ISAG 2025

Conference Program

40th International Society for
Animal Genetics Conference

July 20–25, 2025
Daejeon, Republic of Korea

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Contents

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Animal forensic genetics
Guillermo Giovambattista, Universidad Nacional De La Plata

Animal Genetics Testing Standardization
Leslie Lyons, University of Missouri, Columbia, USA

Applied genetics and genomics in other species of economic importance
Amparo Martinez, Animal Breeding Consulting, S.L., Spain (Chair)

Emiliano Lasagna, University of Perugia, Italy (Co-Chair)

Small Ruminant Genetics and Genomics

Michelle Mousel, USDA/ARS/ADRU, Pullman, Washington, USA (Acting Chair)

Applied genetics of companion animals
Peter Dovc, University of Ljubljana, Biotechnical Faculty, Slovenia (Chair)

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Avian genetics and genomics
Huaijun Zhou, University of California, Davis, USA (Chair)

Min-Sheng Peng, Kunming Institute of Zoology, Kunming, China (Co-Chair)

Cattle molecular markers and parentage testing
Jiansheng Qiu, Neogen GeneSeek, USA (Chair)

Emiliano Lasagna, University of Perugia, Italy (Co-Chair)

Companion animal genetics and genomics
Jeffrey Schoenebeck, Roslin Institute (University of Edinburgh), United Kingdom (Chair)

Comparative and functional genomics
Christa Kühn, FBN Dummerstorf, Germany

Comparative MHC Genetics
John A. Hammond, The Pirbright Institute, United Kingdom

Domestic Animal Sequencing and Annotation
Brenda Murdoch, University of Idaho, USA

Equine genetics and Thoroughbred parentage testing
Leanne Van de Goor, VGL Genetics, Wageningen, The Netherlands

Genetics and genomics of aquaculture species
Maria Saura, INIA, Spain (Chair)

Lior David, The Hebrew University of Jerusalem, Rehovot, Israel (Co-Chair)

Genetics of immune response
Romi Pena, University of Lleida, Spain (Chair)

Sabine Hammer, University of Veterinary Medicine Vienna, Austria (Co-Chair)

Genome edited animals
Xiaolong Wang, Northwest A&F University, China

Horse genetics and genomics
Robin Everts, Etalon Dx, San Diego, California, USA (Chair)

Sebastian Peyrás, Universidad de Cordoba, Spain (Co-Chair)

ISAG-FAO genetic diversity
Juha Kantanen, Natural Resources Institute Finland, Finland (Chair)

Catarina Ginja, CIBIO-InBIO, Universidade do Porto, Portugal (Co-Chair)

Livestock genomics for developing countries
Abdulfatai Tijjani, The Jackson Laboratory, Bar Harbor, Maine, USA (Chair)

Khanyisile Hadebe, Agricultural Research Council, Centurion, South Africa (Co-Chair)

Microbiomes
Oscar Gonzalez-Recio, INIA, Spain (Chair)

Jordi Estelle, INRAE, Jouy-en-Josas, France (Co-Chair)

Pig genetics and genomics
Catherine Larzul, INRAE, Castanet-Tolosan, France (Chair)

Shuhong Zhao, Huazhong Agricultural University, Wuhan, China (Co-Chair)

Ruminant genetics and genomics
Brenda Murdoch, University of Idaho, Moscow, Idaho, USA


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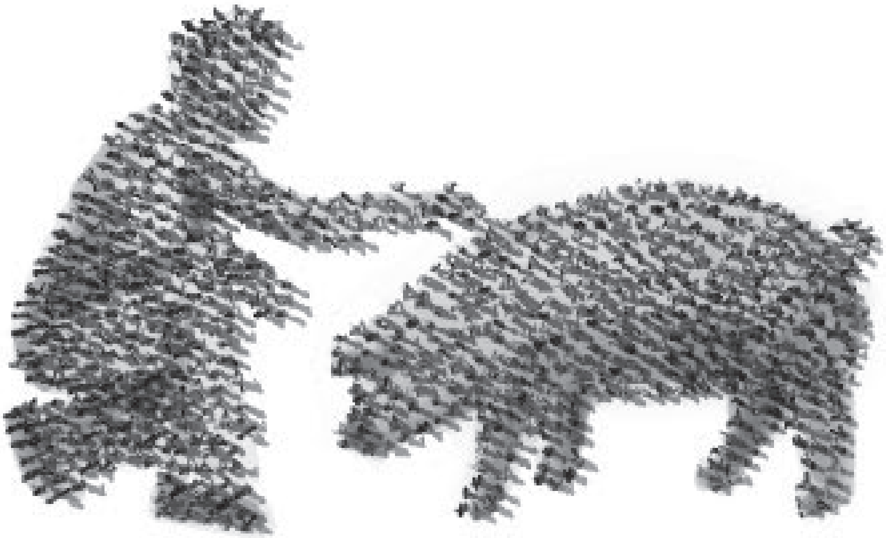

SCHEDULE OF EVENTS

Sunday, July 20, 2025		
14:00-17:00	Poster Setup	Exhibition Hall 109–112
14:00-17:00	Registration	Main Entrance
17:00-17:50	Historical Plenaries: Celebration of 40th ISAG Conference	National Science Museum
18:00-20:00	Welcome Reception	National Science Museum

Monday, July 21, 2025		
08:40-09:00	Welcome Opening	Grand Ballroom 201
09:00-11:10	Plenary I	Grand Ballroom 201
11:10-12:30	Domestic Animal Sequencing and Annotation	Exhibition Hall 109–112
11:10-12:30	Genome Edited Animals	Exhibition Hall 109–112
11:10-12:30	Companion Animal Genetics and Genomics	Exhibition Hall 109–112
11:10-12:30	Cattle Molecular Markers and Parentage Testing	Exhibition Hall 109–112
11:10-12:30	Animal Epigenetics	Exhibition Hall 109–112
11:10-12:30	Ruminant Genetics and Genomics I	Exhibition Hall 109–112
11:10-12:30	Animal Forensic Genetics	Exhibition Hall 109–112
11:10-12:30	Applied Genetics of Companion Animals	Exhibition Hall 109–112
12:30-13:30	Lunch	Exhibition Hall 109–112
13:30-15:30	Companion Animal Genetics and Genomics	Room 101–102
13:30-18:00	Animal Epigenetics	Room 105–106
13:30-18:00	Cattle Molecular Markers and Parentage Testing Committee	Room 103–104
13:30-18:00	Domestic Animal Sequencing and Annotation	Room 107–108
16:00-18:00	Genome Edited Animals	Room 101–102

Tuesday, July 22, 2025		
08:30-10:40	Plenary II	Grand Ballroom 201–202
11:30-12:30	Applied Genetics and Genomics in other Species of Economic Interest	Exhibition Hall 109–112
11:30-12:30	Genetics and Genomics of Aquaculture Species	Exhibition Hall 109–112

11:30-12:30	Genetics of Immune Response and Disease Resistance/Comparative and Functional Genomics	Exhibition Hall 109–112
11:30-12:30	Ruminant Genetics and Genomics II	Exhibition Hall 109–112
11:30-12:30	Equine Genetics and Thoroughbred Parentage Testing	Exhibition Hall 109–112
12:30-13:30	Lunch	Exhibition Hall 109–112
13:30-15:30	Ruminant Genetics and Genomics	Room 103–104
13:30-18:00	Applied Genetics of Companion Animals	Room 101–102
13:30-18:00	Genetics of Immune Response and Disease Resistance	Room 105–106
13:30-18:00	Applied Genetics and Genomics in other Species of Economic Interest	Room 107
13:30-18:00	Genetics and Genomics of Aquaculture Species	Room 108
16:00-18:00	Animal Forensic Genetics	Room 103–104
18:00-20:00	Networking Event for Early Career Scientists	Room 204–205

Wednesday, July 23, 2025

09:00-10:20	Plenary III	Grand Ballroom 201–202
10:20-11:40	Avian Genetics and Genomics I	Exhibition Hall 109–112
10:20-11:40	Pig Genetics and Genomics I	Exhibition Hall 109–112
10:20-11:40	ISAG-FAO Genetic Diversity	Exhibition Hall 109–112
10:20-11:40	Livestock Genomics for Developing Countries	Exhibition Hall 109–112
10:20-11:40	Small Ruminant Genetics and Genomics	Exhibition Hall 109–112
11:40-17:00	Mid-Conference Tours	Main Entrance

Thursday, July 24, 2025

08:30-11:30	Plenary IV	Grand Ballroom 201–202
10:20-11:30	Avian Genetics and Genomics II	Exhibition Hall 109–112
11:30-12:30	Comparative and Functional Genomics	Exhibition Hall 109–112
11:30-12:30	Horse Genetics and Genomics	Exhibition Hall 109–112

11:30-12:30	Microbiomes	Exhibition Hall 109–112
11:30-12:30	Pig Genetics and Genomics II	Exhibition Hall 109–112
12:30-13:30	Lunch	Exhibition Hall 109–112
13:30-15:30	Horse Genetics and Genomics	Room 107
13:30-18:00	Animal Genetic Testing Standardization (AGTS)	Room 105–106
13:30-18:00	Comparative and Functional Genomics	Room 101–102
13:30-18:00	Microbiomes	Room 103–104
16:00-18:00	Small Ruminant Genetics and Genomics	Room 107
16:00-18:00	Early Career Scientist Workshop	Room 108
19:20-20:00	Gala Dinner	Grand Ballroom 201–202

Friday, July 25, 2025		
08:00-11:50	Equine Genetics and Thoroughbred Parentage Testing	Room 101–102
08:00-11:50	Pig Genetics and Genomics	Room 103–104
08:00-10:00	ISAG-FAO Genetic Diversity	Room 105–106
08:00-11:50	Avian Genetics and Genomics	Room 107–108
10:00-11:30	Livestock Genomics for Developing Countries	Room 105–106
12:10-13:20	Business Meeting & Closing	Grand Ballroom 201

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- Variant discovery
- Population structure
- Functional genomics

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- Diversity and haplotype characterization
- Impactful content development
- QTL Mapping

Deploy/Decide
Inform management

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- Genomic selection
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Known variants

Statistical power

Statistical research

Imputation

Multi-omics

Quality assurance

GENERAL INFORMATION

REGISTRATION DESK

Venue: Main Entrance, Convention Center

Dates and Times:

Sunday, 20 July 2025	13:00 – 19:00
Monday, 21 July 2025	08:00 – 19:00
Tuesday, 22 July 2025	08:00 – 19:00
Wednesday, 23 July 2025	08:00 – 19:00
Thursday, 24 July 2025	08:00 – 19:00
Friday, 25 July 2025	08:00 – 13:00

SPEAKER PREPARATION ROOM AND GUIDELINES

Venue: Room 209

Dates and Times:

Monday, 21 July 2025	08:00 – 18:30
Tuesday, 22 July 2025	08:00 – 18:00
Wednesday, 23 July 2025	08:00 – 12:00
Thursday, 24 July 2025	08:00 – 18:00
Friday, 25 July 2025	08:00 – 12:00

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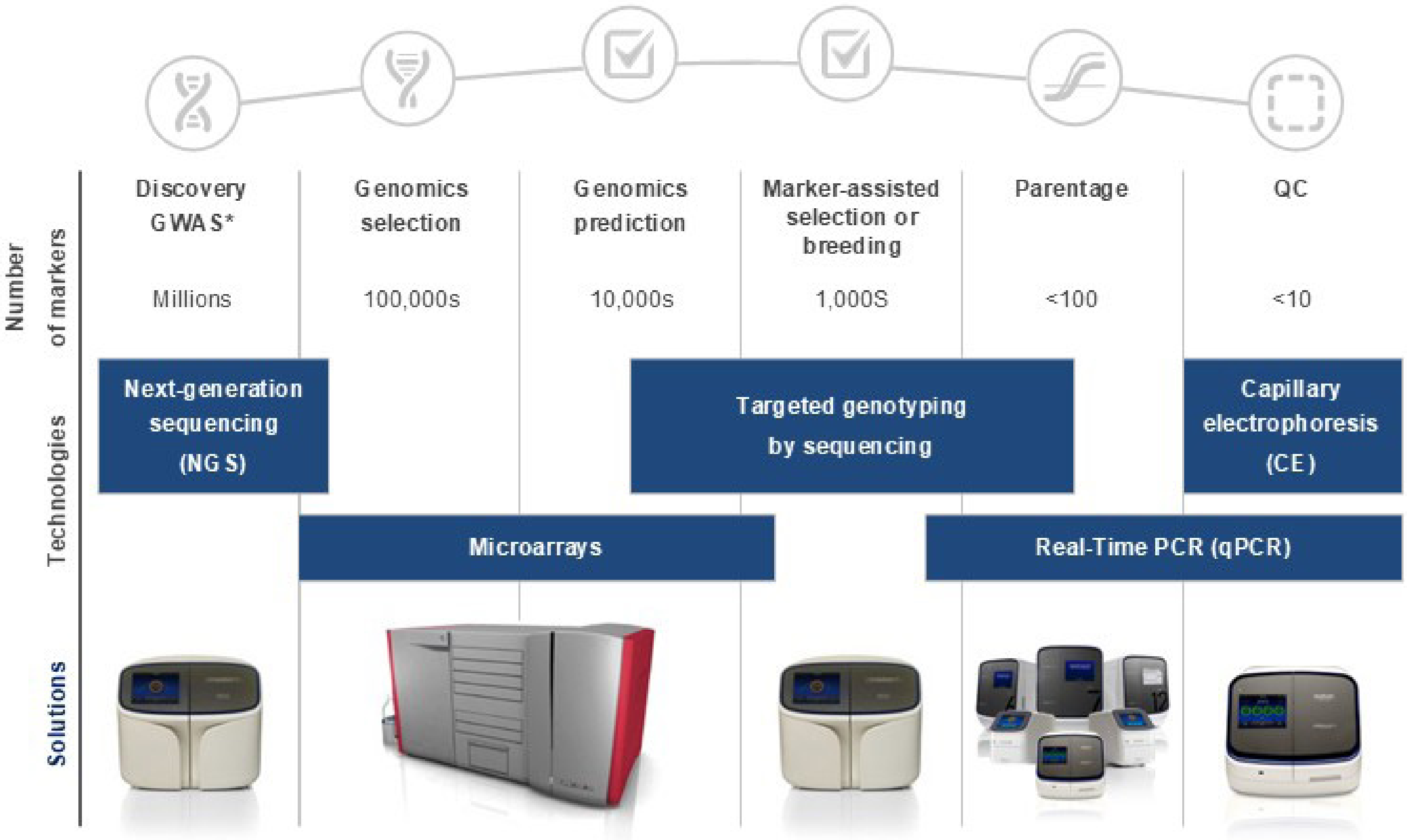
* GWAS = Genome-side association studies



	Discovery GWAS*	Genomics selection	Genomics prediction	Marker-assisted selection or breeding	Parentage	QC
Number of markers	Millions	100,000s	10,000s	1,000S	<100	<10

Technologies

Next-generation sequencing (NGS)

Targeted genotyping by sequencing

Capillary electrophoresis (CE)

Microarrays

Real-Time PCR (qPCR)

Solutions

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SOCIAL PROGRAMME

Welcome Reception
Date: Sunday, 20 July 2025
Venue: National Science Museum
Time: 18:00 – 20:00

Networking Event for Early Career Scientists
Date: Tuesday, 22 July 2025
Venue: Room 204+205
Time: 18:00 – 20:00

Mid-Conference Tours
Date: Wednesday, 23 July 2025
Venue: Various
Time: 11:40

Gala Dinner
Date: Thursday, 6 July 2023
Venue: Room 201+202
Time: 19:00 – 23:00

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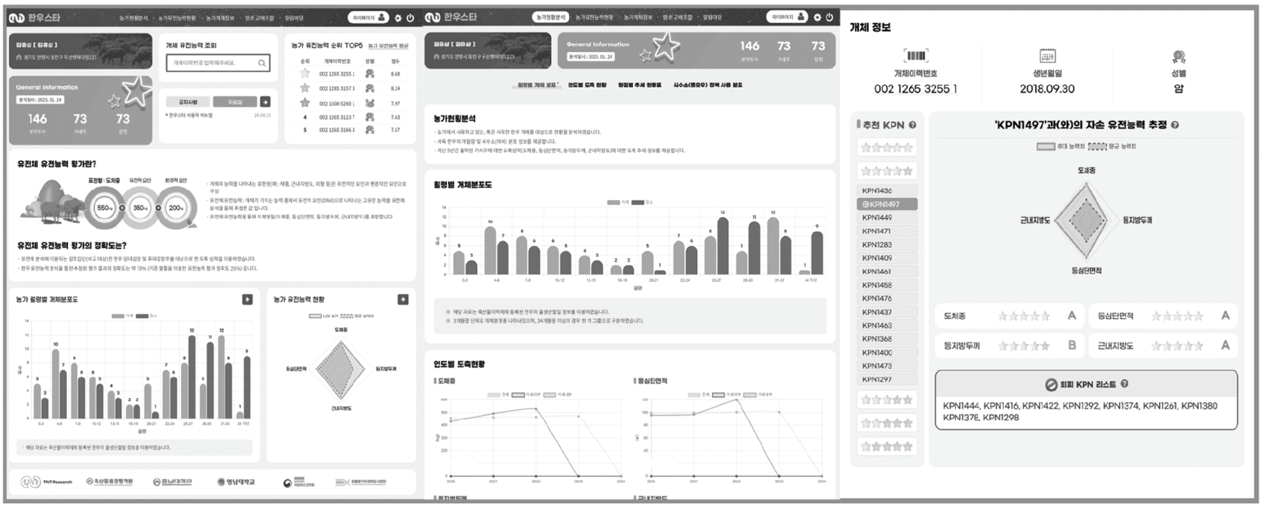

개체 정보

개체이력번호	생년월일	성별
002 1265 3255 1	2018.09.30	암

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POSTER SCHEDULE

POSTER SESSIONS

Poster Room: Exhibition Hall 109–112

All posters will be available for viewing on Monday, Tuesday, Wednesday, and Thursday.

Posters should be mounted to their boards on Sunday between 16:00 and 18:00.

Posters should be removed on Thursday at 18:00.

Poster presenters should make themselves available to discuss their poster during the designated poster session outlined below.

Monday

Presenters of the poster below should make themselves available to discuss their poster from 11:10–12:30 on Monday

Poster Number	**Section**
P100–P121	**Animal Epigenetics**
P122–P124	**Animal Forensic Genetics**
P138–P141	**Applied Genetics of Companion Animals**
P183–P198	**Cattle Molecular Markers and Parentage Testing**
P199–P212	**Companion Animal Genetics and Genomics**
P241–P249	**Domestic Animal Sequencing and Annotation**
P307–P315	**Genome Edited Animals**
P455–P467, P488–P515	**Ruminant Genetics and Genomics I**

Tuesday

Presenters of the poster below should make themselves available to discuss their poster from 11:30–12:30 on Tuesday

Poster Number	**Section**
P125–P137	**Applied Genetics and Genomics in other Species of Economic Interest**
P250–P261	**Equine Genetics and Thoroughbred Parentage Testing**
P262–P272	**Genetics and Genomics of Aquaculture Species**
P273–P306	**Genetics of Immune Response and Disease Resistance/Comparative and Functional Genomics**
P516–P557	**Ruminant Genetics and Genomics II**

Wednesday

Presenters of the poster below should make themselves available to discuss their poster from 10:20–11:40 on Wednesday

Poster Number	**Section**
P142–P166	**Avian Genetics and Genomics I**
P344–P359	**ISAG-FAO Genetic Diversity**
P360–P395	**Livestock Genomics for Developing Countries**
P425–P454	**Pig Genetics and Genomics I**
P558–P580	**Small Ruminant Genetics and Genomics**

Thursday

Presenters of the poster below should make themselves available to discuss their poster from 11:30–12:30 on Thursday

Poster Number	**Section**
P167–P182	**Avian Genetics and Genomics II**
P213–P240	**Comparative and Functional Genomics**
P316–P343	**Horse Genetics and Genomics**
P396–P424	**Microbiomes**
P468–P487	**Pig Genetics and Genomics II**

Sunday, July 20

Poster Setup
Exhibition Hall 109 + 110 + 111 + 112
2:00 PM - 5:00 PM

Registration
Main Entrance
2:00 PM - 5:00 PM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions
Historical Plenaries: Celebration of 40th ISAG Confernce

National Science Museum
5:00 PM - 5:50 PM

5:00 PM	OP100	**International Society for Animal Genetics (ISAG): Reflecting Back and Looking Forward.** N. Cockett*[1] and Joan Lunney[2], [1]*Utah State University*, *Logan, UT, USA*, [2]*USDA-ARS*, *Beltsville, MD, USA*.
5:25 PM	OP101	**Adventures with genetic variation in animals.** F. Nicholas*, *Sydney School of Veterinary Science, University of Sydney*, *Sydney, NSW 2006, Australia*.

OTHER EVENTS

Welcome Reception
National Science Museum
6:00 PM - 8:00 PM

Monday, July 21

Speaker Ready Room
Room 209
8:00 AM - 6:00 PM

Welcome Opening
Grand Ballroom 201
8:40 AM - 9:00 AM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions
Plenary I

Grand Ballroom 201
9:00 AM - 11:10 AM

9:00 AM OP102 **Long-read sequencing, pangenomes and complex variation.**
E. Eichler*[1,2], [1]*Department of Genome Sciences, University of Washington, Seattle, WA, USA*, [2]*Howard Hughes Medical Institute Investigator, Seattle, WA, USA*.

9:50 AM OP103 **Creation of a 12 generation eight breeds intercrossed heterogeneous pig population and its implication in the dissections of complex traits.**
Lusheng Huang*, Congying Chen, Bin Yang, Junwu Ma, Huashui Ai, Zhiyan Zhang, Yuyun Xing, Qiang Yang, Chuanmin Qiao, and Xhijun Xiao, *National Key Laboratory for Swine Genetic Improvement and Germplasm Innovation, Jiangxi Agricultural University, Nanchang, China*.

10:40 AM **Coffee Break.**

POSTER PRESENTATIONS

Animal Epigenetics

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P100 **Impact of maternal overnutrition on GLUT4, C/EBPB, PPARG, and SCD expression in Hanwoo calves at different growth stages.**
Borhan Shokrollahi*, Myungsun Park, Sun-Sik Jang, Gi-Suk Jang, and Youl-Chang Baek, *Hanwoo Research Institute, National Institute of Animal Science, Pyeongchang, 25340, Korea, PyeongChang, Gangwon, Korea*.

P101 **Detection of genomic imprinting signals for birth weight in Rubia Gallega beef cattle population.**
D. López-Carbonell*[1,2], G. Gorjanc[2], C. Hervás-Rivero[1], M. Sánchez-Díaz[1], and L. Varona[1], [1]*Instituto Agroalimentario de Aragón (IA2), University of Zaragoza, Zaragoza, 50013, Spain*, [2]*The University of Edinburgh, The Roslin Institute, Royal (Dick) School of Veterinary Science, Midlothian, EH25 9RG, United Kingdom*.

P102 **The microRNAs at the Gtl2 imprinting site are the main regulatory factors for the coarse wool of newborn Merino lambs.**
Jiankui Wang, Guoying Hua, Jianfei Chen, and Xuemei Deng*, *State Key Laboratory of Animal Biotech Breeding, China Agricultural University, Beijing 100193, China*, *Beijing, China*.

P103 **Research on high-precision in vivo phenotype measurement driven by artificial intelligence methods.**
Yidan Yan*, Lei Wei, Yuzhe Wang, Hanyu Wu, and Xiaoxiang Hu, *State Key Laboratory for Agro-Biotechnology, China Agricultural University*, *Beijing, China*.

P104 **Heat stress effects on the circulating microRNA profile of Iberian purebred and Duroc x Iberian crossbred weaned piglets.**
Paula Aranguren-Rivas[1], Ana Heras-Molina[2], Emilio Gómez-Izquierdo[3], Jose Gomez-Fernández[3], Fabián García[1], Luca Fontanesi[4], Cristina Óvilo[1], Juan María García-Casco[1,5], and María Muñoz*[1], [1]*Animal Breeding & Genetics Department, INIA-CSIC, Madrid, Spain*, [2]*Animal Production Department, UCM, Madrid, Spain*, [3]*Centro de Pruebas de Porcino-ITACYL, Hontalbilla (Segovia), Spain*, [4]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna*, *Bologna, Italy*, [5]*Centro de I+D en cerdo Ibérico, INIA-CSIC, Zafra (Badajoz), Spain*.

P105 **Effect of storage condition on protein and lipid oxidation in chicken and Japanese quails eggs.**
A. S. Babatunde*[1], K. D. Adeyemi[2], and V. O. Chimezei[2], [1]*Grandcereals Limited, Nigeria*, [2]*University of Ilorin, Nigeria*, [3]*University of Ilorin, Nigeria*.

P106 **Decoding the dynamic epigenetic landscapes of *Staphylococcus aureus* challenged bovine cells and enhancing the genomic selection.**
Siqian Chen*, Siyuan Mi, Yue Xing, and Ying Yu, *National Engineering Laboratory for Animal Breeding, State Key Laboratory of Animal Biotech Breeding, Breeding and Reproduction of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University*, *Beijing 100193, China*.

P107 **DNA methylation clock in bull sperm cells reveals the epigenetic aging characteristics and impact on fertility.**
W. Li, Y. Tang, S. Chen, S. An, J. Wang, W. Lai, X. Feng, and Y. Yu*, *Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture & National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University*, *Beijing, China*.

P108 **Identification and differential expression analysis of lncRNAs in relation to mRNA.**
H. Oh*[1], Y. Chung[2], H. Kang[3], P. T. N. Dinh[1], I. Choi[4], and S. H. Lee[4], [1]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, 34134, Republic of Korea*, [2]*Institute of Agricultural Science, Chungnam National University*, *Daejeon 34134, Republic of Korea*, [3]*Dairy Foods and Life Science, Chungnam National University*, *Daejeon, 34134, Republic of Korea*, [4]*Division of Animal & Dairy Science, Chungnam National University*, *Daejeon, 34134, Republic of Korea*.

P109 **Epigenetic biomarkers associated to fetal development during maternal lactation using the RUMIGEN methylation array.**
A. López-Catalina*, M. Gutiérrez-Rivas, and O. González-Recio, *INIA-CSIC, Madrid 28040, Spain*.

P110 **Genome-wide methylation drift and transcriptomic variability in aged beagle dogs.**
D. Kang*[1,2], E.-Y. Bok[3], S.-J. Oh[4], C.-Y. Hong[4], S.-L. Lee[4], and J. Kim[1,2], [1]*Division of Applied Life Science (BK21), Gyeongsang National University*, *Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University*, *Jinju, Republic of Korea*, [3]*Division of Animal Diseases & Health, National Institute of Animal Science, RDA, Wanju 55365, Republic of Korea*, [4]*College of Veterinary Medicine, Gyeongsang National University*, *Jinju, 52828 Republic of Korea*.

P111 **Tissue-specific chromatin accessibility regions and transcription factor binding sites in pig brain and endocrine tissues.**
Siriluck Ponsuksili*, Frieder Hadlich, Nares Trakooljul, Shuaichen Li, Henry Reyer, Michael Oster, and Klaus Wimmers, *Research Institute for Farm Animal Biology (FBN)*, *Dummerstorf, Germany*.

P112 **Epigenetic atlas and long-read transcriptome analysis of sex-specific ESCs and PGCs in chickens.**
Longbin Yang, Tom Porter, and Jiuzhou Song*, *University of Maryland*, *College Park, MD, USA*.

P113 **ISAG Bursary Award: Epigenetic signatures of early-life stress: Investigating stress-induced epigenetic variation in the chicken brain.**
F. Sourani*[1], F. Pértille[1], M. J. Toscano[2], M. B. Petelle[2], and C. Guerrero Bosagna[1], [1]*Department of Organismal Biology, Uppsala University*, *Uppsala, Sweden*, [2]*Center for Proper Housing: Poultry and Rabbits (ZTHZ), Division of Animal Welfare, Veterinary Public Health Institute, University of Bern*, *Zollikofen, Switzerland*.

P114 **Epigenetic signatures associated with myxomatous mitral valve disease in dogs.**
S. Jang*[1,2], C.-O. Yun[3], T.-S. Hwang[3], J. Kim[1,2], and J. Lee[4], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Institute of Animal Medicine, College of Veterinary Medicine, Gyeongsang National University, Jinju, Republic of Korea*, [4]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan-si 31000, Chungcheongnam-do, Republic of Korea*.

P115 **Epitranscriptomics: RNA A-to-I editing sites in porcine brain.**
M. Gòdia*[1], Y. Gang Gang[1], J. E. Bolhuis[2], B. Harlizius[3], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, The Netherlands*, [2]*Adaptation Physiology, Wageningen University & Research, Wageningen, The Netherlands*, [3]*Topigs Norsvin Research Center B.V, ‘s-Hertogenbosch, the Netherlands*.

P116 **DNA methylations associated with promoters and sex chromosomes in vertebrates.**
Y. Lee*[1], H. Kim[2,3], and C. Lee[4], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [2]*Department of Agricultural Biotechnology and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [3]*eGnome Inc, Seoul, Republic of Korea*, [4]*Laboratory of Neurogenetics of Language, The Rockefeller University, New York, NY, USA*.

P117 **Preliminary results of integrating DNA methylation and metabolomic to investigate molecular responses to diverging environmental conditions in the Massese sheep.**
G. Senczuk*[1], M. Di Civita[1], C. Persichilli[1], A. Francioso[2], P. Abbruscato[3], and F. Pilla[1], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso Italy*, [2]*Department of Bioscience and Agro-Food and Environmental Technology, University of Teramo, Teramo Italy*, [3]*Nuova Genetica Italiana, Villa Guardia, Como, Italy*.

P118 **Modular workflow for the custom design of livestock DNA methylation arrays.**
J. Chong*, V. Riggio, J. Prendergast, A. Tenesa, and P. Navarro, *Roslin Institute, University, Edinburgh, Scotland, United Kingdom*.

P119 **Integration of hematological parameters and DNA methylome to identify aging biomarkers in dogs.**
S. J. Kim*[1,2], C.-Y. Hong[3], S.-L. Lee[3], J. Kim[1,2], and E.-Y. Bok[4], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*College of Veterinary Medicine, Gyeongsang National University, Jinju, 52828 Republic of Korea*, [4]*Division of Animal Diseases & Health, National Institute of Animal Science, RDA, Wanju 55365, Republic of Korea*.

P120 **Cross-species conservation of epigenetic markers associated with cardiovascular traits.**
H. Jeong*[1,2], S. Jang[1,2], C.-O. Yun[3], T.-S. Hwang[3], J.-S. Koh[4], J. Kim[1,2], and J. Lee[5], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Institute of Animal Medicine, College of Veterinary Medicine, Gyeongsang National University, Jinju, Republic of Korea*, [4]*Department of Internal Medicine, Gyeongsang National University School of Medicine and Gyeongsang National University Hospital, Jinju, Republic of Korea*, [5]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan-si 31000, Chungcheongnam-do, Republic of Korea*.

P121 **Harnessing epigenetic modifications to decipher complex traits.**
S. van Rhijn*[1], S. Xie[2], S. Khilji[2], C. Stull[1], R. Schnabel[1], B. Murdoch[2], and S. McKay[1], [1]*University of Missouri, Columbia, MO, USA*, [2]*University of Idaho, Moscow, ID, USA*.

Animal Forensic Genetics

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P122 **Effects of *CW-2/NCAPG* genotype and pre-weaning growth rate on early post-weaning growth in Japanese Black Cattle.**
K. Maniwa*[1], T. Gotoh[1], and T. Shimogiri[2], [1]*Hokkaido University, Sapporo, Hokkaido, Japan*, [2]*Kagoshima University, Kagoshima, Kagoshima, Japan*.

P123 **Ancient DNA sheds light on differences between medieval war horses.**
Gabriel Anaya[1], Juan Manuel Garrido[2], Sebastián Demyda Peyrás*[1], Francisco Miró[3], Irene Montilla[4], Antonio Vallejo[5], Antonio de Juan[6], Mercedes Valera[7], Antonio Molina[1], and Jose Antonio Riquelme[2], [1]*Department of Genetics, Veterinary School, University of Córdoba, Spain*, [2]*Department of History, University of Cordoba, Spain*, [3]*Veterinary School, University of Cordoba, Spain*, [4]*Department of Historical Heritage, University of Jaen, Spain*, [5]*Archaeological Site Complex of Madinat al-Zahra, Córdoba, Spain*, [6]*Department of Historical Heritage, University of Castilla la Mancha, Ciudad Real, Spain*, [7]*Department of Agronomics, ETSIA, University of Sevilla, Spain*.

P124 **Speciome: Identification of meat and fish species in complex foods.**
G. Magagna[1], A. Giusti[2], G. Spatola[2], M. Tilola[1], A. Armani[2], and V. Filipello*[1], [1]*Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Brescia, Italy*, [2]*University of Pisa, Pisa, Italy*.

Applied Genetics of Companion Animals

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P138 **Development of a high-density canine microarray for imputation, breed identification, and parentage applications.**
Ali Pirani, Shijie Pang, and Mikyung Park*, *Thermo Fisher Scientific Inc, Seoul, South Korea*.

P139 **Development of a high-density feline microarray for breed and trait identification.**
Ali Pirani, Paola Corrales, and Mikyung Park*, *Thermo Fisher Scientific Inc, Seoul, South Korea*.

P140 **Selective sweep identification in dog populations provides potential candidate genes for trainability.**
S. F. Naghshbandi, A. A. Masoudi*, R. Vaez Torshizi, and A. Maghsoudi, *Department of Animal Science, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran*.

P141 **Transcriptomic profiling of canine gastrointestinal cancer and chronic inflammatory enteropathy: Molecular insights for diagnosis and treatment.**
Maria G. Luigi-Sierra*[1], Janne Graarup-Hansen Lyngby[2], Jennifer M. Jacobsen[1], Ann-Sofie Ingerslev[1], Charlotte Bjørnvad[2], Merete Fredholm[1], Annemarie T. Kristensen[2], Lise Nikolic Nielsen[2], and Susanna Cirera[1], [1]*Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark*, [2]*Department of Veterinary Clinical Sciences, Copenhagen, Denmark*.

Cattle Molecular Markers and Parentage Testing

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P183 **Molecular genetic analyses provide evidence of selection and adaptation of Tanzania shorthorn zebu cattle.**
G. M. Msalya*[1], C. A. Adeola[2], E. S. Kim[3], and Z. Edea[4], [1]*Department of Animal, Aquaculture and Range Sciences, Sokoine University of Agriculture (SUA), PO Box 3004, Chuo Kikuu, Morogoro, Tanzania*, [2]*State Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, 650201, Kunming, Yunan, China*, [3]*Department of Animal Science, Iowa State University, Ames, IA, USA*, [4]*Genomics and Bioinformatics Directorate, Bio and Emerging Technology Institute, Addis Ababa, Ethiopia*.

P184 **Weighted single-step genome-wide association study identifies novel candidate genes for carcass traits and primal cut yield in Hanwoo cattle.**
Jisuk Yu*[1,2] and Hak Kyo Lee[1,2], [1]*Department of Agricultural Convergence Technology, Jeonbuk National University, Jeonju 54896, Korea*, [2]*Department of Animal Biotechnology, Jeonbuk National University, Jeonju 54896, Korea*.

P185 **Neolithic mobile pastoralism—Challenges merging diverse datasets for a genomic analysis of cattle dispersal.**
J. Wankowski*[1], K. Eager[2,3], P. Thomson[3], C. Gondro[4], G. Larson[5], K. Van Damme[6], I. Tammen[3], and J. Lehner[1], [1]*Discipline of Archaeology, Faculty of Arts and Social Sciences, The University of Sydney, Sydney, NSW, Australia*, [2]*Department of Primary Industries and Regional Development, Elizabeth Macarthur Agricultural Institute, Menangle, NSW, Australia*, [3]*Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Sydney, NSW, Australia*, [4]*Department of Animal Science, Michigan State University, East Lansing, MI, USA*, [5]*School of Archaeology, Oxford, UK*, [6]*Mendel University in Brno, Brno, Czechia*.

P186 **Selection increases mitonuclear DNA discordance but reconciles incompatibility in African cattle.**
Xian Shi*[1,3], Olivier Olivier[4], Min-Sheng Peng[1,2], Ya-Ping Zhang[1,5], and Cheng Ma[2], [1]*State Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [2]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China*, [3]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, China*, [4]*Centre for Tropical Livestock Genetics and Health (CTLGH), International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [5]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, School of Life Sciences, Yunnan University, Kunming, China*.

P187 **Genetic analysis of Cárdena Andaluza, an endangered Spanish bovine breed.**
L. Borreguero*[1], M. R. Maya[2], R. Tarifa[2], I. Bonet[2], A. Trigo[2], G. Anaya[3], A. Domingo[4], A. J. Luque[5], and J. A. Bouzada[1], [1]*Laboratorio Central de Veterinaria, Algete, Madrid, Spain*, [2]*Tecnología y Servicios Agrarios (TRAGSATEC), Madrid, Spain*, [3]*Grupo de Investigación PAI-158 (MERAGEM), Universidad de Córdoba, Spain*, [4]*Centro de Selección y Reproducción Animal de Extremadura (CENSYRA), Badajoz, Spain*, [5]*Asociación de Criadores de Raza Cárdena Andaluza, Córdoba, Spain*.

P188 **Comparison of Dinucleotide and Tri- to Hexa-nucleotide microsatellite marker sets for parentage testing in Hanwoo.**
Euiseo Hong*, Nuri Choi, Yusam Kim, Sangwon Yoon, Hee Jung Baek, O-Chul Kwon, Yu Mi Jo, and Dongwon Seo, *TNT Research Ltd, Jeonju 54810, South Korea*.

P189 **Genetic and genomic analysis of heifer fertility traits using imputed whole-genome sequences in Holstein cattle.**
S. Xia*[1,2], W. Li[1,3], Y. Shen[1,2], K. Chen[1,2], Z. An[1,3], Y. Jiang[1,3], J. Zhong[1,2], and H. Wang[1,2], [1]*Jiangsu Academy of Agricultural Sciences, Nanjing, Jiangsu Province, China*, [2]*Jiangsu Province Engineering Research Center of Precision Animal Breeding, Nanjing, Jiangsu Province, China*, [3]*Nanjing Agricultural University, Nanjing, Jiangsu Province, China*.

P190 **Analysis of genetic diversity of Alatau cattle breed by STR-genotyping.**
K. Dossybayev*[1,3], T. Karymsakov[1], A. Torekhanov[1], A. Kozhakhmet[1,3], Z. Bektasov[1,2], and A. Tapelov[1,2], [1]*Kazakh Research Institute of Livestock and Fodder Production, Almaty, Kazakhstan*, [2]*Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan*, [3]*Laboratory of Genetics and Cytogenetics, Institute of Genetics and Physiology, Almaty, Kazakhstan*.

P191 **The population genetic variation of the Red Polish cattle breed in Poland.**
A. Koseniuk*, A. Szumiec, and D. Rubis, *National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland*.

