3]*Czech University of Life Sciences, Prague, Czech Republic*, [4]*Breeding Company CHD Impuls, Bohdalec, Czech Republic*.

P260 **Bimodal haplotype distribution in bovine antibacterial toll-like receptors.**
K. Samaké*[1] and K. Novák[2], [1]*Charles University, Prague, Czech Republic*, [2]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*.

P261 **Breed-associated risk for developing clinical leishmaniasis in dogs: Preliminary results.**
C. Sanz*, J. Sarquis, J. Martínez, and G. Miró, *Animal Health Department, Veterinary Faculty, Complutense University of Madrid, Madrid, Spain*.

P262 **Identification of and validation of loci associated with facial eczema tolerance in New Zealand sheep.**
K. M. McRae*, S. J. Rowe, P. L. Johnson, and S. M. Clarke, *AgResearch Limited, Mosgiel, New Zealand*.

P263 **Transcriptomic analysis of host resistance to tick infestation with *Rhipicephalus microplus* in leukocytes of Brangus cattle.**
E. Mantilla Valdivieso*[1], E. Ross[1], A. Raza[1], B. Hayes[1], N. Jonsson[2], P. James[1], and A. Tabor[1], [1]*Queensland Alliance for Agriculture and Food Innovation, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Queensland, Australia*, [2]*Institute of Biodiversity Animal Health and Comparative Medicine, Institute of Biodiversity Animal Health and Comparative Medicine, Glasgow, UK*.

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P264 **Study on genetic distance according to Mongolian breeds through microsatellite markers analysis.**
J. An*[1], T. Khaliunaa[1], O. Baatartsogt[2], J. Yun[1], G. H. Lee[3], Y. H. Lee[1], J. Seong[4], and H. S. Kong[4], [1]*Major in Applied Biotechnology, The Graduate School of Hankyong National University, Anseong, Korea*, [2]*Department of Biotechnology, Mongolian University of Life Sciences, Ulaanbaatar, Mongolia*, [3]*Department of Animal Life and Environment Science, The Graduate School of Hankyong National University, Anseong, Korea*, [4]*Gyeonggi Regional Research Center, Hankyong National University, Anseong, Korea*.

P265 **Rare and common variant discovery by whole-genome sequencing of 101 Thoroughbred racehorses.**
T. Tozaki*, A. Ohnuma, M. Kikuchi, T. Ishige, H. Kakoi, K.-I. Hirora, and S.-I. Nagata, *Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*.

P266 **Improving the horse Y chromosome reference one step at a time.**
C. Castañeda*, B. Davis, A. Hillhouse, M. Jevit, and T. Raudsepp, *Texas A&M University, College Station, TX, USA*.

P267 **Identification of putative lethal variants using whole-genome sequence data from various horse breeds.**
P. Reich*, C. Falker-Gieske, and J. Tetens, *Department of Animal Sciences, Georg-August-University Göttingen, Göttingen, Germany*.

P268 **Genomic data reveals a serious underestimation of pedigree inbreeding levels in Polo Argentino horses.**
F. Azcona*[1], A. Molina[3], P. Peral-García[1], and S. Demyda-Peyrás[2,4], [1]*IGEVET-CONICET-UNLP, La Plata, La Plata, Buenos Aires, Argentina*, [2]*Departamento de Producción Animal, Facultad de Veterinaria, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, España*, [4]*CONICET-CCT La Plata, La Plata, Buenos Aires, Argentina*.

P269 **Genomic improvement of the horse X chromosome and characterization of the pseudoautosomal boundary.**
M. Jevit*[1], B. Davis[1], C. Casanteda[1], D. Miller[2], and T. Raudsepp[1], [1]*Department of Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [2]*Cornell University, Ithaca, NY, USA*.

P270 **Gene expression of chondrogenic markers to assess the differentiation of equine mesenchymal stem cells in different 3D systems.**
A. Cequier[1], A. Romero[1,2], A. Vitoria[1,2], F. Vázquez[1,2], P. Zaragoza[1], C. Rodellar[1], and L. Barrachina*[1,2], [1]*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza), Instituto Agroalimentario de Aragón– IA, Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

P271 **Genetic variability of 2 native Sardinian horse populations analyzed by microsatellite markers.**
M. C. Cozzi*, P. Valiati, and M. Longeri, *Università degli Studi di Milano, Dipartimento di Medicina Veterinaria, Lodi, Italy*.

P272 **Genetic diversity and phylogenetic relationships among the show Arabian horse populations of special interest to the breeder community.**
M. Machmoum*[1], D. Petit[2], B. Badaoui[3], I. Boujenane[4], and M. Piro[1], [1]*Veterinary Genetic Laboratory, Department of Medicine, Surgery and Reproduction, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco*, [2]*Laboratoire Peirene, EA, Limoges, France*, [3]*Biodiversity, Ecology and Genome Laboratory, Department of Biology, Mohammed V University, Faculty of Science, Rabat, Morocco*, [4]*Department of Animal Production and Biotechnology, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco*.

P273 **Quantitative trait loci associated with alternative gaits in Colombian Paso horses.**
M. Novoa-Bravo*[1,3], F. Serra-Bragança[2], R. Naboulsi[3], M. Sole[3], M. Rhodin[4], and G. Lindgren[3], [1]*Genética Animal de Colombia SAS, Bogotá, Colombia*, [2]*Department of Clinical Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands*, [3]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*, [4]*Department of Anatomy, Physiology and Biochemistry, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

P274 **Transcriptomic markers of recombinant erythropoietin micro-dosing in Thoroughbred racehorses.**
A. Dahlgren*, H. Knych, and C. Finno, *School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*.

P275 **Integration of long-read sequencing technology improves transcriptome annotation of the equine genome.**
S. Peng*[1], T. S. Kalbfleisch[2], R. Bellone[1,3], J. L. Petersen[4], and C. J. Finno[1], [1]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [2]*Department of Veterinary Science, Gluck Equine Research Center, University of Kentucky, Lexington, KY, USA*, [3]*Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California–Davis, Davis, CA, USA*, [4]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA*.

P276 **Assessment of genetic diversity using microsatellite markers to compare donkeys (*Equus asinus*) with horse (*Equus caballus*).**
S. Y. Lee[1] and G. J. Cho*[2], [1]*Racing Laboratory, Korea Racing Authority, Gwacheon, Korea*, [2]*College of Veterinary Medicine and Institute of Equine Medicine, Kyungpook National University, Daegu, Korea*.

P277 **Genetic structure of maternal lines in Przewalski horses based on mtDNA variation.**
A. D. Musial*[1], K. Ropka-Molik[1], M. Stefaniuk-Szmukier[2], G. Mycka[2], A. Fornal[1], and N. Yasynetska[3], [1]*National Research Institute of Animal Production, Balice, Poland*, [2]*University of Agriculture, Krakow, Poland*, [3]*Biosphere Reserve, Askania-Nova, Ukraine*.

P278 **Will selection for elasticity maintain the allele causing fragile foals?**
M. Ablondi*[1,2], M. Johnsson[2], S. Eriksson[2], A. Sabbioni[1], Å. Viklund[2], and S. Mikko[2], [1]*Department of Veterinary, Università degli Studi di Parma Science, Parma, Italy*, [2]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

P279 **Towards a comprehensive horse Y-chromosomal tree: Signatures from local breeds and ancient DNA.**
E. Bozlak*[1,2], L. Radovic[1,2], D. Rigler[2], T. Kunieda[3], R. Juras[4], G. Cothran[4], and B. Wallner[2], [1]*Vienna Graduate School of Population Genetics, Vienna, Austria*, [2]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [3]*Faculty of Veterinary Medicine, Okayama University of Science, Imabari, Japan*, [4]*Department of Integrative Biosciences, College of Veterinary and Biomedical Sciences, Texas A&M University, College Station, TX, USA*.

P280 **Transcriptomic and proteomic profiling of gluteal muscle of Standardbred horses between episodes of recurrent exertional rhabdomyolysis.**
D. Velez-Irizarry*[1], Z. Williams[1], M. Henry[1], H. Iglewski[1], K. Herrick[1], C. Fenger[2], and S. Valberg[1], [1]*Mary Anne MacPhail Equine Performance Center, Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA*, [2]*Equine Integrated Medicine PLC, Lexington, KY, USA*.

P282 **Epigenetic characterization of horse centromeric domains in different tissues and individuals.**
E. Cappelletti*[1], F. M. Piras[1], R. Hijaz[1], L. Sola[1], J. L. Petersen[2], R. R. Bellone[3,4], C. J. Finno[3], T. S. Kalbfleisch[5], E. Bailey[5], S. G. Nergadze[1], and E. Giulotto[1], [1]*Department of Biology and Biotechnology, University of Pavia, Pavia, Italy*, [2]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA*, [3]*University of California–Davis, School of Veterinary Medicine, Department of Population Health and Reproduction, Davis, CA, USA*, [4]*University of California–Davis, School of Veterinary Medicine, Veterinary Genetics Laboratory, Davis, CA, USA*, [5]*University of Kentucky, Gluck Equine Research Center, Lexington, KY, USA*.

P283 **Satellite-less centromeres formation by centric fusion in equids.**
F. M. Piras*, E. Cappelletti, W. A. A. Ahmed, E. Raimondi, S. G. Nergadze, and E. Giulotto, *Department of Biology and Biotechnology, University of Pavia, Pavia, Italy*.