P192 **Analysis of heterozygosity using large-scale microsatellite marker data in Hanwoo cows.**
E. Kim*, C. Dang, J. Cha, H. Chang, H. Seong, S. Lee, M. Alam, D. Lee, E. Ryu, C. Lee, and M. Park, *Animal Genetics & Breeding Division, National Institute of Animal Science, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P193 **Generating parental genotypes from phased half-sib offspring genotypes of Hanwoo cattle using haploid frequency-based imputation.**
N. U. Kim*[1], Y. K. Kim[2], D. H. Lee[2], S. H. Lee[2], and S. H. Lee[1], [1]*Chungnam National University, Daejeon, 34134, Republic of Korea*, [2]*Quantomic Research & Solution, Daejeon, 34134, Republic of Korea*.

P194 **ISAG Bursary Award: Genetic diversity, admixture analysis and pedigree validation in South African smallholder dairy cattle populations using genome-wide SNP data.**
L. C. Mthethwa*[1,4], Y. P. Sanarana[1], M. Malima[2], A. Maiwashe[1], N. Mapholi[4], and C. B. Banga[1,3], [1]*Agricultural Research Council-Animal Production, Pretoria, Irene, 0062, South Africa*, [2]*Agricultural Research Council-Biotechnology Technology Platform, Pretoria, 0110, South Africa*, [3]*Botswana University of Agriculture and Natural Resources, Department of Animal Sciences, 0027, Gaborone, Botswana*, [4]*University of South Africa, Department of Agriculture & Animal Health, Florida, 1709, South Africa*.

P195 **A high-throughput Applied Biosystems™ Axiom™ Bovine Genotyping array with 100,000 markers optimized for dairy evaluation.**
Ali Pirani, Arjun Kandalam, and Mikyung Park*, *Thermo Fisher Scientific Inc, Seoul, South Korea*.

P196 **ISAG Bursary Award: Application of variation graphs for genotyping structural variants in 14 French cattle breeds.**
M. M. Naji*[1], T. Faraut[2], C. Klopp[3], D. Boichard[1], M. P. Sanchez[1], and M. Boussaha[1], [1]*Université Paris Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy en Josas, France*, [2]*GenPhySE, Université de Toulouse, INRAE, ENVT, 31326 Castanet-Tolosan, France*, [3]*Université Fédérale de Toulouse, INRAE, MIAT, Sigenae, BioinfOmics, 31326 Castanet-Tolosan, France*.

P197 **ISAG Bursary Award: Utilisation of genomic parentage verification and discovery techniques in the South African Beefmaster cattle breed.**
J. J. Reding*[1,2], R. R. van der Westhuizen[2], H. E. Theron[2,1], and E. van Marle-Köster[1], [1]*University of Pretoria, Pretoria, Gauteng, South Africa*, [2]*SA Stud Book and Animal Improvement Organisation, Bloemfontein, Free State, South Africa*.

P198 **A case-parent trio WGS study reveals genetic risk factors for abortion in Hanwoo (*Bos taurus coreanae*).**
J. Seo*[1], S. Y. Jhang[2], W. Park[3], and H. Kim[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [2]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [3]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan, Chungcheongnam-do, Republic of Korea*.

Companion Animal Genetics and Genomics

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P199 **Pleiotropic gene *HMGA2* regulates canine social and non-social fear via enhancer activity-dependent regulation of expression.**
Yun Yu*[1], Chao Lilichao[1], Yinyu Su[2], Xuebin Wang[1], Ye Liu[1], James Serpell[3], Shurun Zhang[1], Jinxue Ruan[2], Yanhu Liu[1,4], and Ya-Ping Zhang[1,5], [1]*State Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650201, China*, [2]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan 430070, P. R. China*, [3]*School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA*, [4]*KIZ-CUHK Joint Laboratory of Bioresources and Molecular Research in Common Diseases, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, 650223, China*, [5]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan 650204, China*.

P200 **A combination of alleles in leiomodin 2 on chromosome 14 and in a long non-coding RNA gene on chromosome 13 is strongly associated with high risk of myxomatous mitral valve disease in Cavalier King Charles Spaniels.**
Lisbeth Høier Olsen[1], Arney Eva Gunnlaugsdóttir[5], Majbritt B. Madsen[8], Isabella J. Larsen[7], Maria J. U. Reimann[3], Foteini Papadaki[1], Ingrid Ljungvall[2], Jens Häggström[2], Torben Martinussen[1], Henrik D. Pedersen[6], Torkel Falk[4], Merete Fredholm[1], and Peter Karlskov-Mortensen*[1], [1]*University of Copenhagen, Frederiksberg C, Denmark*, [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [3]*Boehringer Ingelheim Animal Health Nordics, Copenhagen, Denmark*, [4]*Din Veterinär, Helsingborg, Sweden*, [5]*Veterinary Hospital in Garðabær, Garðabær, Iceland*, [6]*Novo Nordisk, Måløv, Denmark*, [7]*Carlsberg Research Laboratory, Copenhagen, Denmark*, [8]*Copenhagen University Hospital, Copenhagen, Denmark*.

P201 **Genetic counseling in veterinary medicine: Towards an evidence-based definition for the small animal practice.**
Laura Adant*[1,2], Virginie Szymczak[3], Sofie F. M. Bhatti[4], Pascale Smets[4], Jimmy Saunders[5], and Bart J. G. Broeckx[1,2], [1]*Department of Veterinary and Biosciences, Faculty of Veterinary Medicine, Merelbeke 9820, Belgium*, [2]*Centre for Clinical Genetics of Companion Animals, Department of Veterinary and Biosciences, Faculty of Veterinary Medicine, Merelbeke 9820, Belgium*, [3]*Center for Medical Genetics, Ghent University, Merelbeke 9820, Belgium*, [4]*Small Animal Department, Small Animal Teaching Hospital, Faculty of Veterinary Medicine, Ghent University, Merelbeke 9820, Belgium*, [5]*Department of Morphology, Imaging, Orthopedics, Rehabilitation, and Nutrition, Faculty of Veterinary Medicine, Ghent University, Merelbeke 9820, Belgium*.

P202 **Identification of differentially expressed genes associated with myxomatous mitral valve disease in companion dogs.**
J. Lee*[1], W. Park[1], H. Go[1], S. Jung[2], S. Choi[2], and D. Kim[2], [1]*Animal Genetics & Breeding Division, National Institute of Animal Science, Cheonan-si, Chungcheongnam-do, Republic of Korea*, [2]*Animal Biotechnology and Genomics Division, Wanju-gun, Jeonbuk-do, Republic of Korea*.

P203 **Exploration of individual identification markers through genetic diversity analysis based on companion dog genome information.**
G. H. Lee[2,4], G. J. Seo[1,5], D. Y. Oh[6], and H. S. Kong*[2,3], [1]*Major in Applied Biotechnology, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [2]*Gyeonggi Regional Research Center, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [3]*Genomic Information Center, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [4]*Hankyong and Genetics, Anseong, Gyeonggi-do, Republic of Korea*, [5]*Korean Gyeongju DongGyeong Dog Association, Gyeongju, Gyeongsangbuk-do, Republic of Korea*, [6]*Gyeongbuk Livestock Research Institute, Yeongju, Gyeongsangbuk-do, Republic of Korea*.

P204 **Canine cutaneous histiocytoma: A model for human pediatric disease?**
C. de Moura*[1,2], K. Sebastino[3,4], K. Pinello[5,6], J. Niza-Ribeiro[5,6], J. Santos[2,7], J. Catarino[2,7], P. Faísca[2,8], and A. J. Amaral[1,3], [1]*University of Évora, Mediterranean Institute for Agriculture, Environment, and Development (MED), Évora, Portugal*, [2]*Faculty of Veterinary Medicine, Lusofona University, Lisbon University Center, Lisbon, Portugal*, [3]*CIISA - Centre for Interdisciplinary Research in Animal Health - Lisbon University, Lisbon, Portugal*, [4]*Faculty of Veterinary Medicine, Lisbon University, Lisbon, Portugal*, [5]*Vet-OncoNet, Population Studies Department, School of Medicine and Biomedical Sciences, ICBAS, University of Porto, Porto, Portugal*, [6]*EPIUnit ITR, Institute of Public Health of the University Porto, University of Porto (ISPUP), Porto, Portugal*, [7]*DNAtech Veterinary Laboratory, Lisbon, Portugal*, [8]*CEVAC-Animal and Veterinary Research Centre, Faculty of Veterinary Medicine, Lusofona University, Lisbon University Center, Lisbon, Portugal*.

P205 **Analysis of canine gene constraint identifies new variants for orofacial clefts and stature.**
Reuben M. Buckley[1], Nüket Bilgen*[2], Alexander C. Harris[1], Peter Savolainen[3], Cafer Tepeli[4], Metin Erdogan[5], Aitor Serres Armero[1], Dayna L. Dreger[1], Frank G. van Steenbeek[6], Marjo K. Hytönen[7,8], Heidi G. Parker[1], Jessica Hale[1], Hannes Lohi[7,9], Bengi Çinar Kul[2], Adam R. Boyko[10,11], [1]*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [2]*Department of Animal Genetics, Faculty of Veterinary Medicine, University of Ankara, Ankara, Türkiye*, [3]*KTH Royal Institute of Technology, School of Chemistry, Biotechnology and Health, Science for Life Laboratory, Stockholm, Sweden*, [4]*Department of Animal Science, University of Selcuk, Faculty of Veterinary Medicine, Konya, Türkiye*, [5]*Department of Veterinary Biology and Genetics, Faculty of Veterinary Medicine, Afyon Kocatepe University, Afyonkarahisar, Türkiye*, [6]*Utrecht University, Faculty of Veterinary Medicine, Dept. of Clinical Sciences, The Netherlands*, [7]*Department of Medical and Clinical Genetics, University of Helsinki, Helsinki, Finland*, [8]*Department of Veterinary Biosciences, University of Helsinki, Helsinki, Finland*, [9]*Folkhälsan Research Center, Helsinki, Finland*, [10]*Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY, USA*, [11]*Embark Veterinary Inc, Boston, MA, USA*.

P206 **A comparative transcriptomic analysis of feline and human hypertrophic cardiomyopathy.**
T. Smedley[1], A. Karagianni[2], O. Sidekli[1], P. Syrris[3], V. Fuentes[1], D. Connolly[1], and A. Psifidi*[1], [1]*Royal Veterinary College, Hatfield, UK*, [2]*University of Surrey, Surrey, UK*, [3]*University College London, London, UK*.

P207 **ROS_Cfam_2.0: A telomere-to-telomere dog reference genome.**
Jeffrey J. Schoenebeck*[1], Juhyun Kim[2], Brandon D. Pickett[2], Arang Rhie[2], Dmitry Antipov[2], Alice C. Young[3], Shelise Y. Brooks[3], Gerard G. Bouffard[3], Chandrindu Abeykoon[1], Melany Jackson[1], Derya Ozdemir[1], Elaine A. Ostrander[4], Sergey Koren[2], and Adam M. Phillippy[2], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, Scotland, UK*, [2]*Genome Informatics Section, Center for Genomics and Data Science Research, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [3]*NIH Intramural Sequencing Center, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [4]*Cancer Genetics and Comparative Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*.

P208 **ISAG Bursary Award: ZMYND10 frameshift deletion in Eurasier dogs with primary ciliary dyskinesia.**
C. Schwarz*[1,2], H. Jainek[3], U. Hetzel[4], V. Jagannathan[1], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Graduate School for Cellular and Biomedical Sciences (GCB), Bern, Switzerland*, [3]*Clinic of Reproductive Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*, [4]*Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*.

P209 **Genomic diversity and selection in the racing Greyhound of Great Britain.**
H. Han*[1], T. A. Blackett[2], M. L. H. Campbell[2,3], A. H. Holtby[1], B. A. McGivney[1], and E. W. Hill[1,4], [1]*Zinto Labs, Dublin, Ireland*, [2]*Greyhound Board of Great Britain, London, United Kingdom*, [3]*Nottingham University, Sutton Bonington, United Kingdom*, [4]*University College Dublin, Dublin, Ireland*.

P210 **Gene expression and regulatory pathways in feline elbow osteoarthritis.**
C. Ley[1], C. J. Ley[2], and Å. Ohlsson*[1], [1]*Department of Animal Biosciences, Swedish University of Agricultural Sciences, Uppsala, Sweden*, [2]*Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

P211 **Myocardial long non-coding RNA profiling for feline hypertrophic cardiomyopathy.**
O. Sidekli*, T. A. Smedley, X. Dai, V. L. Fuentes, D. J. Connolly, and A. Psifidi, *Clinical Sciences and Services, Royal Veterinary College, Hatfield, United Kingdom*.

P212 **ISAG Bursary Award: Beyond the exome: Identifying non-coding driver mutations in canine diffuse large B-cell lymphoma.**
A. D. van der Heiden*[1,2], S. Mäkeläinen[1,2], R. Pensch[1,2], S. V. Kozyrev[1,2], S. Agger[3], C. London[4], J. F. Modiano[5], K. Forsberg Nilsson[1], M. L. Arendt[1,3], and K. Lindblad-Toh[1,6], [1]*Uppsala University, Uppsala, Sweden*, [2]*SciLifeLab, Uppsala, Sweden*, [3]*University of Copenhagen, Copenhagen, Denmark*, [4]*Tufts University, North Grafton, MA, USA*, [5]*University of Minnesota, Minneapolis, MN, USA*, [6]*Broad Institute, Cambridge, MA, USA*.

Domestic Animal Sequencing and Annotation

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P241 **Mechanism of hypothalamic microglia in regulating fear behavior in Shaoxing Ducks.**
Linfang Wang* and Li Chen, *Xianghu Laboratory, The Institute of Seed Industry, Xianghu Laboratory, Qiantang River International Innovation Belt of the Xiaoshan Economic and Technological Development Zone, Hangzhou, China*.

P242 **Targeted genotyping by sequencing with Twist Biosciences target enrichment panels in bovine.**
M. S. Tahir*[1], R. Hatherley[1], C. Reich[1], B. Mason[1], M. Malmberg[1], A. Werner[2], C. Roy[1], I. Macleod[1,3], and A. Chamberlain[1,3], [1]*AgriBio Center, Agriculture Victoria Research, Bundoora, Victoria, Australia*, [2]*Twist Bioscience, South San Francisco, CA, USA*, [3]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.

P243 **Unveiling the Mitochondrial Genome Sequence of Kejobong Goat (*Capra hircus*) by Nanopore Sequencing: Insights into Indonesia's Indigenous Genetic Resources.**
Dela Ayu Lestari*[1], Sutopo1[1], Edy Kurnianto[1], Muhammad Ihsan Andi Dagong[2], Sri Rahma Aprilita Bugiwati[2], Nena Hilmia[3], Hideyuki Mannen[4], Sutikno Sutikno[5], Procula Rudlof Matitaputty[6], and Asep Setiaji[1], [1]*Department of Animal Science, Faculty of Animal and Agricultural Sciences, Universitas Diponegoro, Semarang, Central Java, Indonesia*, [2]*Department of Animal Production, Faculty of Animal Science, Hasanuddin University, South Sulawesi, Makassar, Indonesia*, [3]*Faculty of Animal Husbandry, Padjadjaran University, Jatinangor, Sumedang, Indonesia*, [4]*Graduate School of Agricultural Science, Kobe University, Kobe, Japan*, [5]*Research Center for Biology, National Research and Innovation Agency (BRIN), Bogor, Indonesia*, [6]*Assessment Institute for Agriculture Technology East Nusa Tenggara (AIAT-ENT), Kupang, Indonesia*.

P244 **Structural variations associated with leucism and albinism in Hanwoo cattle.**
S. Ko*[1], Y. Kim[2], P. T. N. Dinh[1], S. H. Lee[3], Y. Ko[4], S. Lee[4], J. Lee[4], and C. Kim[4], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, 34134, Korea*, [2]*Institute of Agricultural Science, Chungnam National University, Daejeon 34134, Republic of Korea*, [3]*Division of Animal & Dairy Science, Chungnam National University, Daejeon, 34134, Korea*, [4]*Animal Genetic Resources Research Center, National Institute of Animal Science, RDA, Hamyang, 50000, Korea*.

P245 **ISAG Bursary Award: Telomere-to-telomere genome assembly of a male goat reveals variants associated with cashmere traits.**
H. Wu*[1,2], L. L. Luo[1], Y. H. Zhang[1], C. H. Zhang[3], Z. H. Liu[3], S. G. Jia[4], and M. H. Li[1], [1]*Frontiers Science Center for Molecular Design Breeding (MOE), State Key Laboratory of Animal Biotech Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*Northern Agriculture and Animal Husbandry Technical Innovation Center, Chinese Academy of Agricultural Sciences, Hohhot, China*, [3]*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China*, [4]*College of Grassland Science and Technology, China Agricultural University, Beijing, China*.

P246 **Chromosome-level genome assemblies and annotation of Finnish native livestock: Finnsheep and Western Finncattle.**
K. Pokharel*[1], M. Weldenegodguad[2], and R. Okwasiimire[3,1], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*Natural Resources Institute Finland (Luke), Helsinki, Finland*, [3]*University of Helsinki, Department of Agricultural Sciences, Helsinki, Finland*.

P247 **Chromosome-scale assembly with improved annotation of an American Shorthair cat.**
Y. Matsumoto[1,2], C. Y. L. Chung[3], S. Isobe[4], M. Sakamoto[5], X. Lin[3], T. F. Chan[3], H. Hirakawa[4], G. Ishikawa[1], H. M. Lam[3], Y. Tanizawa[5], K. Watanabe[1], M. Yagura[5], Y. Niimura[6], and Y. Nakamura*[5], [1]*Research and Development Section, Anicom Specialty Medical Institute Inc, Yokohama, Kanagawa, Japan*, [2]*Data Science Center, Azabu University, Sagamihara, Kanagawa, Japan*, [3]*School of Life Sciences and the Center for Soybean Research of the State Key Laboratory of Agrobiotechnology, The Chinese University of Hong Kong, Shatin, Hong Kong Special Administrative Region*, [4]*Kazusa DNA Research Institute, Kisarazu, Chiba, Japan*, [5]*National Institute of Genetics, Research Organization of Information and Systems, Mishima, Shizuoka, Japan*, [6]*Department of Veterinary Sciences, Faculty of Agriculture, University of Miyazaki, Miyazaki, Miyazaki, Japan*.

P248 **Insights from population scale long read sequencing of cattle.**
A. J. Chamberlain*[1,2], T. V. Nguyen[1], J. Wang[1], and I. M. MacLeod[1,2], [1]*Agriculture Victoria, Centre for AgriBioscience, Bundoora, Victoria, Australia*, [2]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.

P249 **You too can T2T: Democratizing telomere-to-telomere assembly for non-model organisms.**
D. Antipov, J. Kim, A. Rhie, A. M. Phillippy, and S. Koren*, *Genome Informatics Section, Center for Genomics and Data Science Research, National Human Genome Research Institute, Bethesda, MD, USA*.

Genome Edited Animals

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P307 **Effects of the *MC1R* c.741_742insGC frameshift mutation on the regulation of pigmentation in Liang Guang Small Spotted pigs.**
S. Zhu*, J. Lan, X. Shi, W. Jiang, P. Cong, X. Liu, Y. Chen, and Z. He, *State Key Laboratory of Biocontrol, School of Life Sciences, Sun Yat-sen University*, *Guangzhou, Guangdong, China*.

P308 **Evaluation of the resistance of Liang Guang Small Spotted pigs with partial deletion of the CD163 SRCR5 domain to porcine reproductive and respiratory syndrome virus 2 infection.**
Yu Wu, Xiaohong Liu, Yaosheng Chen, Zuyong He, and Sitong Zhu*, *School of Life Sciences, Sun Yat-sen University*, *Guangzhou, Guangdong, China*.

P309 **EXPERT expands prime editing efficiency and range of large fragment edits.**
Y. C. Xiong[1,2], Y. Y. Su*[1,2], R. G. He[1,2], X. S. Han[1,3], H. Wang[1,2], S. S. Xie[1,2], X. W. Xu[1,2], K. Li[6], J. Xu[7], X. Y. Li[1,2], S. H. Zhao[1,2], and J. X. Ruan[1,2], [1]*Frontiers Science Center for Animal Breeding and Sustainable Production, Huazhong Agricultural University*, *Wuhan, PR China*, [2]*Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University*, *Wuhan, PR China*, [3]*Yazhouwan National Laboratory*, *Sanya, PR China*, [4]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agri cultural University*, *Wuhan, PR China*, [5]*Hubei Hongshan Laboratory, Huazhong Agricultural University*, *Wuhan, PR China*, [6]*Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences*, *Shenzhen, PR China*, [7]*Center for Advanced Models for Translational Sciences and Therapeutics, University of Michigan Medical School*, *Ann Arbor, MI, USA*.

P310 **ISAG Bursary Award: Fertility following germline transplantation in sterile *NANOS2* knockout surrogate bulls.**
B. E. Latham*, M. I. Giassetti, M. Ciccarelli, M. J. Oatley, D. Miao, A. Tibary, and J. Oatley, *College of Veterinary Medicine, Washington State University*, *Pullman, WA, USA*.

P311 **Sustainable bioproduction of functional multimeric recombinant human adiponectin in genome-edited chickens.**
Y. Han*[1], E. Yoo[1], H. Choi[1], J. Kim[2], Y. Hong[1], and J. Han[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University*, *Seoul, Republic of Korea*, [2]*Department of International Agricultural Technology & Institute of Green Bioscience and Technology, Seoul National University*, *Pyeongchang, Gangwon, Republic of Korea*.

P312 **Evaluation of the Cytosine Base Editors in chicken somatic cells for Poultry Breeding Applications.**
Pan Li* and Li Chen, *Xianghu Laboratory*, *Hangzhou, Zhejiang, China*.

P313 **Glycosylase-mediated base editors show undetectable off-targets and high on-target editing in mammalian embryos.**
Yinghui Wei[1,2], Kun Xu[1,2], Wenxin Zheng[3], Weiwei Wu[4], and Xiaolong Wang*[1,2], [1]*International Joint Agriculture Research Center for Animal Bio-Breeding of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, Northwest A&F University*, *Yangling, Shaanxi, 712100, China*, [2]*Hainan Institute of Northwest A&F University*, *Sanya, Hainan, 572025, China*, [3]*Institute of Animal Husbandry Quality Standards, Xinjiang Academy of Animal Science*, *Urumqi, Xinjiang, 830011, China*, [4]*Institute of Animal Science, Xinjiang Academy of Animal Science*, *Urumqi, Xinjiang, 830011, China*.

P314 **Expanding the CRISPR toolbox by engineering Cas12a orthologs of metagenomic discovery.**
D. G. Tao[1,3], B. R. Xu[1,2], S. Li[1,3], H. L. Liu[1,3], S. Y. Shi[1,3], Y. Wang[1,2], C. Z. Zhao[3], J. X. Ruan[1,3], L. L. Fu[1,3], X. X. Huang[5], X.Y. Li[1,3], S. H. Zhao[1,4], and S. S. Xie*[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University*, *Wuhan, P. R. China*, [2]*Yazhouwan National Laboratory (YNL)*, *Sanya Hainan, P. R. China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University*, *Wuhan, P. R. China*, [4]*Hubei Hongshan Laboratory, Huazhong Agricultural University*, *Wuhan, P. R. China*, [5]*Laboratory of Pancreatic Disease, The First Affiliated Hospital, Zhejiang University School of Medicine*, *Hangzhou, P. R. China*.

P315 **On-site detection of targeted genome-modification sites and SNPs in agricultural animals via improved RAVI-CRISPR strategy.**
Y. Wang[1,2], L. T. Fu[3], D. G. Tao[1], B. R. Xu[1,2], S. Li[1], X. Y. Li[1], S. H. Zhao[1,2], and S. S. Xie*[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University*, *Wuhan, P. R. China*, [2]*Yazhouwan National Laboratory (YNL)*, *Sanya Hainan, P. R. China*, [3]*Wuhan Shangrui Biotechnology Co., Ltd*, *Wuhan, P. R. China*.

Ruminant Genetics and Genomics I

Exhibition Hall 109 + 110 + 111 + 112
11:10 AM - 12:30 PM

P455 **Assessing structural variants in DSN cattle and their impact on genomic features.**
P. Korkuc, G. B. Neumann, M. Reissmann, and G. A. Brockmann*, *Humboldt-Universität zu Berlin, Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Animal Breeding and Molecular Genetics, Berlin, Germany*.

P456 **Differential expression of circulating microRNAs in lactating Holstein and Jersey cows exposed to heat stress.**
T. Choi*[1], J. Lee[1], D. Kim[1], B. Lim[2], G. Ryu[1], H. Baek[1], J. Kim[3], S. Ha[4], S. Kim[1], S. Lee[5], and I. Choi[5], [1]*Dairy Science Division, National Institute of Animal Science, RDA, Cheonan, Chungnam, South Korea*, [2]*Department of Animal Science and Technology, Chung-Ang University, Anseong, Kyeongki, South Korea*, [3]*Dairy Biotechnology R&D Center, Seoul Milk Cooperation, Yangpyeong, Kyeongki, South Korea*, [4]*Animal Genetic Resources Research Center, National Institute of Animal Science, RDA, Hamyang, Kyeongbuk, South Korea*, [5]*Division of Animal and Dairy Sciences, College of Agriculture and Life Sciences, Chungnam National University, Daejeong, Chungnam, South Korea*.

P457 **From data to decisions: Using genomics and sensors to monitor Holstein behavior and welfare.**
Boris Lukic*[1], Ino Curik[2,5], Karlo Nyarko[3], Tina Bobic[1], Marko Oroz[1], Mihaela Oroz[1], Mario Shihabi[2], David Kranjac[1], Marija Spehar[4], and Nikola Raguz[1], [1]*Faculty of Agrobiotechnical Sciences Osijek, University of Josip Juraj Strossmayer of Osijek, Department for Animal Production and Biotechnology, Osijek, Croatia*, [2]*Faculty of Agriculture, University of Zagreb, Department of Animal Science, Zagreb, Croatia*, [3]*Faculty of Electrical Engineering, Computer Science and Information Technology Osijek, Department of Computer Engineering and Automation, Osijek, Croatia*, [4]*Centre for Livestock Breeding, Department for Genetic Evaluation, Zagreb, Croatia*, [5]*Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences, Kaposvar, Hungary*.

P458 **Genetic control of DNA methylation in bovine sperm cells.**
Y. Tang* and Y. Yu, *Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture & National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*.

P459 **Estimation of genetic parameters for bull conception rate and its genetic correlations with semen production traits in Japanese Black bulls.**
Yoshinobu Uemoto*[1], Rintaro Nagai[1], Masashi Kinukawa[2], Toshio Watanabe[2], Atsushi Ogino[2], Kazuhito Kurogi[3], and Masahiro Satoh[1], [1]*Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan*, [2]*Maebashi Institute of Animal Science, Livestock Improvement Association of Japan Inc, Maebashi, Gunma, Japan*, [3]*Cattle Breeding Department, Livestock Improvement Association of Japan Inc, Tokyo, Japan*.

P460 **ISAG Bursary Award: Oxford Nanopore Technologies reveals age-related genes in beef cattle.**
Yijie Guo, Elizabeth M. Ross, Ben Hayes, and Loan T. Nguyen*, *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia*.

P461 **Structural variations associated with adaptation and coat color in Qinghai-Tibetan Plateau cattle.**
X. T. Xia, F. W. Wang, X. Y. Luo, C. Z. Lei, and N. B. Chen*, *Northwest A&F Unversity, Yangling, Shaanxi, China*.

P462 **Genetic parameters, correlations, and genome-wide association study of cortisol response to LPS challenge in heifers.**
Bruno A. Galindo[1,2], Umesh K. Shandilya[1], Flavio S. Schenkel[1], and Niel A. Karrow*[1], [1]*Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada*, [2]*State University of the Northern Parana, Cornélio Procópio, PR, Brazil*.

P463 **Development of an early prediction model for key swine traits using genomic estimated breeding values and weather data.**
S. W. Yoon*, Y. S. Kim, H. J. Beak, E. S. Hong, O. C. Kwon, N. R. Choi, Y. M. Jo, and D. W. Seo, *TNT Research Co. Ltd, Jeonju-si, Jeollabuk-do, Korea*.

P464 **DaMoS: A cost-effective multi-omic strategy for dairy cattle improvement using low-pass whole-genome sequencing.**
I. Drzaic*[1], V. Brajkovic[1], V. Cubric-Curik[1], M. Ferencakovic[1], M. Shihabi[1], Z. Mijadzikovic[1], N. Raguz[2], B. Lukic[2], N. Mikulec[1], D. Hrsak[3], D. Novosel[4], and I. Curik[1,5], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia*, [2]*J.J. Strossmayer University of Osijek Faculty of Agrobiotechnical Sciences, Osijek, Croatia*, [3]*Ruder Boškovic Institute, Zagreb, Croatia*, [4]*Croatian Veterinary Institute, Zagreb, Croatia*, [5]*Hungarian University of Agriculture and Life Sciences (MATE), Kaposvár, Hungary*.

P465 **GWAS analysis of coccidiosis resistance in Portuguese Merino sheep.**

E. Varela Martínez*[1], A. Afonso[2,3], D. Mainou[4], F. Teixeira[5,6], T. Nunes[7,8], P. Vieira[9], I. Sarraguça[7,8], C. Martins[2], N. Campbell[2,5], R. Cordeiro da Silva[10], T. Perloiro[10], L. Madeira de Carvalho[7,8], A. C. Ferreira[2,9], L. Telo da Gama[7,8], H. Waap[2,7], [1]*Department of Genetics, Physical Anthropology and Animal Physiology, Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Biscay, Spain*, [2]*Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Oeiras, Lisbon District, Portugal*, [3]*Global Health and Tropical Medicine (GHTM), Associate Laboratory in Translation and Innovation Towards Global Health, LA-REAL, Instituto de Higiene e Medicina Tropical (IHMT), Universidade NOVA de Lisboa (UNL), Lisbon, Lisbon District, Portugal*, [4]*Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Central Macedonia, Greece*, [5]*MED—Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute, University of Évora, Évora, Évora District, Portugal*, [6]*School of Science and Technology, University of Evora, Évora, Évora District, Portugal*, [7]*CIISA - Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Lisbon District, Portugal*, [8]*Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Lisbon, Lisbon District, Portugal*, [9]*Faculdade de Medicina Veterinária, Universidade Lusófona de Humanidades e Tecnologias, Centro Universitário de Lisboa, Lisbon, Lisbon District, Portugal*, [10]*Associação Nacional de Criadores de Ovinos de Raça Merina (ANCORME), Évora, Évora District, Portugal*.

P466 **Interplay between microbial and host genes affects methane emission in Nelore cattle rumen.**

J. Afonso[1], J. V. da Silva[2], T. Figueiredo Cardoso[1], J. J. Bruscadin[2], L. C. Conteville[1], L. G. Clemente[3], A. O. de Lima[4], W. J. S. Diniz[5], G. B. Mourao[3], A. Zerlotini[6], M. Tanurdzic[7], L. L. Coutinho[3], M. R. S. Fortes[8], and L. C. A. Regitano*[1], [1]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil*, [2]*Post-graduation Program of Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [3]*Department of Food Science and Technology (ESALQ), University of São Paulo, Piracicaba, São Paulo, Brazil*, [4]*Division of Medical Genetics, Department of Genome Sciences, Department of Medicine, University of Washington, Seattle, WA, USA*, [5]*Department of Animal Sciences, Auburn University, Auburn, AL, USA*, [6]*Bioinformatic Multi-User Laboratory, Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil*, [7]*School of Biological Sciences, The University of Queensland, Brisbane, Queensland, Australia*, [8]*School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Queensland, Australia*.

P467 **Telomere-to-telomere sheep genome assembly identifies variants associated with wool fineness.**

L. Y. Luo*[1], H. Wu[1], L. M. Zhao[2], Y. H. Zhang[1], J. H. Huang[1], Q. Y. Liu[3], H. T. Wang[3], D. X. Mo[1], H. H. Eer[4], L. Q. Zhang[5], H. L. Chen[6], S. G. Jia[7], W. M. Wang[2], and M. H. Li[1], [1]*Frontiers Science Center for Molecular Design Breeding (MOE); State Key Laboratory of Animal Biotech Breeding; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems; Key Laboratory of Grassland Livestock Industry Innovation, Ministry of Agriculture and Rural Affairs, College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, Gansu, China*, [3]*Institute of Genetics and Developmental Biology, The Innovation Academy for Seed Design, Chinese Academy of Sciences, Beijing, China*, [4]*Institute of Animal Science, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan, Ningxia, China*, [5]*Ningxia Shuomuyanchi Tan Sheep Breeding Co. Ltd, Wuzhong, Ningxia, China*, [6]*Beijing Lvyeqingchuan Zoo Co. Ltd, Beijing, China*, [7]*College of Grassland Science and Technology, China Agricultural University, Beijing, China*.

P488 **SNP Chip data analysis of lethal gene carrier frequencies in Holstein and Jersey dairy cattle.**

R. Kim*, C. Dang, J. Cha, H. Chang, H. Seung, S. Lee, E. Kim, M. Alam, D. Lee, E. Ryu, C. Lee, and M. Park, *National Institute of Animal Science, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P489 **Development of an early prediction model for Hanwoo carcass traits using genomic estimated breeding values and weather data.**

S. W. Yoon*, Y. S. Kim, H. J. Beak, E. S. Hong, O. C. Kwon, N. R. Choi, Y. M. Jo, and D. W. Seo, *TNT Research Co., Ltd, Jeonju-si, Jeollabuk-do, Korea*.

P490 **A synonymous SNP in *DGAT1* affects milk fat percentage of dairy sheep by regulating the stability of the mRNA to change the viability, proliferation triglyceride levels of ovine mammary epithelial cells.**

H. Zhen*, J. Wang, Z. Hao, M. Li, and C. Ren, *Gansu Agricultural University, Lanzhou, Gansu, China*.

P491 **Genome-wide signatures of selection and functional characterization of Croatian Holstein cattle.**

M. Shihabi*[2], I. Curik[2,5], T. Bobic[1], M. Oroz[1], D. Kranjac[1], K. Nyarko[3], M. Spehar[4], N. Raguz[1], and B. Lukic[1], [1]*Faculty of Agrobiotechnical Science Osijek, University of Josip Juraj Strossmayer of Osijek, Osijek, Croatia*, [2]*Faculty of Agriculture, University of Zagreb, Zagreb, Croatia*, [3]*Faculty of Electrical Engineering, Computer Science and Information Technology Osijek, Osijek, Croatia*, [4]*Centre for Livestock Breeding, Department for Genetic Evaluation, Zagreb, Croatia*, [5]*Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences, Kaposvár, Hungary*.

P492 **Tracing cattle dispersal through time: Meta-analysis of mitogenome haplogroups and their global phylogeography.**
V. Brajkovic*[1], D. Novosel[1,2], I. Drzaic[1], I. Kersic[1], C. Saliari[3], R. Sosic Klindzic[4], G. Tomac[4], J. Kantanen[5], M. Weldenegodguad[5], J. W. Choi[6], I. Curik[1,8], P. T. Miracle[7], and V Cubric-Curik[1], [1]*University of Zagreb Faculty of Agriculture*, *Zagreb, Croatia*, [2]*Croatian Veterinary Institute*, *Zagreb, Croatia*, [3]*Museum of Natural History Vienna*, *Vienna, Austria*, [4]*University of Zagreb Faculty of Humanities and Social Sciences*, *Zagreb, Croatia*, [5]*Natural Resources Institute Finland*, *Jokioinen, Finland*, [6]*College of Animal Life Sciences, Division of Animal Resource Science*, *Chuncheon, Republic of Korea*, [7]*McDonald Institute for Archaeological Research University of Cambridge*, *Cambridge, UK*, [8]*Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences (MATE)*, *Kaposvár, Hungary*.

P493 **Heart Girth Variability as a Novel, Low-Cost Indicator of Climate Resilience in Smallholder Dairy Systems in Low- and Middle-Income Countries.**
C. C. Ekine-Dzivenu*[1], D. Komwihangilo[3], E. Lyatuu[1], G. Msuta[3], S. Meseret[4], H. Messay[4], J. M. K. Ojango[1], G. Gebreyohanes[1], and R. Mrode[1,2], [1]*International Livestock Research Institute*, *Nairobi, Kenya*, [2]*Scotland Rural College*, *Edinburgh, United Kingdom*, [3]*Tanzania Livestock Research Institute*, *Dodoma, Tanzania*, [4]*International Livestock Research Institute*, *Addis Ababa, Ethiopia*.

P494 **On the genetic architecture of the inbreeding load in the Rubia Gallega beef cattle population.**
C. Hervas Rivero, D. Lopez Carbonell, M. Sanchez Diaz, and L. Varona*, *Universidad de Zaragoza*, *Zaragoza, Spain*.

P495 **Proposing a multi-trait index to select cattle for enhanced fertility.**
Wei L. A. Tan[1], Antonio Reverter[2], Laercio R. Porto Neto[2], and Marina R. S. Fortes*[1], [1]*University of Queensland*, *Brisbane, Queensland, Australia*, [2]*CSIRO Agriculture and Food*, *Brisbane, Queensland, Australia*.

P496 **Identification of key effector genes influencing litter size in Hu sheep.**
Na Zhang*[1,2], Zexuan Liu[1], Daxiang Wang[4], Jianlin Han[3], Yiqiang Zhao[1], and Qiuyue Liu[2], [1]*College of Biology Sciences, China Agricultural University*, *Beijing, China*, [2]*Institute of Genetics and Developmental Biology, Chinese Academy of Sciences*, *Beijing, China*, [3]*Yazhouwan National Laboratory*, *Sanya, China*, [4]*Jiangsu Qianbao Animal Husbandry Co., Ltd*, *Yancheng, China*.

P497 **Update of reference population with other sources of data to increase accuracy of genomic prediction in Hanwoo cattle.**
S. Maeng*[1], Y. Kim[2], Y. Chung[1], D. Lee[2], and S. H. Lee[3], [1]*Institute of Agricultural Science, Chungnam National University*, *Daejeon, Republic of Korea*, [2]*Quantomic Research and Solution*, *Daejeon, Republic of Korea*, [3]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*.

P498 **Identification of lncRNAs involved in the hair follicle cycle transition of cashmere goats in response to photoperiod change.**
M. Yang*[1], Y. Y. Li[1], Y. H. Ma[2], G. Andersson[3], E. Bongcam-Rudloff[3], H. I. Ahmad[4], and J. L. Han[1], [1]*College of Animal Science and Technology, Shihezi University*, *Shihezi, China*, [2]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [3]*Department of Animal Biosciences, Swedish University of Agricultural Sciences*, *Uppsala, Sweden*, [4]*Department of Animal Breeding and Genetics, Faculty of Veterinary and Animal Sciences, Islamia University of Bahawalpur*, *Bahawalpur, Pakistan*.

P499 **Association of the POU class 1 homeobox 1 gene with milk production and reproductive traits of Indonesian Holstein Friesian.**
Ahmad Pramono[1], Muhammad Cahyadi*[1], Zakaria Abdurrahman[2], Suryo Firmanto[3], and Rizwan Friyatna[3], [1]*Department of Animal Science, Universitas Sebelas Maret*, *Surakarta, Jawa Tengah, Indonesia*, [2]*Department of Animal Science, Universitas Boyolali*, *Boyolali, Jawa Tengah, Indonesia*, [3]*PT. Ultra Peternakan Bandung Selatan*, *Kabupaten Bandung, Jawa Barat, Indonesia*.

P500 **ISAG Bursary Award: Integrating GWAS, RNA-seq, and functional annotation to identify causal genes for complex traits in dairy cattle.**
Mohammad Ghoreishifar*[1,2], Amanda Chamberlain[1,2], Jennie Pryce[1,2], and Michael Goddard[1,3], [1]*Agriculture Victoria Research, AgriBio Centre for AgriBioscience*, *Bundoora, VIC 3083, Australia*, [2]*School of Applied Systems Biology, La Trobe University*, *Bundoora, VIC 3083, Australia*, [3]*Faculty of Science, University of Melbourne*, *Parkville, Victoria, 3010, Australia*.

P501 **Effects of *SCD1* A293V and *DGAT1* K232A polymorphisms on milk and fatty acid traits in White Fulani cattle breed.**
Isidore Houaga[1], Yacouba Zaré*[2], Anne W. T. Muigai[3], Fredrick M. Ng'ang'a[4], Eveline M. Ibeagha-Awemu[5], Martina Kyallo[4], Issaka A. K. Youssao[6], and Francesca Stomeo[4], [1]*African Institute of Data Driven Animal and Plant Breeding and Genetics (DATA-GENES-AFRICA)*, *Aplahoue, Benin Republic*, [2]*CNRST/INERA/LaRePSA, Centre National de Recherche Scientifique et Technologique (CNRST)/Institut de l'Environnement et Ouagadougou*, *Burkina Faso*, [3]*Department of Botany, Jomo Kenyatta University of Agriculture and Technology*, *Nairobi, Kenya*, [4]*Biosciences Eastern and Central Africa-International Livestock Research Institute (BecA-ILRI) Hub*, *Nairobi, Kenya*, [5]*Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre*, *Sherbrooke, QC, Canada*, [6]*Laboratory of Animal Biotechnology and Meat Technology, Department of Animal Health and Production, Polytechnic School of Abomey-Calavi University*, *Cotonou, Benin Republic*.

P502 **A TWAS-GTBLUP approach for heritability estimation in Hanwoo cattle.**
Yoonji Chung*[1], Phuong Thanh N. Dinh[2], Suyeon Maeng[1], Hayeong Oh[2], Seunghwan Ko[2], Ju Hyeok Kim[3], and Seung Hwan Lee[3], [1]*Institute of Agricultural Science, Chungnam National University*, *Daejeon, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*.

P503 **Genetic diversity and ancestral genealogy of Hanwoo cattle using ancestral recombination graphs.**
Yoonji Chung*[1], Ju Hyeok Kim[2], Phuong Thanh N. Dinh[3], Suyeon Maeng[1], Hayeong Oh[3], Seunghwan Ko[3], and Seung Hwan Lee[2], [1]*Institute of Agricultural Science, Chungnam National University*, *Daejeon, Republic of Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*.

P504 **Research on adulteration detection of camel milk and milk powder based on near-infrared spectroscopy combined with chemometrics.**
Naqin Bao*, *Inner Mongolia Agricultural University*, *Hohhot, Inner Mongolia, China*.

P505 **Characterization of GDF11 in production, carcass, and meat quality traits in Canadian beef cattle.**
Ezrie Scott[1], Bimol Roy[2], Gregory Penner[1], Heather Bruce[2], and Mika Asai-Coakwell*[1], [1]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*University of Alberta*, *Edmonton, Alberta, Canada*.

P506 **Prediction of Hanwoo body weight and body length using 3D depth image data.**
D. Lee*[1], Y. Kim[1], S. Lee[1], N. Kim[2], J. Lee[3], and S. Lee[2], [1]*Quantomic Research and Solution Co*, *Daejeon, Republic of Korea*, [2]*Department of Animal Science and Biotechnology, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*.

P507 **Estimation of genomic prediction accuracy for reproductive traits in Korean Hanwoo cattle population.**
JongJoo Kim*, Eunbi Jang, Handeul Lee, and Azizul Haque, *Yeungnam University*, *Korea*.

P508 **Evaluation of genomic prediction accuracies for carcass traits in Korean Hanwoo cows using whole-genome SNP chip panels.**
Han-Deul Lee*, Ji-Hee Jang, Azizul Haque, and JongJoo Kim, *Yeungnam University*, *Gyeongsan, South Korea*.

P509 **Assessment of genomic prediction accuracy for carcass traits in Jeju Black cattle using whole-genome SNP chip panels.**
Md Azizul Haque*, Ji-Hee Jang, Han-Deul Lee, and Jong-Joo Kim, *Yeungnam University*, *Gyeongsan, Gyeongbuk, Korea*.

P510 **Genome-wide association study for heifer stayability in *Bos indicus* × *Bos taurus* crossbred cattle.**
J. Davenport and C. A. Gill*, *Texas A&M University*, *College Station, TX, USA*.

P511 **Genome-wide association study identifies SNPs potentially linked to coat pigmentation in Romanian sheep breeds.**
V. A. Bâlteanu*[1], A. Zsolnai[2], and M. Mihaiu[1], [1]*University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca*, *Cluj, Romania*, [2]*Hungarian University of Agriculture and Life Sciences Kaposvár Campus*, *Kaposvár, Hungary*.

P512 **The Argentine-Patagonic Criollo cattle: A tale of genomic divergence after 70 years of natural selection and isolation.**
Enrique Género[1], Luciana Erneta[1], Daniela Estevez[1], Ayelén Karlau[2], Antonio Molina[3], and Sebastián Demyda Peyrás*[3], [1]*IIPAAS, Agricultural Sciences School, National University of Lomas de Zamora*, *Buenos Aires, Argentina*, [2]*Veterinary School, National University of La Plata*, *Buenos Aires, Argentina*, [3]*Department of Genetics, Veterinary School, University of Córdoba*, *Spain*.

P513 **Uncovering the genetic diversity of native bovine from South Angola.**
K. Sebastino*[1,3], H. Chiaia[1,2], P. Afonso[2], J. Gaspar[2], F. Teixeira[2,6], S. Ngola[4], C. Simão[4], J. Casimiro[4], P. Nanga[3], A. Miguel[4], L. Gomes[5], A. Alexandre[2], A. Leitão[1], J. Cordeiro[2], A. Amaral[1,6], [1]*Centre for Interdisciplinary Research in Animal Health (CIISA), Faculdade de Medicina Veterinária da Universidade de Lisboa*, *Lisbon, Portugal*, [2]*Faculdade de Medicina Veterinária do Huambo, Universidade José Eduardo dos Santos (UJES)*, *Huambo, Angola*, [3]*Instituto de Investigação Veterinária (IIV)*, *Huambo, Angola*, [4]*Instituto dos Serviços de Veterinária (ISV)*, *Angola*, [5]*Instituto Técnico Agrário (ITA)*, *Huambo, Angola*, [6]*Universidade de Évora, MED—Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute*, *Évora, Portugal*.

P514 **Comparison of prediction accuracy in Hanwoo beef cattle using pedigree BLUP and single-step genomic BLUP.**
H. Seong*[1], M. Park[1], C. Cho[2], C. Dang[1], S. Lee[1], E. Kim[1], W. Park[1], J. Lee[1], H. Ko[1], J. Cha[1], M. Alam[1], D. Lee[1], E. Ryu[1], C. Lee[1], R. Kim[1], [1]*Animal Breeding and Genetics Division, National Institute of Animal Science, Rural Development Admission*, *Cheonan, Republic of Korea*, [2]*Hanwoo Genetic Improvement Center, NongHyup Agribusiness Group Inc*, *Seosan, Republic of Korea*.

P515 **The effect of MC1R and ASIP genes on coat color of Korean native brindle cattle.**
H. Seong*, M. Park, C. Dang, S. Lee, E. Kim, J. Cha, J. Lee, M. Alam, D. Lee, E. Ryu, C. Lee, and R. Kim, *Animal Breeding and Genetics Division, National Institute of Animal Science, Rural Development Admission*, *Cheonan, Republic of Korea*.

OTHER EVENTS

Lunch
Exhibition Hall 109 + 110 + 111 + 112
12:30 PM - 1:30 PM

SYMPOSIA AND ORAL SESSIONS

Animal Epigenetics

Chair: **(1) George Liu, (2) Luciana Regitano, (1), USDA, Beltsville, MD United States, (2) Embrapa, Sao Carlos, Brazil**
Room 105 + 106
1:30 PM - 6:00 PM

1:30 PM OP104 **ISAG Bursary Award: Epigenetic signatures of early-life stress: Investigating stress-induced epigenetic variation in the chicken brain.**
F. Sourani*[1], F. Pértille[1], M. J. Toscano[2], M. B. Petelle[2], and C. Guerrero Bosagna[1], [1]*Department of Organismal Biology, Uppsala University, Uppsala, Sweden*, [2]*Center for Proper Housing: Poultry and Rabbits (ZTHZ), Division of Animal Welfare, Veterinary Public Health Institute, University of Bern, Zollikofen, Switzerland*.

1:50 PM OP105 **DNA methylations associated with promoters and sex chromosomes in vertebrates.**
Y. Lee*[1], H. Kim[2,3], and C. Lee[4], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [2]*Department of Agricultural Biotechnology and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [3]*eGnome Inc, Seoul, Republic of Korea*, [4]*Laboratory of Neurogenetics of Language, The Rockefeller University, New York, NY, USA*.

2:10 PM OP106 **Cross-species conservation of epigenetic markers associated with cardiovascular traits.**
H. Jeong*[1,2], S. Jang[1,2], C.-O. Yun[3], T.-S. Hwang[3], J.-S. Koh[4], J. Kim[1,2], and J. Lee[5], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Institute of Animal Medicine, College of Veterinary Medicine, Gyeongsang National University, Jinju, Republic of Korea*, [4]*Department of Internal Medicine, Gyeongsang National University School of Medicine and Gyeongsang National University Hospital, Jinju, Republic of Korea*, [5]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan-si 31000, Chungcheongnam-do, Republic of Korea*.

2:30 PM OP107 **DNA methylation clock in bull sperm cells reveals the epigenetic aging characteristics and impact on fertility.**
W. Li, Y. Tang, S. Chen, S. An, J. Wang, W. Lai, X. Feng, and Y. Yu*, *Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture & National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*.

2:50 PM OP108 **Epigenetic biomarkers associated to fetal development during maternal lactation using the RUMIGEN methylation array.**
A. López-Catalina*, M. Gutiérrez-Rivas, and O. González-Recio, *INIA-CSIC, Madrid 28040, Spain*.

3:10 PM OP109 **Epitranscriptomics: RNA A-to-I editing sites in porcine brain.**
M. Gòdia*[1], Y. Gang Gang[1], J. E. Bolhuis[2], B. Harlizius[3], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands*, [2]*Adaptation Physiology, Wageningen University & Research, Wageningen, the Netherlands*, [3]*Topigs Norsvin Research Center B.V, 's-Hertogenbosch, the Netherlands*.

3:30 PM **Coffee Break.**

4:00 PM OP111 **Modular workflow for the custom design of livestock DNA methylation arrays.**
J. Chong*, V. Riggio, J. Prendergast, A. Tenesa, and P. Navarro, *Roslin Institute, University of Edinburgh, Edinburgh, Scotland, United Kingdom*.

4:15 PM OP112 **Preliminary results of integrating DNA methylation and metabolomic to investigate molecular responses to diverging environmental conditions in the Massese sheep.**
G. Senczuk*[1], M. Di Civita[1], C. Persichilli[1], A. Francioso[2], P. Abbruscato[3], and F. Pilla[1], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso Italy*, [2]*Department of Bioscience and Agro-Food and Environmental Technology, University of Teramo, Teramo Italy*, [3]*Nuova Genetica Italiana, Villa Guardia, Como, Italy*.

4:30 PM OP113 **Tissue-specific chromatin accessibility regions and transcription factor binding sites in pig brain and endocrine tissues.**
Siriluck Ponsuksili*, Frieder Hadlich, Nares Trakooljul, Shuaichen Li, Henry Reyer, Michael Oster, and Klaus Wimmers, *Research Institute for Farm Animal Biology (FBN), Wilhelm-Stahl-Allee 2, 18196, Dummerstorf, Germany*.

4:45 PM OP114 **Host-adapted tuberculosis-causing mycobacteria remodel the epigenome of the alveolar macrophage.**
T. Hall*[1], M. Mitermite[2], J. Browne[1], G. McHugo[1], J. O'Grady[1], E. Clark[3,4], M. Salavati[5], S. Gordon[2,6], and D. MacHugh[1,6], [1]*UCD Animal Genomics Laboratory, UCD School of Agriculture and Food Science, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [2]*UCD School of Veterinary Medicine, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [3]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, EH25 9RG, UK*, [4]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush Campus, Roslin EH25 9RG, UK*, [5]*Dairy Research and Innovation Centre, SRUC South and West Faculty, Barony Campus, Parkgate, Dumfries DG1 3NE, UK*, [6]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*.

5:05 PM OP115 **Epigenetic atlas and long-read transcriptome analysis of sex-specific ESCs and PGCs in chickens.**
Longbin Yang, Tom Porter, and Jiuzhou Song*, *University of Maryland, College Park, MD, USA*.

5:25 PM **Business Meeting.**

Cattle Molecular Markers and Parentage Testing
Cattle Molecular Markers and Parentage Testing Committee

Chair: **(1) Jiansheng Qiu, (2) Emiliano Lasagna, (1) Neogen Genomics, Lincoln, NE, USA, (2) University of Perugia, Perugia, Italy**
Room 103 + 104
1:30 PM - 6:00 PM

1:30 PM **Welcoming Remarks.**

1:40 PM **Cattle STR/SNP Comparison Test 2024-2025.**

2:00 PM **Presentation by Duty Lab.**

2:20 PM **Presentation of STR results.**

2:40 PM **Presentation of SNP results.**

3:00 PM **Next Comparison Test (2025-2026).**

3:30 PM **Coffee Break.**

4:00 PM OP116 **A case-parent trio WGS study reveals genetic risk factors for abortion in Hanwoo (*Bos taurus coreanae*).**
J. Seo*[1], S. Y. Jhang[2], W. Park[3], and H. Kim[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [2]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [3]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan, Chungcheongnam-do, Republic of Korea*.

4:20 PM OP117 **ISAG Bursary Award: Utilisation of genomic parentage verification and discovery techniques in the South African Beefmaster cattle breed.**
J. J. Reding*[1,2], R. R. van der Westhuizen[2], H. E. Theron[2,1], and E. van Marle-Köster[1], [1]*University of Pretoria, Pretoria, Gauteng, South Africa*, [2]*SA Stud Book and Animal Improvement Organisation, Bloemfontein, Free State, South Africa*.

4:40 PM OP118 **ISAG Bursary Award: Application of variation graphs for genotyping structural variants in 14 French cattle breeds.**
M. M. Naji*[1], T. Faraut[2], C. Klopp[3], D. Boichard[1], M. P. Sanchez[1], and M. Boussaha[1], [1]*Université Paris Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy en Josas, France*, [2]*GenPhySE, Université de Toulouse, INRAE, ENVT, 31326 Castanet-Tolosan, France*, [3]*Université Fédérale de Toulouse, INRAE, MIAT, Sigenae, BioinfOmics, 31326 Castanet-Tolosan, France*.

5:00 PM **Business Meeting and Closing Remarks.**

Companion Animal Genetics and Genomics

Chair: **Jeffrey Schoenebeck, The Roslin Institute (University of Edinburgh), Midlothian, United Kingdom**
Room 101 + 102
1:30 PM - 3:30 PM

1:30 PM OP119 **Genomic diversity and selection in the racing Greyhound of Great Britain.**
H. Han*[1], T. A. Blackett[2], M. L. H. Campbell[2,3], A. H. Holtby[1], B. A. McGivney[1], and E. W. Hill[1,4], [1]*Zinto Labs, Dublin, Ireland*, [2]*Greyhound Board of Great Britain, London, United Kingdom*, [3]*Nottingham University, Sutton Bonington, United Kingdom*, [4]*University College Dublin, Dublin, Ireland*.

1:43 PM OP120 **A comparative transcriptomic analysis of feline and human hypertrophic cardiomyopathy.**
T. Smedley[1], A. Karagianni[2], O. Sidekli[1], P. Syrris[3], V. Fuentes[1], D. Connolly[1], and A. Psifidi*[1], [1]*Royal Veterinary College, Hatfield, UK*, [2]*University of Surrey, Surrey, UK*, [3]*University College London, London, UK*.

1:56 PM OP121 **Myocardial long non-coding RNA profiling for feline hypertrophic cardiomyopathy.**
O. Sidekli*, T. A. Smedley, X. Dai, V. L. Fuentes, D. J. Connolly, and A. Psifidi, *Clinical Sciences and Services, Royal Veterinary College, Hatfield, United Kingdom*.

2:09 PM OP122 **ISAG Bursary Award: Beyond the exome: Identifying non-coding driver mutations in canine diffuse large B-cell lymphoma.**
A. D. van der Heiden*[1,2], S. Mäkeläinen[1,2], R. Pensch[1,2], S. V. Kozyrev[1,2], S. Agger[3], C. London[4], J. F. Modiano[5], K. Forsberg Nilsson[1], M. L. Arendt[1,3], and K. Lindblad-Toh[1,6], [1]*Uppsala University, Uppsala, Sweden*, [2]*SciLifeLab, Uppsala, Sweden*, [3]*University of Copenhagen, Copenhagen, Denmark*, [4]*Tufts University, North Grafton, MA, USA*, [5]*University of Minnesota, Minneapolis, MN, USA*, [6]*Broad Institute, Cambridge, MA, USA*.

2:22 PM OP123 **Analysis of canine gene constraint identifies new variants for orofacial clefts and stature.**
Reuben M. Buckley[1], Nüket Bilgen*[2], Alexander C. Harris[1], Peter Savolainen[3], Cafer Tepeli[4], Metin Erdogan[5], Aitor Serres Armero[1], Dayna L. Dreger[1], Frank G. van Steenbeek[6], Marjo K. Hytönen[7,8], Heidi G. Parker[1], Jessica Hale[1], Hannes Lohi[7,9], Bengi Çinar Kul[2], Adam R. Boyko[10,11], [1]*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD 20892, USA*, [2]*Department of Animal Genetics, Faculty of Veterinary Medicine, University of Ankara, Ankara 06110, Türkiye*, [3]*KTH Royal Institute of Technology, School of Chemistry, Biotechnology and Health, Science for Life Laboratory, Stockholm, Sweden*, [4]*Department of Animal Science, University of Selcuk, Faculty of Veterinary Medicine, Konya, Türkiye*, [5]*Department of Veterinary Biology and Genetics, Faculty of Veterinary Medicine, Afyon Kocatepe University, Afyonkarahisar, Türkiye*, [6]*Utrecht University, Faculty of Veterinary Medicine, Dept. of Clinical Sciences, The Netherlands*, [7]*Department of Medical and Clinical Genetics, University of Helsinki, 00014 Helsinki, Finland*, [8]*Department of Veterinary Biosciences, University of Helsinki, 00014 Helsinki, Finland*, [9]*Folkhälsan Research Center, 00290 Helsinki, Finland*, [10]*Department of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY 14853, USA*, [11]*Embark Veterinary Inc, Boston, MA 02210, USA*.

2:35 PM OP124 **ISAG Bursary Award: ZMYND10 frameshift deletion in Eurasier dogs with primary ciliary dyskinesia.**
C. Schwarz*[1,2], H. Jainek[3], U. Hetzel[4], V. Jagannathan[1], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Graduate School for Cellular and Biomedical Sciences (GCB), Bern, Switzerland*, [3]*Clinic of Reproductive Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*, [4]*Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*.

2:48 PM OP125 **Gene expression and regulatory pathways in feline elbow osteoarthritis.**
C. Ley[1], C. J. Ley[2], and Å. Ohlsson*[1], [1]*Swedish University of Agricultural Sciences, Department of Animal Biosciences, Uppsala, Sweden*, [2]*Swedish University of Agricultural Sciences, Department of Clinical Sciences, Uppsala, Sweden*.

3:01 PM OP126 **ROS_Cfam_2.0: A telomere-to-telomere dog reference genome.**
Jeffrey J. Schoenebeck*[1], Juhyun Kim[2], Brandon D. Pickett[2], Arang Rhie[2], Dmitry Antipov[2], Alice C. Young[3], Shelise Y. Brooks[3], Gerard G. Bouffard[3], Chandrindu Abeykoon[1], Melany Jackson[1], Derya Ozdemir[1], Elaine A. Ostrander[4], Sergey Koren[2], and Adam M. Phillippy[2], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, Scotland, UK*, [2]*Genome Informatics Section, Center for Genomics and Data Science Research, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [3]*NIH Intramural Sequencing Center, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [4]*Cancer Genetics and Comparative Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*.

3:15 PM **Business Meeting.**

Domestic Animal Sequencing and Annotation

Chair: **Brenda Murdoch, University of Idaho, Moscow, ID United States**
Room 107 + Room 108
1:30 PM - 6:00 PM

1:30 PM OP127 **You too can T2T: Democratizing telomere-to-telomere assembly for non-model organisms.**
D. Antipov, J. Kim, A. Rhie, A. M. Phillippy, and S. Koren*, *Genome Informatics Section, Center for Genomics and Data Science Research, National Human Genome Research Institute, Bethesda, MD, USA*.

1:50 PM OP128 **Chromosome-level genome assemblies and annotation of Finnish native livestock: Finnsheep and Western Finncattle.**
K. Pokharel*[1], M. Weldenegodguad[2], R. Okwasiimire[3,1], and J. Kantanen[1], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*Natural Resources Institute Finland (Luke), Helsinki, Finland*, [3]*University of Helsinki, Department of Agricultural Sciences, Helsinki, Finland*.

2:10 PM OP129 **ISAG Bursary Award: Telomere-to-telomere genome assembly of a male goat reveals variants associated with cashmere traits.**
H. Wu*[1,2], L. L. Luo[1], Y. H. Zhang[1], C. H. Zhang[3], Z. H. Liu[3], S. G. Jia[4], and M. H. Li[1], [1]*Frontiers Science Center for Molecular Design Breeding (MOE); State Key Laboratory of Animal Biotech Breeding; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*Northern Agriculture and Animal Husbandry Technical Innovation Center, Chinese Academy of Agricultural Sciences, Hohhot, China*, [3]*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China*, [4]*College of Grassland Science and Technology, China Agricultural University, Beijing, China*.

2:30 PM OP130 **Structural variations associated with leucism and albinism in Hanwoo cattle.**
S. Ko*[1], Y. Kim[2], P. T. N. Dinh[1], S. H. Lee[3], Y. Ko[4], S. Lee[4], J. Lee[4], and C. Kim[4], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, 34134, Korea*, [2]*Institute of Agricultural Science, Chungnam National University, Daejeon 34134, Republic of Korea*, [3]*Division of Animal & Dairy Science, Chungnam National University, Daejeon, 34134, Korea*, [4]*Animal Genetic Resources Research Center, National Institute of Animal Science, RDA, Hamyang, 50000, Korea*.

2:50 PM OP131 **A telomere-to-telomere assembly unlocks the unique genomic landscape of the Mongolian horse for precision breeding.**
Y. Wang*[1,2], J. Liu[1], Y. Zhao[2], Z. Tang[1], T. Bou[2], H. Liu[1], W. Ding[2], J. Dou[1], S. Zhu[1], L. Yin[1], X. Liu[1,3], M. Yu[1], Y. Fu[1,3], and D. Bai[2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei 430070, PR China*, [2]*Key Laboratory of Equus Germplasm Innovation (Co-construction by Ministry and Province), Ministry of Agriculture and Rural Affairs; Equus Research Center of Inner Mongolia Agricultural University, Hohhot 010018, China*, [3]*Hubei Hongshan Laboratory, Wuhan, Hubei 430070, PR China*.

3:10 PM	OP132	**High-quality genome assembly of Southern Africa Indigenous cattle.** Ntanganedzeni Mapholi*[1], Thendo Tshilate[1], Sinebongo Mdyogolo[1], Rae Smith[1], Tracy Masebe[1], Thomas Raphulu[2], Isidore Houaga[1,3], Annelin Molotsi[1], and Lucky Nesengani[1], [1]*College of Agriculture and Environmental Sciences, UNISA Science Campus, Florida, Johannesburg, South Africa*, [2]*Limpopo Department of Agriculture, Polokwane, 0700, South Africa*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK*.
3:30 PM		**Coffee Break.**
4:00 PM	OP133	**Insights from population scale long read sequencing of cattle.** A. J. Chamberlain*[1,2], T. V. Nguyen[1], J. Wang[1], and I. M. MacLeod[1,2], [1]*Agriculture Victoria, Centre for AgriBioscience, Bundoora, Victoria, Australia*, [2]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.
4:20 PM	OP134	**Construction of *de novo* Japanese wild boar (*Sus scrofa leucomystax)* genome assembly.** D. Gamarra*[1], K. Naito[2], and M. Taniguchi[1], [1]*Institute of Agrobiological Science, National Agriculture and Food Research Organization, Tsukuba 305-8634, Ibaraki, Japan*, [2]*Research Center of Genetic Resources, National Agriculture and Food Research Organization, Tsukuba 305-8602, Ibaraki, Japan*.
4:40 PM	OP135	**Telomere-to-telomere sheep genome assembly identifies variants associated with wool fineness.** L. Y. Luo*[1], H. Wu[1], L. M. Zhao[2], Y. H. Zhang[1], J. H. Huang[1], Q. Y. Liu[3], H. T. Wang[3], D. X. Mo[1], H. H. Eer[4], L. Q. Zhang[5], H. L. Chen[6], S. G. Jia[7], W. M. Wang[2], and M. H. Li[1], [1]*Frontiers Science Center for Molecular Design Breeding (MOE); State Key Laboratory of Animal Biotech Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems; Key Laboratory of Grassland Livestock Industry Innovation, Ministry of Agriculture and Rural Affairs, College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, Gansu, China*, [3]*Institute of Genetics and Developmental Biology, The Innovation Academy for Seed Design, Chinese Academy of Sciences, Beijing, China*, [4]*Institute of Animal Science, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan, Ningxia, China*, [5]*Ningxia Shuomuyanchi Tan Sheep Breeding Co. Ltd, Wuzhong, Ningxia, China*, [6]*Beijing Lvyeqingchuan Zoo Co. Ltd, Beijing, China*, [7]*College of Grassland Science and Technology, China Agricultural University, Beijing, China*.
4:55 PM	OP136	**Tracing the adaptive history of trypanotolerant African cattle using a pangenome graph.** N. Adossa*[1], S. Kambal[1,2], A. Tijjani[1,3], I. Houaga[4,5], A. Ahbara[5], C. Elsik[2], A. Adeola[7], J. Mwacharo[5,8], Y. Li[9], J. Prendergast[4,5], and O. Hanotte[1,10], [1]*LiveGene – CTLGH, International Livestock Research Institute, Addis Ababa, Ethiopia*, [2]*Division of Animal Sciences, University of Missouri, USA*, [3]*Feinstein Institutes for Medical Research, USA*, [4]*The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush Campus, Roslin, Midlothian, EH25 9RG, UK*, [5]*Centre for Tropical Livestock Genetics and Health, Easter Bush, Midlothian, EH25 9RG, UK*, [6]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, The University of South Africa, Cnr Justice Mahomed & Steve Biko Streets, PO Box 392, Pretoria, South Africa*, [7]*Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [8]*International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [9]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, School of Life Sciences, Yunnan University, Kunming, China*, [10]*School of Life Sciences, University of Nottingham, Nottingham, UK*.
5:15 PM	OP137	**Structural variations associated with adaptation and coat color in Qinghai-Tibetan Plateau cattle.** X. T. Xia, F. W. Wang, X. Y. Luo, C. Z. Lei, and N. B. Chen*, *Northwest A&F Unversity, Yangling, Shaanxi, China*.
5:30 PM	OP138	**A graph-based variome uncovers the genetic architecture and breeding potential of commercial pigs.** L. Liu*[1], Y. Qiu[1], S. Deng[1], Y. Liu[1], Z. Yao[1], S. Wang[1], F. Zhou[1], Z. Wu[3], H. Zhang[4], D. Martijn[2], E. Zheng[1], Z. Zhang[1], M. Groenen[2], J. Yang[1], Z. Wu[1], [1]*South China Agricultural University, China*, [2]*Wageningen University & Research, The Netherlands*, [3]*The University of Edinburgh, United Kingdom*, [4]*Anhui Medical University, China*.
5:45 PM		**Business Meeting.**

Genome Edited Animals

Chair: **Xiaolong Wang, Northwest A&F Univ., Yangling, China**
Room 101 + 102
4:00 PM - 6:00 PM

4:00 PM OP139 **Expanding the CRISPR toolbox by engineering Cas12a orthologs of metagenomic discovery.**
D. G. Tao*[1,3], B. R. Xu[1,2], S. Li[1,3], H. L. Liu[1,3], S. Y. Shi[1,3], Y. Wang[1,2], C. Z. Zhao[3], J. X. Ruan[1,3], L. L. Fu[1,3], X. X. Huang[5], X. Y. Li[1,3], S. H. Zhao[1,4], and S. S. Xie[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & Key Lab of Swine Genetics and Breeding, Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, 430070 Wuhan, P. R. China*, [2]*Yazhouwan National Laboratory (YNL), Sanya Hainan 572025, P. R. China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, 430070 Wuhan, P. R. China*, [4]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan 430070, P. R. China*, [5]*Laboratory of Pancreatic Disease, The First Affiliated Hospital, Zhejiang University School of Medicine, Hangzhou 310058, P. R. China*.

4:15 PM OP140 **ISAG Bursary Award: Fertility following germline transplantation in sterile *NANOS2* knockout surrogate bulls.**
B. E. Latham*, M. I. Giassetti, M. Ciccarelli, M. J. Oatley, D. Miao, A. Tibary, and J. Oatley, *College of Veterinary Medicine, Washington State University, Pullman, WA, USA*.

4:30 PM OP141 **Glycosylase-mediated base editors show undetectable off-targets and high on-target editing in mammalian embryos.**
Yinghui Wei[1,2], Kun Xu*[1,2], Wenxin Zheng[3], Weiwei Wu[4], and Xiaolong Wang[1,2], [1]*International Joint Agriculture Research Center for Animal Bio-Breeding of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, 712100, China*, [2]*Hainan Institute of Northwest A&F University, Sanya, Hainan, 572025, China*, [3]*Institute of Animal Husbandry Quality Standards, Xinjiang Academy of Animal Science, Urumqi, Xinjiang, 830011, China*, [4]*Institute of Animal Science, Xinjiang Academy of Animal Science, Urumqi, Xinjiang, 830011, China*.

4:45 PM OP142 **Evaluation of the resistance of Liang Guang Small Spotted pigs with partial deletion of the CD163 SRCR5 domain to porcine reproductive and respiratory syndrome virus 2 infection.**
Sitong Zhu*, Xiaohong Liu, Yaosheng Chen, Zuyong He, and Yu Wu, *School of Life Sciences, Sun Yat-sen University, Guangzhou, Guangdong, China*.

5:00 PM OP143 **Evaluation of the cytosine base editors in chicken somatic cells for poultry breeding applications.**
Pan Li* and Li Chen, *Xianghu Laboratory, Hangzhou, Zhejiang, China*.

5:15 PM OP144 **Sustainable bioproduction of functional multimeric recombinant human adiponectin in genome-edited chickens.**
Y. Han*[1], E. Yoo[1], H. Choi[1], J. Kim[2], Y. Hong[1], and J. Han[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [2]*Department of International Agricultural Technology & Institute of Green Bioscience and Technology, Seoul National University, Pyeongchang, Gangwon, Republic of Korea*.

5:30 PM OP145 **On-site detection of targeted genome-modification sites and SNPs in agricultural animals via improved RAVI-CRISPR strategy.**
Y. Wang*[1,2], L. T. Fu[3], D. G. Tao[1], B. R. Xu[1,2], S. Li[1], X. Y. Li[1], S. H. Zhao[1,2], and S. S. Xie[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, 430070, P. R. China*, [2]*Yazhouwan National Laboratory (YNL), Sanya Hainan, 572025, P. R. China*, [3]*Wuhan Shangrui Biotechnology Co., Ltd, Wuhan, 430070, P. R. China*.

5:45 PM **Business Meeting.**

OTHER EVENTS

Networking Event for Early Career Scientists
Room 204 + 205
6:00 PM - 8:00 PM

Tuesday, July 22

Speaker Ready Room
Room 209
8:00 AM - 6:00 PM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions
Plenary II

Grand Ballroom 201 + 202
8:30 AM - 10:40 AM

8:30 AM	OP146	**Advancing the standards for variant classification: Updates from ClinGen and ACMG.** S. Harrison*[1,2], [1]*Ambry Genetics, Aliso Viejo, CA, USA*, [2]*ACMG/AMP/CAP/ClinGen Sequence Variant Classification WG*.
9:20 AM	OP147	**Usage of single-cell gene regulatory networks for the fine-mapping and interpretation of genetic variation.** Monique G. P. van der Wijst*, *University Medical Center Groningen, Groningen, Groningen, the Netherlands*.
10:10 AM		**Coffee Break.**
10:40 AM	OP148	**Learning from African cattle and the vertebrate genome projects.** H. Kim*[1,2], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [2]*Department of Agricultural Biotechnology and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*.

POSTER PRESENTATIONS

Applied Genetics and Genomics in other Species of Economic Interest

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P125	**ISAG Bursary Award: DNA metabarcoding approach, a promising tool for disentangling the precise dietary spectrum of pangolins.** Stanislas Zanvo* and Brice Sinsin, *Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Abomey-Calavi, Benin*.
P126	**TempO-Seq platform for animal genotyping and pathogen detection.** M. Hernandez, G. Montis, S. Camiolo, D. House, J. McComb*, J. M. Yeakley, B. Seligmann, and Z. Chen, *BioSpyder Technologies Inc, Carlsbad, CA, USA*.
P127	**Genetic diversity and population structure of the asiatic black bears restoring in South Korea based on genome sequence polymorphism.** S. H. Han*[1], C. H. Myung[2], H. C. Kang[2], J. Y. Kim[2], T. W. Kim[1], S. H. Lee[1], and H. T. Lim[2,3], [1]*National Park Institute for Wildlife Conservation, Korea National Park Service, Yeongju 36015, Korea*, [2]*Department of Animal Science, Gyeongsang National University, Jinju 52828, Korea*, [3]*Institute of Agriculture and Life Science, Gyeongsang National University, Jinju 52828, Korea*.

P128 **High-quality alpaca genome VicPac4 and Oligo-FISH reveal large-scale satellite repeat clusters specific to South American camelids.**
M. N. Mendoza Cerna*, B. W. Davis, and T. Raudsepp, *Texas A&M University*, *College Station, TX, USA*.

P129 **Soil microbiota dynamics associated with different forage systems under winter swathgrazing in Western Canada.**
O. N. Durunna*[1,2], S. Obiora[2], N. Malmuthuge[3], J. Nowosad[1], O. Oyedeji[4], C. Vandenberg[1], D. B. Holman[5], and H. A. Lardner[2], [1]*Lakeland College*, *Vermilion, Alberta, Canada*, [2]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [3]*University Calgary*, *Calgary, Alberta, Canada*, [4]*Agriculture and Irrigation, Government of Alberta*, *Edmonton, Alberta, Canada*, [5]*Agriculture and Agri-Food Canada*, *Lacombe, Alberta, Canada*.

P130 **Impact of garlic-infused mineral supplements on the rumen microbiome and resistome of feedlot cattle.**
O. N. Durunna*[1], N. Malmuthuge[2], D. B. Holman[3], T. A. McAllister[4], I. Cheang-Deis[5], C. Vandenberg[1], O. Oyedeji[6], E. Gonzalez[7], and H. A. Lardner[8], [1]*Lakeland College*, *Vermilion, Alberta, Canada*, [2]*University of Calgary*, *Calgary, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada*, *Lacombe, Alberta, Canada*, [4]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*, [5]*Cenovus Energy*, *Lloydminster, Alberta, Canada*, [6]*Agriculture and Irrigation, Government of Alberta*, *Edmonton, Alberta, Canada*, [7]*McGill University*, *Montreal, Quebec, Canada*, [8]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

P131 **Generation of polyclonal antibodies in chickens against Dengue, Zika, and Chikungunya virus antigens for diagnostic applications.**
H. Choi*[1], J. Kim[2], and J. Han[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences*, *Gwanak-gu, Seoul, Republic of Korea*, [2]*Department of International Agricultural Technology & Institute of Green Bioscience and Technology*, *Pyeongchang, Gangwon-do, Republic of Korea*.

P132 **Genetic diversity and population structure among suri and huacaya alpacas bred in Poland – Preliminary study.**
A. Masior*, J. Wolkowicz, M. Domagala, and K. Zygmunt, *National Research Institute of Animal Production*, *Balice, Poland*.

P133 **ISAG Bursary Award: Advancing hilsa genomics: Refining genome assembly and identifying novel genes with multi-tissue RNA-seq.**
M. B. R. Mollah*, M. G. Q. Khan, M. S. Islam, and M. S. Alam, *Bangladesh Agricultural University*, *Mymensingh, Bangladesh*.

P134 **Allele sequencing of microsatellite markers for parentage verification in sheep.**
Agnieszka Szumiec, Agata Piestrzynska-Kajtoch*, and Anna Radko, *National Research Institute of Animal Production, Department of Animal Molecular Biology*, *Balice, Poland*.

P135 **Exploring the genetics of coat color and fleece type in alpacas using the improved VicPac4 reference genome.**
A. Letko*[1], M. Mendoza Cerna[2], G. Lühken[3], T. Raudsepp[2], B. W. Davis[2], and C. Drögemüller[1], [1]*Institute of Genetics, University of Bern*, *Bern, Switzerland*, [2]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University*, *College Station, TX, USA*, [3]*Institute for Animal Breeding and Genetics, Justus Liebig University Giessen*, *Giessen, Germany*.

P136 **Analyzing of ranking correlation with GEBV and DGV using Hanwoo reference population for genomic evaluation.**
Mina Park*[1], Haseung Seong[1], Eunho Kim[1], Chungil Cho[2], Changgwon Dang[1], Jaebeom Cha[1], Hyukkee Chang[1], Sangmin Lee[1], Mahboob Alam[1], Dongkyu Lee[1], Eunah Ryu[1], and Chaeyoung Lee[1], [1]*National Institute of Animal Science*, *Sibang, Seonghwan-eup, Seobuk-gu, Cheonan-si, Chungcheongnam-do, 31000, Republic of Korea*, [2]*Hanwoo Genetic Improvement Center*, *Haeun-ro, Unsan-myeon, Seosan, Chungcheongnam-do, 31948, Republic of Korea*.

P137 **GWAS and fine-mapping analysis for identifying positional candidate genes influencing blood cortisol levels in pigs.**
In-Cheol Cho*, Hyeon-ah Kim, Yong Jun Kang, Sang-Geum Kim, and Su-Yeon Kim, *National Institute of Animal Science*, *Sanrokbukro, Jeju-si, Jejudo, Republic of Korea*.

Equine Genetics and Thoroughbred Parentage Testing

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P250 **Genomic hotspots of oxidative stress: Age-related DNA damage in equine spermatozoa.**
C. Jenkins*[1,2], B. Velie[3], R. Griffin[1], A. Swegen[1], N. Hamilton[2], and Z. Gibb[1], [1]*The University of Newcastle*, *Newcastle, NSW, Australia*, [2]*Equine Genetics Research Centre*, *Scone, NSW, Australia*, [3]*University of Sydney*, *Sydney, NSW, Australia*.