P284 **Transcriptome analysis of 8 priority tissues in 2 Thoroughbred stallions for the Functional Annotation of Animal Genomes project.**
A. Barber*[1], S. Peng[2], A. Fuller[1], E. Giulotto[3], T. Kalbfleisch[4], C. Finno[2], R. Bellone[2], and J. Petersen[1], [1]*University of Nebraska–Lincoln, Lincoln, NE, USA*, [2]*University of California–Davis, Davis, CA, USA*, [3]*University of Pavia, Pavia, Italy*, [4]*University of Kentucky, Lexington, KY, USA*.

P285 **Debunking the genetic origins of the Mangalarga through Turbante J.O.**
L. Patterson Rosa*[1], F. Araujo[1], M. Vierra[1], S. Brooks[2], and C. Lafayette[1], [1]*Etalon Inc, Menlo Park, CA, USA*, [2]*University of Florida, Gainesville, FL, USA*.

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P286 **Demographic history and genetic diversity of wild African harlequin quail (*Coturnix delegorguei*) populations of Kenya.**
S. Ogada[1], N. Otecko[2], G. Kennedy[1], J. Musina[3], B. Agwanda[3], V. Obanda[4], J. Lichoti[5], M.-S. Peng[2], Y.-P. Zhang[2], and S. Ommeh*[1], [1]*Institute For Biotechnology Research (IBR), Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi, Kenya*, [2]*State Key Laboratory of Genetic Resources and Evolution, Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Germplasm Bank of Wild Species, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [3]*Department of Zoology, National Museums of Kenya, Nairobi, Kenya*, [4]*Department of Veterinary Services, Kenya Wildlife Service, Nairobi, Kenya*, [5]*State Department of Livestock, Ministry of Agriculture, Livestock, Fisheries and Irrigation, Nairobi, Kenya*.

P287 **Donkey worldwide diversity based on control-region data and entire mitochondrial genomes.**
D. Bigi[1], N. Rambaldi Migliore[2], M. Milanesi[3,4], P. Zambonelli[1], R. Negrini[3], A. Verini-Supplizi[5], L. Liotta[6], F. Chegdani[7], S. Agha[8], A. Torroni[2], P. Ajmone-Marsan[3,9], A. Achilli[2], and L. Colli*[3,10], [1]*Dipartimento di Scienze e Tecnologie Agro-Alimentari (DISTAL), Alma Mater Studiorum University of Bologna, Bologna, BO, Italy*, [2]*Dipartimento di Biologia e Biotecnologie "Lazzaro Spallanzani," University of Pavia, Pavia, PV, Italy*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti (DIANA), Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [4]*Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo, VT, Italy*, [5]*Dipartimento di Medicina Veterinaria, University of Perugia, Perugia, PG, Italy*, [6]*Dipartimento di Scienze Veterinarie, University of Messina, Messina, ME, Italy*, [7]*Department of Biology, Faculty of Sciences Aïn Chock, University Hassan II, Casablanca, Morocco*, [8]*Animal Production Department, Faculty of Agriculture, Ain Shams University, Cairo, Egypt*, [9]*PRONUTRIGEN Centro Ricerca Nutrigenomica e proteomica, Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [10]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del S. Cuore, Piacenza, PC, Italy*.

P288 **Historical biogeography of Philippine native pigs and the perplexing mitochondrial DNA variation in Philippine wild pigs.**
J. Layos*[1,2], C. Godinez[1,3], L. Liao[4], Y. Yamamoto[1], and M. Nishibori[1], [1]*Laboratory of Animal Genetics, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*, [2]*College of Agriculture and Forestry, Capiz State University, Capiz, Philippines*, [3]*Department of Animal Science, Visayas State University, Leyte, Philippines*, [4]*Laboratory of Aquatic Ecology, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*.

P289 **Reassessing phylogeny and Bayesian divergence dating provide new insights on the evolutionary history of chickens in Southeast Asia.**
C. J. P. Godinez*[1,2], J. K. N. Layos[1,3], Y. Yamamoto[1], L. M. Liao[4], M. Duangjinda[5], and M. Nishibori[1,2], [1]*Laboratory of Animal Genetics, Hiroshima University, Higashi-Hiroshima, Japan*, [2]*Visayas State University, Leyte, Philippines*, [3]*Capiz State University, Capiz, Philippines*, [4]*Laboratory of Aquatic Ecology, Hiroshima University, Higashi-Hiroshima, Japan*, [5]*Khon Kaen University, Khon Kaen, Thailand*.

P290 **Genetic diversity and runs of homozygosity in Rendena cattle.**
E. Somenzi*[1], N. Franceschi[1], M. Barbato[1], L. Colli[1], E. Partel[2], M. Komjanch[2], A. Achilli[3], H. C. Hauffe[2], and P. Ajmone Marsan[1], [1]*Università Cattolica del Sacro Cuore, Piacenza, Italy*, [2]*Edmund Mach Foundation, San Michelle all'Adige, Trento, Italy*, [3]*Pavia University, Pavia, Italy*.

P291 **Genetic relationships among Canarian, African, and European goats using SNPs.**
M. Macri*[1,2], A. Martínez[2], M. G. Luigi[3], J. Capote[4], A. Canales[1,2], M. Amills[3], J. V. Delgado[2], and M. R. Fresno[4], [1]*Animal Breeding Consulting, S.L, Cordoba, Cordoba, Spain*, [2]*Department of Genetics, University of Córdoba, Cordoba, Cordoba, Spain*, [3]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, University of Barcelona, Bellaterra, Barcelona, Spain*, [4]*ICIA, Canary Islands Institute for Agricultural Research, San Cristóbal de La Laguna, Santa Cruz de Tenerife, Spain*.

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P292 **Genetic basis of thermotolerance in African indigenous chickens.**
A. A. Gheyas*[1], M. Rachman[2], A. Vallejo-Trujillo[2], O. Bamidele[3,4], A. Kebede[3,5], T. Dessie[3], J. Smith[1], and O. Hanotte[2,3], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Midlothian, Scotland, UK*, [2]*School of Life Sciences, University of Nottingham, Nottingham, UK*, [3]*LiveGene – CTLGH, International Livestock Research Institute, Addis Ababa, Ethiopia*, [4]*Kings University, Ode Omu, Nigeria*, [5]*Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia*.

P293 **A within- and across-country assessment of the genomic diversity and autozygosity in South African and Eswatini Nguni cattle.**
S. Lashmar[1], C. Visser*[1], M. Okpeku[2], N. Mapholi[3], and E. Van Marle-Köster[1], [1]*University of Pretoria, Pretoria, South Africa*, [2]*University of KwaZulu-Natal, Durban, South Africa*, [3]*University of South Africa, Pretoria, South Africa*.

P294 **Signatures of selection in South African Nguni and Bonsmara cattle breeds.**
B. Bhika Kooverjee*[1,2], P. Soma[1], M. A. van der Nest[3], F. W. C. Neser[2], M. M. Scholtz[1], and M. D. MacNeil[4], [1]*Agricultural Research Council-Animal Production, Irene, South Africa*, [2]*Department of Animal, Wildlife, and Grassland Sciences, University of Free State - Bloemfontein, South Africa*, [3]*Agricultural Research Council-Biotechnology Platform, Onderstepoort, South Africa*, [4]*Delta G, Miles City, MT, USA*.

P295 **Whole-genome sequence analysis to detect potential candidate genes for reproduction in South African beef cattle.**
K. Nxumalo*[1,2], M. B. Malima[1], J. Grobler[2], M. Makgahlela[1,3], J. Kantanen[4], C. Ginja[5], D. R. Kugonza[6], N. Mohamed[7], R. P. M. A. Crooijmans[8], and A. A. Zwane[1], [1]*Animal Breeding and Genetics, Agricultural Research Council-Animal Production, Pretoria, South Africa*, [2]*Department of Genetics, University of the Free State, Bloemfontein, Free State, Bloemfontein, South Africa*, [3]*Department of Animal, Wildlife and Grassland Sciences, University of Free State, Bloemfontein, Bloemfontein, South Africa*, [4]*Animal Production Research, Agricultural Research Centre (MTT), Jokioinen, Finland*, [5]*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*, [6]*Department of Agricultural Production, School of Agricultural Sciences, College of Agricultural and Environmental Sciences, Makerere University, Kampala, Uganda*, [7]*Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt*, [8]*Animal Breeding and Genomics Group, Wageningen University and Research, Wageningen, the Netherlands*.

P296 **Genetics of base coat color variations and coat color patterns of the South African Nguni cattle investigated using high-density SNP genotypes.**
L. Kunene*[1], F. Muchadeyi[2], K. Hadebe[2], G. Mészáros[3], J. Sölkner[3], and E. Dzomba[1], [1]*University of KwaZulu-Natal, Scottsville, South Africa*, [2]*Agricultural Research Council, Onderstepoort, South Africa*, [3]*University of Natural Resources and Life Sciences, Vienna, Austria*.

P297 **Copy number variations and their association with coat color phenotypes in South African Nguni cattle.**
N. M. Dlamini*[1,2], E. F. Dzomba[2], and F. C. Muchadeyi[1], [1]*Biotechnology Platform, Agricultural Research Council – Onderstepoort Veterinary Institute, Onderstepoort, Pretoria, South Africa*, [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa*.

P298 **Population structure, inbreeding and admixture for indigenous goats within a pilot community-based breeding program in Pella, North West, South Africa.**
T. Mtshali*[1,3], F. Muchadeyi[2], O. Mapholi[3], E. Dzomba[4], and K. Hadebe[2], [1]*Agricultural Research Council, Vegetable and Ornamental Plants, Pretoria, South Africa*, [2]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, South Africa*, [3]*University of South Africa, Florida, Johannesburg, South Africa*, [4]*University of KwaZulu-Natal, Scottsville, Pietermaritzburg, South Africa*.

P299 **Correlation between resilience and tolerance in Angus females exposed to *Rhipicephalus* (*Boophilus*) *microplus*.**
C. D. S. Arce*[1], F. R. Araújo Neto[2], A. M. Maiorano[1], L. G. Albuquerque[1], and H. N. Oliveira[1], [1]*Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, Sao Paulo, Brazil*, [2]*Instituto Federal Goiano, Rio Verde, Goias, Brazil*.

P300 **Candidate positive signature of selection and environmental adaptation in indigenous African cattle: A review.**
S. Kambal*[1,2], A. Tijjani[3], and O. Hanotte[3,4], [1]*National University Biomedical Research Institute, National University, Sudan*, [2]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [3]*LiveGene – CTLGH, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [4]*School of Life Sciences, University of Nottingham, Nottingham, UK*.

Microbiomes

P301 **The effect of a total fishmeal replacement by *Athrospira platensis* on the microbiome of African catfish (*Clarias gariepinus*).**
S. Rosenau*[1], E. Oertel[1], A. C. Mott[1], and J. Tetens[1,2], [1]*Department of Animal Science, Goettingen, Germany*, [2]*Center of Integrated Breeding Research, Goettingen, Germany*.

P302 **Response to selection on fecal microbiota composition in Large White piglets.**
C. Larzul*[1], M. Borey[2], Y. Billon[3], M.-N. Rossignol[2], G. Lemonnier[2], J. Estelle[2], and C. Rogel-Gaillard[2], [1]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*INRAE, GenESI, Surgères, France*.

P303 **The impact of host genetics, independently of environmental factors, on porcine gut microbiota composition.**
A. Heras-Molina*[1], J. Estellé[2], A. López-García[1], J. L. Pensantez-Pacheco[1,3], S. Astiz[1], C. Garcia-Contreras[1], M. Vazquez-Gomez[4,5], B. Isabel[4], A. Gonzalez-Bulnes[6], and C. Ovilo[1], [1]*INIA (CSIC), Madrid, Spain*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*School of Veterinary Medicine and Zootechnics, Faculty of Agricultural Sciences, University of Cuenca, Cuenca, Ecuador*, [4]*Faculty of Veterinary Medicine, UCM, Madrid, Spain*, [5]*Nutrition and Obesities: Systemic Approaches Research Unit (NutriOmics), INSERM, Sorbonne Université, Paris, France*, [6]*Departamento de Producción y Sanidad Animal, Facultad de Veterinaria, Universidad Cardenal Herrera-CEU, Valencia, Spain*.

P304 **Assessment of the fecal microbiota from sow to piglet and the impact of different ratios of dietary polyunsaturated fatty acids.**
M. Cau*[1,2], A. Agazzi[3], T. X. Nguyen[3], M. McLaughlin[2], and A. S. Bonastre[1], [1]*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain*, [2]*College of Medical, Veterinary and Life Sciences, School of Veterinary Medicine, University of Glasgow, Glasgow, UK*, [3]*Department of Health, Animal Science and Food Safety "Carlo Cantoni" (VESPA), Universitá degli Studi di Milano, Lodi, Italy*.

P305 **Mapping the livestock microbiome.**
M. Watson*, L. Glendinning, A. Warr, and J. Mattock, *The Roslin Institute, Edinburgh, UK*.

P306 **Cecal microbiota composition of experimental laying hens infected with infectious bronchitis virus differs according to genetics and vaccination.**
M. Borey*[1], B. Bed'Hom[1,2], N. Bruneau[1], J. Estellé[1], F. Larsen[3], F. Blanc[1], M.-H. Pinard-van der Laan[1], T. Dalgaard[3], and F. Calenge[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, UMR GABI, Jouy-en-Josas, France*, [2]*Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France*, [3]*Aarhus University, Department of Animal Science, Tjele, Denmark*.

P307 **Microbiota characterization of traditional cattle breeds.**
R. Gonzalez-Prendes[1], R. Gomez Exposito[2], T. Reilas[3], M. Makgahlela[4], J. Kananen[3], C. Ginja[5], D. Kugonza[6], N. Ghanem[7], H. Smidt[2], and R. Crooijmans*[1], [1]*Animal Breeding and Genomics Group, Wageningen University and Research, Wageningen, the Netherlands*, [2]*Micriobiology group, Wageningen University and Research, Wageningen, Wageningen, the Netherlands*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*, [4]*Agricultural Research Council-Animal Production Institute, Pretoria, South Africa*, [5]*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*, [6]*Department of Agricultural Production, School of Agricultural Sciences, College of Agricultural and Environmental Sciences, Makerere University, Kampala, Uganda*, [7]*Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt*.

P308 **Characterization of cecum microbiome between Silky Fowl and White Leghorns in the late laying period.**
X. Yang*, Y. Tai, Y. Ma, and X. Deng, *Laboratory of Animal Genetic Resources and Molecular Breeding, China Agricultural University, Beijing, China*.

P309 **Rumen eukaryotes are the main risk factors for larger methane emissions in dairy cattle.**
A. Saborío-Montero*[1,2], M. Gutiérrez-Rivas[1], R. Atxaerandio[3], A. García-Rodríguez[3], I. Goiri[3], J. López-Paredes[4], J. A. Jiménez-Montero[4], and O. González-Recio[1,5], [1]*Departamento de Mejora Genética Animal, Instituto Nacional de Tecnología Agraria y Alimentaria, Madrid, Spain*, [2]*Centro de Investigación en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San Pedro, San José, Costa Rica*, [3]*Department of Animal Production NEIKER-Basque Institute for Agricultural Research and Development, Basque Research and Technology Alliance (BRTA), Campus Agroalimentario de Arkaute s/n, País Vasco, Spain*, [4]*Departamento Técnico de Confederación de Asociaciones de Frisona Española (CONAFE), Valdemoro, Madrid, Spain*, [5]*Departamento de Producción Agraria, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, Madrid, Spain*.

P310 **Could the gut microbiome modulate environmental variance and animal resilience?**
C. Casto-Rebollo*[1], M. Argente[2], M. García[2], A. Blasco[1], and N. Ibáñez-Escriche[1], [1]*Institute for Animal Science and Technology, Universitat Politècnica de València, València, Spain*, [2]*Departamento de Tecnología Agroalimentaria, Universidad Miguel Hernández de Elche, Orihuela, Spain*.

P311 **The potential of using rumen microbial profiles for the prediction of enteric methane emissions traits for commercial livestock breeding.**
T. Bilton*[1], M. Bastiaanse[1], M. Hess[1], J. Budel[2], G. Noronha[2], H. Henry[1], S. Hickey[3], G. Pile[1], P. Janssen[4], J. McEwan[1], and S. Rowe[1], [1]*AgResearch*, *Mosgiel, New Zealand*, [2]*Universidade Federal do Pará (UFPa)*, *Belém Do Pará, Brazil*, [3]*AgResearch*, *Ruakura, New Zealand*, [4]*AgResearch*, *Palmerston North, New Zealand*.

P312 **Overcoming host contamination in bovine vaginal metagenomics studies with efficient host depletion, extraction and sequencing methods.**
C. Ong*[1], C. Turni[1], P. Blackall[1], G. Boe-Hansen[2], E. Ross[1], B. Hayes[1], and A. Tabor[1,3], [1]*The University of Queensland, Centre of Animal Science, Queensland Alliance for Agriculture and Food Innovation*, *Brisbane, Queensland, Australia*, [2]*The University of Queensland, School of Veterinary Science*, *Brisbane, Queensland, Australia*, [3]*The University of Queensland, School of Chemistry and Molecular Biosciences*, *Brisbane, Queensland, Australia*.

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P313 **Global analysis of the association between pig muscle fatty acid composition and gene expression using RNA-seq.**
J. Valdés-Hernández*[1,2], L. Criado-Mesas[1], Y. Ramayo-Caldas[3], A. Castelló[1], M. Passols[1], A. Sanchez[1,2], and J. M. Folch[1,2], [1]*Centre for research in agricultural Genomics (CRAG), Plant and Animal Genomics, CSIC-IRTA-UAB-UB Consortium, UAB Campus*, *Bellaterra, Spain*, [2]*Autonomous University of Barcelona (UAB), Department of Animal and Food Science, Faculty of Veterinary Medicine*, *Bellaterra, Spain*, [3]*Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Departament de Genètica i Millora Animal, Torre Marimon*, *Caldes de Montbui, Barcelona, Spain*.

P314 **Genetic analysis of protein efficiency in Swiss Large White pigs.**
E. O. Ewaoluwagbemiga*[1,3], G. Bee[2], H. Pausch[3], and C. Kasper[2], [1]*Animal GenoPhenomics Group, Agroscope*, *Posieux, Switzerland*, [2]*Swine Research Unit*, *Posieux, Switzerland*, [3]*Animal Genomics, ETH Zurich*, *Lindau, Zurich, Switzerland*.

P315 **An exon-intron split framework to prioritize miRNA-driven regulatory signals and its application to study energy homeostasis in pigs.**
E. Mármol-Sánchez*[1], S. Cirera[2], M. J. Jacobsen[2], Y. Ramayo-Caldas[3], C. B. Jørgensen[2], M. Fredholm[2], and M. Amills[1,4], [1]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen*, *Copenhagen, Denmark*, [3]*Animal Breeding and Genetics Program, IRTA, Torre Marimón*, *Caldes de Montbui, Barcelona, Spain*, [4]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*.

P316 **E2-ER system positive feedback induces *CYP19A1* expression to inhibit porcine granulosa cells apoptosis.**
Q. Li*, X. Du, Q. Zeng, L.-F. Wang, and Q.-F. Li, *Nanjing Agriculture University*, *Nanjing, China*.