P251 **Pairwise statistical algorithm for likelihood-based paternity analysis.**
Mahmoud Amiri Roudbar*[1] and Seyedeh Fatemeh Mousavi[2], [1]*Agricultural Research, Education and Extension Organization (AREEO), Tehran, Tehran, Iran*, [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden*.

P252 **Genetic diversity and population structure of baroque horse breeds: Insights from genomic data.**
R. I. Alvarez-Quiñónez[1], G. Senczuk[2], C. Persichilli[2], S. Capomaccio[3], M. Silvestrelli[3], A. M. Martinez[4], J. L. Rivero[1], and J. L. Vega-Pla*[5], [1]*Laboratorio de Biopatologia Muscular, Departamento de Anatomia, Anatomia Patologica Comparadas y Toxicologia, School of Veterinary Medicine, University of Cordoba, Cordoba, Spain*, [2]*Dipartimento di Agricoltura, Ambiente e Alimenti, University of Molise, Campobasso, Italy*, [3]*Dipartimento di Medicina Veterinaria, University of Perugia, Perugia, Italy*, [4]*Departamento de Genetica, University of Cordoba, Cordoba, Spain*, [5]*Laboratorio de Investigacion Aplicada, Cria Caballar de las Fuerzas Armadas, Cordoba, Spain*.

P253 **Optimization of thoroughbred horse parentage testing system.**
Daeha Choi*[1], Sun-Young Lee[1], Shin-Wook Kang[1], Giljae Cho[2], and Jundong Yu[1], [1]*Racing Laboratory, Korea Racing Authority, Gwacheon-Si, Gyeonggi-Do, Korea*, [2]*College of Veterinary Medicine, Kyungpook National University, Buk-gu, Daegu, Korea*.

P254 **A novel kit for individual identification and parentage test of thoroughbred horses.**
Daeha Choi[1], Sun-Young Lee[1], Shin-Wook Kang*[1], Giljae Cho[2], and Jundong Yu[1], [1]*Racing Laboratory, Korea Racing Authority, Gwacheon-Si, Gyeonggi-Do, Korea*, [2]*College of Veterinary Medicine, Kyungpook National University, Buk-gu, Daegu, Korea*.

P255 **Microsatellite DNA polymorphism of the Felin Pony—Preliminary studies.**
A. Bieniek* and A. Szumiec, *National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland*.

P256 **Assessment of the potential of a breed-specific SNP panel for parentage testing in Pura Raza Español horse.**
N. Laseca[1,2], M. Valera[1], T. Marshall[3], P. J. Azor*[2], I. González[2], and A. Molina[4], [1]*Department of Agronomy, School of Agricultural Engineering, University of Seville, Seville, Spain*, [2]*Royal Purebred Spanish Horse Breeders' Association, Seville, Spain*, [3]*Field Genetics Ltd, London, United Kingdom*, [4]*Department of Genetics, University of Cordoba, Cordoba, Spain*.

P257 **Assessment of the reliability of genomic evaluation for reproductive traits in the Pura Raza Española Horses.**
Chiraz Ziadi[1], Sebastián Demyda Peyrás*[1], Mercedes Valera[2], Nora Laseca[2], Davinia Perdomo Gonzales[3], Juan Pablo Sanchez[1], Arancha Rodríguez-Sainz de los Terreros[3], and Antonio Molina[1], [1]*Department of Genetics, Veterinary School, University of Córdoba, Spain*, [2]*Department of Agronomy, ETSIA, University of Sevilla, Spain*, [3]*Royal National Association of Spanish Horse Breeders, Sevilla, Spain*.

P258 **Candidate gene investigation for equine disorders of sex development.**
H. C. Anderson*, S. C. Stroupe, R. Juras, B. W. Davis, and T. Raudsepp, *College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*.

P259 **Development of a robust across breed equine parentage ISAG SNP panel.**
R. R. Bellone*[1,2], E. Esdaile[1], F. Avila[1], B. J. Till[1], B. Wallner[3], T. Raudsepp[4], S. Hughes[1], J. Hughes[1], R. Grahn[1], S. Chadaram[5], S. Shrestha[5], A. S. Grulikowski[1], M. McCue[6], P. Flynn[7], T. Mansour[2], [1]*Veterinary Genetics Laboratory, University California Davis, Davis, CA, USA*, [2]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, CA, USA*, [3]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [4]*Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, School of Veterinary Medicine and Biomedical Sciences, College Station, TX, USA*, [5]*Thermo Fisher Scientific, Waltham, MA, USA*, [6]*Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, MN, USA*, [7]*Weatherbys, Kildare, Ireland*.

P260 **Genetic diversity and the evaluation of the effectiveness of single nucleotide polymorphisms compared to microsatellite markers for parentage verification in horse breeds.**
Daeha Choi[1], Sun-Young Lee[1], Shin-Wook Kang[1], and Giljae Cho*[2], [1]*Racing Laboratory, Korea Racing Authority, Gwacheon-Si, Gyeonggi-Do, Korea*, [2]*College of Veterinary Medicine, Kyungpook National University, Buk-gu, Daegu, Korea*.

P261 **Evaluation of SNP markers for parentage testing in Taishu horse population.**
Taichiro Ishige*[1], Tomoko Yoshihara[2], Koki Kawate[1], Mio Kikuchi[1], Risako Furukawa[1], Teruaki Tozaki[1], and Hironaga Kakoi[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya-shi, Tochigi, Japan*, [2]*Joint Faculty of Veterinary Medicine, Kagoshima University, Kagoshima-shi, Kagoshima, Japan*.

Genetics and Genomics of Aquaculture Species

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P262 **Genetic insights into bacterial disease resistance in olive flounder (*Paralichthys olivaceus*): A multi-trait GWAS approach.**
Chaehyeon Lim*, Jong-Won Park, Minhwan Jeong, Dain Lee, Julan Kim, Hyejin Kim, Ju-won Kim, and Hee Jeong Kong, *Genetics and Breeding Research Center, National Institute of Fisheries Science*, *Geoje, Republic of Korea*.

P263 **Bulk segregation method with transcriptomics is an innovative method for identifying true SNPs and functional genes in a breeding line of specific pathogen resistant (SPR) WSSV-resistant Madagascar-Malaysia *Penaeus monodon*.**
Subha Bhassu* and Farhana Mohd Ghani, *Animal Genetics and Genome Evolutionary Biology Lab, Institute of Biological Sciences, Faculty of Science, University of Malaya*, *Kuala Lumpur, Malaysia*.

P264 **Transcriptome-wide in vivo identification of miRNA target genes in Atlantic salmon.**
R. Andreassen* and S. Ramberg, *Oslo Metropolitan University*, *Oslo, Norway*.

P265 **Invited Workshop Presentation: Can early-life priming improve stress and disease resistance?**
Tamsyn M. Uren Webster*, *Biosciences, Faculty of Science and Engineering, Swansea University*, *Swansea, Wales, UK*.

P266 **Occurrence of inbreeding depression for pigmentation in a farmed population of turbot.**
M. Saura*[1], D. Costas-Imbernón[1], S. Otero[1], P. García-Fernández[2], P. Touriñán[2], R. Tur[2], D. Chavarrías[2], and J. Rotllant[1], [1]*Instituto de Investigaciones Marinas IIM-CSIC*, *Vigo, Spain*, [2]*Pescanova Biomarine Center*, *O Grove, Spain*.

P267 **ISAG Bursary Award: De novo assembly of a Mozambique Tilapia (*Oreochromis mossambicus*): An update using high-accuracy technology.**
T. S. Tshilate*[1], L. T. Nesengani[1], S. Mdyongolo[2], A. H. Smith[2], T. Molotsi[1], C. Masebe[2], N. Rhode[3], and N. Mapholi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, UNISA Science Campus*, *Johannesburg, Gauteng, South Africa*, [2]*Department of Life and Consumer Sciences, College of Agriculture and Environmental Sciences, UNISA Science Campus*, *Johannesburg, Gauteng, South Africa*, [3]*Department of Genetics, Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*.

P268 **ISAG Bursary Award: De novo assembly of a Mozambique Tilapia (*Oreochromis mossambicus*): An update using high-accuracy technology.**
T. S. Tshilate*[1], L. T. Nesengani[1], S. Mdyongolo[2], A. H. Smith[2], T. Molotsi[1], C. Masebe[2], N. Rhode[3], and N. Mapholi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, UNISA Science Campus*, *Johannesburg, Gauteng, South Africa*, [2]*Department of Life and Consumer Sciences, College of Agriculture and Environmental Sciences, UNISA Science Campus*, *Johannesburg, Gauteng, South Africa*, [3]*Department of Genetics, Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*.

P269 **High-resolution genome assemblies and variant analysis for advancing olive flounder (*Paralichthys olivaceus*) breeding.**
J. Kim*[1], Y. Kim[2], J.-W. Park[1], M. Jeong[1], D. Lee[1], H. Kim[1], C. Lim[1], H.-C. Kim[1], J.-H. Lee[1], S. H. Lee[3], and J. Kim[4], [1]*Genetics and Breeding Research Center, National Institute of Fisheries Science*, *Geoje, Republic of Korea*, [2]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Division of Animal & Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*, [4]*Department of Convergent Bioscience and Informatics, Chungnam National University*, *Daejeon, Republic of Korea*.

P270 **Genomic insights into Korean olive flounder population structure and breeding potential.**
J. Kim*[1], Y. Chung[2], H.-C. Kim[1], J.-H. Lee[1], P. T. N. Dinh[3], E. Hong[4], W. Jeong[5], W. Ekanayake[5], H. J. Kong[1], and S. H. Lee[6], [1]*Genetics and Breeding Research Center, National Institute of Fisheries Science*, *Geoje, Republic of Korea*, [2]*Institute of Agricultural Science, Chungnam National University*, *Daejeon, Republic of Korea*, [3]*Department of Bio-AI Convergence, Chungnam National University*, *Daejeon, Republic of Korea*, [4]*Bigdata Center, TNT Research Co., Ltd*, *Jeonju, Republic of Korea*, [5]*Department of Bio-Big Data and Precision Agriculture, Chungnam National University*, *Daejeon, Republic of Korea*, [6]*Division of Animal & Dairy Science, Chungnam National University*, *Daejeon, Republic of Korea*.

P271 **Complex genetic architecture underlying sex determination in common carp.**
Eldad Gamliel, Roni Tadmor-Levi, Bayan Abdelkader, Evgenia Marcos-Hadad, and Lior David*, *The Hebrew University of Jerusalem*, *Rehovot, Israel*.

P272 **Predicting fatty acid composition in Atlantic salmon using Raman spectroscopy: Genetic and phenotypic validation from crude fat to individual fatty acids.**
J. Park*[1], G. F. Difford[1], S. S. Horn[2], H. Moghadam[3], B. Hillestad[3], A. K. Sonesson[2], P. Berg[1], J. P. Wold[2], and N. K. Afseth[2], [1]*Norwegian University of Life Sciences (NMBU), Ås, Akershus, Norway*, [2]*Nofima, Ås, Akershus, Norway*, [3]*Benchmark Genetics, Bergen, Vestland, Norway*.

Genetics of Immune Response and Disease Resistance/Comparative and Functional Genomics

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P273 **Evaluation of mastitis resistance and milk production traits in Holstein Friesian and zebu dairy cattle breeds in Pakistan.**
Mustafa Kamal[1,3], Guillermo Martinez-Boggioc[3], Naseem Rafiq[2], Ying Yu[4], Francisco Peñagaricano[3], and Tahir Usman*[1], [1]*College of Veterinary Sciences and Animal Husbandry, Abdul Wali Khan University Mardan, Mardan, Pakistan, Mardan, Pakistan*, [2]*Department of Zoology, Abdul Wali Khan University Mardan, Mardan, Pakistan, Mardan, Pakistan*, [3]*Department of Animal and Dairy Sciences, University of Wisconsin Madison, Madison, USA, Madison, WI, USA*, [4]*Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China, Beijing, China*.

P274 **Integration of cell death related mRNA-miRNA approach reveals multi-miRNA phenomena in stimulated ovine mammary epithelial cells.**
Ghulam Asghar Sajid*[1], Muhammad Jasim Uddin[2,3], Saif Adil Abbood Al-Janabi[1], Mustafa Özdemir[1], Abdiaziz Nur[1], and Mehmet Ulas Cinar[1,4], [1]*Erciyes University, Talas, Kayseri, Turkiye*, [2]*Center for Biosecurity and One Health, Harry Butler Institute, Murdoch, WA 6150, Australia*, [3]*School of Veterinary Medicine, Murdoch University, Murdoch, WA 6150, Australia*, [4]*Department of Veterinary Microbiology & Pathology, College of Veterinary Medicine, Washington State University, Pullman, WA 99164, USA*.

P275 **Genetic basis of production and disease resistance traits in indigenous chicken ecotypes across Africa: A comprehensive review.**
S. Ndatsha*[1], L. T. Nesengani[1], N. Mapholi[1], T. S. Tshilate[1], and I. Houaga[1,2], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Pretoria, South Africa*, [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, Easter Bush Campus, University of Edinburgh, Midlothian, UK*.

P276 **Identification of CALR as a host target gene for inhibiting RNA virus infection via porcine CRISPR screening.**
Yonghui Zhang*[1,2], Jinyan Zhang[1,2], Rui Jiang[1,2], Yuan Wang[1,2], Liuxing Qin[1,2], Jingpei Han[1,2], Ping Qian[2], and Shengsong Xie[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei, P. R. China*, [2]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hubei, P. R. China*.

P277 **Polymorphism of bovine major histocompatibility complex (BoLA)-*DRB3* of progeny derived from semen with resistance and susceptibility to bovine leukemia virus proviral load.**
A. Bao*[1], S. Watanuki[1], R. Matsuura[1], Y. Matsumoto[1,2], H. Shimizu[3], A. Niwano[3], R. Kawata[3], and Y. Aida[1], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Laboratory of Global Animal Resource Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [3]*KAWATA Animal Clinic, Saitama, Japan*.

P278 **An indicine X-linked CYBBL237M can suppress intracellular infection with tubercle bacilli.**
Haoxin Wang, Zhaolei Chu, and Ningbo Chen*, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaan Xi, China*.

P279 **Validation of candidate markers for resilient response upon PRRSV outbreaks in sows.**
R. N. Pena*[1,2], A. M. M. Stoian[1,2], and L. J. Fraile[1,2], [1]*Departament de Ciència Animal, Universitat de Lleida, Lleida, Spain*, [2]*AGROTECNIO-CERCA Center, Lleida, Spain*.

P280 **Dissecting the bovine host response to *Mycobacterium bovis* infection using network biology and integrative genomics.**
Adnan Khan*[1], Dermot J. Kelly[1], John F. O'Grady[1], Gillian P. McHugo[1], Thomas J. Hall[1], John A. Browne[1], Eamonn Gormley[2], Kieran G. Meade[1,4], Isobel C. Gormley[5], Stephen V. Gordon[3,4], and David E. MacHugh[1,4], [1]*UCD School of Agriculture and Food Science, University College Dublin, Ireland*, [2]*UCD School of Veterinary Medicine, University College Dublin, Ireland*, [3]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Ireland*, [4]*UCD One Health Centre, University College Dublin, Ireland*, [5]*UCD School of Mathematics and Statistics, University College Dublin, Ireland*.

P281 **Knockout of EMC6 and SEC63 inhibits Japanese encephalitis virus proliferation by regulating ER-phagy.**
Y. Q. Yang*, H. L. Liu, D. G. Tao, and S. S. Xie, *Huazhong Agricultural University, Wuhan, P. R. China*.

P282 **Genetic and transcriptomic characterisation of bovine digital dermatitis using *in vivo* and *in vitro* data.**
A. Hinsu*[1], A. Sato[2], K. Bao[2], E. Attree[1], A. Anagnostopoulos[2], N. Siachos[2], A. Gillespie[2], D. Guest[1], D. Xia[1], D. Werling[1], N. Evans[2], G. Banos[3], G. Oikonomou[2], and A. Psifidi[1], [1]*Royal Veterinary College, Hatfield, Hertfordshire, UK*, [2]*University of Liverpool, Neston, Cheshire, UK*, [3]*Scotland's Rural College, Easter Bush Campus, Midlothian, UK*.

P283 **IL-6, -1β, and TNFα levels in dairy cattle udder parenchyma of healthy quarters adjacent to the infected with staphylococci.**
A. Szprynca*[1], M. Zalewska[2], M. Rzewuska[3], T. Sakowski[1], K. Pawlina-Tyszko[4], T. Zabek[4], and E. Bagnicka[1], [1]*Institute of Genetics and Animal Biotechnology PAS, Jastrzebiec, Poland*, [2]*University of Warsaw, Faculty of Biology, Warsaw, Poland*, [3]*Warsaw University of Life Sciences, Institute of Veterinary, Warsaw, Poland*, [4]*The National Research Institute of Animal Production, Balice, Poland*.

P284 **Single-cell transcriptomic profiling of BALF in PRRSV infections with differential virulence.**
Byeonghwi Lim*[1], Seung-Chai Kim[2], Do-Young Kim[1], Chiwoong Lim[1], Tae-Hong Min[1], Min-Ki Seok[1], Nae-Ho Park[1], Chang-Hyeon Ham[1], Sang-Hyeop Lee[1], Kyung-Tai Lee[3], Won-Il Kim[2], and Jun-Mo Kim[1], [1]*Functional Genomics & Bioinformatics Laboratory, Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do 17546, Republic of Korea*, [2]*College of Veterinary Medicine, Jeonbuk National University, Iksan, Jeonbuk-do 54596, Republic of Korea*, [3]*Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju, Jeonbuk-do 54896, Republic of Korea*.

P285 **Opportunities for reducing respiratory disease in sheep through selective breeding.**
K. M. McRae* and S. C. Clarke, *AgResearch Invermay, Mosgiel, New Zealand*.

P286 **Single-cell RNA sequencing of innate immune cell populations in *RAG1*$^{-/-}$ chickens: A novel platform for exploring avian immunology.**
Seung Je Woo*[1], Jin-Kyoo Kim[1], Eui Shin Lee[1], Thirubasyini Songodan[1], Hyemin Na[1], and Jae Yong Han[1,2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [2]*Department of International Agricultural Technology & Institute of Green Bioscience and Technology, Pyeongchang, Republic of Korea*.

P287 **Comprehensive analysis on genetic variations of Suidae immunome from 10 suids reveals the presence of lineage- or species-specific loss-of-function mutations.**
J. Shin*[1], B. Ahn[1], M. Kang[1], H. Dinka[2], D. Hailu[2], and C. Park[3], [1]*Konkuk University, Seoul, Republic of Korea*, [2]*Adama University, Adama, Ethiopia*, [3]*Bio and Emerging Technology Institute, Addis Ababa, Ethiopia*.

P288 **Protein sequences based phylogenomic insights into the evolutionary history and adaptive traits of Nguni sheep (Zulu ecotype).**
N. Nxumalo*[2,1], R. Clint[1], N.W. Kunene[4], and A.H. Molotsi[3,1], [1]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [2]*University of Mpumalanga, Mbombela, Mpumalanga, South Africa*, [3]*University of South Africa, Johannesburg, Gauteng, South Africa*, [4]*University of Zululand, Kwadlangezwa, KwaZulu-Natal, South Africa*.

P289 **ISAG Bursary Award: Genome-wide CRISPR screening identified TIRAP as a critical host factor facilitating *Brucella* intracellular survival.**
Yige Ding[1,4], Jiayuan Sun[1,4], Shuhong Huang[1], Wenxin Zhang[3,4], Jiabo Ding[4], and Xiaolong Wang*[1,2], [1]*International Joint Agriculture Research Center for Animal Bio-Breeding of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*, [2]*Hainan Institute of Northwest A&F University, Sanya, Hainan, China*, [3]*College of Animal Science and Veterinary Medicine, Shandong Agricultural University, Tai'an, Shandong, China*, [4]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*.

P290 **Handling errors in the response: Considerations for leveraging unsupervised or incomplete data for genetic evaluations.**
X.-L. Wu*[1,2], J. B. Cole[1,3], A. Legarra[1,4], K. L. Parker Gaddis[1], and J. W. Durr[1], [1]*Council on Dairy Cattle Breeding, Bowie, MD, USA*, [2]*Department of Animal and Dairy Sciences, University of Wisconsin, Madison, WI, USA*, [3]*Department of Animal Science, North Carolina State University, Raleigh, NC, USA*, [4]*Department of Animal and Dairy Science, University of Georgia, Athens, GA, USA*.

P291 ***In silico* homology modelling of MHC class 1 BF2 gene in Korean native chickens: Structural validation and molecular docking potential.**
R. Fernando*[1,2], T. N. Agulto[1], E. Cho[1], and J. H. Lee[1], [1]*Chungnam National University, Daejeon, Republic of Korea*, [2]*University of Peradeniya, Peradeniya, Sri Lanka*.

P292 **Use of 600K SNP to study LD pattern and evidence for recombinant hotspots in chicken MHC-*B* region.**
P. Manjula*, *Uva Wellassa University, Badulla, Sri Lanka*.

P293 **ISAG Bursary Award: High-resolution genotyping reveals the crucial role of SLA in PRRSV resistance.**
L. Yang*[1], Q. Wu[1], W. Liu[1], Q. Su[1], X. Zhou[1,2], and B. Liu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, China*, [2]*Hubei Hongshan Laboratory*, *Wuhan, China*.

P294 **Comparative analysis of immune-related gene expression in Korean native chickens.**
S. G. Lee*[1,2], T. J. Choi[1], J. H. Lee[1], G. L. Ryu[1], D. S. Kim[1], H. U. Baek[1], and S. H. Sohn[2], [1]*National Institute of Animal Science*, *Cheonan, Chungcheongnam-do, Republic of Korea*, [2]*Gyeongsang National University*, *Jinju, Gyeongsangnam-do, Republic of Korea*.

P295 **Effect of Galectin-9 on the expression of genes involved in bovine innate and adaptive immune responses in blood.**
M. Worku*, R. Uzzaman, P. Pande, and S. Ghimre, *North Carolina Agricultural and Technical State University*, *Greensboro, NC, USA*.

P296 **Genomic basis of the host response to the porcine respiratory disease complex.**
H. Laghouaouta*[1,2], L. Fraile[1,2], and R. N. Pena[1,2], [1]*Departament de Ciència Animal, Universitat de Lleida*, *Lleida, Spain*, [2]*AGROTECNIO-CERCA Center*, *Lleida, Spain*.

P297 **Identification and validation of novel SNPs associated with BLV-induced lymphoma and proviral load using genome-wide association study.**
Y. Aida*[1], S. Watanuki[1], Y. Ye[1], F. Nagata[1], R. Matsuura[1], C. Lo[1], S. Saito[1], Y. Matsumoto[1], Y. Miyazaki[2], S. Sasaki[3], and S. Takeshima[4], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo*, *Tokyo, Japan*, [2]*Livestock improvement association of Japan, Inc*, *Gunma, Japan*, [3]*Faculty of Agriculture, University of the Ryukyus*, *Okinawa, Japan*, [4]*Department of Food and Nutrition, Jumonji University*, *Saitama, Japan*.

P298 **ISAG Bursary Award: Integration of CRISPR screening and proteomic analysis of WDR91 manipulation of endosome-to-cytosol transport of African swine fever virus.**
H. L. Liu*[1], Y. L. Guo[2], Z. S. Guo[1], G. Q. Peng[2], S. H. Zhao[1], and S. S. Xie[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University*, *Wuhan, Hubei, China*, [2]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University*, *Wuhan, Hubei, China*.

P299 **Host-adapted tuberculosis-causing mycobacteria remodel the epigenome of the alveolar macrophage.**
T. Hall*[1], M. Mitermite[2], J. Browne[1], G. McHugo[1], J. O'Grady[1], E. Clark[3,4], M. Salavati[5], S. Gordon[2,6], and D. MacHugh[1,6], [1]*UCD Animal Genomics Laboratory, UCD School of Agriculture and Food Science, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [2]*UCD School of Veterinary Medicine, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [3]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, EH25 9RG, UK*, [4]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush Campus, EH25 9RG, UK*, [5]*Dairy Research and Innovation Centre, SRUC South and West Faculty, Barony Campus, Parkgate, Dumfries DG1 3NE, UK*, [6]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*.

P300 **The inflammatory state and energy metabolism of porcine immune cells are closely connected.**
E. Murani[1], W. Ma[1,2], J. Brenmoehl[1], N. Trakooljul[1], F. Hadlich[1], B. Fuchs[1], C. Galuska[1], and K. Wimmers*[1,2], [1]*Research Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock*, *Rostock, Germany*.

P301 **Assessing immune competence phenotypes in New Zealand sheep.**
K. M. McRae*[1], K. G. Dodds[1], N. Haack[2], A. Heiser[2], J. Peers-Adams[1], S. Coll[1], and P. J. Johnson[1], [1]*AgResearch Invermay*, *Mosgiel, New Zealand*, [2]*AgResearch Grasslands*, *Palmerston North, New Zealand*.

P302 **Single-cell RNA sequencing reveals immune response dynamics and infection mechanisms in PRRSV-infected porcine alveolar macrophages.**
Jiang Bo Jiang, Chen Xin Chen, Chen Xu Chen, and Zhengcao Li Li*, *Sun Yat-Sen University*, *Guangzhou, China*.

P303 **ISAG Bursary Award: Development of a blood-based transcriptional biosignature for accurate discrimination of *M. bovis* infected and control non-infected cattle.**
J. F. O'Grady*[1], A. Ivich[2], G. P. McHugo[1], J. A. Ward[1], T. J. Hall[1], S. L. F. O'Donnell[1], C. N. Correia[1], J. A. Browne[1], M. McDonald[1], A. Khan[1], E. Gormley[3,4], V. Riggio[5,6], J. G. D. Prendergast[5,6], E. L. Clarke[5,6], H. Pausch[7], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus, Aurora, CO, USA*, [3]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*, [4]*UCD One Health Centre, University College Dublin, Belfield, Dublin, Ireland*, [5]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, UK*, [6]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Midlothian, UK*, [7]*Animal Genomics, ETH Zurich, Zurich, Switzerland*, [8]*UCD School of Mathematics and Statistics, University College Dublin, Belfield, Dublin, Ireland*.

P304 **Validation of genetic biomarkers and immune phenotypes as indicators of the immune response to E2-CD154 subunit classical swine fever virus (CSFV) vaccine.**
M. Ballester*[1], C. Hernández-Banqué[1], T. Jové-Juncà[1], O. González-Rodríguez[1], L. Coronado[2], L. Ganges[2], J. Reixach[3], S. Gol[3], R. Quintanilla[1], and J. Tarres[1], [1]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*, [2]*Centre de Recerca en Sanitat Animal (CReSA), Unitat Mixta d'Investigació IRTA-UAB en Sanitat Animal, Campus Universitat Autònoma de Barcelona (UAB), Barcelona, Bellaterra, Spain*, [3]*Selección Batalle SA, Riudarenes, Spain*.

P305 **Cyprinid fish species appear to be both disease resistant and infection resistant to cyprinid herpes virus type 3 (CyHV-3).**
B. Dorfman*[1], J. Marcos-Hadad[1], R. Tadmor-Levi[1], O. Liffmann[1], B. Abd Elkader[1], E. Myara[1], S. Lamichhane[2], B. Gorgoglione[2], and L. David[1], [1]*Dept. of Animal Sciences, R.H. Smith Faculty of Agricultural, The Hebrew University of Jerusalem, Israel, Rehovot, Israel*, [2]*Fish Pathobiology and Immunology Laboratory, Dept. Pathobiology and Diagnostic Investigation (CVM)/Dept. Fisheries and Wildlife (CANR), Michigan State University, East Lansing, MI, USA*.

P306 **Genetic analysis of the major histocompatibility complex class I BF2 gene of Korean native chickens.**
T. N. Agulto*[1], M. Kim[1], P. Manjula[2], R. Fernando[1,3], and J. H. Lee[1], [1]*Chungnam National University, Daejeon, Republic of Korea*, [2]*Uva Wellassa University, Badulla, Sri Lanka*, [3]*University of Peradeniya, Peradeniya, Sri Lanka*.

Ruminant Genetics and Genomics II

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P516 **Analysis of *KRTAP6-1* transcriptional regulation in Gansu alpine fine-wool sheep.**
H. X. Sun, Z. H. He, F. F. Zhao, J. Hu, J. Q. Wang, X. Liu, Z. D. Zhao, M. N. Li, Y. Z. Luo, and S. B. Li*, *Gansu Agricultural University, Lanzhou, China*.

P517 **Exploring the genetic structure of economic traits in Hu sheep through low-coverage sequencing.**
Z. Liu*[1], L. Tan[1], Q. Liu[2], and Y. Zhao[1], [1]*College of Biological Sciences, China Agricultural University, Beijing, China*, [2]*State Key Laboratory of Molecular Developmental Biology, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China*.

P518 **Simulation of genetic gain enhancement in Hanwoo cattle through genomic selection of females.**
H. J. Kim*[1], S. Jin[1], S. H. Lee[2], and J. H. J. Van der Werf[3], [1]*Hanwoo Research Center, Pyeongchang, Korea*, [2]*Chungnam National University, Daejeon, Korea*, [3]*University of New England, Armidale, NSW, Australia*.

P519 **Leveraging genomic and RNA-seq data to decode dynamic genetic basis underlying cattle feed intake across lactation.**
C. James*[1], L. Fang[2], E. Wall[1], M. Coffey[1], and B. Li[1], [1]*Animal and Veterinary Sciences, Scotland's Rural College (SRUC), Easter Bush, Midlothian, United Kingdom*, [2]*Center for Quantitative Genetics and Genomics, Aarhus University, Aarhus, Denmark*.

P520 **Integrative multi-omics analysis reveals regulatory networks underlying body weight variation in Hanwoo (Korean native cattle).**
T. Jeong*[1], S. Hwang[1], J. Lee[1], W. Park[2], S. Jang[2], and D. Lim[1], [1]*Department of Animal Resources Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon, Republic of Korea*, [2]*National Institute of Animal Science, Wanju, Republic of Korea*.

P521 **Genomic insights into coat color variation in Hanwoo: A whole-genome perspective.**
J. W. Shin*[1], Y. S. Kim[2], S. H. Lee[3], Y. G. Ko[4], S. Y. Lee[4], J. Y. Lee[4], C. L. Kim[4], and Y. J. Chung[2], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Korea*, [2]*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*, [3]*Institute of Agricultural Science, Chungnam National University, Daejeon, Republic of Korea*, [4]*Animal Genetic Resources Research Center, National Institute of Animal Science, RDA, Gyeongsangnam-do, Hamyang-gun, Seosang-myeon, Deogyuwolseong-ro, Republic of Korea*.

P522 **Development of prediction equations for immunoglobulin A, G, and M concentrations in mature milk from Holstein cows using milk infrared spectral data.**
Y. Satake*[1], T. Katsura[1], T. Zhuang[1], M. Urakawa[1], T. Baba[2], G. Yoshida[3], H. Kitazawa[1], H. Shirakawa[1], T. Nakamura[1], T. Nochi[1], Y. Sakai[1], M. Satoh[1], S. Haga[1], H. Aso[1], Y. Uemoto[1], [1]*Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan*, [2]*Holstein Cattle Association of Japan, Hokkaido Branch, Sapporo, Hokkaido, Japan*, [3]*Shihoro Agricultural Cooperative, Kato District, Hokkaido, Japan*.

P523 **Identification of common gene modules in fat and muscle tissues in Hanwoo (Korean native cattle) using weighted gene co-expression network analysis (WGCNA).**
Suk Hwang*[1], Taejoon Jeong[1], Junyoung Lee[1], Woncheoul Park[2], Sunsik Jang[2], and Dajeong Lim[1], [1]*Department of Animal Resources Science, College of Agriculture and Life Sciences, Chungnam National University, Yuseong District, Daejeon, Republic of Korea*, [2]*National Institute of Animal Science, Wanju, Jeonbuk State, Republic of Korea*.

P524 **ISAG Bursary Award: Comparative analysis of whole-genome amplification methods and genotyping strategies for preimplantation embryo genomic selection in cattle.**
S. H. Yan*, S. N. Yan, Y. W. L. Cheng, H. Y. Cui, D. M. Dai, Y. G. He, J. F. Si, S. M. Zeng, and Y. Zhang, *China Agricultural University, Beijing, China*.

P525 **Genome-wide expression QTL analysis based on transcriptome data in kidney fat of Hanwoo (Korean Native Cattle).**
Junyoung Lee*[1], Taejoon Jeong[1], Suk Hwang[1], Woncheoul Park[2], Sunsik Jang[2], and Dajeong Lim[1], [1]*Department of Animal Resources Science College of Agriculture and Life Sciences Chungnam National University, Yuseong District, Daejeon, Republic of Korea*, [2]*National Institute of Animal Science, Wanju, Jeonbuk State, Republic of Korea*.

P526 **Enhancing genomic prediction through text mining-based SNP selection in Hanwoo cattle.**
Youngjae Choi*[1], Seung Hwan Lee[2], and Yoshinobu Uemoto[1], [1]*Tohoku University, Sendai, Miyagi, Japan*, [2]*Chungnam National University, Yuseung-gu, Daejeon, South Korea*.

P527 **Unraveling the cellular and molecular landscape of bovine corpus luteum using single-cell RNA sequencing.**
D. Becker*[1], V. S. Baddela[1], P. K. Chitneedi[1], A. Vernunft[1], C. Klein[2], G. Neufeld[2], and J. Vanselow[1], [1]*Research Institute for Farm Animal Biology, Dummerstorf, Germany*, [2]*Federal Research Institute for Animal Health, Neustadt, Germany*.

P528 **Genome-wide variant filtering discovers likely causal variants for 3 emerging inherited diseases affecting Australian livestock.**
K. L. M. Eager*[1,2], L. K. Johnson[1,2], K. Atkinson[3], R. W. Cook[1], X. Gao[2], H. Xian[2], Z. Xu[2], C. E. Willet[4], B. A. O'Rourke[1], and I. Tammen[2], [1]*Elizabeth Macarthur Agricultural Institute, NSW DPIRD, Menangle, NSW, Australia*, [2]*Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Sydney, NSW, Australia*, [3]*Central West Local Land Services, Coonabarabran, NSW, Australia*, [4]*Sydney Informatics Hub, The University of Sydney, Sydney, NSW, Australia*.

P529 **ISAG Bursary Award: Validation of the effects of gene polymorphisms on BTA19 on fatty acid composition revealed a common QTL in 3 Japanese Black populations.**
C. Toiguchi*, H. Mannen, S. Sasazaki, and F. Kawaguchi, *Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Hyogo, Japan*.

P530 **Cattle breed differences and similarities in fat trait candidate genes identified by GWAS and meta-analysis.**
J. Yao*, R. A. McEwin, W. S. Pitchford, C. D. K. Bottema, and M. S. Khatkar, *Davies Livestock Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Adelaide, SA, Australia*.

P531 **Comprehensive multi-omics insights into Yangtze Valley water buffalo (*Bubalus bubalis*): Diversity and molecular genetic basis.**
Yangyang Shen*[1,2], Zhenjiang An[1,2], Shuwen Xia[1,2], Qiang Ding[1,2], Kunlin Chen[1,2], Yilong Miao[1,2], Jifeng Zhong[1,2], Jianbin Li[3], Xiao Wang[3], and Huili Wang[1,2], [1]*Institute of Animal Science, Jiangsu Academy of Agriculture Science, Nanjing, Jiangsu, China*, [2]*Jiangsu Provincial Engineering Research Center of Precision Animal Breeding, Nanjing, Jiangsu, China*, [3]*Institute of Animal Science and Veterinary Medicine, Shandong Academy of Agricultural Sciences, Jinan, Shandong, China*.

P532 **Leveraging non-additive GWAS to identify deleterious mutations for height accumulated through inbreeding in Brown Swiss.**
Q. He*[1], J. Deuber[1], F. R. Seefried[2], H. Pausch[1], and N. Kadri[1], [1]*Eidgenössische Technische Hochschule Zürich, Zürich, Switzerland*, [2]*Qualitas AG, Zug, Switzerland*.

P533 **Genetics underlying congenital adrenal hyperplasia in Australian female cattle.**
R. Hofmeyer*, T. Chen, L. Hampton, W. L. Low, W. S. Pitchford, M. S. Khatkar, K. Petrovski, and C. D. K. Bottema, *Davies Livestock Research Centre, School of Animal and Veterinary Sciences, Roseworthy Campus, University of Adelaide, Roseworthy SA, Australia*.

P534 **ISAG Bursary Award: Multi-ancestry meta-analysis of genome-wide association studies for udder confirmation traits and stature in 4 cattle breeds.**
N. W. Watson*, Q. H. He, N. K. Kadri, and H. P. Pausch, *ETH Zurich, Zurich, Switzerland*.

P535 **Family-based genetic evaluation and genome-wide association analysis of carcass traits in Hanwoo.**
J. Y. Kim*[1], H. C. Kang[1], C. H. Myung[1], E. H. Kim[2], and H. T. Lim[1,3], [1]*Department of Animal Science, Gyeongsang National University, Jinju 52828, Korea*, [2]*Animal Genetics and Breeding Division, National Institute of Animal Science, Cheonan 31000, Korea*, [3]*Institute of Agriculture and Life Science, Gyeongsang National University, Jinju 52828, Korea*.

P536 **Estimating genetic parameters for carcass traits and marbling fineness in Hanwoo steers.**
Shil Jin*[1], Hyoun Ju Kim[1], Jeong Il Won[1], Sung-Sik Kang[1], Sung Woo Kim[1], Yeong Kuk Kim[2], Doo Ho Lee[2], Soo Hyun Lee[2], and Seung Hwan Lee[3], [1]*Hanwoo Research Center, National Institute of Animal Science, Pyeongchang, Republic of Korea*, [2]*Quantomic Research and Solution Co, Daejeon, Republic of Korea*, [3]*Department of Animal Science and Biotechnology, Chungnam National University, Daejeon, Republic of Korea*.

P537 **Exploration of genetic polymorphisms related to Wagyu beef aroma using whole genome resequencing data.**
Kanna Nakamura*, Fuki Kawaguchi, Hideyuki Mannen, Shuji Ueda, and Shinji Sasazaki, *Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Nada, Kobe, Japan*.

P538 **ISAG Bursary Award: Genome-wide analysis of selection signatures and genetic variants associated with economic traits in Karan Fries cattle.**
P. Pal*, A. Mukherjee, G. Gowane, and S. Mukherjee, *Animal Genetics and Breeding Division, ICAR-National Dairy Research Institute, Karnal, Haryana, India*.

P539 **Characterization of pivotal metabolites influencing the formation of milk components in dairy goats.**
Mengke Ni, Xinran Luo, Jun Luo, and Cong Li*, *Northwest A&F University, Yangling, Shaanxi, China*.

P540 **Construction of goat milk metabolite map and identification of key metabolites in goat milk at different lactation stages.**
X. Gong, X. Luo, J. Luo, and C. Li*, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaan Xi, China*.

P541 **Analysis of expression patterns during adipocyte differentiation of candidate genes for fatty acid composition in beef.**
S. Okuno*, H. Mannen, S. Sasazaki, and F. Kawaguchi, *Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Hyogo, Japan*.