P317 **A SYBR Green qPCR for evaluation of factors affecting porcine semen sex ratio.**
N. R. Sahoo*[1,2], A. Santhosh[1], V. Yadav[1],[3], M. V. Darji[1], N. Srivastava[1], P. Kumar[1], and G. K. Gaur[1], [1]*ICAR-Indian Veterinary Research Institute*, *Bareilly, Uttar Pradesh, India*, [2]*ICAR-DFMD-ICFMD*, *Bhubaneswar, Odisha, India*, [3]*ICAR-National Dairy Research Institute*, *Karnal, Haryana, India*.

P318 **Association of LEP and CTSF genotypes with levels of meat quality of Large White pig breed.**
V. Balatsky*, Y. Oliinychenko, K. Pochernyaev, A. Saienko, T. Buslyk, and I. Bankovska, *Institute of Pig Breeding and Agro-Industrial Production, National Academy of Agricultural Sciences of Ukraine*, *Poltava, Ukraine*.

P319 **The common warthog (*Phacochoerus africans*) reference genome and sequence variation.**
L. Eory[1], P. Wiener[1], H. A. Finlayson[1], K. Gharbi[2], S. Girling[3], C. Palgrave[1], E. Okoth[4], T. Burdon[1], M. Watson[1], and A. L. Archibald*[1], [1]*The Roslin Institute and R(D)SVS, University of Edinburgh*, *Midlothian, UK*, [2]*Edinburgh Genomics, University of Edinburgh*, *Edinburgh, UK*, [3]*The Royal Zoological Society of Scotland*, *Edinburgh, UK*, [4]*International Livestock Research Institute*, *Nairobi, Kenya*.

P320 **GBLUP-GWAS identifies candidate genes and polymorphisms for age at puberty in gilts.**
H. R. Wijesena*, D. J. Nonneman, W. M. Snelling, G. A. Rohrer, B. N. Keel, and C. A. Lents, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE, USA*.

P321 **A pangenome of commercial pig breeds.**
M. Derks*[1,3], B. Harlizius[2], M. van Son[2], M. Lopes[1], E. Grindflek[2], E. Knol[1], E. Sell-Kubiak[4], and A. Gjuvsland[2], [1]*Topigs Norsvin Research Center*, *Beuningen, the Netherlands*, [2]*Norsvin SA*, *Hamar, Norway*, [3]*Wageningen University and Research*, *Wageningen, the Netherlands*, [4]*Poznan University of Life Sciences*, *Poland*.

P322 **Density gradient centrifugation to purify ejaculated sperm has a mild but noticeable impact on the pig semen transcriptome.**
Y. Lian*[1], M. Gòdia[1], A. Castello[1,2], J. E. Rodriguez-Gil[3], S. Balasch[4], A. Sanchez[1,2], and A. Clop[1,5], [1]*Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Barcelona, Catalonia, Spain*, [2]*Unit of Animal Science, Department of Animal and Food Science, Autonomous University of Barcelona*, *Barcelona, Catalonia, Spain*, [3]*Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Autonomous University of Barcelona*, *Barcelona, Catalonia, Spain*, [4]*Grup Gepork S.A*, *Barcelona, Catalonia, Spain*, [5]*Consejo Superior de Investigaciones Científicas (CSIC)*, *Barcelona, Catalonia, Spain*.

P323 **Genomic variations of porcine cathelicidin PR-39 and determination of copy numbers using real-time PCR.**
B. Ahn, H. Jeon, M. T. Le, M. Kang, and C. Park*, *Department of Stem Cell and Regenerative Biotechnology, Konkuk University*, *Seoul, South Korea*.

P324 **Native pigs from Angola: Insights into their origins and unique genetic features.**
P. Sá[1], D. Santos[1], A. Leitão[1], J. M. M. Cordeiro[2], L. T. Gama[1], and A. J. Amaral*[1], [1]*CIISA - Centro de Investigação Interdisciplinar Em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa*, *Lisbon, Portugal*, [2]*Faculdade de Medicina Veterinária do Huambo*, *Huambo, Angola*.

P325 **TGFBR2 is a novel substrate and indirect transcription target of deubiquitylase USP9X in granulosa cells.**
L. Yang*, X. Du, and Q. Li, *Nanjing Agricultural University*, *Nanjing, JiangSu, China*.

P326 **Differentiating pigs from wild boars from Poland based on *NR6A1* and *MC1R* gene polymorphisms.**
A. Koseniuk*, G. Smolucha, M. Natonek-Wisniewska, A. Radko, and D. Rubis, *National Research Institute of Animal Production, Department of Animal Molecular Biology*, *Balice, Poland*.

P327 **The genomic inbreeding trends in Italian heavy pig breeds over the last 25 years.**
G. Schiavo*[1], S. Bovo[1], A. Ribani[1], S. Tinarelli[1,2], V. Utzeri[1], M. Cappelloni[2], M. Gallo[2], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna*, *Bologna, Italy*, [2]*Associazione Nazionale Allevatori Suini (ANAS)*, *Roma, Italy*.

P328 **Identifying muscle transcriptional regulatory elements in the pig genome.**
D. Crespo-Piazuelo*[1], O. González-Rodríguez[1], M. Mongellaz[2], H. Acloque[2], M.-J. Mercat[3], M. C. A. M. Bink[4], A. E. Huisman[5], Y. Ramayo-Caldas[1], J. P. Sánchez[1], and M. Ballester[1], [1]*Animal Breeding and Genetics Program, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain*, [2]*Institut national de recherche pour l'agriculture, l'alimentation et l'environnement (INRAE), Génétique animale et biologie intégrative (GABI), Jouy-en-Josas, France*, [3]*IFIP-Institut du porc and Alliance R&D, Le Rheu, France*, [4]*Hendrix Genetics Research Technology and Services B.V, Boxmeer, the Netherlands*, [5]*Hypor B.V, Boxmeer, the Netherlands*.

P329 **Characterization of circulating microRNAs profile in Iberian pigs with and without heat stress.**
M. Muñoz*[1], A. Fernández-Rodríguez[2], F. García[1], A. García-Cabrero[1], C. Caraballo[1,3], G. Gómez[4], G. Matos[4], C. Óvilo[1], and J. García-Casco[1,3], [1]*Animal Breeding Department, INIA (CSIC), Madrid, Spain*, [2]*Unit of Viral Infection and Immunity, National Center for Microbiology, Institute of Health Carlos III, Majadahonda (Madrid), Spain*, [3]*Centro de Investigación en cerdo Ibérico INIA-Zafra (INIA, CSIC), Zafra (Badajoz), Spain*, [4]*Sánchez Romero Carvajal—Jabugo, SRC, Huelva, Spain*.

P330 **Rate of rejection of first-degree relationships for assigning parent-offspring relationships and estimation of genotyping errors with an HD array in pigs.**
L. Gomez-Raya*[1], E. Gomez Izquierdo[2], E. de Mercado[1], and W. M. Rauw[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*ITACyL, Hontalbilla, Spain*.

P331 **SNP discovery and association study for growth and fatness traits in crossbred Iberian pigs.**
C. Ovilo*[1], N. Trakooljul[2], F. Hadlich[2], E. Murani[2], M. Ayuso[1], C. García-Contreras[1], M. Vázquez-Gomez[3], R. Benítez[1], Y. Núñez[1], A. Rey[3], A. González-Bulnes[1], B. Isabel[3], K. Wimmers[2], and M. Muñoz[1], [1]*INIA (CSIC), Madrid, Spain*, [2]*FBN, Dummerstorf, Germany*, [3]*UCM, Madrid, Spain*.

P332 **Transcriptomics integrated with metabolomics reveal the complex molecular regulatory network involved in meat quality in Enshi Black iigs.**
Y. Ma*, H. Zhan, S. Xie, X. Li, and S. Zhao, *Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of the Ministry of Education and Key Laboratory of Swine Genetics and Breeding of the Ministry of Agriculture, Huazhong Agricultural University*, *Wuhan, Hubei, China*.

P333 **MSTN regulates fat distribution in different pathways through GR.**
Y. Niu*, X. Wen, W. Lin, L. Zhang, and J. Chen, *College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, China*.

P334 **Alteration of expression of miRNA and mRNA transcripts in fetal muscle tissue in the context of sex, mother, and variable fetal weight.**
S. Ponsuksili*[1], A. Ali[1], F. Hadlich[1], E. Murani[1], and K. Wimmers[1,2], [1]*Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*.

P335 **Integrated transcriptomes and functional analyses in porcine oviductal tissue through porcine estrous cycle.**
M.-J. Jang*, C. Lim, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.

P336 **Time serial ovarian transcriptome analysis for entire porcine estrous cycle reveals changes of steroid metabolism and corpus luteum development.**
Y. Park*, Y.-B. Park, S.-W. Lim, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.

P337 **Overview of long noncoding RNA and mRNA annotation throughout swine estrous cycle in reproductive tissues.**
Y.-B. Park*, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.

P338 **Signature of stress-related characteristics according to changes in pig breeding condition through transcriptome analysis.**
S.-W. Lim*, B. Lim, and J.-M. Kim, *Functional Genomics and Bioinformatics Lab, Department of Animal Science and Technology, Chung-Ang University, Anseong, Republic of Korea*.

P339 **Muscle proteomics of preweaning piglets from sows fed diets with extreme ω-6/ω-3 fatty acid ratios.**
Y. Manaig*[1,3], A. Agazzi[3], S. Panseri[3], G. Tedeschi[3], J. Folch[1,2], A. Sanchez[1,2], and G. Savoini[3], [1]*Universitat Autònoma de Barcelona, Barcelona, Spain*, [2]*Centre for Research in Agricultural Genomics, Barcelona, Spain*, [3]*Università degli Studi di Milano, Milan, Italy*.

P340 **Structural genetic basis of differential gene expression in loin muscle of Iberian pigs.**
A. López-García*[1], R. Peiro[1], M. Muñoz[1], C. García-Contreras[1], M. Vázquez-Gómez[2], B. Isabel[3], A. Rey[3], A. González-Bulnes[1], and C. Óvilo[1], [1]*INIA (CSIC), Madrid, Spain*, [2]*INSERM (UPS), Paris, France*, [3]*UCM, Madrid, Spain*.

P341 ***AGPAT5* gene influences fat content and composition in pigs.**
E. Molinero*, R. N. Pena, J. Estany, and R. Ros-Freixedes, *Departamento de Ciencia Animal, Universidad de Lleida – AGROTECNIO-CERCA Center, Lleida, Spain*.

P342 **Functional variant identification of cis-eQTL associated with pig *NUDT7* gene and its association analysis with meat color traits.**
X. Xu*[1,2], L. Liu[1,2], L. Liu[1,2], T. Ma[1,2], Z. Zheng[1,2], and X. Xu[1,2], [1]*Huazhong Agricultural University, Huazhong Agricultural University, Wuhan, Hubei Province, China*, [2]*Key Lab of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei Province, China*.

P343 **Integration analysis of molecular phenotype QTLs speeds up the identification of functional mutations affecting pork quality.**
Y. Liu*[1,2], T. Ma[1,2], Z. Zheng[1,2], and X. Xu[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education and College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China*, [3]*Key Lab of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Wuhan, China*.

P344 **Genetic architecture underlying nascent speciation: The evolution of Eurasian pigs under domestication.**
H.-B. Xie*[1], L.-G. Wang[2], C.-Y. Fan[3], L.-C. Zhang[2], A. C. Adeola[1], X. Yin[3], Z.-B. Zeng[4], L.-X. Wang[2], and Y.-P. Zhang[1,5], [1]*State Key Laboratory of Genetic Resources and Evolution, Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [2]*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [3]*State Key Laboratory for Conservation and Utilization of Bio-resource in Yunnan, School of Life Science, Yunnan University, Kunming, China*, [4]*Bioinformatics Research Center, Department of Horticultural Science, North Carolina State University, Raleigh, NC, USA*, [5]*Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China*.

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P345 **Genetic and genomic factors influencing gestational length in beef cattle.**
H. Bolen* and M. Asai-Coakwell, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

P346 **Genomic regions of polygenic selection in Nelore cattle revealed by whole-genome sequencing.**
A. M. Maiorano*, C. D. S. Arce, W. B. Santos, F. C. Silvério, L. G. Albuquerque, and H. N. Oliveira, *Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, Sao Paulo, Brazil.*

P347 **The genetic complexity of scurs development in cattle.**
I. A. S. Randhawa*[1], R. E. Lyons[2,1], B. J. Hayes[3], and M. R. McGowan[1], [1]*The University of Queensland, Gatton, QLD, Australia*, [2]*Agri-Genetics Consulting, QLD, Australia*, [3]*Centre for Animal Science, Queensland Alliance for Agriculture and Food Innovation, University of Queensland, St Lucia, QLD, Australia.*

P348 **Genome-wide investigations reveal the population structure and selection signatures of Nigerian cattle adaptation in the sub-Saharan tropics.**
D. H. Mauki[1,3], A. Tijjani[4,5], C. Ma[1,3], S. I. Ng'ang'a[1,3], A. I. Mark[6], O. J. Sanke[7], A. M. Abdussamad[13], S. C. Olaogun[8], P. M. Dawuda[9], R. R. Kazwala[10], P. S. Gwakisa[11], Y. Li[12], M.-S. Peng[1,2], A. C. Adeola*[2,13], Y.-P. Zhang[1,14], [1]*State Key Laboratory of Genetic Resources and Evolution and Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [2]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, China, Kunming, China*, [3]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China*, [4]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [5]*Centre for Genomics Research and Innovation, National Biotechnology Development Agency, Kunming*, [6]*Ministry of Agriculture and Rural Development, Secretariat, Ibadan, Nigeria*, [7]*Taraba State Ministry of Agriculture and Natural Resources, Jalingo, Nigeria*, [8]*Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria*, [9]*Department of Veterinary Surgery and Theriogenology, College of Veterinary Medicine, University of Agriculture Makurdi, Makurdi, Nigeria*, [10]*Faculty of Veterinary Medicine, Sokoine University of Agriculture, Morogoro, Tanzania*, [11]*Sokoine University of Agriculture, Department of Microbiology, Parasitology and Biotechnology/ Genome Science Center, Morogoro, Tanzania*, [12]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, School of Life Sciences, Yunnan University, Kunming, China*, [13]*Centre for Biotechnology Research, Bayero University, Kano, Nigeria*, [14]*Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China.*

P349 **A comprehensive catalog of regulatory variants in the cattle transcriptome: A case study for the FarmGTEx Project.**
G. E. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD, USA.*

P350 **Confirmation of quantitative trait locus location on BTA19 for the percentage of oleic acid in beef based on effects of 5 polymorphisms and linkage disequilibrium analysis in 2 Japanese Black cattle populations.**
F. Kawaguchi*[1], F. Kakiuchi[1], K. Oyama[2], H. Mannen[1], and S. Sasazaki[1], [1]*Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Hyogo, Japan*, [2]*Food Resources Education and Research Center, Kobe University, Kasai, Hyogo, Japan.*

P351 **Whole-genome sequencing reveals selection signals among Chinese, Pakistani and Nepalese goats.**
Y. Li*[1,2], S. Song[1,3], X. Liu[1,2], Y. Zhang[1,2], D. Wang[1,2], X. He[1,2], Q. Zhao[1,2], Y. Pu[1,2], W. Guan[1,2], E. Guangxin[4], C. Kumer[5], Y. Ma[1,2], and L. Jiang[1,2], [1]*Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, P. R. China*, [2]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, P. R. China*, [3]*State Key Laboratory of Cardiovascular Disease Fuwai Hospital, National Center for Cardiovascular Diseases, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, P. R. China*, [4]*College of Animal Science and Technology, Chongqing Key Laboratory of Forage and Herbivore, Chongqing Engineering Research Centre for Herbivores Resource Protection and Utilization, Southwest University, Chongqing, P. R. China*, [5]*Department of Animal Breeding and Genetics, Faculty of Animal Husbandry and Veterinary Sciences, Sindh Agriculture University, Tando Jam, Pakistan.*

P352 **Long-terminal repeat insertion as potential origin of allele-biased expression of the *APOB* gene in cholesterol deficiency carriers.**
D. Becker[1], A. Heimes[1], R. Weikard[1], M. Meyerholz[2,3], W. Petzl[2], H. Zerbe[2], H.-J. Schuberth[3], M. Hoedemaker[4], M. Schmicke[5], S. Engelmann[6,7], and C. Kühn*[1,8], [1]*Research Institute for Farm Animal Biology, Dummerstorf, MV, Germany*, [2]*Clinic for Ruminants with Ambulatory and Herd Health Services, Ludwig-Maximilians-University Munich, Oberschleißheim, Germany*, [3]*Institute of Immunology, University of Veterinary Medicine Foundation, Hannover, Germany*, [4]*Clinic for Cattle, University of Veterinary Medicine Foundation, Hannover, Germany*, [5]*Faculty of Natural Sciences III, Martin-Luther University Halle-Wittenberg, Halle, Germany*, [6]*Institute for Microbiology, Technical University Braunschweig, Braunschweig, Germany*, [7]*Microbial Proteomics, Helmholtz Centre for Infection Research, Braunschweig, Germany*, [8]*Agricultural and Environmental Faculty, University of Rostock, Rostock, Germany.*

P353 **Comparison of sequencing and assembly strategies for the cattle pangenome effort.**
A. Leonard*[1], Z.-H. Fang[1], B. Rosen[2], D. Bickhart[2], T. Smith[2], and H. Pausch[1], [1]*ETH Zürich, Zürich, Switzerland*, [2]*ARS, USDA, Beltsville, MD, USA*.

P354 **Genome-wide association analyses for maternal weaning weight in South African Bonsmara cattle.**
J. Reding[1], E. van Marle-Köster*[1], and D. Berry[1,2], [1]*University of Pretoria, Hatfield, South Africa*, [2]*Teagasc, Dublin, Ireland*.

P355 **Investigating gene and allele-specific expression in early development in sheep to identify functional variants associated with growth traits.**
S. Woolley*, M. Salavati, and E. Clark, *The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, UK*.

P356 **Whole-genome gene expression profiling of muscle tissue of Nellore cattle with divergent meat cooking loss.**
M. Serna-García*[1], L. F. S. Fonseca[1], D. B. S. Silva[1], P. I. Schmidt[1], A. F. B. Magalhães[2], N. A. Marín-Garzón[1], B. M. Salatta[1], G. B. Frezarim[1], and L. G. Albuquerque[1,3], [1]*Faculty of Agricultural and Veterinary Sciences, São Paulo State University, FCAV/UNESP, Jaboticabal, São Paulo, Brazil*, [2]*APTA Beef Cattle Center, Animal Science Institute, Sertaozinho, São Paulo, Brazil*, [3]*National Council for Science and Technological Development (CNPq), Brasília, Brazil*.

P357 **The eastward dispersal of domestic goats and their introgression, population stratification, and genetic adaptation in East Asia.**
Y. Cai*, W. Fu, Z. Zheng, X. Liu, Y. Jiang, and X. Wang, *Northwest A&F University, Yangling, Shaanxi, China*.