P542 **ISAG Bursary Award: Nepalese wild and domestic buffaloes: A whole-genome based insight into genetic relationship.**
A. Dhakal*[1,2], J. F. Si[1], S. Sapkota[3], A. Pauciullo[4], J. L. Han[5], N. Amatya Gorkhali[6], X. B. Zhao[1], and Y. Zhang[1], [1]*National Engineering Laboratory for Animal Breeding, Key Laboratory of Animal Genetics, Breeding and Reproduction of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*Nepal Polytechnic Institute Ltd., College of Engineering, Agriculture, Veterinary and Medical Sciences, Chitwan, Nepal*, [3]*National Animal Breeding and Genetics Research Centre, Nepal Agricultural Research Council, Lalitpur, Nepal*, [4]*Department of Agricultural, Forest and Food Sciences, University of Torino, Grugliasco, Italy*, [5]*Yazhouwan National Laboratory, Sanya, China*, [6]*National Animal Science Research Institute, Nepal Agricultural Research Council, Lalitpur, Nepal*.

P543 **Establishing a genomic-driven conservation of a cattle genetic resource: The case of the Parmigiano-Reggiano cheese iconic breed.**
Giuseppina Schiavo[1], Samuele Bovo[1], Francesca Bertolini[1], Matteo Bolner[1], Anisa Ribani[1], Valeria Taurisano[1], Stefania Dall'Olio[1], Jessica Maranzani[2], Massimo Bonacini[2], and Luca Fontanesi*[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy*, [2]*ANABoRaRe - National Association of Reggiana Cattle Breeders, Reggio Emilia, Italy*.

P544 **Establishing a genomic-driven conservation of a cattle genetic resource: The case of the Parmigiano-Reggiano cheese iconic breed.**
G. Schiavo[1], S. Bovo[1], F. Bertolini[1], M. Bolner[1], A. Ribani[1], V. Taurisano[1], S. Dall'Olio[1], J. Maranzani[2], M. Bonacini[2], and L. Fontanesi*[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy*, [2]*ANABoRaRe - National Association of Reggiana Cattle Breeders, Reggio Emilia, Italy*.

P545 **The Y-linked PRAME gene regulates sperm function, fertilization, and epigenetic dynamics in bovine embryogenesis.**
C. H. Kern and W.-S. Liu*, *Department of Animal Science, Center for Reproductive Biology and Health (CRBH). College of Agricultural Sciences, The Pennsylvania State University*, *University Park, PA, USA*.

P546 **Evaluation of animal identification performance using deep learning-based image embedding models.**
H. Chang*, *National Institute of Animal Science*, *Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P547 **Comparison of artificial neural network and GBLUP applications for genomic prediction of growth and carcass traits in the Brangus heifers.**
S. Peters*[1], K. Kizilkaya[2], and M. Sinecen[2], [1]*Berry College*, *Mount Berry, GA, USA*, [2]*Aydin Adnan Menderes University*, *Aydin, Turkey*.

P548 **Establishment of an immunofluorescence method based on fluonanobody for sensitive and rapid detection of aflatoxin M_1 residues in dairy products.**
Li Yi*[1], Yisi Ai[2], Qinghui Li[1], Liang Ming[1], and Rimutu Ji[1], [1]*Key Laboratory of Dairy Biotechnology and Engineering, Ministry of Education, College of Food Science and Engineering, Inner Mongolia Agricultural University*, *Hohhot, Inner Mongolia, China*, [2]*Inner Mongolia Autonomous Region International Mongolian Hospital*, *Hohhot, Inner Mongolia, China*.

P549 **Relationship between fatty acid composition and intramuscular fat content in Hanwoo steers.**
D. Lee*[1], M. Alam[1], C. Dang[1], S. Lee[1], H. Seong[1], J. Cha[1], E. Kim[1], H. Jang[1], E. Ryu[1], C. Lee[1], A. Jang[2], C. Cho[3], and M Park[1], [1]*Animal Genetics and Breeding Division, National Institute of Animal Science*, *Cheonan, Chungcheongnam-do, Rep. of Korea*, [2]*Department of Applied Animal Science, College of Animal Life Sciences, Kangwon National University*, *Chuncheon, Gangwon, Rep. of Korea*, [3]*Hanwoo Genetic Improvement Center, National Agricultural Cooperative Federation Agribusiness Group Inc*, *Seosan, Chungcheongnam-do, Rep. of Korea*.

P550 **Estimation of genomic breeding values for slaughter traits and carbon emission intensity of Hanwoo populations.**
Dohyun Kim*, Jisuk Yu, and Hakkyo Lee, *Jeonbuk National University*, *Jeonju-si, Jeollabuk-do, Republic of Korea*.

P551 **Integrating genome-wide and targeted sequencing: TELP-WGS enables high-accuracy genotyping for precision cattle breeding.**
Feng Liu*[1], Keke Shi[1], Le Li[1], Tian Chen[1], Xinming Liang[1], Jingbo Tang[1], Dou Hu[1], Yanyan Zhang[1], and Lin Yang[1,2], [1]*MGI Tech Co., Ltd*, *Shenzhen, China*, [2]*College of Life Sciences, University of Chinese Academy of Sciences*, *Beijing, China*.

P552 **Responses related to host's ion, actin and intestinal metabolism to short-term heat stress in Hanwoo cattle.**
Hana Kim*[1], Jong-Eun Park[2], Woncheoul Park[3], and Donghyun Shin[1], [1]*Jeonbuk National University*, *Jeonju, Jeonbuk, Republic of Korea*, [2]*Jeju National University*, *Jeju, Jeju, Republic of Korea*, [3]*National Institute of Animal Science*, *Wanju, Jeonbuk, Republic of Korea*.

P553 **Genome-enabled prediction of linear body measurement traits using single-step genomic best linear unbiased prediction in Hanwoo beef cows.**
M. Naserkheil*[1], H. Mehrban[1], Y. J. Han[2], and D. M. Lee[2], [1]*Animal Science Research Institute of Iran*, *Karaj, Alborz, Iran*, [2]*Hankyong National University*, *Anseong, Gyeonggi, Republic of Korea*.

P554 **Investigation of genomic prediction accuracy for carcass traits using linear type traits in Hanwoo beef cows.**
H. Mehrban*[1], M. Naserkheil[1], Y. J. Han[2], and D. M. Lee[2], [1]*Animal Science Research Institute of Iran*, *Karaj, Alborz, Iran*, [2]*Hankyong National University*, *Anseong, Gyeonggi, Republic of Korea*.

P555 **Screening of *Staphylococcus aureus*-specific nanobodies and their application in sandwich ELISA.**
N. Su*[1], L. Yi[1], and R. Ji[1,2], [1]*Key Laboratory of Dairy Biotechnology and Engineering, Ministry of Education, College of Food Science and Engineering, Inner Mongolia Agricultural University*, *Hohhot, Inner Mongolia, China*, [2]*Inner Mongolia China-Kazakhstan Camel Research Institute*, *Alxa, Inner Mongolia, China*.

P556 **Study on runs-of-homozygosity and genomic inbreeding using Axiom Bovine Genotyping V3 array in Korean Holstein Cattle.**
M. Alam*, D. Lee, C. Dang, E. Kim, H. Chang, M. Park, J. Cha, H. Seong, S. Lee, C. Lee, and E. Ryu, *Animal Breeding and Genetics Division, National Institute of Animal Science*, *Cheonan-si, Chungnam, Republic of Korea*.

P557 **Enrichment of fertility-related quantitative trait loci in regulatory regions of the bovine placenta.**
M. D. Wagle*[1], H. L. Neibergs[1], T. E. Spencer[2,3], and K. M. Davenport[1], [1]*Department of Animal Sciences, Washington State University*, *Pullman, WA, USA*, [2]*Division of Animal Sciences, University of Missouri*, *Columbia, MO, USA*, [3]*Department of Obstetrics, Gynecology, and Women's Health, University of Missouri*, *Columbia, MO, USA*.

OTHER EVENTS

Lunch
Exhibition Hall 109 + 110 + 111 + 112
12:30 PM - 1:30 PM

SYMPOSIA AND ORAL SESSIONS

Applied Genetics and Genomics in other Species of Economic Interest

Chair: **Amparo Martinez, University of Cordoba, Cordoba, Spain**
Room 107
1:30 PM - 6:00 PM

1:30 PM **Welcoming remarks.**

1:35 PM **Pig CT Discussion.**

1:55 PM **Dromedary CT Discussion.**

2:15 PM **Alpaca/Llama CT Discussion.**

2:35 PM **Pigeon CT Discussion.**

2:55 PM **Goat CT Discussion.**

3:10 PM **Sheep CT Discussion.**

3:30 PM **Coffee Break.**

4:00 PM **Election of committee and any other business.**

4:10 PM OP149 **Exploring the genetics of coat color and fleece type in alpacas using the improved VicPac4 reference genome.**
A. Letko*[1], M. Mendoza Cerna[2], G. Lühken[3], T. Raudsepp[2], B. W. Davis[2], and C. Drögemüller[1], [1]*Institute of Genetics, University of Bern, Bern, Switzerland*, [2]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University*, *College Station, TX, USA*, [3]*Institute for Animal Breeding and Genetics, Justus Liebig University Giessen*, *Giessen, Germany*.

4:30 PM OP151 **Allele sequencing of microsatellite markers for parentage verification in sheep.**
Agnieszka Szumiec, Agata Piestrzynska-Kajtoch*, and Anna Radko, *National Research Institute of Animal Production, Department of Animal Molecular Biology*, *Balice, Poland*.

4:50 PM OP152 **Impact of garlic-infused mineral supplements on the rumen microbiome and resistome of feedlot cattle.**
O. N. Durunna*[1], N. Malmuthuge[2], D. B. Holman[3], T. A. McAllister[4], I. Cheang-Deis[5], C. Vandenberg[1], O. Oyedeji[6], E. Gonzalez[7], and H. A. Lardner[8], [1]*Lakeland College, Vermilion, Alberta, Canada*, [2]*University of Calgary*, *Calgary, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Lacombe, Alberta, Canada*, [4]*Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*, [5]*Cenovus Energy, Lloydminster, Alberta, Canada*, [6]*Agriculture and Irrigation, Government of Alberta, Edmonton, Alberta, Canada*, [7]*McGill University*, *Montreal, Quebec, Canada*, [8]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

Applied Genetics of Companion Animals

Chair: (1), Peter Dovc, (2) Jiansheng Qiu, (1) University of Ljubljana, Biotechnical Faculty, Ljubljana, Slovenia, (2) Neogen Genomics, Lincoln, NE United States

Room 101 + 102

1:30 PM - 6:00 PM

1:30 PM **Introduction.**

1:40 PM **Ethical concerns of Fashion dog breeds (David J. Menor-Campos).**

2:10 PM OP154 **Development of a high-density feline microarray for breed and trait identification.**
Ali Pirani, Paola Corrales, and Mikyung Park*, *Thermo Fisher Scientific Inc*, *Seoul, South Korea*.

2:26 PM OP155 **Transcriptomic profiling of canine gastrointestinal cancer and chronic inflammatory enteropathy: Molecular insights for diagnosis and treatment.**
Maria G. Luigi-Sierra*[1], Janne Graarup-Hansen Lyngby[2], Jennifer M. Jacobsen[1], Ann-Sofie Ingerslev[1], Charlotte Bjørnvad[2], Merete Fredholm[1], Annemarie T. Kristensen[2], Lise Nikolic Nielsen[2], and Susanna Cirera[1], [1]*Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark*, [2]*Department of Veterinary Clinical Sciences*, *Copenhagen, Denmark*.

2:42 PM OP156 **Selective sweep identification in dog populations provides potential candidate genes for trainability.**
S. F. Naghshbandi, A. A. Masoudi*, R. Vaez Torshizi, and A. Maghsoudi, *Department of Animal Science, Faculty of Agriculture, Tarbiat Modares University*, *Tehran, Iran*.

2:58 PM OP157 **A wolf is not a dog—Man's best friends interactome.**
D. Schwochow*[1], C. Kálmán[2], R. Carlsson Norlin[1], S. Dasgupta[1], A. Karadagi[3], E. Ellis[3], K. Enikö[2], P. Savolainen[1], and P. Sahlén[1], [1]*KTH Royal Institute of Technology, Science for Life Laboratory, School of Engineering Sciences in Chemistry, Biotechnology and Health, Division of Gene Technology*, *Solna, Sweden*, [2]*Eötvös Loránd University, 2 Department of Ethology*, *Budapest, Hungary*, [3]*Karolinska Institutet/ ME Transplantation, Karolinska University Hospital, 3Department of Clinical Science, Intervention and Technology, (CLINTEC), Division of Transplantation surgery*, *Huddinge, Sweden*.

3:14 PM OP158 **Chromosome-scale assembly with improved annotation of an American Shorthair cat.**
Y. Matsumoto[1,2], C. Y. L. Chung[3], S. Isobe[4], M. Sakamoto[5], X. Lin[3], T. F. Chan[3], H. Hirakawa[4], G. Ishikawa[1], H. M. Lam[3], Y. Tanizawa[5], K. Watanabe[1], M. Yagura[5], Y. Niimura[6], and Y. Nakamura*[5], [1]*Research and Development Section, Anicom Specialty Medical Institute Inc*, *Yokohama, Kanagawa, Japan*, [2]*Data Science Center, Azabu University*, *Sagamihara, Kanagawa, Japan*, [3]*School of Life Sciences and the Center for Soybean Research of the State Key Laboratory of Agrobiotechnology, The Chinese University of Hong Kong*, *Shatin, Hong Kong Special Administrative Region*, [4]*Kazusa DNA Research Institute*, *Kisarazu, Chiba, Japan*, [5]*National Institute of Genetics, Research Organization of Information and Systems*, *Mishima, Shizuoka, Japan*, [6]*Department of Veterinary Sciences, Faculty of Agriculture, University of Miyazaki*, *Miyazaki, Miyazaki, Japan*.

3:30 PM **Coffee Break.**

4:00 PM OP159 **Epigenetic signatures associated with myxomatous mitral valve disease in dogs.**
S. Jang*[1,2], C.-O. Yun[3], T.-S. Hwang[3], J. Kim[1,2], and J. Lee[4], [1]*Division of Applied Life Science (BK21), Gyeongsang National University*, *Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University*, *Jinju, Republic of Korea*, [3]*Institute of Animal Medicine, College of Veterinary Medicine, Gyeongsang National University*, *Jinju, Republic of Korea*, [4]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA*, *Cheonan-si 31000, Chungcheongnam-do, Republic of Korea*.

4:15 PM OP160 **Integration of hematological parameters and DNA methylome to identify aging biomarkers in dogs.**
S. J. Kim*[1,2], C.-Y. Hong[3], S.-L. Lee[3], J. Kim[1,2], and E.-Y. Bok[4], [1]*Division of Applied Life Science (BK21), Gyeongsang National University*, *Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University*, *Jinju, Republic of Korea*, [3]*College of Veterinary Medicine, Gyeongsang National University*, *Jinju, 52828 Republic of Korea*, [4]*Division of Animal Diseases & Health, National Institute of Animal Science, RDA*, *Wanju 55365, Republic of Korea*.

4:30 PM **Proposal of data format for SNP data exchange.**
Leanne van de Goor, Dr. van Haeringen Laboratorium B.V., The Netherlands.

4:45 PM **A new cat SNP panel proposal.**
Leanne van de Goor, Dr. van Haeringen Laboratorium B.V., The Netherlands.

5:00 PM **Dog 2025 CT report.**
Robert A. Grahn, University of California-Veterinary Genetics Laboratory, Davis, CA, USA.

5:15 PM **Cat 2025 CT report.**
Hubert Bauer, LABOKLIN, Bad Kissingen, Germany.

5:30 PM **General Discussion.**

5:45 PM **Elections.**

Genetics and Genomics of Aquaculture Species

Chair: **Lior David (1), Maria Saura (2), (1) The Hebrew University of Jerusalem, Rehovot, Israel; (2) Instituto de Investigaciones Marinas IIM-CSIC, Vigo, Spain**
Room 108
1:30 PM - 6:00 PM

Presentations assigned 20 minutes will be 15 minutes each + 5 minutes Q&A. Presentations assigned 10 minutes are considered poster pitch presentations and will have no Q&A.

1:30 PM OP161 **Invited Workshop Presentation: Can early-life priming improve stress and disease resistance?**
Tamsyn M. Uren Webster*, *Biosciences, Faculty of Science and Engineering, Swansea University*, *Swansea, Wales, UK*.

2:30 PM OP162 **Complex genetic architecture underlying sex determination in common carp.**
Eldad Gamliel, Roni Tadmor-Levi, Bayan Abdelkader, Evgenia Marcos-Hadad, and Lior David*, *The Hebrew University of Jerusalem*, *Rehovot, Israel*.

2:50 PM OP163 **Genetic insights into bacterial disease resistance in olive flounder (*Paralichthys olivaceus*): A multi-trait GWAS approach.**
Chaehyeon Lim*, Jong-Won Park, Minhwan Jeong, Dain Lee, Julan Kim, Hyejin Kim, Ju-won Kim, and Hee Jeong Kong, *Genetics and Breeding Research Center, National Institute of Fisheries Science*, *Geoje, Republic of Korea*.

3:10 PM OP164 **Bulk segregation method with transcriptomics is an innovative method for identifying true SNPs and functional genes in a breeding line of specific pathogen resistant (SPR) WSSV-resistant Madagascar-Malaysia *Penaeus monodon*.**
Subha Bhassu* and Farhana Mohd Ghani, *Animal Genetics and Genome Evolutionary Biology Lab, Institute of Biological Sciences, Faculty of Science, University of Malaya*, *Kuala Lumpur, Malaysia*.

3:30 PM **Coffee Break.**

4:00 PM OP165 **Occurrence of inbreeding depression for pigmentation in a farmed population of turbot.**
M. Saura*[1], D. Costas-Imbernón[1], S. Otero[1], P. García-Fernández[2], P. Touriñán[2], R. Tur[2], D. Chavarrías[2], and J. Rotllant[1], [1]*Instituto de Investigaciones Marinas IIM-CSIC, Vigo, Spain*, [2]*Pescanova Biomarine Center*, *O Grove, Spain*.

4:20 PM OP166 **Transcriptome-wide in vivo identification of miRNA target genes in Atlantic salmon.**
R. Andreassen* and S. Ramberg, *Oslo Metropolitan University*, *Oslo, Norway*.

4:40 PM OP167 **Predicting fatty acid composition in Atlantic salmon using Raman spectroscopy: Genetic and phenotypic validation from crude fat to individual fatty acids.**
J. Park*[1], G. F. Difford[1], S. S. Horn[2], H. Moghadam[3], B. Hillestad[3], A. K. Sonesson[2], P. Berg[1], J. P. Wold[2], and N. K. Afseth[2], [1]*Norwegian University of Life Sciences (NMBU), Ås, Akershus, Norway*, [2]*Nofima, Ås, Akershus, Norway*, [3]*Benchmark Genetics*, *Bergen, Vestland, Norway*.

5:00 PM OP168 **Genomic insights into Korean olive flounder population structure and breeding potential.**
J. Kim*[1], Y. Chung[2], H.-C. Kim[1], J.-H. Lee[1], P. T. N. Dinh[3], E. Hong[4], W. Jeong[5], W. Ekanayake[5], H. J. Kong[1], and S. H. Lee[6], [1]*Genetics and Breeding Research Center, National Institute of Fisheries Science, Geoje, Republic of Korea*, [2]*Institute of Agricultural Science, Chungnam National University, Daejeon, Republic of Korea*, [3]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Republic of Korea*, [4]*Bigdata Center, TNT Research Co., Ltd, Jeonju, Republic of Korea*, [5]*Department of Bio-Big Data and Precision Agriculture, Chungnam National University, Daejeon, Republic of Korea*, [6]*Division of Animal & Dairy Science, Chungnam National University, Daejeon, Republic of Korea*.

5:20 PM OP169 **ISAG Bursary Award: De novo assembly of a Mozambique Tilapia (*Oreochromis mossambicus*): An update using high-accuracy technology.**
T. S. Tshilate*[1], L. T. Nesengani[1], S. Mdyongolo[2], A. H. Smith[2], T. Molotsi[1], C. Masebe[2], N. Rhode[3], and N. Mapholi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, UNISA Science Campus, Johannesburg, GAuteng, South Africa*, [2]*Department of Life and Consumer Sciences, College of Agriculture and Environmental Sciences, UNISA Science Campus, Johannesburg, GAuteng, South Africa*, [3]*Department of Genetics, Stellenbosch University, Stellenbosch, Western Cape, South Africa*.

5:40 PM **Workshop Business Meeting.**

Genetics of Immune Response and Disease Resistance

Chair: **(1) Romi Pena, (2), Sabine Hammer, (3) John Hammond, (1), University of Lleida, Lleida, Spain, (2), University of Veterinary Medicine Vienna, Vienna, Austria, (3) The Pirbright Institute, UK**
Room 105 + 106
1:30 PM - 6:00 PM

1:30 PM OP171 **Assessing immune competence phenotypes in New Zealand sheep.**
K. M. McRae*[1], K. G. Dodds[1], N. Haack[2], A. Heiser[2], J. Peers-Adams[1], S. Coll[1], and P. J. Johnson[1], [1]*AgResearch Invermay, Mosgiel, New Zealand*, [2]*AgResearch Grasslands, Palmerston North, New Zealand*.

2:00 PM OP172 **Cyprinid fish species appear to be both disease resistant and infection resistant to cyprinid herpes virus type 3 (CyHV-3).**
B. Dorfman*[1], J. Marcos-Hadad[1], R. Tadmor-Levi[1], O. Liffmann[1], B. Abd Elkader[1], E. Myara[1], S. Lamichhane[2], B. Gorgoglione[2], and L. David[1], [1]*Dept. of Animal Sciences, R.H. Smith Faculty of Agricultural, The Hebrew University of Jerusalem, Israel, Rehovot, Israel*, [2]*Fish Pathobiology and Immunology Laboratory, Dept. Pathobiology and Diagnostic Investigation (CVM)/Dept. Fisheries and Wildlife (CANR), Michigan State University, East Lansing, MI, USA*.

2:12 PM OP176 **Validation of genetic biomarkers and immune phenotypes as indicators of the immune response to E2-CD154 subunit classical swine fever virus (CSFV) vaccine.**
M. Ballester*[1], C. Hernández-Banqué[1], T. Jové-Juncà[1], O. González-Rodríguez[1], L. Coronado[2], L. Ganges[2], J. Reixach[3], S. Gol[3], R. Quintanilla[1], and J. Tarres[1], [1]*Animal breeding and genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*, [2]*Centre de Recerca en Sanitat Animal (CReSA), Unitat Mixta d'Investigació IRTA-UAB en Sanitat Animal, Campus Universitat Autònoma de Barcelona (UAB), Barcelona, Bellaterra, Spain*, [3]*Selección Batalle SA, Riudarenes, Spain*.

2:24 PM OP174 **Effect of Galectin-9 on the expression of genes involved in bovine innate and adaptive immune responses in blood.**
M. Worku*, R. Uzzaman, P. Pande, and S. Ghimre, *North Carolina Agricultural and Technical State University, Greensboro, NC, USA*.

2:36 PM OP175 **Decoding the dynamic epigenetic landscapes of *Staphylococcus aureus* challenged bovine cells and enhancing the genomic selection.**
Siqian Chen*, Siyuan Mi, Yue Xing, and Ying Yu, *National Engineering Laboratory for Animal Breeding, State Key Laboratory of Animal Biotech Breeding, Breeding and Reproduction of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing 100193, China*.

2:48 PM OP179 **Genetic analysis of the major histocompatibility complex class I BF2 gene of Korean native chickens.**
T. N. Agulto*[1], M. Kim[1], P. Manjula[2], R. Fernando[1,3], and J. H. Lee[1], [1]*Chungnam National University, Daejeon, Republic of Korea*, [2]*Uva Wellassa University, Badulla, Sri Lanka*, [3]*University of Peradeniya, Peradeniya, Sri Lanka*.

3:00 PM		**Workshop Joint Activity.**
3:30 PM		**Coffee Break.**
4:00 PM	OP178	**The inflammatory state and energy metabolism of porcine immune cells are closely connected.** E. Murani[1], W. Ma[1,2], J. Brenmoehl[1], N. Trakooljul[1], F. Hadlich[1], B. Fuchs[1], C. Galuska[1], and K. Wimmers*[1,2], [1]*Research Institute for Farm Animal Biology (FBN), 18196 Dummerstorf, Germany*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, 18059 Rostock, Germany*.
4:20 PM	OP177	**Genetic parameters, correlations and genome-wide association study of cortisol response to LPS challenge in heifers.** Bruno A. Galindo[1,2], Umesh K. Shandilya[1], Flavio S. Schenkel[1], and Niel A. Karrow*[1], [1]*Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada*, [2]*State University of the Northern Parana, Cornélio Procópio, PR, Brazil*.
4:40 PM	OP173	**Heat stress effects on the circulating microRNA profile of Iberian purebred and Duroc x Iberian crossbred weaned piglets.** Paula Aranguren-Rivas[1], Ana Heras-Molina[2], Emilio Gómez-Izquierdo[3], Jose Gomez-Fernández[3], Fabián García[1], Luca Fontanesi[4], Cristina Óvilo[1], Juan María García-Casco[1,5], and María Muñoz*[1], [1]*Animal Breeding & Genetics Department, INIA-CSIC, Madrid, Spain*, [2]*Animal Production Department, UCM, Madrid, Spain*, [3]*Centro de Pruebas de Porcino-ITACYL, Hontalbilla (Segovia), Spain*, [4]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [5]*Centro de I+D en cerdo Ibérico, INIA-CSIC, Zafra (Badajoz), Spain*.
4:52 PM	OP180	**ISAG Bursary Award: Development of a blood-based transcriptional biosignature for accurate discrimination of *M. bovis* infected and control non-infected cattle.** J. F. O'Grady*[1], A. Ivich[2], G. P. McHugo[1], J. A. Ward[1], T. J. Hall[1], S. L. F. O'Donnell[1], C. N. Correia[1], J. A. Browne[1], M. McDonald[1], A. Khan[1], E. Gormley[3,4], V. Riggio[5,6], J. G. D. Prendergast[5,6], E. L. Clarke[5,6], H. Pausch[7], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [2]*Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus, Aurora, CO, USA*, [3]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [4]*UCD One Health Centre, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [5]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, EH25 9RG, UK*, [6]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Midlothian, EH25 9RG, UK*, [7]*Animal Genomics, ETH Zurich, 8006, Zurich, Switzerland*, [8]*UCD School of Mathematics and Statistics, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*.
5:05 PM	OP181	**Identification and validation of novel SNPs associated with BLV-induced lymphoma and proviral load using genome-wide association study.** Y. Aida*[1], S. Watanuki[1], Y. Ye[1], F. Nagata[1], R. Matsuura[1], C. Lo[1], S. Saito[1], Y. Matsumoto[1], Y. Miyazaki[2], S. Sasaki[3], and S. Takeshima[4], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Livestock Improvement Association of Japan Inc, Gunma, Japan*, [3]*Faculty of Agriculture, University of the Ryukyus, Okinawa, Japan*, [4]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*.
5:17 PM	OP182	**Genomic basis of the host response to the porcine respiratory disease complex.** H. Laghouaouta*[1,2], L. Fraile[1,2], and R. N. Pena[1,2], [1]*Departament de Ciència Animal, Universitat de Lleida, Lleida, Spain*, [2]*AGROTECNIO-CERCA Center, Lleida, Spain*.
5:30 PM	OP183	**ISAG Bursary Award: Integration of CRISPR screening and proteomic analysis of WDR91 manipulation of endosome-to-cytosol transport of African swine fever virus.** H. L. Liu*[1], Y. L. Guo[2], Z. S. Guo[1], G. Q. Peng[2], S. H. Zhao[1], and S. S. Xie[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, Hubei, China*.
5:45 PM		**Genetics of Immune Response and Disease Resistance Business Meeting.**

Ruminant Genetics and Genomics

Chair: **Brenda Murdoch, University of Idaho, Moscow, ID, USA**
Room 103 + 104
1:30 PM - 3:30 PM

1:30 PM OP184 **Invited Workshop Presentation: Assessing structural variants in DSN cattle and their impact on genomic features.**
P. Korkuc, G. B. Neumann, M. Reissmann, and G. A. Brockmann*, *Humboldt-Universität zu Berlin, Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Animal Breeding and Molecular Genetics*, *Berlin, Germany*.

1:50 PM OP185 **Interplay between microbial and host genes affects methane emission in Nelore cattle rumen.**
J. Afonso[1], J. V. da Silva[2], T. Figueiredo Cardoso[1], J. J. Bruscadin[2], L. C. Conteville[1], L. G. Clemente[3], A. O. de Lima[4], W. J. S. Diniz[5], G. B. Mourao[3], A. Zerlotini[6], M. Tanurdzic[7], L. L. Coutinho[3], M. R. S. Fortes[8], and L. C. A. Regitano*[1], [1]*Embrapa Pecuária Sudeste*, *São Carlos, São Paulo, Brazil*, [2]*Post-graduation Program of Evolutionary Genetics and Molecular Biology, Federal University of São Carlos*, *São Carlos, São Paulo, Brazil*, [3]*Department of Food Science and Technology (ESALQ), University of São Paulo*, *Piracicaba, São Paulo, Brazil*, [4]*Division of Medical Genetics, Department of Genome Sciences, Department of Medicine, University of Washington*, *Seattle, WA, USA*, [5]*Department of Animal Sciences, Auburn University*, *Auburn, AL, USA*, [6]*Bioinformatic Multi-User Laboratory, Embrapa Informática Agropecuária*, *Campinas, São Paulo, Brazil*, [7]*School of Biological Sciences, The University of Queensland*, *Brisbane, Queensland, Australia*, [8]*School of Chemistry and Molecular Biosciences, The University of Queensland*, *Brisbane, Queensland, Australia*.

2:10 PM OP186 **Estimation of genetic parameters for bull conception rate and its genetic correlations with semen production traits in Japanese Black bulls.**
Yoshinobu Uemoto*[1], Rintaro Nagai[1], Masashi Kinukawa[2], Toshio Watanabe[2], Atsushi Ogino[2], Kazuhito Kurogi[3], and Masahiro Satoh[1], [1]*Graduate School of Agricultural Science, Tohoku University*, *Sendai, Miyagi, Japan*, [2]*Maebashi Institute of Animal Science, Livestock Improvement Association of Japan Inc*, *Maebashi, Gunma, Japan*, [3]*Cattle Breeding Department, Livestock Improvement Association of Japan Inc*, *Tokyo, Japan*.

2:30 PM OP187 **Genetics underlying congenital adrenal hyperplasia in Australian female cattle.**
R. Hofmeyer*, T. Chen, L. Hampton, W. L. Low, W. S. Pitchford, M. S. Khatkar, K. Petrovski, and C. D. K. Bottema, *Davies Livestock Research Centre, School of Animal and Veterinary Sciences, Roseworthy Campus, University of Adelaide*, *Roseworthy SA, Australia*.

2:50 PM OP188 **Genome-wide association study for heifer stayability in *Bos indicus* × *Bos taurus* crossbred cattle.**
J. Davenport and C. A. Gill*, *Texas A&M University*, *College Station, TX, USA*.

3:05 PM OP189 **From data to decisions: Using genomics and sensors to monitor Holstein behavior and welfare.**
Boris Lukic*[1], Ino Curik[2,5], Karlo Nyarko[3], Tina Bobic[1], Marko Oroz[1], Mihaela Oroz[1], Mario Shihabi[2], David Kranjac[1], Marija Spehar[4], and Nikola Raguz[1], [1]*Faculty of Agrobiotechnical Sciences Osijek, University of Josip Juraj Strossmayer of Osijek, Department for Animal Production and Biotechnology*, *Osijek, Croatia*, [2]*Faculty of Agriculture, University of Zagreb, Department of Animal Science*, *Zagreb, Croatia*, [3]*Faculty of Electrical Engineering, Computer Science and Information Technology Osijek, Department of Computer Engineering and Automation*, *Osijek, Croatia*, [4]*Centre for Livestock Breeding, Department for Genetic Evaluation*, *Zagreb, Croatia*, [5]*Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences*, *Kaposvar, Hungary*.

3:20 PM **Business Meeting.**

Animal Forensic Genetics

Chair: **Guillermo Giovambattista, Universidad Nacional De La Plata, La Plata, Argentina**
Room 103 + 104
4:00 PM - 6:00 PM

4:00 PM	OP190	**Genome-wide methylation drift and transcriptomic variability in aged beagle dogs.** D. Kang*[1,2], E.-Y. Bok[3], S.-J. Oh[4], C.-Y. Hong[4], S.-L. Lee[4], and J. Kim[1,2], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Division of Animal Diseases & Health, National Institute of Animal Science, RDA, Wanju 55365, Republic of Korea*, [4]*College of Veterinary Medicine, Gyeongsang National University, Jinju, 52828 Republic of Korea*.
4:20 PM	OP191	**ISAG Bursary Award: Oxford nanopore technologies reveals age-related genes in beef cattle.** Yijie Guo, Elizebeth M. Ross, Ben Hayes, and Loan T. Nguyen*, *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia*.
4:40 PM	OP192	**Speciome: Identification of meat and fish species in complex foods.** G. Magagna[1], A. Giusti[2], G. Spatola[2], M. Tilola[1], A. Armani[2], and V. Filipello*[1], [1]*Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia Romagna, Brescia, Italy*, [2]*University of Pisa, Pisa, Italy*.
5:00 PM		**Results of 2024-2025 Comparison Test.**
5:20 PM		**Election of Committee Members.**
5:40 PM		**Design of the 2025-2026 CT. Other business.**

OTHER EVENTS

Editorial Board and Associate Editors Meeting
Room 204
6:00 PM - 9:00 PM

Wednesday, July 23

Speaker Ready Room
Room 209
8:00 AM - 12:00 PM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions
Plenary III

Grand Ballroom 201 + 202
9:00 AM - 10:20 AM

9:00 AM OP193 **A novel method to unravel direct and indirect genetic effects on complex traits: Implications for identifying causal variants and enhancing genomic prediction.**
S. H. Lee*[1,2] and L. D. Amente[1,2], [1]*Australian Centre for Precision Health, University of South Australia, Adelaide, SA 5000, Australia*, [2]*UniSA Allied Health and Human Performance, University of South Australia, Adelaide, SA 5000, Australia*, [3]*South Australian Health and Medical Research Institute, Adelaide, SA 5000, Australia*.

9:50 AM **Coffee Break.**

POSTER PRESENTATIONS

Avian Genetics and Genomics I

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:40 AM

P142 **Genomic insights into adaptation and local selection in South and Southeast Asian chicken breeds.**
A. Hinsu*[1], I. Syndicus[1], P. Koringa[2], M. A. Hoque[3], H. T. T. Pham[4], R. Kalupahana[5], G. Fournié[1], D. Blake[1], F. Tomley[1], and A. Psifidi[1], [1]*Royal Veterinary College, Hatfield, UK*, [2]*Kamdhenu University, Anand, India*, [3]*Chattogram Veterinary and Animal Sciences University, Chattogram, Bangladesh*, [4]*CIRAD, Hanoi, Vietnam*, [5]*University of Peradeniya, Peradeniya, Sri Lanka*.

P143 **Host transcriptome response of meat-type chickens reared under chronic heat stress with or without glucose supplementation.**
Samuel E. Aggrey*, Marie C. Milfort, Ahmed F. A. Ghareeb, Alberta L. Fuller, and Romdhane Rekaya, *University of Georgia, Athens, GA, USA*.

P144 **Structural variations cause population gene expression and complex trait variation in Beijing-You chickens.**
X. Yang*, L. Bai, Y. Zhang, X. Ma, W. Xing, G. Zhao, J. Wen, and R. Liu, *State Key Laboratory of Animal Biotech Breeding, State Key Laboratory of Animal Nutrition and Feeding, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*.

P145 **Analysis the molecular mechanism of melanin-related flavor substances and melanin deposition in black-bone chicken based on multi-omics.**
Ziyi Fang*, Zhengxiao He, Yaxiong Jia, and Guiping Zhao, *State Key Laboratory of Animal Biotech Breeding, State Key Laboratory of Animal Nutrition and Feeding, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

P146 **GWAS analysis for selective breeding in Korean native ducks using customized SNP chip.**
J. Kim*, E. Cho, M. Kim, J. Kim, and J. H. Lee, *Chungnam National University*, *Daejeon, Republic of Korea*.

P147 **Transcriptomic characterisation of growth rate and Newcastle disease virus antibody response in tropically adapted chickens raised in smallholder farm conditions.**
O. Sidekli*[1], A. Hinsu[1], K. M. Morris[2], K. Sutton[2], M. Girma[3], W. Esatu[3], B. Solomon[3], T. Dessie[3], L. Vervelde[2], O. Hanotte[3,4], G. Banos[2,5], and A. Psifidi[1,2], [1]*Clinical Sciences and Services, Royal Veterinary College*, *Hatfield, United Kingdom*, [2]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh*, *Edinburgh, United Kingdom*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), ILRI Ethiopia*, *Addis Ababa, Ethiopia*, [4]*School of Life Sciences, University of Nottingham*, *Nottingham, United Kingdom*, [5]*Scotland's Rural College (SRUC)*, *Midlothian, United Kingdom*.

P148 **Inbreeding levels and selection signatures of two endangered Italian duck breeds.**
Francesco Perini*[1], Filippo Cendron[2], Emiliano Lasagna[1], Maristella Baruchello[3], and Martino Cassandro[2,4], [1]*Department of Agricultural, Food and Environmental Sciences, University of Perugia*, *Perugia, Italy*, [2]*Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova*, *Legnaro, Italy*, [3]*Veneto Agricoltura*, *Legnaro, Italy*, [4]*Federazione delle Associazioni Nazionali di Razza e Specie*, *Rome, Italy*.

P149 **ISAG Bursary Award: Prevalence and genetic diversity of *Haemoproteus* and *Leucocytozoon* in raptors and other captive birds at the National Zoological Garden, South Africa.**
R. M. Gaorekwe*[1,2], V. Phetla[2], D. P. Malatji[1], and M. Chaisi[1,3], [1]*South African National Biodiversity Institute*, *Pretoria, Gauteng, South Africa*, [2]*University of South Africa*, *Johannesburg, Gauteng, South Africa*, [3]*University of Pretoria*, *Pretoria, Gauteng, South Africa*.

P150 **Investigating germline-specific gene regulation in chicken primordial germ cells.**
Jeong Hoon Han* and Tae Hyun Kim, *The Pennsylvania State University*, *University Park, Pennsylvania, USA*.

P151 **A cataloging of nucleotide variants in the toll-like receptor (TLR) 13 gene in the turkey, *Meleagris gallopavo*.**
C. Bank, R. Jordan, K. Rawlings-Cole, J. Xu, and E. Smith*, *Virginia Tech*, *Blacksburg, VA, USA*.

P152 **Chromosome-level genome assembly of Korean long-tailed chicken and pangenome of 40 *Gallus gallus* assemblies.**
H. D. Shin*[1], W. Park[2], H. Chai[2], Y. Lee[1], J. Jung[1], B. J. Ko[3], and H. Kim[1,3], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University*, *Seoul, Republic of Korea*, [2]*Animal Genomics & Bioinformatics Division, National Institute of Animal Science*, *Wanju, 55365, Republic of Korea*, [3]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences*, *Seoul, Republic of Korea*.

P153 **CRISPR-based insights into chicken antiviral defense.**
E. A. Weaver*, G. E. Schmidt, J. H. Han, and T. H. Kim, *Pennsylvania State University*, *Pennsylvania, USA*.

P154 **Beyond traditional GWAS: Machine learning uncovers novel genetic variants of flavor compounds in Korean native chickens.**
E. Cho*, M. Kim, and J. H. Lee, *Chungnam National University*, *Daejeon, Republic of Korea*.

P155 **Metabolome genome-wide association analyses identify a splice mutation in *AADAT* affects lysine degradation in duck skeletal muscle.**
Dapeng Liu*, Wenlei Fan, Youyou Yang, Shuisheng Hou, and Zhengkui Zhou, *State Key Laboratory of Animal Biotech Breeding, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, P.R. China*.

P156 **Functional characterization of noncoding SNP regions identified by GWAS for taste-related nucleotide compounds in chicken meat using the CRISPRa toolkit.**
J. Kim*[1], J. H. Han[2], M. Kim[1], G. Schmidt[2], E. Cho[1], Y. Kim[1], T. H. Kim[2], and J. H. Lee[1], [1]*Chungnam National University*, *Daejeon, South Korea*, [2]*The Pennsylvania State University*, *University Park, PA, USA*.

P157 **Structural variations highlight selection for environmental adaptability and productivity in indigenous chickens.**
A. Vallejo-Trujillo*[1], O. Hanotte[2,3], and J. Smith[1], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh*, *Easter Bush Campus, Edinburgh, Midlothian, EH25 9RG, United Kingdom*, [2]*International Livestock Research Institute (ILRI)*, *P.O. Box - 5689, Addis Ababa, Ethiopia*, [3]*School of Life Sciences, University of Nottingham*, *Nottingham, NG7 2RD, United Kingdom*.

P158 **ISAG Bursary Award: Enhancing genomic prediction accuracy through molecular phenotyping in ducks.**
Wentao Cai*, Zhengkui Zhou, and Shuisheng Hou, *Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P159 **Telomere-to-telomere genome assembly of eight chicken breeds and its application.**
R. Liu*[1], Y. Zhang[1], X. Yang[1], L. Bai[1], K. Li[2], G. Zhao[1], and J. Wen[1], [1]*State Key Laboratory of Animal Biotech Breeding, State Key Laboratory of Animal Nutrition and Feeding, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [2]*Huazhi Biotechnol Co Ltd, Changsha, China*.

P160 **The Duck 1000 Genomes Project.**
Zhengkui Zhou*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

P161 **Incorporating cecal microbial data improves the accuracy of chicken feed efficiency phenotype estimation.**
Zhengxiao He*[1,2], Alan Fahey[2], Jie Wen[1], Ranran Liu[1], and Guiping Zhao[1], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*.

P162 **Meta-analysis and metabolite-based genome-wide studies reveal the genetic basis of lipid accumulation in chickens.**
Na Luo[1,2], Peihao Liu[1], Limin Wei[3,4], Jie Wen[1], Bingxing An[1], and Guiping Zhao*[1,3], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*College of Animal Science and Technology, Henan University of Animal Husbandry and Economy, Zhengzhou, China*, [3]*Sanya Research Institute of Hainan Academy of Agricultural Sciences (Hainan Provincial Laboratory Animal Research Center), Sanya, China*, [4]*Institute of Animal Husbandry and Veterinary Medicine, Hainan Academy of Agricultural Sciences, Haikou, China*.

P163 **Functional analysis of chicken *IRF9* in the innate anti-viral immune response.**
G. E. Schmidt*, E. A. Weaver, J. H. Han, and T. H. Kim, *Penn State University, University Park, PA, USA*.

P164 **A multiomics characterisation of chicken resistance to avian influenza infection.**
A. Hinsu[1], T. Bremmer[1], C. Cuffe[1], M. A. Hoque[2], M. A. Samad[3], H. T. T. Pham[4], P. T. Ngoc[5], S. Butt[1], G. Fournié[1], D. Blake[1], F. Tomley[1], and A. Psifidi*[1], [1]*Royal Veterinary College, Hatfield, UK*, [2]*Chattogram Veterinary and Animal Sciences University, Chattogram, Bangladesh*, [3]*Bangladesh Livestock Research Institute, Ashulia, Bangladesh*, [4]*CIRAD, Hanoi, Vietnam*, [5]*National Institute of Veterinary Research, Hanoi, Vietnam*, [6]*French National Institute for Agricultural Research INRAE, Paris, France*.

P165 **Single-cell cross-species perspective reveals the synergistic mechanism of muscle tissue development in chickens.**
Y. Wang, H. Cui, Y. Chen, J. Zhuang, H. Yang, G. Zhao, and J. Wen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*.

P166 **Meta GWAS reveal novel growth trait loci in chicken using Global Chicken Reference Panel V2.0.**
Chenghao Zhai*[1,2] and Yuzhe Wang[1,2], [1]*State Key Laboratory of Animal Biotech Breeding, College of Biological Sciences, China Agricultural University, Beijing, China*, [2]*National Research Facility for Phenotypic and Genotypic Analysis of Model Animals (Beijing), China Agricultural University, Beijing, China*.

ISAG-FAO Genetic Diversity

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:40 AM

P344 **ISAG Bursary Award: Microsatellite marker analysis of Tswana cattle kept under *in situ* conservation at Botswana University of Agriculture and Natural Resources.**
T. Bakae*, *Botswana University of Agriculture and Natural Resources, Gaborone, Botswana*.

P345 **ISAG Bursary Award: Probabilities that 2 alleles between individuals are identity-by-state at unobserved loci can be predicted by observed SNPs in simulated and real cattle populations.**
R. Nagai*[1], T. Honda[2], M. Satoh[1], and Y. Uemoto[1], [1]*Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan*, [2]*Food resources Education and research Center, Kobe University, Kasai, Hyogo, Japan*.

P346 **Maternal and paternal analyses for indigenous goats around the Spice Islands in Indonesia.**
Sakura Akao*[1], Ryo Masuko[1], Fuki Kawaguchi[1], Shinji Sasazaki[1], Muhammad I. A. Dagong[2], Sri R. A. Bugiwati[2], and Hideyuki Mannen[1], [1]*Laboratory of Animal Breeding and Genetics, Graduates School of Agricultural Science, Kobe University, Kobe, Japan*, [2]*Faculty of Animal Science, Hasanuddin University, Makassar, South Sulawesi, Indonesia*.

P347 **Inferring of population structure and migration routes of Island Southeast Asian goats by mtDNA, SRY and 50K SNP array analyses.**
Ryo Masuko*[1], Fuki Kawaguchi[1], Shinji Sasazaki[1], Muhammad I. A. Dagong[2], Sri R. A. Bugiwati[2], Joseph S. Masangkay[3], Jiaqu Wu[4], Takahiro Yonezawa[4], and Hideyuki Mannen[1], [1]*Laboratory of Animal Breeding and Genetics, Graduates School of Agricultural Science, Kobe University, Kobe, Japan*, [2]*Faculty of Animal Science, Hasanuddin University, Makassar, South Sulawesi, Indonesia*, [3]*College of Veterinary Medicine, University of the Philippines, Los Baños, Philippines*, [4]*Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*.

P348 **Genetic distance among Criollo sheep populations.**
J. S. Cappello Villada[1], M. A. Revidatti*[1], S. A. De la Rosa[1], V. N. Morales[1], E. R. Tejerina[1], REZGEN-IBA-BIOVIS Consortium2[2], and A. Martínez Martínez[3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional del Nordeste, Corrientes, Corrientes, Argentina*, [2]*Córdoba, Córdoba, España*, [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, Córdoba, España*.

P349 **Influence of genetic map usage on genomic inbreeding estimation in Holstein cattle.**
M. Shihabi*[1], T. Druet[2], M. Ferencakovic[1], V. Cubric Curik[1], M. Špehar[3], N. Raguz[4], B. Lukic[4], and I. Curik[1,5], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia*, [2]*Unit of Animal Genomics, GIGA-R and Faculty of Veterinary Medicine, University of Liège, Liège, Belgium*, [3]*Croatian Agency for Agriculture and Food, Zagreb, Croatia*, [4]*Faculty of Agrobiotechnical Sciences Osijek, Osijek, Croatia*, [5]*Hungarian University of Agriculture and Life Sciences (MATE), Kaposvár, Hungary*.

P350 **Genetic characterization of Kyrgyz yaks based on haplotypes of the mitochondrial DNA.**
Seungchang Kim*, Daehyeok Jin, Huimang Song, and Bonghwan Choi, *National Institute of Animal Science, Deogyuwolseong-ro, Seosang-myeon, Hamyang-gun, Gyeongsangnam-do, Republic of Korea*.

P351 **ISAG Bursary Award: Why should we care about Portuguese native dog breeds?—A genome-wide perspective.**
Ludmilla Blaschikoff*[1,2], Octávio Serra[4], Dayna Dreger[5], Gabriella J. Spatola[5], Fernanda Simões[4], Heidi G. Parker[5], Elaine A. Ostrander[5], Catarina Ginja[2,3], and Ana Elisabete Pires[2,3], [1]*Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal*, [2]*CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal*, [3]*BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal*, [4]*INIAV, Instituto Nacional de Investigação Agrária e Veterinária - Unidade de Biotecnologia e Recursos Genéticos, Oeiras, Portugal*, [5]*Cancer Genetics and Comparative Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*, [6]*CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal*, [7]*Faculdade de Medicina Veterinária, Universidade Lusófona-Centro Universitário de Lisboa; I-MVET Investigação Medicina Veterinária; CECAV - Centro de Ciência Animal e Veterinária, Portugal*.

P352 **Study of Iberian sheep biodiversity and population structure.**
Amparo Martínez*[1], Águeda Pons Barro[2], Catarina Ginja[3,4], Daniel Gaspar[5,6], Carolina B. Sousa[4], and José Luis Vega Pla[7], [1]*Universidad de Córdoba, Córdoba, Spain*, [2]*Instituto de Investigación y Formación Agroalimentaria y Pesquera de Illes Balears, Palma, Spain*, [3]*CIISA-Centro Interdisciplinar em investigação em Sanidade Animal, Faculdade de Medicina Veterinária de Lisboa, Lisboa, Portugal*, [4]*CIBIO Universidade do Porto, CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO - Laboratório Associado, Campus de Vairão, Vairão, Portugal*, [5]*5BIOPOLIS, Universidade do Porto, Campus de Vairão, Vairão, Portugal*, [6]*Universidade do Porto, Departamento de Biologia, Faculdade de Ciências, Porto, Portugal*, [7]*Laboratorio de Investigación Aplicada, Cría Caballar de las Fuerzas Armadas, Cordoba, Spain*, [8]*REZGEN-IBA Consortium, REZGEN-IBA Consortium*.

P353 **Developing novel genetic erosion footprint for livestock in life cycle assessment.**
Ira Bhattarai* and Kirsi Usva, *Natural Resources Institute Finland, Jokioinen, Finland*.

P354 **Genetic diversity and population structure of heritage Finnish landrace chickens using whole-genome sequencing data.**
Melak Weldenegodguad*[1], Petra Tuunainen[2], Kisun Pokharel[3], and Juha Kantanen[3], [1]*Natural Resources Institute Finland, Helsinki, Finland*, [2]*Natural Resources Institute Finland, Maaninka, Finland*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*.

P355 **Genomic diversity and selection signatures in Portuguese coarse wool sheep breeds.**
D. Gaspar*[1,2], A. Usié[3,4], C. Bruno de Sousa[2,5], J. Matos[6], C. Matos[7], A. E. Pires[2,8], and C. Ginja[2,5], [1]*Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal*, [2]*BIOPOLIS/CIBIO, Program in Genomics, Biodiversity and Land Planning, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Vairão, Portugal*, [3]*Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo (CEBAL)/ Instituto Politécnico de Beja, Beja, Portugal*, [4]*MED- Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute, CEBAL – Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Beja, Portugal*, [5]*CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal*, [6]*Instituto Nacional de Investigação Agrária E Veterinária, I.P. (INIAV, I.P.), Oeiras, Portugal*, [7]*ACOS-Agricultores do Sul, Beja, Portugal*, [8]*Faculdade de Medicina Veterinária, Universidade Lusófona, Lisboa, Portugal*.

P356 **Estimation of contemporary and historical effective population size in horses.**

I. Curik*[1,2], N. Moravcikova[3], E. Santiago[4], A. Caballero[5], M. Shihabi[1], R. Kasarda[3], H. Vostra-Vydrova[6], V. Cubric-Curik[1], and L. Vostry[6], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia*, [2]*Hungarian University of Agriculture & Life Sciences (MATE), Kaposvár, Hungary*, [3]*Slovak University of Agriculture in Nitra, Institute of Nutrition & Genomics, Nitra, Slovakia*, [4]*Universidad de Oviedo, Facultad de Biología, Oviedo, Spain*, [5]*Universidade de Vigo, Facultade de Bioloxía, Vigo, Spain*, [6]*Czech University of Life Sciences Prague, Prague, Czech Republic*.

P357 **The VarGoats 1000 genome project dataset: An alternative approach for WGS data filtering for large-scale analysis of livestock diversity.**

L. Colli*[1,2], B. Lazzari[1,3], Y. Li[4], A. Bionda[5], M. Milanesi[6], A. Talenti[7], A. Stella[3], G. Tosser-Klopp[8], P. Crepaldi[5], and The VarGoats Consortium9[9], [1]*DIANA Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [2]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [3]*Istituto di Biologia e Biotecnologia Agraria, CNR National Research Council, Milano, MI, Italy*, [4]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, P. R. China*, [5]*Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia, Università degli Studi di Milano, Milano, MI, Italy*, [6]*Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo, VT, Italy*, [7]*The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, United Kingdom*, [8]*GenPhySE, Université de Toulouse, INRA, ENVT, Castanet Tolosan, France*, [9]*http://www.goatgenome.org/vargoats.html*.

P358 **Genomic insights into cattle domestication and aurochs legacy in the Balkans.**

V. Cubric-Curik*[1], R. Sosic-Klindzic[2], G. Tomac[2], I. Drzaic[1], V. Brajkovic[1], I. Kersic[1], I. Curik[1], and P. T. Miracle[3], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia*, [2]*University of Zagreb Faculty of Humanities and Social Sciences, Zagreb, Croatia*, [3]*McDonald Institute for Archaeological Research University of Cambridge, Cambridge, UK*.

P359 **REZGEN-IBA: Ibero-American network on zoogenomic resources and their resilience.**

C. Ginja*[1,2], REZGEN-IBA Consortium3[3], and A. Martínez[4], [1]*CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal*, [2]*BIOPOLIS -Program in Genomics, Biodiversity and Land Planning, Universidade do Porto, CIBIO, Campus de Vairão, Vairão, Portugal*, [3]*REZGEN-IBA Consortium, https://www.cyted.org/web_redes.php?id_rede=511*, [4]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*.

Livestock Genomics for Developing Countries

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:40 AM

P360 **Genome wide association and functional genomic analyses for various type traits and production traits in Kankrej cattle.**

A. B. Chaudhari*[1], J. P. Gupta[2], B. P. Brahmkshtri[3], J. D. Chaudhari[4], S. K. Mohapatra[5], A. C. Mahajan[6], and M. V. Darji[7], [1]*Department Of Animal Genetics and Breeding College of Veterinary Science and Animal Husbandry Kamdhenu University, Sardarkrushinagar, Gujarat, India*, [2]*Department of Animal Genetics and Breeding, Bihar Veterinary College, Bihar Animal Sciences University (BASU), Patna, Bihar, India*, [3]*Department of Animal Genetics and Breeding College of Veterinary Science and Animal Husbandry Kamdhenu University, Himmatnagar, Gujarat, India*, [4]*Department of Animal Genetics and Breeding College of Veterinary Science and Animal Husbandry Kamdhenu University, Sardarkrushinagar, Gujarat, India*, [5]*Department of Animal Biotechnology, College of Veterinary Science and A.H., Kamdhenu University, Sardarkrushinagar, Gujarat, India*, [6]*National Dairy Development Board (NDDB), Anand, Gujarat, India*, [7]*Gujarat Biotechnology Research Center (GBRC), Gandhinagar, Gujarat, India*.

P362 **Ovary transcriptome analysis of Ethiopian indigenous chicken ecotypes living at high and low altitudes.**

B. Solomon*[1,2], N. Seboka[2,3], A. Vallejo-Trujillo[4], J. Smith[4], C. Jacobson[2], L. Nesengani[1], O. Hanotte[2,5], and M. Ntanganedzeni[1], [1]*University of South Africa, UNISA, Pretoria, South Africa*, [2]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [3]*Addis Ababa University, Addis Ababa, Ethiopia*, [4]*Roslin Institute, University of Edinburgh, UK, Easter Bush, Scotland, UK*, [5]*School of Life Sciences, University of Nottingham, UK, Nottingham, UK*.

P363 **Genome-wide scan identified genes for local adaptation and fat deposition in Ethiopian sheep populations.**

H. D. Melka*[1,5], Z. E. Bedada[1], T. Dessie[2], M. Worku[3], and K.-S. Kim[4], [1]*Bio and Emerging Technology Institute, Addis Ababa, Ethiopia*, [2]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [3]*North Carolina Agricultural and Technical State University, Greensboro, NC, USA*, [4]*Chungbunk National University, Cheongju, South Korea*, [5]*Addis Ababa Science and Technology University, Addis Ababa, Ethiopia*.

P364 **Genome-wide selection scan identified genes for local adaptation and fat deposition in Ethiopian sheep populations.**
H. D. Melka*[1,5], Z. E. Bedada[1], T. Dessie[2], M. Worku[3], and K-S. Kim[4], [1]*Bio and Emerging Technology Institute*, *Addis Ababa, Ethiopia*, [2]*International Livestock Research Institute*, *Addis Ababa, Ethiopia*, [3]*North Carolina Agricultural and Technical State University*, *Greensboro, NC, USA*, [4]*Chungbunk National University*, *Cheongju, South Korea*, [5]*Addis Ababa Science and Technology University*, *Addis Ababa, Ethiopia*.

P365 **Genome-wide selection scan identified genes for local adaptation and fat deposition in Ethiopian fat-tailed sheep populations.**
H. D. Melka*[1,5], Z. E. Bedada[1], T. Dessie[2], M. Worku[3], and K.-S. Kim[4], [1]*Bio and Emerging Technology Institute*, *Addis Ababa, Ethiopia*, [2]*International Livestock Research Institute*, *Addis Ababa, Ethiopia*, [3]*North Carolina Agricultural and Technical State University, Department of Animal Science*, *Greensboro, NC, USA*, [4]*Chungbunk National University*, *Cheongju, South Korea*, [5]*Addis Ababa Science and Technology University*, *Addis Ababa, Ethiopia*.

P366 **Uncovering the genetics underlying economic traits of Bangladeshi indigenous chickens.**
M. A. G. Rabbani*[1,2], A. Vallejo-Trujillo[1], K. Miedzinska[1], Z. Wu[1], S. Faruque[2], K. A. Watson[1], and J. Smith[1], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh*, *Midlothian, UK*, [2]*Poultry Production Research Division, Bangladesh Livestock Research Institute (BLRI)*, *Savar, Dhaka, Bangladesh*.

P367 **Distribution of PRDM9 haplotypes among Mongolian native horse breeds.**
Onontuul Ganbaatar*[1,2], Nu Anh Thu Le[3], Thanh Thuy Nguyen[4], Liushiqi Borjigin[3], Yu Okuda[3], Saipolda Togtorbay[2], Rentsenkhand Jargalsaikhan[2], Enkhmanlai Ganbaatar[2], Badamsuren Batsukh[2], Takehito Tsuji[1], and Tetsuo Kunieda[1], [1]*Graduate School of Environmental, Life, Natural Science and Technology, Okayama University*, *Okayama, Japan*, [2]*School of Animal Science and Biotechnology, Mongolian University of Life Sciences*, *Ulaanbaatar, Mongolia*, [3]*Faculty of Veterinary Medicine, Okayama University of Science*, *Ehime, Japan*, [4]*Faculty of Animal Sciences and Veterinary Medicine, University of Agriculture and Forestry, Hue University*, *Hue City, Vietnam*.

P368 **ISAG Bursary Award: ABC-random forest machine learning estimates admixture and migration timing of indicine cattle into Africa.**
Mulusew Kassa Bitew*[1], Christian Persichilli[1], Marika Di Civita[1], Slim Ben Jemaa[2], Salvatore Mastrangelo[3], Joram M. Mwacharo[4,5], Olivier Hanotte[6,7], Fabio Pilla[1], and Gabriele Senczuk[1], [1]*Department of Agriculture, Environmental and Food Sciences, University of Molise*, *Campobasso, Italy*, [2]*Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Université de Carthage*, *Ariana, Tunisia*, [3]*Dipartimento Scienze Agrarie, Alimentari e Forestali, University of Palermo*, *Palermo, Italy*, [4]*Dryland Livestock Genomics, International Centre for Agricultural Research in the Dry Areas (ICARDA)*, *Addis Ababa, Ethiopia*, [5]*Animal and Veterinary Sciences, SRUC and Centre for Tropical Livestock Genetics and Health (CTLGH)*, *Midlothian, Scotland*, [6]*School of Life Sciences, University of Nottingham*, *Nottingham, UK*, [7]*CTLGH–LiveGene, International Livestock Research Institute*, *Addis Ababa, Ethiopia*.

P369 **In silico analyses of the Prolactin (*PRL*) gene in locally adapted Muscovy and Mallard ducks reveal genetic conservatism and SNPs potentially associated with functionality.**
O. H. Osaiyuwu[1], M. O. Oyebanjo*[2,1], O. M. Coker[1], and A. E. Salako[1], [1]*University of Ibadan*, *Ibadan, Oyo, Nigeria*, [2]*University of Bradford*, *Bradford, West Yorkshire, UK*.

P370 **Gene set enrichment analysis (GSEA) based on random forest algorithm to identify candidate genes associated with reproductive traits in Holstein cattle.**
Jeyran Jabbari-Tourchi*[1], Sadegh Alijani[1], Seyed Abbas Rafat[1], and Mohammadreza Afrazandeh[2], [1]*Tabriz*, *Tabriz, East Azerbaijan Province, Iran*, [2]*Azad Karaj University*, *Karaj, Alborz, Iran*.

P371 **ISAG Bursary Award: Detecting signatures of selection to environmental drivers of adaptation in Indigenous cattle in Tigray, Northern Ethiopia.**
Tsadkan Zegeye*[1,2], Gurja Belay[2], Adriana Vallejo-Trujillo[4], Jianlin Han[3,5], and Olivier Hanotte[3,4], [1]*Mekelle Agricultural Research Center, Tigray Agricultural Research Institute*, *Mekelle, Tigray, Ethiopia*, [2]*Department of Microbial, Cellular and Molecular Biology, Addis Ababa University*, *Addis Ababa, Addis Ababa, Ethiopia*, [3]*Live Gene–CTLGH, International Livestock Research Institute (ILRI)*, *Addis Ababa, Addis Ababa, Ethiopia*, [4]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh*, *Edinburgh, UK*, [5]*Yazhouwan National Laboratory*, *Sanya, China*, [6]*Cells, Organism and Molecular Genetics, School of Life Sciences, University of Nottingham*, *Nottingham, UK*.

P372 **Extreme phenotype sampling-based GWAS for milk yield in Sahiwal cattle.**
Y. Koul*[1], U. Surati[1], S. Ahlawat[2], V. Vohra[1], and S. K. Niranjan[2], [1]*ICAR–National Dairy Research Institute*, *Karnal, Haryana, India*, [2]*ICAR–National Bureau of Animal Genetic Resources*, *Karnal, Haryana, India*.

P373 **Climate factors drive the local adaptation of Old World cattle.**
Luyang Sun, Xiaoting Xia, Chuzhao Lei, and Ningbo Chen*, *College of Animal Science and Technology, Northwest A&F University*, *Yangling, Shaan Xi, China*.

P374 **ISAG Bursary Award: The landscape of genomic structural variation in East Asian cattle.**
Xiwen Guan, Chuzhao Lei, and Ningbo Chen*, *Northwest A&F University*, *Yangling, Shannxi, China*.

P375 **Signatures of selection in Sumba Ongole cattle reveal candidate genes involved in economic traits and tropical adaptation.**
Pita Sudrajad[1,2], Dyah Maharani*[1], Sigit Bintara[1], Tri Satya Mastuti Widi[1], Tety Hartatik[1], Endang Baliarti[1], and Panjono Panjono[1], [1]*Faculty of Animal Science, Universitas Gadjah Mada*, *Yogyakarta, Indonesia*, [2]*Research Center for Animal Husbandry, Research Organization for Agriculture and Food, National Research and Innovation Agency*, *Bogor, Indonesia*.

P376 **Genome-wide genotyping uncovers genetic profiles and history of Northern African sheep breeds in global context.**
I. Baazaoui*[1], S. Bedhiaf-Romdhani[2], S. Mastrangelo[3], J. A. Lenstra[4], A. Da Silva[5], B. Benjelloun[6], and E. Ciani[7], [1]*Centre de Recerca Agrigenòmica (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Spain*, [2]*Laboratory of Animal and Fodder Production, National Institute of Agronomic Research of Tunisia, Ariana, Tunisia*, [3]*Dipartimento Scienze Agrarie, Alimentari e Forestali, University of Palermo, Palermo, Italy*, [4]*Faculty of Veterinary Medicine, Utrecht University, the Netherlands*, [5]*Faculté des Sciences et Techniques de Limoges, E2LIM, Limoges, France*, [6]*National Institute of Agronomic Research (INRA Maroc), Regional Centre of Agronomic Research, Beni-Melal Morocco*, [7]*Dipartamento Bioscienze, Biotecnologie, Biofarmaceutica, University of Bari Aldo Moro, Bari, Italy*.

P377 **Genomic insights into genetic diversity and population structure of pastoral Belahi cattle of north Himalayan (Shivalik) foothills.**
A. Yadav*[1], K. D. Khan[1], S. Chavan[1], R. Paul[1], V. N. Sahana[1], R. K. Gahlyan[2], R. ALEX[1], V. Vohra[1], and G. R. Gowane[1], [1]*ICAR–National Dairy Research Institute, Karnal, Haryana, India*, [2]*Animal Husbandry and Dairying Department*, *Haryana, India*.

P378 **Evaluation of performances and genomic architecture of upgraded cattle populations of Bangladesh.**
M. S. A. Bhuiyan*[1], S. A. Siddiqua[1], A. K. F. H. Bhuiyan[1], S. H. Lee[2], and J. H. Lee[2], [1]*Department of Animal Breeding and Genetics, Bangladesh Agricultural University*, *Mymensingh, Mymensingh, Bangladesh*, [2]*Division of Animal and Dairy Science, Chungnam National University*, *Daejeon, Daejeon, South Korea*.

P379 **From ancient origins to modern resilience: Unraveling the genomic characteristics of Philippine native cattle.**
J. M. Dominguez*[1,2], M. G. Jr. Yebron[2], J. Banayo[2], A. Salces[2], and K. S. Kim[1], [1]*Department of Animal Science, College of Agriculture, Life & Environment Sciences, Chungbuk National University*, *Cheongju-si, Chungbuk-do, South Korea*, [2]*Institute of Animal Science, College of Agriculture and Food Science, University of the Philippines Los Baños, College, Laguna, Philippines*.

P380 **Genetic signatures of selection in southern Angolan sheep unravel adaptation for maternal and body conformation traits.**
F. Teixeira*[1,2], H. Chiaia[2,3], K. Sebastino[5,3], J. Gaspar[2], P. Afonso[2], S. Ngola[6], C. Simão[6], P. Nanga[5], D. Santos[7], A. Leitão[3,4], J. Morais[2], J. M. Cordeiro[2], L. T. Gama[3,4], J. Sölkner[8], A. J. Amaral[1,3], [1]*Universidade de Évora, MED (Mediterranean Institute for Agriculture, Environment and Development) & CHANGE (Global Change and Sustainability Institute), Pólo da Mitra, Évora, Portugal*, [2]*Faculty of Veterinary Medicine, University José Eduardo dos Santos, Huambo, Angola*, [3]*CIISA–Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal*, [4]*AL4AnimalS–Associate Laboratory for Animal and Veterinary Sciences, Lisbon, Portugal*, [5]*IIV–Instituto de Investigação Veterinária, Angola*, [6]*ISV–Veterinary Services Institute, Angola*, [7]*BE, Bioinsight & Ecoa, Odivelas, Lisbon, Portugal*, [8]*Department of Sustainable Agricultural Systems, University of Natural Resources and Life Sciences Vienna (BOKU), Vienna, Austria*.

P381 **The population structure and genetic diversity analysis of South African Bosvelder sheep.**
N. S. Zulu[1], K. C. Lehloenya[1], M. Segakoeng[2], T. C. Chokoe[7], P. J. Sebei[4], T. Raphulu[4], B. Mtileni[5], M. Nkadimeng[6], T. Matelele[6], T. Mphahlele[6], F. V. Ramukhithi[6], and K. Hadebe*[2], [1]*Department of Agriculture, University of Zululand*, *South Africa*, [2]*Biotechnology Platform, Agricultural Research Council*, *South Africa*, [3]*Limpopo Department of Agriculture, Land Reform and Rural Development, Mara Research Station*, *South Africa*, [4]*Department of Animal Sciences, Tshwane University of Technology*, *South Africa*, [5]*Germplasm Conservation and Reproductive Biotechnologies, Agricultural Research Council*, *South Africa*, [6]*Department of Agriculture Land Reform and Rural Development, Farm Animal Genetic Resources*, *South Africa*, [7]*Agriculture Land Reform, Rural Development and Environment, Gauteng Provincial Legislature*, *South Africa*.

P382 **Genomic insights into the diversified selective sweeps for potential genes and QTLs related to dairy traits in Indian Sahiwal cattle with high breeding values.**
Satish Kumar Illa*[1], Sabyasachi Mukherjee[2], Sapna Nath[3], and Anupama Mukherjee[2], [1]*Livestock Research Station, Sri Venkateswara Veterinary University, Garividi, Andhra Pradesh, India*, [2]*Indian Council of Agricultural Research–National Dairy Research Institute, Karnal, Harayana, India*, [3]*College of Veterinary Science, Garividi, Sri Venkateswara Veterinary University, Garividi, Andhra Pradesh, India*.

P383 **ISAG Bursary Award: Genomic diversity, population structure and admixture in native cattle breeds of Benin.**
Loukaiya Zorobouragui*[1,2], Kathiravan Periasamy[2,3], Isidore Houaga[4,5], Alassan Assani Seidou[1], Christophe Iwaka[1], and Ibrahim T. Alkoiret[1], [1]*Laboratory of Ecology, Health and Animal Production (LESPA), Faculty of Agronomy, University of Parakou, Parakou, Benin*, [2]*Animal Production and Health Laboratory, Department of Nuclear Applications, Joint Food and Agriculture Organization/International Atomic Energy Agency (FAO/IAEA), Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria*, [3]*Indian Council of Agricultural Research–National Research Centre on Mithun, Medziphema, Nagaland, India*, [4]*Roslin Institute and Centre for Tropical Livestock Genetics and Health (CTLGH), Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush Campus, Edinburgh, UK*, [5]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Pretoria, South Africa*.

P384 **A homozygosity-focused assessment of genomic inbreeding in two provincially separated, nondescript cattle subpopulations of South Africa.**
S. F. Lashmar*, B. B. Kooverjee, and P. Soma, *Agricultural Research Council, Irene, Gauteng, South Africa*.

P385 **Spermatozoa motility at different thawing temperatures of Jersey, Holstein Friesian, and Murrah bulls at National Livestock Breeding Office, Pokhara, Nepal.**
Rajesh Gautam*[1,2] and Bhajuram Mahato[3], [1]*Tribhuvan University, Kirtipur, Bagmati, Nepal*, [2]*Institute of Agriculture and Animal Science, Rupandehi, Lumbini, Nepal*, [3]*National Livestock Breeding Office, Pokhara, Gandaki, Nepal*.

P386 **Virginia Tech's post-baccalaureate research education program (VT PREP): Outcomes and training activities as models for genetics and genomics training in developing countries.**
E. J. Smith*, *Virginia Tech, Blacksburg, VA, USA*.

P388 **Genetic diversity of native sheep (*Ovis aries*) from Southern Angola.**
H. Chiaia*[1,2], K. Sebastino[1,3], P. Afonso[2], J. Gaspar[2], F. Teixeira[2,8], S. Ngola[4], C. Simão[4], L. Gomes[5], D. Santos[6], J. Morais[2], A. Leitão[1], J. M. Cordeiro[2], L. T. Gama[1], J. Sölkner[7], A. J. Amaral[1,8], [1]*Centre for Interdisciplinary Research in Animal Health (CIISA) and AL4Animals, Faculdade de Medicina Veterinária, Universidade de Lisboa, Portugal*, [2]*Faculdade de Medicina Veterinária do Huambo, Universidade José Eduardo dos Santos (UJES), Angola*, [3]*Instituto de Investigação Veterinária (IIV), Angola*, [4]*Instituto dos Serviços de Veterinária (ISV), Angola*, [5]*Instituto Técnico Agrário (ITA), Huambo, Angola*, [6]*BE, Bioinsight & Ecoa, Odivelas, Lisbon, Portugal*, [7]*Department of Sustainable Agricultural Systems, University of Natural Resources and Life Sciences Vienna (BOKU), Vienna, Austria*, [8]*Universidade de Évora, MED (Mediterranean Institute for Agriculture, Environment and Development) & CHANGE (Global Change and Sustainability Institute), Évora, Portugal*.

P389 **Identification of selection signatures associated with adaptation in nondescript cattle from South African smallholding systems.**
M. P. Ramoroka*[1,2], M. D. MacNeil[3], F. W. C. Neser[1], S. L. Lashmar[2], and M. L. Makgahlela[1,2], [1]*Department of Animal Science, University of the Free State, Bloemfontein, Free State, South Africa*, [2]*Agricultural Research Council, Animal Production-Irene, Pretoria, Gauteng, South Africa*, [3]*Delta G, Miles City, MT, USA*.

P390 **Comparative analysis of the indigenous Venda chicken genome versus the reference chicken genome to identify structural variants involved in adaptation.**
A. H. Molotsi*, J. Rees, L. Nesengani, S. Mdyogolo, R. Smith, T. S. Tshiliate, and N. O. Mapholi, *University of South Africa, Florida, Gauteng, South Africa*.

P391 **ISAG Bursary Award: Population structure and genetic diversity of native African cattle using whole-genome sequence data: A case of five breeds from Uganda.**
R. Okwasiimire*[1,2], D. Kugonza[3], M. Weldenegodguad[2], N. Ghanem[4], M. L. Makgahlela[5], C. Ginja[6], R. Crooijmans[7], J. Kantanen[2], P. Uimari[1], and K. Pokharel[2], [1]*University of Helsinki, Department of Agricultural Sciences, Helsinki, Finland*, [2]*Natural Resources Institute Finland, Jokioinen, Finland*, [3]*Makerere University, College of Agricultural and Environmental Sciences, Kampala, Uganda*, [4]*University of Cairo, Department of Animal Reproduction, Cairo, Egypt*, [5]*Agricultural Research Council, Animal Breeding and Genetics, Pretoria, South Africa*, [6]*CIISA, Faculty of Veterinary Medicine, University of Lisbon and BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal*, [7]*Wageningen University and Research, Animal Breeding and Genomics, Wageningen, the Netherlands*.

P392 **High-quality genome assembly of Southern Africa Indigenous cattle.**
Ntanganedzeni Mapholi*[1], Thendo Tshilate[1], Sinebongo Mdyogolo[1], Rae Smith[1], Tracy Masebe[1], Thomas Raphulu[2], Isidore Houaga[1,3], Annelin Molotsi[1], and Lucky Nesengani[1], [1]*College of Agriculture and Environmental Sciences, UNISA Science Campus, Florida, Johannesburg, South Africa*, [2]*Limpopo Department of Agriculture, Polokwane, South Africa*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK*.

P393 **Annotation of African indigenous sheep reveals high-quality ovine genome with unique structure.**
Lucky Nesengani*[1], Thendo Tshilate[1], Sinebongo Mdyogolo[1], Rae Smith[1], Tracy Masebe[1], Thomas Raphulu[2], Isidore Houaga[1,3], and Ntanganedzeni Mapholi[1], [1]*College of Agriculture and Environmental Sciences, UNISA Science Campus, Florida, Johannesburg, South Africa*, [2]*Limpopo Department of Agriculture, Polokwane, South Africa*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK*.

P394 **Integrative analysis of transcriptome and microRNA profiling in the mammary gland of Indian dairy goats across lactation stages.**
A. Kumar*, S. P. Singh, D. Sharma, B. Kumari, Pooja, G. K. Gupta, R. P. Pandey, and M. Anand, *U.P. Pt. Deen Dayal Upadhyay Pashu Chikitsa Vigyan Vishwavidyalaya Evam Go-Ansundhan Sansthan, (DUVASU), Mathura, UP, India*.

P395 **Tracing the adaptive history of trypanotolerant African cattle using a pangenome graph.**
N. Adossa*[1], S. Kambal[1,2], A. Tijjani[1,3], I. Houaga[4,5], A. Ahbara[5], C. Elsik[2], A. Adeola[7], J. Mwacharo[5,8], Y. Li[9], J. Prendergast[4,5], and O. Hanotte[1,10], [1]*LiveGene–CTLGH, International Livestock Research Institute, Addis Ababa, Ethiopia*, [2]*Division of Animal Sciences, University of Missouri, USA*, [3]*Feinstein Institutes for Medical Research, USA*, [4]*Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush Campus, Midlothian, UK*, [5]*Centre for Tropical Livestock Genetics and Health, Easter Bush, Midlothian, UK*, [6]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Pretoria, South Africa*, [7]*Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [8]*International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [9]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, School of Life Sciences, Yunnan University, Kunming, China*, [10]*School of Life Sciences, University of Nottingham, Nottingham, UK*.

Pig Genetics and Genomics I

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:40 AM

P425 **Integrated mitogenome and Y-chromosome analysis corroborates a complex origin of African indigenous pigs.**
Adeniyi C. Adeola*[1,2], Lameck A. Odongo[1,3], George M. Msalya[4], Olawale F. Olaniyan[5], Shuhong Zhao[6], Chadi A. M. S. Djagoun[7], Pam D. Luka[8], George Niba[9], Olufunke O. Oluwole[10], Elliot Greiner[11], Philip M. Dawuda[12], Joram M. Mwacharo[13], Jian–Lin Han[14], Min–Sheng Peng[1,3], Ya–Ping Zhang[1,3], [1]*Key Laboratory of Genetic Evolution and Animal Models and Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*Department of Veterinary Physiology and Biochemistry, Faculty of Veterinary Medicine, Bayero University, Kano, Nigeria*, [3]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan, China*, [4]*Sokoine University of Agriculture, Department of Animal, Aquaculture, and Range Sciences, Morogoro, Tanzania*, [5]*School of Agriculture and Environmental Sciences, University of the Gambia, Serrekunda, Gambia*, [6]*Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of the Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei, China*, [7]*Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey–Calavi, Cotonou, Benin*, [8]*National Veterinary Research Institute, Vom, Nigeria*, [9]*National Centre for Animal Husbandry, Veterinary and Halieutic Training, Jakiri, Cameroon*, [10]*Institute of Agricultural Research and Training, Obafemi Awolowo University, Ibadan, Nigeria*, [11]*The Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany*, [12]*Department of Animal Science, Faculty of Agriculture National University of Lesotho, Roma, Lesotho*, [13]*Dryland Livestock Genomics, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [14]*Yazhouwan National Laboratory, Sanya, Hainan, China*.