P358 **Single-cell transcriptomic analyses of cattle ruminal epithelial cells before and after weaning.**
Y. Gao[1], L. Fang[3], R. L. Baldwin[1], E. E. Connor[4], J. B. Cole[1], C. P. Van Tassell[1], L. Ma[2], C. J. Li*[1], and G. E. Liu[1], [1]*ARS, USDA, Beltsville, MD, USA*, [2]*University of Maryland, College Park, MD, USA*, [3]*University of Edinburgh, Edinburgh, UK*, [4]*University of Delaware, Newark, DE, USA*.

P359 **The detection of transmission ratio distortion signals in the goat genome is strongly affected by SNP calling quality.**
M. Luigi-Sierra[1], J. Casellas[2], A. Martínez[3], J. Delgado[3], J. Alvarez[3], F. Such[2], J. Jordana[2], and M. Amills*[1,2], [1]*Centre for Research in Agricultural Genomics (CRAG), Bellaterra, Spain*, [2]*Universitat Autònoma de Barcelona, Bellaterra, Spain*, [3]*Universidad de Córdoba, Córdoba, Spain*.

P360 **miR-2382-5p regulates lipid metabolism by targeting *NDRG2* and *KLF6* genes in bovine mammary epithelial cells.**
L. Xia*[1], Z. Zhao[2], X. Fang[1], and R. Yang[1], [1]*College of Animal Science, Jilin University, Changchun, Jilin, China*, [2]*College of Coastal Agricultural Sciences, Guangdong Ocean University, Zhanjiang, Guangdong, China*.

P361 **Genome-wide association analysis for milk production traits in German Black Pied cattle (DSN).**
P. Korkuc*[1], D. Arends[1], K. May[2], S. König[2], and G. Brockmann[1], [1]*Humboldt University Berlin, Berlin, Germany*, [2]*Justus-Liebig-University of Giessen, Giessen, Germany*.

P362 **Assessing the impact of genome assemblies on livestock genomic analyses.**
A. Lloret-Villas*, M. Bhati, N. K. Kadri, A. S. Leonard, and H. Pausch, *Animal Genomics, Institute of Agricultural Sciences, ETH, Zürich, Switzerland*.

P363 **Long noncoding RNA-420 competitively binds to miR-129-5p and targets *DLK1* inhibiting lipid metabolism in bovine preadipocytes.**
J. Mi*, W. He, X. Lu, X. Fang, and R. Yang, *College of Animal Science, Jilin University, Changchun, Jilin, China*.

P364 **Isolation of bovine milk-derived exosomes and identification of miRNAs associated with mastitis.**
X. Lu*, X. Zhang, J. Mi, W. He, X. Fang, and R. Yang, *College of Animal Science, Jilin University, Changchun, Jilin, China*.

P365 **Identification and characterization of miRNAs in spleens of animals subjected to repetitive vaccination.**
E. Varela-Martínez[1], M. Bilbao-Arribas[1], N. Abendaño[1], A. Guisasola-Serrano[1], J. Asín[2,3], M. M. Pérez[2], L. Luján[2], and B. M. Jugo*[1], [1]*University of the Basque Country (UPV/EHU), Leioa (Bizkaia) Spain*, [2]*University of Zaragoza, Zaragoza, Spain*, [3]*University of California, Davis, CA, USA*.

P366 **Genetic history and convergent evolution of the northernmost cattle from Siberia.**
L. Buggiotti[1], A. A. Yurchenko[2,9], N. S. Yudin[2,9], C. J. Vander Jagt[3], N. V. Vorobieva[4], M. Kusliy[4], S. K. Vasiliev[5], A. N. Rodionov[6], O. I. Boronetskaya[7], N. A. Zinovieva[6], A. S. Graphodatsky[4], H. D. Daetwyler[3,8], and D. M. Larkin*[1,9], [1]*Royal Veterinary College, University of London, London, UK*, [2]*The Federal Research Center Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia*, [3]*Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, Victoria, Australia*, [4]*Department of the Diversity and Evolution of Genomes, Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia*, [5]*Paleometal Archeology Department, Institute of Archaeology and Ethnography SB RAS, Novosibirsk, Russia*, [6]*L. K. Ernst Federal Research Centre for Animal Husbandry, Podolsk, Russia*, [7]*Timiryazev Russian State Agrarian University, Moscow Agrarian Academy, Moscow, Russia, Moscow, Russia*, [8]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia, Bundoora, Victoria, Australia*, [9]*Kurchatov Genomic Center, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Science, Novosibirsk, Russia*.

P367 **Genome-wide association studies in the Reggiana cattle breed identify several candidate genes affecting pigmentation-related traits, stature and udder defects.**
S. Bovo*[1], G. Schiavo[1], H. Kazemi[1], G. Moscatelli[1], A. Ribani[1], M. Ballan[1], M. Bonacini[2], M. Prandi[2], S. Dall'Olio[1], and L. Fontanesi[1], [1]*Department of Agricultural and Food Science, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Associazione Nazionale Allevatori Bovini di Razza Reggiana (ANABORARE), Reggio Emilia, Italy*.

P368 **An integrated long noncoding RNA transcriptome during the sheep immune system activation.**
M. Bilbao-Arribas*, E. Varela-Martínez, and B. M. Jugo, *Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Basque Country, Spain*.

P369 **Online Mendelian Inheritance in Animals (OMIA): Updated variant tables for key livestock species.**
I. Tammen*[1], K. L. M. Eager[1,2], S. A. Woolley[1,2], S. M. Y. Shields[1], S. Hermesch[3], B. A. O'Rourke[2], and F. W. Nicholas[1], [1]*The University of Sydney, Sydney School of Veterinary Science, Sydney, NSW, Australia*, [2]*The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, NSW, Australia*, [3]*University of New England, Animal Genetics Breeding Unit, Armidale, NSW, Australia*.

P370 **Single-cell RNA sequencing reference datasets of isolated bovine milk cells and cultured primary mammary epithelial cells.**
D. Becker*[1], R. Weikard[1], F. Hadlich[1], and C. Kühn[1,2], [1]*Leibniz Institute of Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany*, [2]*University of Rostock, Faculty of Agricultural and Environmental Sciences, Rostock, Germany*.

P371 **RNA sequencing transcriptomic analysis of Maedi-Visna and scrapie coinfected sheep.**
A. Hernaiz*[1], D. Martínez[1], B. Marín[2], B. Ranera[3], P. Zaragoza[1], J. J. Badiola[2], R. Bolea[2], B. Moreno[2], and I. Martín-Burriel[1,2], [1]*Laboratorio de Genética Bioquímica (LAGENBIO), Facultad de Veterinaria, Universidad de Zaragoza-IA, Zaragoza, Spain*, [2]*Centro de Encefalopatías y Enfermedades Transmisibles Emergentes (CEETE), Facultad de Veterinaria, Universidad de Zaragoza-IA, Zaragoza, Spain*, [3]*Facultad de Ciencias de la Salud, Universidad San Jorge, Zaragoza, Spain*.

P372 **Differential allele-specific expression in SNPs related to meat quality traits in *Bos indicus* muscle.**
J. Bruscadin*[1], T. Cardoso[2], M. De Souza[3], J. Afonso[2], J. Malheiros[4], T. Porto[1], J. Petrini[5], and L. Regitano[2], [1]*Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [2]*Embrapa Southeast Livestock, São Carlos, São Paulo, Brazil*, [3]*Iowa State University, Ames, IA, USA*, [4]*Federal University of Latin American Integration, Foz do Iguaçu, Paraná, Brazil*, [5]*University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil*.

P373 **The intronic branch point sequence is depleted for mutations in the bovine and human genome.**
N. K. Kadri* and H. Pausch, *ETH Zurich, Zurich, Switzerland*.

P374 **Genome-wide local ancestry and direct evidence for cytonuclear disequilibria in hybrid African cattle populations (*Bos taurus/indicus*).**
J. A. Ward*[1], G. P. McHugo[1], M. J. Dover[1], T. J. Hall[1], S. I. Ng'ang'a[2,3], T. S. Sonstegard[4], D. G. Bradley[5], L. A. F. Frantz[2,3], M. Salter-Townshend[6], and D. E. MacHugh[1,7], [1]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilian University, Munich, Germany*, [3]*School of Biological and Chemical Sciences, Queen Mary University of London, London, UK*, [4]*Acceligen, Eagan, MN, USA*, [5]*Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland*, [6]*UCD School of Mathematics and Statistics, University College Dublin, Dublin, Ireland*, [7]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland*.

P375 **Genome-wide scan reveals pleiotropic effects on carcass and meat quality traits in crossbred beef cattle.**
F. Rezende*[1], E. Rodriguez[1], J. Leal-Gutiérrez[2], M. Elzo[1], D. Johnson[1], C. Carr[1], and R. Mateescu[1], [1]*University of Florida, Gainesville, FL, USA*, [2]*University of California, San Diego, CA, USA*.

P376 **Imputation to whole-genome sequence by using a small reference population.**
J. Petrini*[1], B. G. N. Andrade[2], T. F. Cardoso[3], A. S. M. Cesar[4], B. Silva-Vignato[1], G. Morota[5], M. L. Spangler[6], L. C. A. Regitano[3], L. L. Coutinho[1], and G. B. Mourão[1], [1]*Department of Animal Science, College of Agriculture "Luiz de Queiroz," University of São Paulo/ESALQ, Piracicaba, SP, Brazil*, [2]*Department of Computer Science, Munster Technological University, Cork, Munster, Ireland*, [3]*Embrapa Southeast Livestock, São Carlos, SP, Brazil*, [4]*Department of Agroindustry, Food and Nutrition, College of Agriculture "Luiz de Queiroz," University of São Paulo/ESALQ, Piracicaba, SP, Brazil*, [5]*Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA*, [6]*Animal Science Department, University of Nebraska–Lincoln, Lincoln, NE, USA*.

P377 **C2C12 myotubes promote the migration of 3T3-L1 preadipocytes via the CCL5/CCR5 axis under coculture condition.**
W. Yu*, Y. Zhao, Y. Tian, M. Yan, W. Wei, L. Zhang, and J. Chen, *College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, Jiangsu Province, China*.

P378 **Mutations in transcription factors and cofactors associated with gene expression and feed efficiency-related traits in Nelore cattle.**
T. F. Cardoso*[1], J. J. Bruscadin[2], J. Afonso[1], J. Petrini[3], B. G. N. Andrade[4], P. S. N. de Oliveira[2], J. M. Malheiros[5], T. Porto[2], A. Zerlotini[6], G. B. Mourão[3], L. L. Coutinho[3], and L. C. A. Regitano[1], [1]*Embrapa Southeast Livestock, São Carlos, São Paulo, Brazil*, [2]*Postgraduate Program on Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [3]*Department of Animal Science, "Luiz de Queiroz" College of Agriculture, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil*, [4]*Munster Technological University, Ireland*, [5]*Federal University of Latin American Integration, Foz do Iguaçu, Paraná, Brazil*, [6]*Embrapa Agricultural Informatics, Campinas, São Paulo, Brazil*.

P379 **Bovine horn bud structure and gene expression at 58 days of fetal development.**
J. Aldersey*[1], Y. Ren[1], W. Low[1], R. Tearle[1], K. Petrovski[1], T. Chen[1], J. Williams[1,2], T. Sonstegard[3], and C. Bottema[1], [1]*Davies Livestock Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, Australia*, [2]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del Sacro Cuore, Piacenza, Italy*, [3]*Acceligen, Eagan, MN, USA*.

P380 **Genomic breeding values from low-coverage Nanopore sequencing.**
H. J. Lamb, B. J. Hayes, L. T. Nguyen, and E. M. Ross*, *The Queensland Alliance for Agriculture and Food Innovation, St Lucia, Queensland, Australia*.

P381 **Expression (e)QTL study to determine the association between omics and phenotypes for Warner-Bratzler shear force of longissimus dorsi in Hanwoo cattle.**
Y. Chung*[1], D. Seo[1], K.-Y. Chung[2], and S. H. Lee[1], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, South Korea*, [2]*Department of Beef Science, Korea National College of Agriculture and Fisheries, South Korea*.

P382 **Whole-genome resequencing points to candidate variants and genes for body temperature maintenance under the cold stress in Siberian cattle populations.**
A. V. Igoshin*[1], N. S. Yudin[1,2], R. B. Aitnazarov[1], A. A. Yurchenko[1,2], and D. M. Larkin[1,3], [1]*The Federal Research Center Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences (ICG SB RAS), Novosibirsk, Russia*, [2]*Kurchatov Genomic Center, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Science, Novosibirsk, Russia*, [3]*Royal Veterinary College, University of London, London, UK*.

P383 **Rare casein variants in goats identified by capture sequencing.**
S. Rahmatalla*[1,2], D. Arends[1], A. S. Ahmed[1], L. Hassan[3], S. Krebs[4], M. Reissmann[1], and G. Brockmann[1], [1]*Humboldt University, Berlin, Germany*, [2]*University of Khartoum, Khartoum, Sudan*, [3]*Wildlife Research Center, Khartoum, Sudan*, [4]*Ludwig Maximilian University, Munich, Germany*.

P384 **Simulating the likely impact of genome editing using a real multigeneration pedigree of genotyped animals.**
A. Reverter*, L. Porto-Neto, and J. Kijas, *CSIRO Agriculture and Food, Brisbane, Queensland, Australia*.

P385 **Bovine circSGCB regulates *KLF3* through the ceRNA mechanism and affects the development of bovine myoblasts.**
J. Xu, Y. Wen, X. Li, X. Ding, S. Zhang, P. Yang, Z. Yao, C. Lei, H. Chen, and Y. Huang*, *Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*.

P386 **Genome-wide association and genetic parameter estimation studies for coat color of Chikso.**
J. M. Kang*[1], Y. K. Kim[1], D. H. Lee[1], S. H. Lee[2], T. J. Choi[2], M. N. Park[2], and S. H. Lee[1], [1]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea*, [2]*Animal Genetic Improvement Division, National Institute of Animal Science, Korea*.

P387 **Multi breed genome-wide association for male fertility traits in tropical cattle.**
L. Porto-Neto*[1], J. Bertram[2], M. Fortes[3,4], P. Alexandre[1], M. McGowan[5], B. Hayes[4], and A. Reverter[1], [1]*Commonwealth Scientific and Industrial Research Organisation, Agriculture and Food, Brisbane, QLD, Australia*, [2]*Agriculture Consultant, Livestock management and breeding, Toowoomba, QLD, Australia*, [3]*The University of Queensland, School of Chemistry and Molecular Biosciences, Brisbane, QLD, Australia*, [4]*The University of Queensland, Queensland Alliance of Agriculture and Food Innovation, Brisbane, QLD, Australia*, [5]*The University of Queensland, School of Veterinary Sciences, Gatton, QLD, Australia*.

P388 **Assessing genomic diversity and signatures of selection in Pinan cattle using whole-genome sequencing data.**
S. Zhang, Z. Yao, X. Ding, X. Li, Y. Wen, J. Xu, P. Yang, C. Lei, H. Chen, and Y. Huang*, *Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*.

P389 **Genotyping of *PRNP* gene in Spanish local goat breeds.**
A. Canales*[1,2], M. Macri[1,2], J. V. Delgado[2], and A. M. Martínez[2], [1]*Animal Breeding Consulting, S.L, Cordoba, Cordoba, Spain*, [2]*Department of Genetics, University of Córdoba, Cordoba, Cordoba, Spain*.

P390 **Single nucleotide polymorphisms in the calpain 1 gene (*CAPN1*) are associated with production traits in Irish beef cattle.**
K. Quigley*[1], D. F. G. Flores[1], L. O'Kane[1], R. D. Evans[2], T. J. Hall[3], D. E. MacHugh[3,4], and M. P. Mullen[1], [1]*Bioscience Research Institute, Athlone Institute of Technology, Athlone, Co. Westmeath, Ireland*, [2]*Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland*, [3]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, Belfield, Dublin, Ireland*, [4]*UCD Conway Institute of Biomolecular and Biomedical Research, Belfield, Dublin, Ireland*.

P391 **MicroRNA profiles in colostrum and newborn calves after colostrum ingestion.**
D. T. Hue*[1,2], Y. Ren[1], W. Y. Low[1], T. Chen[1], K. Petrovski[1], J. L. Williams[1,3], R. Tearle[1], and C. D. K. Bottema[1], [1]*Davies Livestock Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, Australia*, [2]*Faculty of Animal Science, Vietnam National University of Agriculture, Trau Quy, Gia Lam, Hanoi, Vietnam*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del Sacro Cuore, Piacenza, Italy*.

P392 **Prediction of Hanwoo cattle phenotypes from genotypes using machine learning methods.**
B. I. Lopez*, S. Srivastava, M. Jang, H. Kumar, W. Park, H.-H. Chai, J.-E. Park, and D. Lim, *Division of Animal Genomics and Bioinformatics, National Institute of Animal Science, Wanju, Republic of Korea*.

P393 **Pregnancy in goats induces a strong transcriptomic change in the olfactory bulb.**
M. G. Luigi-Sierra*[1], D. Guan[1], M. López-Béjar[2], E. Casas[2], S. Olvera[2], J. Gardela[2], M. J. Palomo[3], U. I. Osuagwuh[3], U. L. Ohaneje[3], E. Mármol-Sanchez[1], and M. Amills[1,4], [1]*Centre de Recerca Agrigenòmica (CRAG), Bellaterra, Barcelona*, [2]*Department of Health and Animal Anatomy, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [3]*Department of Animal Medicine and Surgery, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [4]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*.

P394 **Integrative QTL mapping and selection signature analysis identify positional candidate genes influencing headed white spotting in Groningen White Headed cattle breed.**
R. Gonzalez-Prendes*[1], C. Ginja[2], J. Kantanen[3], N. Ghanem[4], D. R. Kugonza[5], M. I. Makgahlela[6], M. A. M. Groenen[1], and R. P. M. A. Crooijmans[1], [1]*Animal Breeding and Genomics, Wageningen University and Research, Wageningen, the Netherlands*, [2]*CIBIO/InBIO-Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*, [4]*Animal Production Department, Cairo University, Cairo, Egypt*, [5]*Makekere University, Kampala, Uganda*, [6]*Agricultural Research Council, Pretoria, South Africa*.

P395 **The distinct morphological phenotypes of domestic sheep are shaped by introgressions from their sibling wild species.**
H. Cheng*, J. Wen, Z. Zhang, and Y. Jiang, *Northwest A&F University, Yangling, Shaanxi, China*.

P396 **Resequencing the Yaroslavl cattle genomes reveals signatures of selection and young genetic variants likely to be related to the breed phenotypes.**
D. Ruvisnkiy*[1,2], N. S. Yudin[1,2], and D. M. Larkin[1,3], [1]*The Federal Research Center Institute of Cytology and Genetics, Novosibirsk, Russia*, [2]*Kurchatov Genomic Center, Institute of Cytology and Genetics, Novosibirsk, Russia*, [3]*Royal Veterinary College, London, UK*.