P426 **ISAG Bursary Award: ZBED6 is a key regulator of lipogenesis in pig and mouse.**
Dandan Wang*[1,2], Leif Andersson[2], and Lin Jiang[1], [1]*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*.

P427 **ISAG Bursary Award: A genome-wide association study examining 24 hematological traits at two different ages in production pigs.**
J. Sun*, E. Ibragimov, M. K. Morsing, M. P. Rydal, J. P. Nielsen, M. Fredholm, and P. Karlskov-Mortensen, *Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark*.

P428 **ISAG Bursary Award: Exploring genomic regions regulating the liver transcriptome and energy homeostasis in pigs.**
F. Llobet-Cabau*[1,2], J. Liu[3], T. Jové-Juncà[3], A. Castelló[1,2], A. Sánchez[1,2], M. Ballester[3], and J. M. Folch[1,2], [1]*Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Barcelona, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain*, [3]*Animal Breeding and Genetics Program, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain*.

P429 **Differential expression of salivary miRNAs during the suckling-to-weaning transition in piglets.**
G. H. Jeong*[1], S. H. Lee[2], and K. S. Lim[1], [1]*Department of Animal Resources Science, Kongju National University, Yesan, Chungcheongnam-do, Republic of Korea*, [2]*Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea*.

P430 **ISAG Bursary Award: Genetic architecture of vitamin D metabolism and bone turnover in pigs.**
Dipanwita Paul*[1,2], Henry Reyer[1], Michael Oster[1], Siriluck Ponsuksili[1], and Klaus Wimmers[1,2], [1]*Research Institute for Farm Animal Biology (FBN), Dummerstorf, Mecklenburg-Vorpommern, Germany*, [2]*University of Rostock, Rostock, Mecklenburg-Vorpommern, Germany*.

P431 **Selection associated with domestication targeted both tissue-specific and ubiquitously expressed genes.**
D. Vargas Donayre*[1,2], S. Ramos Onsins[1], A. Noce[1], A. Clop[1], and M. Amills[1,2], [1]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Spain*, [2]*Department of Health and Animal Anatomy, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

P432 **Identification and characterization of GDPD2 as a novel antiviral target against swine enteric coronaviruses.**
Yajing Zhou*, Haifei Wang, and Wenbin Bao, *College of Animal Science and Technology, Yangzhou University, Yangzhou, Jiangsu, China*.

P433 **Integrated analysis of mRNA and miRNA transcriptomes reveals the mechanism of PRRSV induced thymocyte cell cycle arrest.**
Y. Hei*[1], X. Shi[1], X. Meng[1], W. Liu[3], B. Liu[1,2], and X. Zhou[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Wuhan, Hubei, China*, [3]*School of Computer Science and Artificial Intelligence, Wuhan University of Technology, Wuhan, Hubei, China*.

P434 **A molecular mechanism for trunk vertebra number variation in domestic pigs.**
Jianbo Li*[1,4], Ligang Wang[2], Dawei Yu[3], Haibing Xie[1,4], and Yaping Zhang[1,4], [1]*Kunming Institute of Zoology, Kunming, China*, [2]*Institute of Animal Science, Beijing, China*, [3]*Institute of Zoology, Beijing, China*, [4]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Kunming, China*, [5]*Institute of Biophysics, Beijing China*.

P435 **Genomic insights into dual domestication origins and pre-divergence hybridization of Chinese indigenous pigs.**
Yuzhan Wang*[1,2] and Yiqiang Zhao[1,2], [1]*National Research Facility for Phenotypic and Genotypic Analysis of Model Animals, Beijing, China*, [2]*China Agricultural University, Beijing, China*.

P436 **ISAG Bursary Award: Genome-wide association study identified new QTL and candidate genes on SSC2 associated with teat number in Large White Tongcheng crossed pigs.**
Qinghua Yang*[1], Fang Ma[1], Jiao Yuan[1], Yang Shen[1], Xiangge Meng[1], Songyu Li[1], Zining Yuan[1], Ping Zhou[1], Weizhen Liu[3], Bang Liu[1,2], and Xiang Zhou[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Wuhan, Hubei, China*, [3]*School of Computer Science and Artificial Intelligence, Wuhan University of Technology, Wuhan, Hubei, China*.

P437 **Comprehensive differential gene expression and genomic variant profiling using RNA-seq data from the pituitary gland of Iberian piglets exposed to in utero heat stress.**
P. Vázquez-Ortego*[1], Y. Núñez[1], F. García[1], H. Laviano[2], A. Magro[2], R. Escudero[2], F. Sánchez-Esquiliche[3], A. de las Heras-Molina[2], C. Óvilo[1], J. M. García-Casco[4], and M. Muñoz[1], [1]*Animal Breeding and Genetics Department, INIA-CSIC, Madrid, Spain*, [2]*Animal Production Department, UCM, Madrid, Spain*, [3]*Sánchez Romero Carvajal, Jabugo, Spain*, [4]*Centro de I+D en Cerdo Ibérico, INIA-CSIC, Zafra, Spain*.

P438 **Genomic evaluation of productive and reproductive traits in Duroc pigs: A comparison between ssGBLUP and PBLUP.**
S. Lee*, C. Dang, J. Cha, H. Chang, H. Seong, E. Kim, M. Alam, D. Lee, E. Ryu, C. Lee, and M. Park, *Animal Genetics & Breeding Division, National Institute of Animal Science, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P439 **Investigation of specific gene in improved Nanchukmacdon through population genetic analysis with other pig breeds.**
W. Park*[1], C. Dang[1], H. Ko[1], Y. Kang[2], I. Cho[2], and J. Lee[1], [1]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan, Chungcheongnam-do, Republic of Korea*, [2]*Subtropical Livestock Research Institute, National Institute of Animal Science, RDA, Jeju, Republic of Korea*.

P440 **Multi-omics approaches for understanding efficient pig production traits.**
Maria G. Luigi-Sierra*[1], Marta Gòdia[2], Ole Madsen[2], and Peter Karlskov-Mortensen[1], [1]*Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark*, [2]*Animal Breeding and Genomics, Wageningen University and Research, Wageningen, the Netherlands*.

P441 **Key gene screening and mechanism analysis of lactation traits in pigs.**
Lijun Shi* and Lixian Wang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P442 **STR marker-based study of genetic diversity and population structure in five Polish pig breeds.**
G. Smolucha*, A. Koseniuk, and A. Radko, *National Research Institute of Animal Production, Department of Animal Molecular Biology*, *Balice, Poland*.

P443 **Transcriptome profile of porcine CD8$^+$ and CD8$^-$ γδ T cells in response to PRRSV infection.**
Seung-Hoon Lee*, Byeonghwi Lim, Min-Jae Jang, Young-Jun Seo, and Jun-Mo Kim, *Department of Animal Science and Technology, Chung-Ang University*, *Anseong, Gyeonggi-do, Republic of Korea*.

P444 **A comprehensive landscape of pig long noncoding RNA.**
Hang Liu[1], Ligang Wang[2], Ya-Ping Zhang[1], and Zhong-Yin Zhou*[1], [1]*Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, Yunnan, China*, [2]*Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P445 **Origins, dispersal, and impact: Bidirectional introgression between Chinese and European pig populations.**
Yibin Qiu*[1,4], Langqing Liu[1,2], Zebin Zhang[1,2], Enqin Zheng[1,2], Sixiu Huang[1,2], Huaqiang Yang[1,3], Zicong Li[1,2], Gengyuan Cai[1,3], Zhenfang Wu[1,5], and Jie Yang[1,2], [1]*State Key Laboratory of Swine and Poultry Breeding Industry, College of Animal Science and National Engineering Research Center for Breeding Swine Industry, South China Agricultural University*, *Guangzhou, Guangdong, China*, [2]*National and Regional Livestock Genebank, Guangdong Gene Bank of Livestock and Poultry, South China Agricultural University*, *Guangzhou, Guangdong, China*, [3]*Guangdong Zhongxin Breeding Technology Co. Ltd*, *Guangzhou, Guangdong, China*, [4]*Guangdong Provincial Key Laboratory of Agro-animal Genomics and Molecular Breeding, South China Agricultural University*, *Guangzhou, Guangdong, China*, [5]*Yunfu Subcenter of Guangdong Laboratory for Lingnan Modern Agriculture*, *Yunfu, Guangdong, China*.

P446 **ISAG Bursary Award: Enhancing prime editing efficiency through modulation of methylation on the newly synthesized DNA strand and prolonged expression.**
X. S. Han[1,2], X. H. Xu*[1], Y. C. Xiong[1], G. X. Zhao[1], R. G. He[1], Y. Y. Su[1], S. Li[1], C. Z. Zhao[1,2], X. N. Xi[1], Y. X. Zhao[1,2], X. W. Xu[1], S. S. Xie[1,3], X. Y. Li[1,3], S. H. Zhao[1,2], J. X. Ruan[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University*, *Wuhan, P. R. China*, [2]*Yazhouwan National Laboratory*, *Sanya, P. R. China*, [3]*Frontiers Science Center for Animal Breeding and Sustainable Production, Huazhong Agricultural University*, *Wuhan, P. R. China*, [4]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production*, *Wuhan, P. R. China*.

P447 **Genetic characterization of Woori-Heukdon (WRH) using whole-genome sequencing: Insights into genetic diversity, selection signatures, and parental contributions.**
Bongsang Kim*[1,2], Jongan Lee[3], Young-Shin Kim[4], and Seoae Cho[2], [1]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University*, *Seoul, Republic of Korea*, [2]*eGnome Inc*, *Seoul, Republic of Korea*, [3]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA*, *Cheonan, Korea*, [4]*Swine Science Division, National Institute of Animal Science, RDA*, *Cheonan, Korea*.

P448 **Combining metabolomics and genomics to describe genetic factors affecting the metabolism in growing Duroc male pigs.**
S. Bovo*[1], M. Bolner[1], C. Lewis[2], J. Holl[3], B. Valente[3], G. Schiavo[1], F. Bertolini[1], and L. Fontanesi[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna*, *Bologna, Italy*, [2]*PIC Europe, Genus*, *Sant Cugat del Valles, Barcelona, Spain*, [3]*PIC North America, Genus*, *Hendersonville, TN, USA*.

P449 **The domestication model of Chinese domestic pigs.**
S. Y. Wang* and L. Q. Liu, *South China Agricultural University*, *Guangzhou, China*.

P450 **Transcriptome profiling of the digestive tract and hypothalamus reveals differentially expressed genes involved in feed resilience in Piétrain-sired pigs.**
E. U. Nwosu[1], R. Meyermans[1], B. Chakkingal-Bhaskaran[1], E. Kowalski[2,3], W. Gorssen[1,4], S. Janssens[1], S. Millet[2], M. Aluwé[2], S. De Smet[3], and N. Buys*[1], [1]*KU Leuven, Department of Biosystems, Center for Animal Breeding and Genetics*, *Leuven, Belgium*, [2]*ILVO*, *Merelbeke-Melle, Belgium*, [3]*Ghent University, Laboratory for Animal Nutrition and Animal Product Quality*, *Ghent, Belgium*, [4]*Animal Genomics, ETH Zürich*, *Zürich, Switzerland*.

P451 **Assessing inbreeding and declining genetic diversity in South African village pigs using SNP-based runs of homozygosity analysis.**
N. L. Hlongwane*[1], M. G. Mbuyazi[2,3], M. Van Der Nest[4], E. F. Dzomba[3], F. C. Muchadeyi[5], L. T. Nesengani[1], T. C. Matelele[6], and N. O. Mapholi[1], [1]*Department of Agriculture and Animal Health, University of South Africa, Florida, South Africa*, [2]*Agricultural Research Council, Biotechnology Platform, Pretoria, Gauteng, South Africa*, [3]*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*, [4]*Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa*, [5]*International Atomic Energy Agency, Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria*, [6]*Department of Agriculture and Rural Development, Farm Animal Genetic Resources, Pretoria, South Africa*.

P452 **Integrated transcriptomic and lipidomic analyses revealed the role of lipid metabolism in PRRSV replication.**
S. Lu*[1], X. Wu[1], B. Liu[1,2], and X. Zhou[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Wuhan, China*.

P453 **The *Pecari tajacu* genome: A tool for its conservation and the study of the *Suoidea* superfamily.**
A. J. Amaral*[1,2], L. Eory[3], D. Santos[4], F. L. B. Toral[5], I. Delgado[6,7], A. Leitão[2,6], L. T. Gama[2,6], and A. L. Archibald[3], [1]*Universidade de Évora, Escola de Ciência e Tecnologia, Department of Animal Production, University of Évora, Évora, Portugal*, [2]*Centre of Interdisciplinary Research, Faculty of Veterinarian Medicine, University of Lisbon, Lisbon, Portugal*, [3]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK*, [4]*Bioinsight & Ecoa, Odivelas, Portugal*, [5]*Departamento de Zootecnia, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil*, [6]*Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Lisbon Portugal*, [7]*Faculty of Veterinary Medicine, Lusofona University–Lisbon University Center, Lisbon Portugal*.

P454 **Genome-wide association study for sow lifetime productivity related traits in purebred Landrace and Yorkshire pigs.**
Yu-Ju Lee*[1], Tae-Hee Kim[2], Min-Ho Jeong[2], Dong-Bin Hwang[2], Joon-Ki Hong[1], Young-Sin Kim[1], and Hee-Bok Park[2], [1]*Swine Science Division, National Institute of Animal Science, Rural Development Administration, Cheonan-si, Chungcheongnam-do, Republic of Korea*, [2]*Department of Animal Resources Science, Kongju National University, Yesan-eup, Chungcheongnam-do, Republic of Korea*.

Small Ruminant Genetics and Genomics

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:40 AM

P558 **Polymorphisms in GH and CAST genes and their association with meat productivity traits in sheep breeds in Kazakhstan.**
A. Mussayeva, Sh. Bakhtybekkyzy*, Z. Orazymbetova, S. Alayeva, A. Bekitayeva, and A. Aryngaziyev, *Institute of Genetics and Physiology, Almaty, Kazakhstan*.

P559 **The impact of heat stress on growth and resilience phenotypes of sheep raised in a semi-arid environment of sub-Saharan Africa.**
E. Oyieng*[1,2], J. M. K. Ojango[2], M. Gauly[3], C. C. Ekine-Dzivenub[2], R. Oloo[2], R. Mrode[2,4], E. Clark[5], and S. König[1], [1]*Institute of Animal Breeding and Genetics, Justus-Liebig-University Gießen, Gießen, Germany*, [2]*International Livestock Research Institute, Nairobi, Kenya*, [3]*Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen–Bolzano, Bolzano, Italy*, [4]*Animal and Veterinary Science, Scotland's Rural College, Edinburgh, UK*, [5]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*.

P560 **The North being cold, the South warm: Selection signature of local sheep breeds in contrasting environmental conditions.**
C. Persichilli[1], A. Cesarani[2,3], S. Mastrangelo[4], M. Di Civita[1], S. Ben Jemaa[4], F. Pilla[1], and G. Senczuk*[1], [1]*Department of Agriculture, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Department of Agricultural Science, University of Sassari, Sassari, Italy*, [3]*Department of Animal and Dairy Science, University of Georgia, GA, USA*, [4]*Department of Agricultural and Forestry Sciences, University of Palermo, Italy*.

P561 **A genome-wide association study demonstrates that the polymorphism of the melanocortin 1 receptor (*MC1R*) gene determines the black vs. red pigmentation of Palmera goats.**
I. Baazaoui*[1], A. Castelló[1,2], B. Cabrera[1,2], E. Vega[1], E. Badosa[1,2], and M. Amills[1], [1]*Centre de Recerca Agrigenòmica (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Spain*, [2]*Departament de Ciència Animal i dels Aliments Universitat Autònoma de Barcelona, Bellaterra, Spain*.

P562 **Genome-wide scan for adaptive differentiation along altitudinal gradients within breed: Case study on two Italian sheep breeds.**
Slim Ben Jemaa*[1], Gabriele Senczuk[2], Federica Carta[1], Silvia Riggio[1], Alessia Benanti[1], Maria Teresa Sardina[1], Alberto Cesarani[3], and Salvatore Mastrangelo[1], [1]*University of Palermo, Palermo, Sicily, Italy*, [2]*University of Molise, Campobasso, Molise, Italy*, [3]*University of Sassari, Sassari, Sardinia, Italy*.

P563 **Assessment of genetic diversity in Korean native black goats (KNBG) using microsatellite (MS) marker.**
H. C Kang*[1], C. H. Myung[1], J. Y. Kim[1], D. H. Jin[3], S. C. Kim[3], and H. T. Lim[1,2], [1]*Department of Animal Science, Gyeongsang National University, Jinju, Korea*, [2]*Institute of Agriculture and Life Science, Gyeongsang National University, Jinju, Korea*, [3]*Animal Genetic Resources Research Center, National Institute of Animal Science, Rural Development Administration, Hamyang, Korea*.

P564 **Genetic parameters of production traits in Abergelle goats under community-based breeding program scale up villages.**
Yeshiwas Walle[1,3], Zeleke Tesema[2], and Wossenie Mebratie*[3], [1]*Sekota Dry land Agricultural Research Center, Sekota, Ethiopia*, [2]*Debrebirhan Agricultural Research center, Debrebrhan, Ethiopia*, [3]*Bahir Dar University, Bahir Dar, Ethiopia*.

P565 **Genotyping analysis uncovers genetic diversity patterns in three native sheep breeds in the Kingdom of Saudi Arabia.**
Areej Almuhayya*[1], Abdulrahman Aldawish[1,2], Afrah Alsulami[1], Ahmad Farag[1], Faisal Alsubaie[1], Fheed Alrashedi[1], Hatim Almutairi[1], Quaiser Saquib[2], Yara Alabboud[1], Mohammed Alarwi[1], and Mohammed Albeshr[2], [1]*National Livestock & Fisheries Development Program, Ministry of Environment, Water & Agriculture, Riyadh, Riyadh, Saudi Arabia*, [2]*Department of Zoology, College of Science, King Saud University, Riyadh, Riyadh, Saudi Arabia*.

P566 **Diversity and evolutionary patterns in South African Dorper sheep affected with wet-carcass syndrome.**
B. Bhika Kooverjee*[1,2], P. Soma[1], M. Maalima[3], F. W. C. Neser[2], and M. M. Scholtz[1,2], [1]*Agricultural Research Council–Animal Production, Irene, South Africa*, [2]*University of the Free State, Department of Animal, Wildlife and Grassland Sciences, Bloemfontein, South Africa*, [3]*Agricultural Research Council–Biotechnology platform, Onderstepoort, South Africa*.

P567 **Nucleotide diversity in South African Dorper and Ile de France sheep using whole-genome sequencing.**
P. Soma*[1], B. B. Kooverjee[1], M. Malima[1], and M. van der Nest[2], [1]*Agricultural Research Council, Pretoria, Gauteng, South Africa*, [2]*University of Pretoria, Pretoria, Gauteng, South Africa*.

P568 **Prospective genes for coat and eye color traits in Punjab goat breeds using identified by GWAS.**
Muhammad Moaeen-ud-Din*[1] and Raja Muner[2], [1]*PMAS-Arid Agriculture University Rawalpindi, Rawalpindi, Punjab, Pakistan*, [2]*Department of Animal Breeding & Genetics, Faculty of Veterinary and Animal Sciences, University of Agriculture, Dera Ismail Khan, Pakistan*.

P569 **Cox1 gene diversity of Nigerian indigenous goats.**
A. A. Adepoju*[1,2], [1]*Federal College of Horticulture, Dadinkowa, Gombe State, Nigeria*, [2]*Federal University of Kashere, Kashere, Gombe State, Nigeria*, [3]*National Centre for Genetic Resources and Biotechnology, Ibadan Oyo State, Nigeria*, [4]*Bauchi State College of Agriculture, Yelwa Bauchi State, Nigeria*.

P570 **ISAG Bursary Award: Uncovering the role of structural variants in genetic selection for New Zealand sheep.**
R. M. Clarke*[1], R. Brauning[1], H. Baird[1], K. G. Dodds[1], M. A. Lee[2,3], and S. M. Clarke[1], [1]*AgResearch, Invermay, Mosgiel, New Zealand*, [2]*Beef+Lamb NZ Genetics, Dunedin, New Zealand*, [3]*Department of Mathematics and Statistics, University of Otago, Dunedin, New Zealand*.

P571 **Impact of differential degrees of runs of homozygosity and haplotype sharing extents across breeds on body size traits in Korean indigenous goats.**
S. Kim*[1,2], H. Jeong[1,2], G.-E. Kim[3], K.-W Kim[3], W. Park[4], J. Kim[1,2], and B.-H. Choi[3], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Animal Genetic Resources Research Center, National Institute of Animal Science, Rural Development Administration, Deogyuwolseong-ro, Seosang-myeon, Hamyang-gun, Gyeongsangnam-do, Republic of Korea*, [4]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P572 **Genomic diversity and population structure of Thuringian goats.**
A. W. Omar[1], P. Korkuc[1,2], G. B. Neumann[2], E.M. Strucken[1], D. Arends[3], J. Conington[4], M. Reissmann[1], A. Martinez[5], S. Carolan[6], J. A. Lenstra[7], G. A. Brockmann[1], and S. Rahmatalla*[1], [1]*Humboldt-Universität zu Berlin, Berlin, Germany*, [2]*Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany*, [3]*Northumbria University, Newcastle upon Tyne, UK*, [4]*Scotland's Rural College, Roslin Institute Building, Easter Bush, Midlothian, UK*, [5]*University of Cordoba, Andalusia, Spain*, [6]*Old Irish Goat Society, Mulranny, Ireland*, [7]*Utrecht University, Utrecht, the Netherlands*.

P573 **Analysis of the genetic relationship between native black goats and foreign breeds using microsatellite markers.**
K. Tseveen[1], G. H. Lee[2,4], Z. Byambasuren[1], and H. S. Kong*[2,3], [1]*Major in Applied Biotechnology, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [2]*Gyeonggi Regional Research Center, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [3]*Laboratory of Molecular Genetics, Hankyong National University, Anseong, Gyeonggi-do, Republic of Korea*, [4]*Hankyong and Genetics, Anseong, Gyeonggi-do, Republic of Korea*.

P574 **Leveraging genomic insights for livestock breeding optimization: A robust pipeline for trait score analysis and animal ranking.**
Hatim Almutairi*, Areej Almuhayya, Nouf Alharbi, and Mohammed Alarwi, *National Livestock & Fisheries Development Program, Riyadh, Riyadh, Saudi Arabia*.

P575 **Evaluation of the current breeding program of stud Kalahari Red goats across breeders in South Africa.**
K. P. Nkgapele*[1], E. Bhebhe[2], and O. Tada[1], [1]*University of Limpopo, Polokwane, Limpopo, South Africa*, [2]*University of Venda, Venda, Limpopo, South Africa*.

P576 **Landscape genomics reveal signatures of environmental adaptation in goats.**
Y. Li*[1,2], P. Su[1], Y. Gong[1], L. Tang[2], Z. Zhang[3], Q. Ren[1], Z. Wang[1,4], Y. Pu[1], Y. Ma[1], and L. Jiang[1], [1]*National Germplasm Center of Domestic Animal Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, PR China*, [2]*GIGA & Faculty of Veterinary Medicine, University of Liège, Liège, Belgium*, [3]*Wageningen University and Research, Animal Breeding and Genomics, Wageningen, the Netherlands*, [4]*College of Animal Science, Shanxi Agricultural University, Taigu, Shanxi, PR China*.

P577 **Spatio-temporal expression of the *KRT86* gene and the effect of its genetic variation on wool traits.**
Zhanzhao Chen* and Hongxian Sun, *Gansu Agricultural University, College of Animal Science and Technology, Lanzhou, Gansu, China*.

P578 **Genetic diversity, selection signatures, and genome-wide association studies identify candidate genes related to functional longevity in Cyprus Chios sheep.**
Theodoulakis Christofi* and Georgia Hadjipavlou, *Agricultural Research Institute, Nicosia, Cyprus*.

P579 **Worldwide analysis of the variability of microRNA genes in domestic goats.**
E. Marmol Sanchez[1], P. Bardou[2], L. Colli[3,4], VarGoats Consortium2[2], M. Luigi-Sierra[5], G. Tosser-Klopp[2], and M. Amills*[5,6], [1]*Center for Evolutionary Hologenomics, Copenhagen, Denmark*, [2]*GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet Tolosan, France*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Univ. Cattolica del S. Cuore di Piacenza, Piacenza, Italy*, [4]*Centro di Ricerca sulla Biodiversità e sul DNA antico BioDNA, Univ. Cattolica del S. Cuore di Piacenza, Piacenza, Italy*, [5]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Bellaterra, Spain*, [6]*Departament de Ciència Animal i dels Aliments, Universitat Autonoma de Barcelona, Bellaterra, Spain*.

P580 **An atlas of gene expression in goats.**
M.J. Wang*[1,2], A. Noce[1], M. Luigi Sierra[1], D. Vargas[1], E. Mármol-Sánchez[1], K. Wang[1], E. Petretto[1], S. Olvera Maneu[3,4], P. Serres[4], J. Gardela[4], M. López Béjar[4], and M. Amills[1,2], [1]*Centre de Recerca Agrigenòmica (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [3]*Department of Veterinary Medicine, University of Nicosia, School of Veterinary Medicine, Nicosia, Cyprus*, [4]*Department of Animal Health and Anatomy, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*.

OTHER EVENTS

Mid-Conference Tours
Main Entrance
11:40 AM - 5:00 PM

Thursday, July 24

Speaker Ready Room
Room 209
8:00 AM - 6:00 PM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions
Plenary IV

Grand Ballroom 201 + 202
8:30 AM - 11:30 AM

8:30 AM OP194 **Genomic Diversity, Adaptation, and Priority Strategies for Animal Genetic Resources Conservation.**
J. Kantanen*, *Natural Resources Institute Finland, Jokioinen, Finland*.

9:20 AM OP195 **Once upon a time, I was carrying an rDNA.**
Arang Rhie*, *Genome Informatics Section, Computational and Statistical Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA*.

10:10 AM **Coffee Break.**

10:40 AM OP196 **Antimicrobial peptidomics towards improving animal health.**
H.-S. Cho, D. Kim, H. Jeon, M. Kang, B. Ahn, P. Somasundaram, N. Soundararajan, and C. Park*, *Department of Stem Cell and Regenerative Biotechnology, Konkuk University, Seoul, Republic of Korea*.

POSTER PRESENTATIONS

Avian Genetics and Genomics II

Exhibition Hall 109 + 110 + 111 + 112
10:20 AM - 11:30 AM

P167 **Initiative for African Muscovy Ducks Genome Conservation Project.**
O. A. Yusuf*[1], C. A. Adeola[2,3], F. E. Sola-Ojo[1], A. O. Oguntunji[4], L. M. Nneji[5], M. K. Ewuola[6], S. F. Bello[7], W. A. Olaniyi[8], A. T. Adesoji[9], O. J. Sanke[10], and E. L. Daniel[11], [1]*Department of Animal Production, Faculty of Agriculture, University of Ilorin, Ilorin, Kwara State, Nigeria*, [2]*State Key Laboratory of Genetic Evolution & Animal Models and Yunnan Key Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650201, China*, [3]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, Yunnan, China*, [4]*Department of Animal Science and Fisheries Management, Bowen University, Iwo, Osun, Nigeria*, [5]*Department of Ecology and Evolutionary Biology, Princeton University, Princeton, New Jersey, USA*, [6]*Animal Breeding and Genetics Unit/Department of Animal Science, University of Ibadan, Ibadan, Oyo, Nigeria*, [7]*Agriculture Research Group, Organization of African Academic Doctors (OAAD), P.O. Box 25305-00100, Langata, Nairobi, Kenya*, [8]*Department of Animal Science, Faculty of Agriculture, Adekunle Ajasin University, Akungba Akoko, Ondo State, Nigeria*, [9]*Department of Agricultural Education, Federal College of Education, Bichi, Kano, Nigeria*, [10]*Taraba State Ministry of Agriculture and Natural Resources, Jalingo, Taraba, Nigeria*, [11]*Department of Animal Science, University of Benin, Benin City, Nigeria*.

P168 **Estimation of genetic diversity in Nigerian domestic pigeons (*Columba livia domestica*) using mitochondria cytochrome C oxidase 1 gene.**
I. A. Abubakar*[1], F. E. Sola-Ojo[1], and C. A. Adeola[2], [1]*University of Ilorin, Ilorin, Kwara state, Nigeria*, [2]*University of Ilorin, Ilorin, Kwara state Nigeria*, [3]*Kumming Institute of Zoology, Chinese Academy of Sciences, Kumming, China*.

P169 **Genetics and cellular transcriptomics regulating pigmentation patterns in chicken feathers.**
P. J. Hsin*[1], Z. Li[2], L. Andersson[2], and B. W. Davis[1], [1]*Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA*, [2]*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*.

P170 **Genetic and phenotypic parameter estimates for the selection of body weight and egg production traits of Tilili chicken of Ethiopia.**
Birhan Kassa*[1,2], Mengistie Taye[1,4], Wondmeneh Esatu[3], Adebabay Kebede[5], Mekonnen Girma[3], Fasil Getachew[6], Georgios Banos[7], Kellie Watson[6], Tadelle Dessie[3], and Olivier Hanotte[3,8], [1]*College of Agriculture and Environmental Science, Bahir Dar University, Bahir Dar, Ethiopia*, [2]*ANdassa Livestock Research Centre, Bahir Dar, Ethiopia*, [3]*Live Gene, International Livestock Research Institute, Addis Ababa, Ethiopia*, [4]*Institute of Biotechnology, Bahir Dar University, Bahir Dar, Ethiopia*, [5]*Amahra Regional Agricultural Research Institute, Bahir Dar, Ethiopia*, [6]*The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, EH25 9RG, UK*, [7]*Scotland's Rural College, Easter Bush, Midlothian EH25 9RG, UK*, [8]*Cells, Organisms, and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, NG7 2RD, UK*.

P171 **ISAG Bursary Award: Exploring expressional and regulative pattern of paternal alleles in *Cairina moschata* using haplotype-resolved assemblies.**
Te Li*[1], Yiming Wang[1], Mengfei Ning[1], Zhou Zhang[2], and Yinhua Huang[1], [1]*China Agricultural University, Beijing, China*, [2]*Jiangxi Agricultural University, Nanchang, China*.

P172 **ISAG Bursary Award: Dynamic embryonic skeletal muscle development atlas and its foundation model at single-cell resolution across different chicken breeds.**
Chong Li*[1], Yidan Yan[1], Xiarui Zhu[1], Lingzhao Fang[3], Hao Qu[2], Xiaoxiang Hu[1], and Yuzhe Wang[1], [1]*China Agricultural University, Beijing, China*, [2]*Guangdong Academy of Agricultural Sciences, Guangzhou, China*, [3]*Aarhus University, Aarhus, Denmark*.

P173 **Influence of defatted winged termite inclusion levels on gut microbial community of broiler chickens.**
Sekobane Daniel Kolobe*, Nthabiseng Amenda Sebola, Emmanuel Malematja, and Monnye Mabelebele, *University of South Africa, University of South Africa Florida Science Campus, Johannesburg, Gauteng, South Africa*.

P174 **Multivariate GWAS reveals pleiotropic effects for taste-active compounds in Korean native chicken meat.**
M. Kim*, E. Cho, and J. H. Lee, *Chungnam National University, Daejeon, Republic of Korea*.

P175 **Molecular detection and characterization of avian haemosporidian parasites in village chickens in selected villages of Limpopo and North-West Provinces, South Africa.**
T. Matloa, M. B. Ledwaba, and D. P. Malatji*, *University of South Africa, Florida, Gauteng, South Africa*.

P176 **Genetic basis of yellow skin in chickens revealed by *BCO2* mutation.**
L. Rong*[1], X. Wu[1], J. Li[1], J. Nan[2], L. Yang[1], W. Fan[1], Y. Pan[1], X. Wang[1], and S. Li[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*The Second Affiliated Hospital & Liangzhu Laboratory, Zhejiang University School of Medicine, Hangzhou, Zhejiang, China*, [3]*Key Laboratory of Smart Farming for Agricultural Animals, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*.

P177 **Genetic mechanisms of indigenous chickens adapted to high and low altitudinal environments in Tigray, Ethiopia.**
Gebreslassie Berhe*[1,2], Gurja Belay[2], Tsadkan Zegeye[1,2], Tadelle Dessie[3], Minister Birhane[1], Mulalem Zenebe[1], Morris Katrina[4], Olivier Hanotte[3,4], and Adriana Vallejo-Trujillo[5], [1]*Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia*, [2]*Addis Ababa University, College of Natural Resource; Department of Microbial, Cellular and Molecular Biology, Addis Ababa, Addis Ababa, Ethiopia*, [3]*International Livestock Research Institute, Addis Ababa, Addis Ababa, Ethiopia*, [4]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK*, [5]*School of Life Sciences, University of Nottingham, NG7 2RD, Nottingham, United Kingdom, Nottingham, Nottinghamshire, UK*.

P178 **Oct4-driven enhancer activation regulate germ cell migration and oogonial stem cell derivation in chickens.**
L. Meng*[1], C. Wang[2], X. Cao[1], X. Huang[1], Q. Man[1], and G. Zhu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, College of Animal Science and Veterinary Medicine, Shandong Agricultural University, Taian, Shandong, China*.

P179 **Multiple transcriptome analysis reveals liver-targeted regulation of plasma exosome miR-30c-5p in chicken acute heat stress response.**
Zi Mei*, Zhenquan Song, Bin Zheng, Zheya Sheng, and Yanzhang Gong, *Huazhong Agricultural University, Wuhan, Hubei, China*.

P180 **Exploring population characteristics of Korean native chickens and foreign breeds through Runs of Homozygosity analysis.**
H. Ko*[1], J. Cha[2], J. Lee[1], and W. Park[1], [1]*Animal Genetics and Breeding Division, National Institute of Animal Science, Rural Development Administration, Cheonan, Republic of Korea*, [2]*Research Policy Planning Division, Research Policy Bureau, Rural Development Administration, Wanju, Republic of Korea*.

P181 **Adaptive evolution of mitochondrial genomes facilitated chicken colonization of the hypoxic Tibetan plateau.**
Zheng-Fei Cai[1,2], Li-Jiao Gu[1,3], Cheng Ma[1,4], Ting-Ting Yin[1,3], Rui Bi[1,3], Xun-He Huang[5], Shu-Run Zhang[1], Ya-Ping Zhang[1,2], and Min-Sheng Peng*[1,3], [1]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*Yunnan University, Kunming, Yunnan, China*, [3]*University of Chinese Academy of Sciences, Beijing, China*, [4]*Uppsala University, Uppsala, Sweden*, [5]*Jiaying University, Meizhou, Guangdong, China*.

P182 **Genomic diversity and adaptation to extreme climatic conditions in indigenous chickens.**
Nigussie Seboka*[1,4], Gurja Belay[1], Helen Nigussie[1], Feleke Woldeyes[4], Bersabhe Solomon[2,3], Adriana Vallejo-Trujillo[3], Christian Jacobson[2], Jacqueline Smith[3], and Olivier Hanotte[2,3], [1]*Addis Ababa University, Department of Microbial Sciences and Genetics, Addis Ababa, Ethiopia*, [2]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, EH25 9RG, UK*, [4]*Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia*.

Comparative and Functional Genomics

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P213 **ISAG Bursary Award: Comparative transcriptome analysis of ovarian tissues from high and low prolific ewes of South African Merino sheep using RNA-seq.**
J. Mamutse*[1], A. H. Molotsi[2,1], C. U. Braz[3], and K. Dzama[1], [1]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [2]*University of South Africa (UNISA), Florida, Johannesburg, South Africa*, [3]*University of Illinois at Urbana-Champaign, Urbana-Champaign, IL, USA*.

P214 **Investigating functional variation in testis tissue of pre- and postpubertal bulls.**
M. Osbahr*, X. M. Mapel, A. Leonard, and H. Pausch, *ETH Zurich, Zurich, Switzerland*.

P215 **Introducing ontology-based clinical synopses and pathogenicity labels of variants for single gene diseases in Online Mendelian Inheritance in Animals (OMIA).**
I. Tammen*[1], M. Mather[2], T. White[2], X. Luo[2], S. Shields[1], and F. W. Nicholas[1], [1]*Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Sydney, NSW, Australia*, [2]*Sydney Informatics Hub, The University of Sydney, Sydney, NSW, Australia*.

P216 **Elucidating breed-specific variants of native pigs in Korea: insights into pig breeds' genomic characteristics.**
Young-Sup Lee*[1,2], Seung-woo Son[2,1], Hak-Kyo Lee[3,2], Ra Ham Lee[4,1], and Donghyun Shin[5,2], [1]*Department of Animal Biotechnology, Jeonju, Jeola-bukdo, Republic of Korea*, [2]*Department of Agricultural Convergence Technology, Jeonju, Jeola-bukdo, Republic of Korea*, [3]*Department of Animal Biotechnology, Department of Agricultural Convergence Technology, Jeonju, Jeola-bukdo, Republic of Korea*, [4]*Deparment of Animal Biotechnology, Jeonbuk National University, Jeonju, Jeola-bukdo, Republic of Korea*, [5]*Department of Agricultural Convergence Technology, Jeonbuk National University, Jeonju, Jeola-bukdo, Republic of Korea*.

P217 **The effects of wind speed on the growth performance, physiology, and transcriptome of Ross 308 broiler under high temperature humidity index condition.**
Y. Park*[1], S. Lee[1], M. M. Hossain[1], W. Park[2], H. Kim[3], Y. Ko[1], and J-E. Park[1], [1]*Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, Jeju-si, Jeju-do, Republic of Korea*, [2]*Animal Biotechnology and Genomics Division, National Institute of Animal Science, RDA, Wanju-gun, Jellabuk-do, Republic of Korea*, [3]*Precision Animal Nutrition Division, National Institute of Animal Science, RDA, Wanju-gun, Jellabuk-do, Republic of Korea*.

P218 **Effect of glutathione peroxidase and superoxide dismutase activity levels on bulk gene expression of blood during transition period in Holstein.**
Francisco Calcaterra[1,2], Olivia Marcuzzi[1,2], Maria E. Fernandez[1,2], Leonidas H. Olivera[1,2], Sebastian J. Picco[1], and Guillermo Giovambattista*[1,2], [1]*National University of La Plata, La Plata, Buenos Aires, Argentina*, [2]*Consejo Nacional de Investigaciones Científicas y Técnicas, La Plata, Buenos Aires, Argentina*.

P219 **Characterization of heavy chain antibody gene repertoires in Bactrian camels.**
Yuexing Liu*[1,2], Li Yi[3], Yixue Li[1,2], and Zhen Wang[1], [1]*Shanghai Institute of Nutrition and Health, University of Chinese Academy of Sciences, Chinese Academy of Sciences, Shanghai, China*, [2]*Guangzhou Laboratory, Guangzhou 510005, Guangdong Province, Guangzhou, 510005, China, Guangzhou, China*, [3]*Inner Mongolia Agricultural University, Huhhot, China*.