P397 **Preliminary genome-wide association study with sialyl oligosaccharides content in 4 cattle breeds.**
M. Milanesi*[1], C. Lovallo[2], C. Marchitelli[3], S. Claps[2], G. Chillemi[1], and A. Crisà[3], [1]*Dipartimento per la Innovazione nei sistemi Biologici, Agroalimentari e Forestali (DIBAF), University of Tuscia, Viterbo, VT, Italy*, [2]*Centro Ricerca Zootecnia e Acquacoltura (CREA), Consiglio per la Ricerca in agricoltura e l'analisi dell'economia agraria, Bella Muro, PZ, Italy*, [3]*Centro Ricerca Zootecnia e Acquacoltura (CREA), Consiglio per la Ricerca in agricoltura e l'analisi dell'economia agraria, Monterotondo, RM, Italy*.

P398 **Can SNPs associated with variation in the level of stress biomarkers be used for the selection of stress-resilient dairy cows?**
M. M. Passamonti*[1], M. Milanesi[4], J. Ramirez Diaz[1], A. Stella[2], M. Barbato[1], M. Premi[1], R. Negrini[1], A. Cecchinato[3], E. Trevisi[1], J. L. Williams[1], and P. Ajmone Marsan[1], [1]*Universitá Cattolica del Sacro Cuore, Piacenza, Italy*, [2]*Consiglio Nazionale della Ricerca, Milan, Italy*, [3]*Universitá di Padova, Padua, Italy*, [4]*Università della Tuscia, Viterbo, Italy*.

P399 **Comparison of variant calling programs with short-read sequences from U.S. sheep.**
M. Stegemiller*[1], R. Redden[2], D. Notter[3], J. Taylor[4], N. Cockett[5], M. Heaton[6], T. Kalbfleisch[7], and B. Murdoch[1], [1]*Department of Animal, Veterinary and Food Sciences, University of Idaho, Moscow, Idaho, USA*, [2]*Department of Animal and Veterinary Science, University of Idaho, San Angelo, TX, USA*, [3]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA, USA*, [4]*United States Sheep Experiment Station, United States Department of Agriculture, Agricultural Research Service, Dubois, ID, USA*, [5]*Utah State University, Logan, UT, USA*, [6]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA*, [7]*Maxwell Gluck Equine Research Center, College of Agriculture and Veterinary Sciences, Lexington, KY, USA*.

P400 **Validation of selection signatures for coat color in an Italian grey beef cattle breed.**
G. Rovelli[1], V. Landi[2], F. Sbarra[3], A. Quaglia[3], F. Pilla[4], E. Lasagna*[1], and E. Ciani[5], [1]*Department of Agricultural, Food and Environmental Sciences (DSA, Perugia, Perugia, Italy*, [2]*Department of Veterinary Medicine, University of Bari, Valenzano, Bari, Italy*, [3]*National Association of Italian Beef-Cattle Breeders (ANABIC), San Martino in Colle, Perugia, Italy*, [4]*Department of Agricultural, Environment and Food, University of Molise, Campobasso, Campobasso, Italy*, [5]*Department of Biosciences, Biotechnologies and Biopharmaceutics, University of Bari, Bari, Bari, Italy*.

P401 **Gene network for thermotolerance in Brangus cattle.**
K. M. Sarlo Davila*, E. E. Rodriguez, F. M. Rezende, A. N. Nunez Andrade, and R. G. Mateescu, *University of Florida, Gainesville, FL, USA*.

P402 **A comparative framework for comparing Hi-C datasets across ruminant livestock species.**
C. MacPhillamy*[1], H. Alinejad-Rokny[2,3], W. Pitchford[1], and W. Low[1], [1]*Davies Livestock Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, Australia*, [2]*Biological and Medical Machine Learning Lab, The Graduate School of Biomedical Engineering, University of New South Wales, Sydney, NSW, Australia*, [3]*School of Computer Science and Engineering, The University of New South Wales, Sydney, NSW, Australia*.

P403 **Dissection of the scurs phenotype to refine the mapping of scurs.**
G. Wang* and C. Gill, *Texas A&M University, College Station, TX, USA*.

P404 **Comparing genomic prediction of an individual bull's contribution to cow fertility using individual or pooled genotypes.**
Y. Li*[1], L. Porto-Neto[1], R. McCulloch[1], S. McWilliam[1], P. Alexandre[1], J. McDonald[2], C. Smith[2], A. Reverter[1], and S. Lehnert[1], [1]*CSIRO Agriculture and Food, St Lucia, QLD, Australia*, [2]*MDH Pty Ltd, Cloncurry, QLD, Australia*.

P405 **Genome-wide association study in bull semen production traits: A review.**
M. Modiba*[1,2], J. Wang[1], K. A. Nephawe[2], L. Wenfa[1], and B. J. Mtileni[2], [1]*Jilin Agricultural University, Jilin, China*, [2]*Tshwane University of Technology, Pretoria, South Africa*.

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P406 **Identification of novel SNPs in litter size–associated genes in indigenous goat of Bangladesh.**
A. Das*, M. Shaha, and G. Miah, *Department of Genetics and Animal Breeding, Chattogram Veterinary and Animal Sciences University, Khulshi, Chattogram, Bangladesh*.

P407 **Study on fiber characteristics of different Inner Mongolia Cashmere goats.**
Z. Chongyan, X. Yuchun, G. Juntao, S. Xin, Z. Cun, Q. Qing, D. Dongliang, W. Zhixin, L. Jinquan, and L. Zhihong*, *Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China*.

P408 **Machine learning algorithm to predict coagulating milk factor through milk traits in 2 sheep breeds.**
H. Marina*, B. Gutiérrez-Gil, R. Pelayo, A. Suárez-Vega, C. Esteban-Blanco, and J. Arranz, *Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, Campus de Vegazana, León, Spain*.

P409 **Design of a low-density panel of SNPs to detect fraud in cured goat cheese.**
A. M. Martínez*[1], A. Canales[1,2], M. Macri[1,2], and J. V. Delgado[1], [1]*University of Cordoba, Cordoba, Spain*, [2]*Animal Breeding Consulting S.L, Cordoba, Spain*, [3]*Instituto Canario de Investigaciones Agrarias, Tenerife, Spain*.

P410 **Extended haplotype homozygosity analysis reveals positive selection patters in 6 Spanish goat breeds.**
T. E. Ziegler[1,2], A. Molina[3], G. Anaya[3], and S. Demyda-Peyrás*[2,4], [1]*IGEVET, Instituto de Genética Veterinaria, La Plata, Buenos Aires, Argentina*, [2]*FCV-UNLP, Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*, [4]*CONICET, Consejo Superior de Investigaciones Científicas y Tecnológicas, La Plata, Buenos Aires, Argentina*.

P411 **Unveiling genomic regions that underlie footrot resistance in Portuguese sheep Merino.**
D. Gaspar*[1,2], A. Usié[1,3], C. Leão[3,4], C. Matos[5], L. Padre[3], C. Dias[3], C. Ginja[2], and A. M. Ramos[1,3], [1]*CEBAL – Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Beja, Portugal*, [2]*CIBIO/InBIO – Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, Porto, Portugal*, [3]*MED-Mediterranean Institute for Agriculture, Environment and Development, University of Évora, Évora, Portugal*, [4]*INIAV – Instituto Nacional de Investigação Agrária e Veterinária, Santarém, Portugal*, [5]*ACOS – Agricultores do Sul, Beja, Portugal*.

P412 **Comparative transcriptome analysis between suckling lambs with different levels of perirenal adipose tissue in the carcass.**
M. Alonso-García[1], A. Suárez-Vega[1], J. Mateo[2], H. Marina[1], R. Pelayo[1], C. Esteban-Blanco[1], J. J. Arranz[1], and B. Gutiérrez-Gil*[1], [1]*Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, León, Spain*, [2]*Departamento de Higiene y Tecnología de los Alimentos, Facultad de Veterinaria, Universidad de León, León, León, Spain*.

P413 **Exploring differentially expressed genes in hypothalamic transcriptome in different sexual behavior phenotypes in rams using RNA-seq.**
K. Lakhssassi*[1,2], I. Ureña[3], B. Marín[4], M. P. Sarto[1], B. Lahoz[1], J. L. Alabart[1], J. Folch[1], M. Serrano[3], and J. H. Calvo[1,5], [1]*Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA)-IA, Zaragoza, Spain*, [2]*Institut National de la Recherche Agronomique, Rabat, Morocco*, [3]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain*, [4]*Universidad de Zaragoza, Zaragoza, Spain*, [5]*Fundación Agencia Aragonesa para la Investigación y el Desarrollo (ARAID), Zaragoza, Spain*.

P414 **Identification of a novel loss-of-function variant in the ovine *TMCO6* gene associated with motor neuron disease of North Country Cheviot sheep.**
A. Letko*[1], I. M. Häfliger[1], E. Corr[2], F. Brulisauer[2], S. Scholes[2], and C. Drögemüller[1], [1]*Institute of Genetics, Bern, Switzerland*, [2]*SRUC Consulting Veterinary Services, Penicuik, Midlothian, UK*.

P415 **Molecular marker in *MC4R* gene for local goat of Indonesia.**
T. Hartatik*[1], L. Latifah[1], F. A. Z. Chairunissa[1], D. Maharani[1], and A. Kustantinah[2], [1]*Department of Animal Breeding and Reproduction, Faculty of Animal Science, Universitas Gadjah Mada, Yogyakarta, Indonesia*, [2]*Department of Animal Nutrition and Feed, Faculty of Animal Science, Universitas Gadjah Mada, Jogjakarta, Indonesia*.

P416 **The difference of lipid metabolism based on intestinal microbiome and transcriptome between Dorper and Tan sheep.**
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P417 **Identification of novel SNPs associated to litter size in Rasa Aragonesa sheep breed.**
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