P220 **Estimates of effective population size and linkage disequilibrium in South African beef cattle.**
Khathutshelo Nephawe*, Bohani Mtileni, and Mamokoma Modiba, *Tshwane University of Technology, Pretoria, Gauteng, South Africa*.

P221 **Inbreeding coefficients in South African beef cattle using runs of homozygosity.**
B. Mtileni*, M. Modiba, and K. Nephawe, *Tshwane University of Technology, Pretoria, South Africa*.

P222 **Genomic insights into Yanbian cattle: Breed-specific selective-sweeps identified by whole-genome sequencing data.**
Qingshan Gao[1], Jihye Baek*[2], Seungwoo Son[2], Hak-Kyo Lee[2], Donghyun Shin[2], and Chang-Guo Yan[1], [1]*Yanbian University, Yanji, Jilin, China*, [2]*Jeonbuk National University, Jeonju, Jeonbuk, Republic of Korea*.

P223 **Transcriptome analysis and quality assessment for muscle tissue of native livestock in Jeju Island.**
J-E. Park*[1], S. Lee[1], N. Kim[1,2], Y. Ryu[1], and I. Cho[2], [1]*Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, Jeju-si, Jeju-do, Republic of Korea*, [2]*Subtropical Livestock Research Center, National Institute of Animal Science, RDA, Jeju-si, Jeju-do, Republic of Korea*.

P224 **Comparative genomic analysis of the T2T genomes of nine chicken breeds.**
Yapeng Zhang*, Lu Bai, Xinting Yang, Jie Wen, Ranran Liu, and Guiping Zhao, *State Key Laboratory of Animal Nutrition; Key Laboratory of Animal (Poultry) Genetics Breeding and Reproduction, Ministry of Agriculture, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*.

P225 **ISAG Bursary Award: Chromosomal divergences between the small red brocket deer *Mazama rufa toba* (Lonnberg, 1919) and *Mazama rufa* (Illiger, 1815): Evidence for a potentially valid species of Neotropical deer.**
Eluzai Dinai Pinto Sandoval*[1], Agda Maria Bernegossi[1], Miluse Vozdova[2], Halina Cernohorska[2], Svatava Kubickova[2], Juan Pablo Juliá[3], and José Mauricio Barbanti Duarte[1], [1]*Deer Research and Conservation Center (NUPECCE), School of Agricultural and Veterinarian Sciences. São Paulo State University (UNESP), Jaboticabal, São Paulo, Brazil*, [2]*Veterinary Research Institute, Brno, Czech Republic*, [3]*Facultad de Ciencias Naturales. Universidad Nacional de Tucumán, Argentina*.

P226 **Cross-species transcriptomic profiling of milk somatic cells using single-cell RNA sequencing.**
Minja Zorc*[1], Mateja Dolinar[1], Jurica Levatic[2], Sašo Džeroski[2], and Peter Dovc[1], [1]*University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Ljubljana, Slovenia, Slovenia*, [2]*Jožef Stefan Institute, Department of Knowledge Technologies, Ljubljana, Slovenia, Slovenia*.

P227 **The MIDAS Project: Are mitonuclear genomic interactions hidden drivers of adaptation and selection in animal species?**
E. Petretto[1], J. K. Layos[1], S. Capomaccio[2], and L. Colli*[1,3], [1]*DIANA Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del S. Cuore, Piacenza, PC, Italy*, [2]*Dipartimento di Medicina Veterinaria, Università di Perugia, Perugia, PG, Italy*, [3]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del S. Cuore, Piacenza, PC, Italy*.

P228 **Sex-specific cardiac transcriptomic differences in camelized mice (Nrapc.255ins78) and their implications for mammalian adaptation.**
S. Y. Lee[1,2], B. Lim[3], B. Y. Lee[4], M. Kim[5], and K. S. Kim*[6], [1]*Macrogen Inc, Seoul, Republic of Korea*, [2]*Seoul National University, Seoul, Republic of Korea*, [3]*Chung-Ang University, Anseong, Republic of Korea*, [4]*University of New Hampshire, Durham, NH, USA*, [5]*Kyungpook National University, Daegu, Republic of Korea*, [6]*Chungbuk National University, Cheongju, Republic of Korea*.

P229 **Gene expression study on marbling fineness profiling by genomic breeding value in Hanwoo cattle.**
P. T. N. Dinh*[1], Y. Chung[2], S. Maeng[3], H. Oh[1], S. Ko[1], J. H. Kim[3], and S. H. Lee[3], [1]*Department of Bio-AI Convergence, Chungnam National University, Daejeon, Republic of Korea*, [2]*Institute of Agricultural Science, Chungnam National University, Daejeon, Republic of Korea*, [3]*Division of Animal & Dairy Science, Chungnam National University, Daejeon, Republic of Korea*.

P230 **Genomic selection signatures In selected South African beef cattle reveal candidate genes related to body conformation, reproduction, and meat quality.**
Mamokoma Modiba*, Bohani Mtileni, and Khathutshelo Nephawe, *Tshwane University Of Technology, Pretoria, Gauteng, South Africa*.

P231 **A wolf is not a dog—Man's best friends interactome.**
D. Schwochow*[1], C. Kálmán[2], R. Carlsson Norlin[1], S. Dasgupta[1], A. Karadagi[3], E. Ellis[3], K. Enikö[2], P. Savolainen[1], and P. Sahlén[1], [1]*KTH Royal Institute of Technology, Science for Life Laboratory, School of Engineering Sciences in Chemistry, Biotechnology and Health, Division of Gene Technology*, *Solna, Sweden*, [2]*Eötvös Loránd University, Department of Ethology*, *Budapest, Hungary*, [3]*Karolinska Institutet/ME Transplantation, Karolinska University Hospital, 3Department of Clinical Science, Intervention and Technology, (CLINTEC), Division of Transplantation Surgery*, *Huddinge, Sweden*.

P232 **Chromatin activation direct asymmetrical gonadal development in female but not male chickens.**
Z. L. Peng*, Y. Q. Jiang, Y. L. Liao, X. Y. Li, and H. Wang, *Huazhong Agricultural University*, *Wuhan, Hubei, China*.

P233 **Identification of goat molQTL based on large-scale transcriptome data.**
Min Tian[1], Meiwen Song[1], Zhen Zhang[1], Yifan Li[1], Xueqing Han[1], Jun Luo[1], Lingzhao Fang[2], and Cong Li*[1], [1]*College of Animal Science and Technology, Northwest A&F University*, *Yangling, Shaanxi, China*, [2]*Center for Quantitative Genetics and Genomics, Aarhus University*, *Aarhus, Denmark*.

P234 **Deep learning deciphers the regulatory grammar of transcription initiation in non-model immune cells.**
C. Zhu*, R. Owen, T. Connelley, L. Morrison, M. Hassan, D. Macqueen, R. Zhao, and J. Prendergast, *Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh*, *Edinburgh, Scotland, UK*.

P235 **European Network on Livestock Phenomics: An international initiative to enhance genome to phenome integration in all livestock species for applications in animal breeding.**
Luca Fontanesi*[1], Tomas Norton[2], and EU-LI-PHE Consortium1[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna*, *Bologna, Italy*, [2]*M3-BIORES Research Group, Division of Animal and Human Health Engineering, De-partment of Biosystems, KU Leuven*, *Leuven, Belgium*.

P236 **Cross-species integration of single-cell RNA sequencing reveals conserved mechanisms in bovine and ovine placentation.**
M. L. Leavitt[1], W. C. Warren[2,3], T. E. Spencer[2,4], and K. M. Davenport*[1], [1]*Department of Animal Sciences, Washington State University*, *Pullman, WA, USA*, [2]*Division of Animal Sciences, University of Missouri*, *Columbia, MO, USA*, [3]*Institute for Data Science and Informatics, University of Missouri*, *Columbia, MO, USA*, [4]*Department of Obstetrics, Gynecology, and Women's Health, University of Missouri*, *Columbia, MO, USA*.

P237 **Decoding the bovine regulatory landscape: Genome-wide high-resolution mapping of regulatory elements in cattle.**
R. Zhao*[1], R. Owen[1], L. Pagie[2], M. Marr[1], K. Jensen[1], V. Bisht[2], T. Connelley[1], L. Morrison[1], J. van Arensbergen[2], M. Hassan[1], and J. Prendergast[1], [1]*Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh*, *Edinburgh, United Kingdom*, [2]*Annogen B.V., Science Park 406, 1098XH*, *Amsterdam, the Netherlands*.

P238 **Comparison of pig, human, and mouse transcriptomes: Implications for complex traits and disease modeling.**
Jingwen Dou*[1], Xin Huang[1], Jingjin Li[1], Hong Liu[1], Yong Liao[1], Yue Wang[1], Jingya Xu[1], Zhengshuang Tang[1], Xinyun Li[1,2], Shuhong Zhao[1,2], Xiaolei Liu[1,2], and Yuhua Fu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University*, *Wuhan, Hubei 430070, PR China;*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production*, *Wuhan, Hubei 430070, PR China*, [3]*Hubei Hongshan Laboratory*, *Wuhan, Hubei 430070, PR China*.

P239 **ISAG Bursary Award: RNA-editing, a potential mechanism to influence gene expression, is regulated by genomic variation in *Bos taurus* and *Bos indicus* cattle.**
M. S. Tahir*[1], M. Goddard[1,4], B. Hayes[2], C. Van der Jagt[1], R. Xiang[1], B. Mason[1], M. Forutan[2], E. Ross[2], L. T. Nguyen[2], I. van den Berg[1], S. Meier[3], C. Phyn[3], C. Burke[3], and A. Chamberlain[1,5], [1]*AgriBio Center, Agriculture Victoria Research*, *Bundoora, Victoria, Australia*, [2]*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland*, *St Lucia, Queensland, Australia*, [3]*DairyNZ*, *Newstead, Hamilton, New Zealand*, [4]*University of Melbourne*, *Parkville, Victoria, Australia*, [5]*School of Applied Systems Biology, La Trobe University*, *Bundoora, Victoria, Australia*.

P240 **A comprehensive miRNA resource for livestock genomics.**
K. Pokharel*[1], A. J. Amaral[2], B. Liang[3], C. Anthon[3], G. Corsi[3], S. Marthey[4], A. Hoffman[5], J. Lagnel[6], F. Haack[7], O. Palasca[3], S. Seemann[3], L. T. Gama[2], M. A. M. Groenen[8], J. Kantanen[1], R. P. M. A. Crooijmans[8], [1]*Natural Resources Institute Finland (Luke)*, *Jokioinen, Finland*, [2]*Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon*, *Lisbon, Portugal*, [3]*Center for Noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen*, *Frederiksberg C, Denmark*, [4]*GABI, AgroParisTech, INRA, Université Paris Saclay*, *Jouy-en-Josas, France*, [5]*Bioinformatics Group, Department of Computer Science, University of Leipzig*, *Leipzig, Germany*, [6]*INRA PACA*, *Montfavet Cedex, France*, [7]*Leibniz Institute for Farm Animal Biology*, *Dummerstorf, Germany*, [8]*Wageningen University & Research*, *Wageningen, the Netherlands*, [9]*Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University*, *College Station, TX, USA*, [10]*Veterinary Science Department, Martin-Gatton College of Agriculture, Food, and Environment*, *Lexington, KY, USA*.

Horse Genetics and Genomics

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P316 **Potential of circulating microRNAs as biomarkers in horses.**
M. Kikuchi*[1,2], K. Kizaki[2], T. Ishiguro-Oonuma[2], H. Murase[3], K. Urata[3], T. Ishige[1], T. Tozaki[1], and H. Kakoi[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [2]*Graduate School of Veterinary Sciences, Iwate University, Morioka, Iwate, Japan*, [3]*Equine Science Division, Hidaka Training and Research Center, Urakawa, Hokkaido, Japan*.

P317 **Detection using chamber digital PCR with a DNA extraction-free method for gene doping control.**
R. Furukawa*[1], T. Tozaki[1], K. Kawate[1], M. Kikuchi[1], T. Ishige[1], Y. Takahashi[2], E. Fukui[3], and H. Kakoi[1], [1]*Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [2]*Equine Research Institute, Japan Racing Association, Shimotsuke, Tochigi, Japan*, [3]*Utsunomiya University, Utsunomiya, Tochigi, Japan*.

P318 **Genomic and pedigree-based inbreeding analysis in the Taishu horse.**
Tomoko Yoshihara*[1], Taichiro Ishige[2], Koki Kawate[2], Mio Kikuchi[2], Risako Furukawa[2], Teruaki Tozaki[2], Hironaga Kakoi[2], and Seiji Hobo[1], [1]*Joint Graduate School of Veterinary Medicine, Kagoshima University, Kagoshima, Japan*, [2]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*.

P319 **The effect of the LCORL gene on the body conformation of the Kazakh Mughaljar horse breed.**
R. B. Uskenov[1], K. Zh. Iskhan[2], S. K. Bostanova[1], K. Nurgulsim*[1], A. K. Smakova[1], and A. Zhumalin[1], [1]*S. Seifulin Kazakh Agrotechnical Research University, Republic of Kazakhstan, Astana*, [2]*Kazakh National Agrarian University, Republic of Kazakhstan, Almaty*.

P320 **A comprehensive database of genetic variants in Arabian horse genome of various origins.**
T. Szmatola[1,2], T. Zabek*[2], M. Stefaniuk-Szmukier[2], S. Almarzook[3], K. Ropka-Molik[2], A. Gurgul[1], I. Jasielczuk[1], E. Norton[4], and C. J. Finno[5], [1]*Department of Basic Sciences, Faculty of Veterinary Medicine, University of Agriculture, Krakow, Poland*, [2]*Department of Animal Molecular Biology, National Research Institute of Animal Production, Balice, Poland*, [3]*Faculty of Applied Sciences, University of Applied Sciences Europe, Berlin, Germany*, [4]*Department of Animal and Comparative Biomedical Sciences, University of Arizona, Tuscon, AZ, USA*, [5]*Department of Population Health and Reproduction, University of California, Davis School of Veterinary Medicine, Davis, CA, USA*.

P321 **Simulation of genome-wide exonic variants in equine genomes determines agreement of variant annotation and theoretical deleterious variant burden.**
J. L. Marlowe*[1], L. Hughes[2], M. E. McCue[2], and S. A. Durward-Akhurst[1], [1]*University of Minnesota, Department of Veterinary Clinical Sciences, St. Paul, MN, USA*, [2]*University of Minnesota, Department of Veterinary Population Medicine, St. Paul, MN, USA*.

P322 **Transcriptome-wide association studies for performance traits in Thoroughbred horses identify functionally relevant genes for exercise.**
M. Feng*[1], T. J. Hall[1], J. Francis O. Grady[1], D. E. MacHugh[1,2], L. M. Katz[3], and E. W. Hill[1,4], [1]*UCD School of Agriculture and Food Science, Belfield, Dublin, D04 V1W8, Ireland*, [2]*UCD Conway Institute of Biomolecular and Biomedical Research, Belfield, Dublin, D04 V1W8, Ireland*, [3]*UCD School of Veterinary Medicine, Belfield, Dublin, D04 V1W8, Ireland*, [4]*Zinto Labs Ltd, The Highline, Pottery Rd, Dun Laoghaire, Co. Dublin, Ireland*.

P323 **Analysis of expression characteristics of exercise-related transcripts in Jeju horses.**
Jae-Young Choi*, Hyeonah Kim, Yong-Jun Kang, In-Cheol Cho, and Nam-Young Kim, *Subtropical Livestock Research Center, National Institute of Animal Science, Sallokbuk-ro, Jeju-si, Jeju-do, Republic of Korea*.

P324 **Comparative gene expression of equine iMSCs and BM-MSCs: Profiling their immune properties in vitro.**
B. Serrano[1], E. Bernad[1], A. Cequier[1,2], F. J. Vazquez[1,2], A. Romero[1,2], A. Vitoria[1,2], P. Zaragoza[1], L. Barrachina[1,2], and C. Rodellar*[1], [1]*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza); Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA); Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

P325 **Unravelling the epigenetic and transcriptomic interplay of exercise and maternal care in Thoroughbred horses.**
T. Hall*[1], M. Fiang[1], A. Moss[2], A. Byrne[2], J. Browne[1], L. Katz[2], and E. Hill[1,3], [1]*UCD Animal Genomics Laboratory, UCD School of Agriculture and Food Science, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [2]*UCD School of Veterinary Medicine, UCD College of Health and Agricultural Sciences, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland*, [3]*Zinto Labs Ltd, Dun Laoghaire, Co. Dublin, Ireland*.

P326 **Identifying candidate genes associated with equine xylazine metabolism.**
E. Bacon*[1], C. Donnelly[2,3], B. Haase[4], H. Knych[5], C. Finno[2], and B. Velie[1], [1]*Equine Genetics and Genomics Group, School of Life and Environmental Sciences, University of Sydney, Sydney, NSW, Australia*, [2]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, CA, USA*, [3]*Department of Clinical Sciences, College of Veterinary Medicine, Cornell University, Ithica, NY, USA*, [4]*Sydney School of Veterinary Science, University of Sydney, Sydney, NSW, Australia*, [5]*5Pharmacology and Toxicology Graduate Group, Environmental Toxicology, University of California, Davis, CA, USA*.

P327 **The revolution in PRE horse genomics: New Axiom EQUIGENE medium-density array.**
P. J. Azor*[1], A. Molina[2], A. Rodríguez Sainz de los Terreros[1], N. Laseca[1,3], S. Demyda-Peyras[2], A. Gil[1], C. Ziadi[2], D. I. Perdomo-González[4], A. Encina[1], G. Anaya[2], I. González[1], J. Poyato[1], C. Medina[2], M. Ripollés-Lobo[3], M. Valera[3], [1]*Royal Purebred Spanish Horse Breeders' Association (ANCCE), Seville, Spain*, [2]*Department of Genetics, University of Cordoba, Cordoba, Spain*, [3]*Department of Agronomy, School of Agricultural Engineering, University of Seville, Seville, Spain*, [4]*Complutense University of Madrid, Madrid, Spain*.

P328 **Bioinformatic analysis of Bosnian Mountain Horse genome.**
Peter Dovc*[1], Marko Cotman[2], Matjaz Mesaric[2], and Minja Zorc[1], [1]*University of Ljubljana, Biotechnical Faculty, Ljubljana, Slovenia*, [2]*University of Ljubljana, Veterinary Faculty, Ljubljana, Slovenia*.

P329 **ISAG Bursary Award: Moving towards personalized pangenomic veterinary medicine in equids.**
S. C. Stroupe*[1], J. N. Cullen[2], S. A. Durward-Akhurst[3], M. Paini[4], M. Delledonne[4], J. L. Petersen[5], T. Kalbfleisch[6], M. E. McCue[2], and B. W. Davis[1], [1]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, USA*, [2]*Department of Veterinary Population Medicine, University of Minnesota, Minneapolis, Minnesota, USA*, [3]*Department of Veterinary Clinical Sciences, University of Minnesota, St. Paul, Minnesota, USA*, [4]*Department of Biotechnology, University of Verona, Verona, Italy*, [5]*Institute of Agriculture and Natural Resources, University of Nebraska–Lincoln, Lincoln, Nebraska, USA*, [6]*Department of Veterinary Science, Martin Gatton-College of Agriculture, Food and Environment, University of Kentucky, Lexington, Kentucky, USA*.

P330 **Ancient inbreeding and selection signatures revealed by runs of homozygosity in Kazakh horse populations.**
K. Dossybayev*[1,3], A. Kozhakhmet[2,3], T. Kapassuly[1,2], Z. Kozhanov[1,4], U. Akhmetov[1,4], K. Yergali[1,3], A. Torekhanov[1,4], and B. Bekmanov[1,2], [1]*Kazakh Research Institute of Livestock and Fodder Production, Almaty, Kazakhstan*, [2]*Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan*, [3]*Laboratory of Genetics and Cytogenetics, Institute of Genetics and Physiology, Almaty, Kazakhstan*, [4]*Faculty of Veterinary Medicine and Zooengineering, Kazakh National Agrarian Research University, Almaty, Kazakhstan*.

P331 **Genetic structure and breed composition of the modern Criollo horse.**
F. Azcona[1,2], A. Karlau[1,2], A. Molina[3], P. Trigo[1,2], and S. Demyda Peyrás*[3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*CONICET, La Plata, Buenos Aires, Argentina*, [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, España*.

P332 **Origin of the Criollo Argentino horse through SNP-based genomic characterization.**
A. Karlau[1,2], F. Azcona[1,2], A. Molina[3], P. Trigo[1,2], and S. Demyda Peyrás*[3], [1]*Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET), La Plata, Buenos Aires, Argentina*, [2]*Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [3]*Departamento de Genética, Universidad de Córdoba, Córdoba, España*.

P333 **Boosting the accuracy of genetic evaluations for dressage aptitude in young Pura Raza Española horses using genomic information.**
Chiraz Ziadi[1], Mercedes Valera[2], Sebastián Demyda-Peyrás*[1], Davinia Perdomo-Gonzalez[3], Nora Laseca[2], Juan Pablo Sanchez[1], Ana Encima[4], Pedro Azor[4], and Antonio Molina[1], [1]*Department of Genetics, Veterinary School, University of Córdoba, Spain*, [2]*Department of Agronomy, ETSIA, University of Sevilla, Spain*, [3]*Department of Animal Production, Complutense University of Madrid, Spain*, [4]*Royal National Association of Spanish Horse Breeders, Sevilla, Spain*.

P334 **mtDNA variability in SNCT produced cloned horses: Are they so identical genomically?**
Ayelén Karlau[1], Gabriel Anaya[1], Pablo Trigo[2], Florencia Azcona[2], Maria Yuzhi Arjona[1], Juan Pablo Sanchez Serrano[1], Antonio Molina[1], and Sebastián Demyda Peyrás*[1], [1]*Department of Genetics, Veterinary School, University of Córdoba, Spain*, [2]*Veterinary School, National University of La Plata, La Plata, Buenos Aires, Argentina*.

P335 **ISAG Bursary Award: Structural variation and breed evolution in the equine pangenome.**
J. N. Cullen*[1], S. Stroupe[2], S. A. Durward-Akhurst[1], M. Paini[3], M. Delledonne[3], J. L. Petersen[4], T. Kalbfleisch[5], B. W. Davis[2], and M. E. McCue[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, Minneapolis, MN, USA*, [2]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, USA*, [3]*Department of Biotechnology, University of Verona, Verona, Italy*, [4]*Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln, Lincoln, Nebraska, USA*, [5]*Department of Veterinary Science, Martin Gatton-College of Agriculture, Food and Environment, University of Kentucky, Lexington, KY, USA*.

P336 **Changing references: How breed-specific genomes impact measures of diversity in the horse.**
J. L. Petersen*[1], J. Ciosek[2], K. Li[2], N. P. Balasubramaniam[1,2], E. Bailey[2], and T. Kalbfleisch[2], [1]*University of Nebraska-Lincoln*, *Lincoln, NE, USA*, [2]*University of Kentucky*, *Lexington, KY, USA*.

P337 **ISAG Bursary Award: Galloping towards an equid pangenome.**
J. L. Ciosek*[1], L. C. Johnson[1], K. Li[1], E. D. Robyn[1], N. Hussien AbouEl Ela[1], N. Subramaniam[1], J. Cullen[2], S. Stroupe[3], J. L. Petersen[4], S. A. Durward-Akhurst[2], M. E. McCue[2], B. W. Davis[3], and T. S. Kalbfleisch[1], [1]*University of Kentucky*, *Lexington, KY, USA*, [2]*University of Minnesota*, *St. Paul, MN, USA*, [3]*Texas A&M University*, *College Station, TX, USA*, [4]*University of Nebraska–Lincoln*, *Lincoln, NE, USA*.

P338 **A combination of spectrophotometric and genotypic data with a machine learning approach as a potential tool for effective prediction of coat colour in horses.**
Jelena Kotišcak*[1], Minja Zorc[2], Matjaž Mesaric[3], and Marko Cotman[1], [1]*University of Ljubljana, Veterinary Faculty, Institute for Preclinical Sciences*, *Ljubljana, Slovenia*, [2]*University of Ljubljana, Biotechnical Faculty, Department of Animal Science*, *Ljubljana, Slovenia*, [3]*University of Ljubljana, Veterinary Faculty, Clinic for Reproduction and Large Animals*, *Ljubljana, Slovenia*.

P339 **A telomere-to-telomere assembly unlocks the unique genomic landscape of the Mongolian horse for precision breeding.**
Y. Wang*[1,2], J. Liu[1], Y. Zhao[2], Z. Tang[1], T. Bou[2], H. Liu[1], W. Ding[2], J. Dou[1], S. Zhu[1], L. Yin[1], X. Liu[1,3], M. Yu[1], Y. Fu[1,3], and D. Bai[2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University*, *Wuhan, Hubei, PR China*, [2]*Key Laboratory of Equus Germplasm Innovation (Co-construction by Ministry and Province), Ministry of Agriculture and Rural Affairs. Equus Research Center of Inner Mongolia Agricultural University*, *Hohhot, China*, [3]*Hubei Hongshan Laboratory*, *Wuhan, Hubei, PR China*.

P340 **ISAG Bursary Award: A telomere-to-telomere assembly of the horse Y chromosome reveals its complete repeat structure.**
K. Li[1], J. L. Ciosek[1], E. D. Robyn*[1], N. Hussien AbouEl Ela[1], L. C. Johnson[1], J. N. Cullen[2], S. C. Stroupe[3], S. A. Durward-Akhurst[2], M. E. McCue[2], B. W. Davis[3], S. C. Loux[4], J. L. Petersen[5], T. S. Kalbfleisch[1], and T. Raudsepp[3], [1]*University of Kentucky*, *Lexington, KY, USA*, [2]*University of Minnesota*, *St. Paul, MN, USA*, [3]*Texas A&M University*, *College Station, TX, USA*, [4]*Louisiana State University*, *Baton Rouge, LA, USA*, [5]*University of Nebraska–Lincoln*, *Lincoln, NE, USA*.

P341 **Further insight into the genetics behind hypermobility in horses.**
M. Ablondi[1,2], Å Gelinder-Viklund[2], S. Eriksson[2], and S. Mikko*[2], [1]*Parma University*, *Parma, Italy*, [2]*Swedish University of Agricultural Sciences*, *Uppsala, Sweden*.

P342 ***LMF1* frameshift deletion in Franches-Montagnes horses with hypertriglyceridemia-induced pancreatitis.**
M. Drögemüller[1], N. Fouché[2], M. Wyler[2], C. Gurtner[3], S. L. Meister[3], M. Neuditschko[4], V. Jagannathan[1], V. Gerber[2], and T. Leeb*[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern*, *3001 Bern, Switzerland*, [2]*Swiss Institute of Equine Medicine, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern*, *3001 Bern, Switzerland*, [3]*Institute of Animal Pathology, Vetsuisse Faculty, University of Bern*, *3001 Bern, Switzerland*, [4]*Animal GenoPhenomics, Agroscope*, *1725 Posieux, Switzerland*.

P343 **Germline mutations identified by whole-genome sequencing in Thoroughbreds.**
Teruaki Tozaki*[1], Risako Furukawa[1], Koki Kawate[1], Mio Kikuchi[1], Taichiro Ishige[1], Yukihide Momozawa[2], and Hironaga Kakoi[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry*, *Utsunomiya, Tochigi, Japan*, [2]*Laboratory for Genotyping Development, RIKEN Center for Integrative Medical Sciences*, *Yokohama, Kanagawa, Japan*.

Microbiomes

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P396 **Rumen microbiota for cattle performance and greenhouse gas mitigation across the world.**
A. Ayemele Gnetegha* and H. Jianlin, *Yazhouwan National Laboratory*, *Sanya, Hainan, China*.

P397 **Effects of insect meal as a substitute for zinc bacitracin for microbiome modulation, hematology, and performance in broiler chicks at the starter phase.**
E. Malematja*, S. D. Kolobe, N. A. Sebola, and M. Mabelebele, *University of South Africa*, *Johannesburg, South Africa*.

P398 **Microbiome-metabolome interactions under prolonged social stress in a porcine model.**
R. Río-López*[1], I. T. Voularki[2], A. Clavell-Sansalvador[2], A. Valdés[3], L. Padilla[1], J. García-Gil[4], X. Xifró[5], F. X. Prenafeta-Boldú[6], M. Ballester[2], R. Quintanilla[2], A. Dalmau[1], and Y. Ramayo-Caldas[2], [1]*Animal Welfare Program, Institute of Agrifood Research and Technology (IRTA), Monells, Girona, Spain*, [2]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*, [3]*Department of Bioactivity and Food Analysis, Food Science Research Institute (CIAL) and Spanish National Research Council (CSIC), Madrid, Madrid, Spain*, [4]*Digestive Diseases and Microbiota Group, Biomedical Research Institute of Girona (IDIBGI), Girona, Girona, Spain*, [5]*New Therapeutic Targets Laboratory Research Group, Medical Sciences Department, Faculty of Medicine, University of Girona (UdG), Girona, Girona, Spain*, [6]*Sustainability in Biosystems, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*.

P399 **Genomic insights into the probiotic potential of *Bifidobacterium thermophilum* and *Lactobacillus acidophilus*.**
S. Mani*, *Agricultural Research Council–Animal Production, Irene, Gauteng, South Africa*.

P400 **Rumen microbiome profiling of indigenous goats in the North West and Limpopo for optimal health and production.**
S. Mani*, *Agricultural Research Council–Animal Production, Irene, Gauteng, South Africa*.

P401 **Gut-liver metabolic synergy mediated by *Enterococcus* and *Streptococcus* improves heat tolerance in chickens via energy homeostasis regulation.**
Haobo Zhou*, Bin Zheng, Chenglong Wang, Yanzhang Gong, and Zheya Sheng, *College of Animal Science and Technology and College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, Hubei, China*.

P402 **Synergistic dynamics of antimicrobial resistance and virulence in indigenous chicken microbiomes across Gauteng, Limpopo, and KwaZulu-Natal, South Africa.**
M. Nene*[1], N. Molete[1], T. Mthembu[1], A. Rotimi[2], R. Pierneef[3], and K. Hadebe[1], [1]*Agricultural Research Council–Biotechnology Platform, Ondestepoort, South Africa*, [2]*Inqaba Biotechnical Industries, Muckleneuk, Pretoria, South Africa*, [3]*Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa*.

P403 **The diversity of the gastrointestinal tract microbiome is associated with body weight in Hanwoo cattle.**
S.-W. Woo*[1,2], S. J. Kim[1,2], M. Kim[2], J. Kim[1,2], and W. Park[3], [1]*Division of Applied Life Science (BK21), Gyeongsang National University, Jinju, Republic of Korea*, [2]*Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea*, [3]*Animal Genetics & Breeding Division, National Institute of Animal Science, RDA, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P404 **Exploring the influence of fecal microbiota transfer from a chronic stress porcine model on axenic mice.**
A. Clavell-Sansalvador*[1], R. Martín-Rosique[2], S. Chadi[2], R. Río-López[3], J. García-Gil[4], X. Xifró[5], and Y. Ramayo-Caldas[1], [1]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*, [2]*INRAE, AgroParisTech, Micalis Institut, Jouy-en-Josas, Île-de-France, France*, [3]*Animal Welfare Subprogram, Institute of Agrifood Research and Technology (IRTA), Monells, Girona, Spain*, [4]*Digestive diseases and microbiota group. Biomedical Research Institute of Girona (IDIBGI), Salt, Girona, Spain*, [5]*New Therapeutic Targets Group, Department of Medical Science, Faculty of Medicine, Universitat de Girona, Girona, Girona, Spain*.

P405 **Comparative analysis of the gut microbiome in broilers exposed to high temperatures under different wind conditions.**
M. M. Hossain*[1], S. Lee[1], Y. Park[1], Y. Ko[1], W. Park[2], H. Kim[3], and J-E. Park[1], [1]*Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, Jeju-si, Jeju-do, Republic of Korea*, [2]*Animal Biotechnology and Genomics Division, National Institute of Animal Science, Rural Development of Administration, Wanju-gun, Jeollabuk-do, Republic of Korea*, [3]*Precision Animal Nutrition Division, National Institute of Animal Science, Rural Development of Administration, Wanju-gun, Jeollabuk-do, Republic of Korea*.

P406 **Genomic and functional analysis of *Lactiplantibacillus plantarum* EG037 for enhanced antimicrobial applications.**
J. Kim*, J.S. Lim, and H. Kim, *Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*.

P407 **Metagenomics analysis of Boschveld chickens fed sorghum-based diets.**
N. Nemukondeni*[1], C. A. Mbajiorgu[2], K. A. Nephawe[1], T. Mafuna[3], and M. Mabelebele[2], [1]*Tshwane University of Technology, Pretoria, South Africa*, [2]*University of South Africa, Florida, South Africa*, [3]*University of Johannesburg, Auckland Park, South Africa*.

P408 **Identification of lactic acid bacteria strains from traditional fermented foods with cognitive-enhancing properties in animals.**
J. S. Lim*, J. Kim, and H. Kim, *Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*.

P409 **Long-read sequencing of the 16S-23S rRNA operon reveals microbiome diversity in Dokdo shrimp.**
S. Y. Jhang*[1], B. Koh[2,3], C. E. Lim[4], Y. Hong[4], and H. Kim[1,2], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [2]*Department of Agricultural Biotechnology, Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*, [3]*eGnome Inc, Seoul, Republic of Korea*, [4]*Climate Change and Environmental Biology Research Division, National Institute of Biological Resources, Incheon, Republic of Korea*.

P410 **Integrative analysis between the gene expression of liver and fecal microbiota profile reveals hub genes in response to different diets.**
C. Oliveira[1], S. Fanalli[1], T. dos Santos[1], A. Felício-Ament[1], B. Silva-Vignato[1], L. Brito[2], V. de Almeida[3], and A. Cesar*[1], [1]*University of São Paulo, Piracicaba, São Paulo, Brazil*, [2]*Purdue University, West Lafayette, IN, USA*, [3]*Federal University of Goiás, Goiânia, Goiás, Brazil*.

P411 **Microbiomes and holobionts as genetic resources for agroecology.**
Gwendal Restoux[1], Jordi Estellé[1], Catherine Larzul[2], Paul Cotter[3], Nichole Ginnan[4], Kelly Eversole[5], and Claire Rogel-Gaillard*[1], [1]*Université Paris Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [3]*Teagasc Food Research Centre, APC Microbiome Ireland, VistaMilk, Ireland*, [4]*One Health Microbiome Center, Huck Institute of the Life Sciences, Pennsylvania State University, University Park, PA, USA*, [5]*Animal Microbiome Working Group, International Alliance for Phytobiomes Research, Eau Claire, WI, USA*.

P412 **HolomiRA: Insights into the regulatory influence of host-derived miRNAs on human and bovine gut microbiota.**
T. F. Cardoso[1], J. J. Bruscadin[2,1], L. C. Conteville[1], J. V. da Silva[2,1], A. M. G. Ibelli[1], G. A. C. Pena[1], T. Porto[2,1], P. S. N. de Oliveira[2,1], B. G. N. Andrade[3], A. Zerlotini[4], and L. C. de A. Regitano*[1], [1]*Embrapa Southeastern Livestock, São Carlos, São Paulo, Brazil*, [2]*Center of Biological and Health Sciences–Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [3]*Munster Technological University, Bishopstown, Cork, Ireland*, [4]*Embrapa Digital Agriculture, Campinas, São Paulo, Brazil*.

P413 **Sustained response after four generations of selection for porcine fecal microbiota composition.**
C. Larzul[1], F. Blanc[2], G. Lemonnier[2], D. Jardet[2], M. N. Rossignol[2], C. Niort[3], C. Rogel-Gaillard[2], and J. Estellé*[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*.

P414 **Differential response to an *in vivo* infectious challenge in pigs genetically selected for contrasting enterotypes.**
A. Ucero-Carretón[1], H. Argüello[1], G. Lemonnier[2], A. Carvajal[1], C. Niort[3], C. Rogel-Gaillard[2], C. Larzul[4], F. Blanc[2], and J. Estellé*[2], [1]*Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, León, Spain*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*INRAE, GenESI, Surgères, France*, [4]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*.

P415 **The gut microbiome influences the porcine hepatosomatic index by regulating hepatic lipid metabolism.**
P. Zhou*[1], J. Yuan[1], Y. Wang[1], T. Wang[1], Z. Liu[1], M. Fu[1], X. Zhou[1,2], and B. Liu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Wuhan, China*.

P416 **Investigating correlations of poultry SCFAs in duodenum, cecum, liver and serum with cecum microbiota and feed efficiency traits.**
Zhengxiao He*[1,2], Alan Fahey[2], Jie Wen[1], Ranran Liu[1], and Guiping Zhao[1], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*.

P417 **Influence of the leptin receptor gene on the gut microbiota in pigs.**
R. Suárez-Mesa[1,2], H. Laghouaouta[1,2], R. Ros-Freixedes[1,2], R. N. Pena[1,2], and J. Estany*[1,2], [1]*University of Lleida, Lleida, Spain*, [2]*Agrotecnio-CERCA Center, Lleida, Spain*.

P418 **Impact of host inbreeding on vaginal microbiota diversity and pregnancy rate in sheep.**
E. L. Reinoso-Peláez[1,2], M. Serrano[1], A. Fernández[1], B. Villanueva[1], and M. Saura*[3], [1]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA-CSIC), Madrid, Spain*, [2]*Universidad Politécnica de Madrid (UPM), Madrid, Spain*, [3]*Instituto de Investigacións Mariñas (IIM-CSIC), Vigo, Spain*.

P419 **Effects of multigenerational early-life metabolic disruption in the intestinal microbiome of mouse.**
V. de Anca Prado*[1], J. C. Jiménez-Chillarón[2], M. Gódia Perello[3], and C. Guerrero Bosagna[1], [1]*Uppsala University, Uppsala, Uppsala, Sweden*, [2]*University of Barcelona, Barcelona, Catalunya, Spain*, [3]*Wageningen University and Research, Wageningen, the Netherlands*.

P420 **A comprehensive view of the rumen microbiome and virome to accelerate reduction of enteric methane production through selective breeding.**
O. González-Recio*[1], C. N. Marcos[2], B. J. Sepulveda[3], M. Gutierrez-Rivas[1], J. E. Pryce[3], and A. J. Chamberlain[3], [1]*INIA-CSIC, Madrid, Spain*, [2]*Facultad de Veterinaria. Universidad Complutense de Madrid, Madrid, Spain*, [3]*Agriculture Victoria Research, AgriBio, Centre for AgriBioscience*, *Victoria, Australia*.

P421 **Microbiome as boosters of the genetic potential of beef cattle.**
P. A. Alexandre*[1], A. Wilson[2], T. P. R. A. Legrand[1], R. J. Farr[2], S. E. Denman[1], and A. Reverter[1], [1]*CSIRO Agriculture & Food*, *St. Lucia, Queensland, Australia*, [2]*CSIRO Health & Biosecurity*, *Geelong, Victoria, Australia*.

P422 **Metagenomes, methylation, and methane: Using quantitative microbiology to tackle livestock emissions.**
E. M. Ross*, L. T. Nguyen, Z. Chen, Y. Li, and C. T. Ong, *University of Queensland, Queensland Alliance for Agriculture and Food Innovation*, *Queensland, Australia*.

P423 **ISAG Bursary Award: Microbial signatures as predictors of fatty acid composition in Iberian pigs.**
L. Azouggagh*[1], C. Casto-Rebollo[1], P. Hernández[1], L. Varona[2], J. Casellas[3], S. Negro[4], and N. Ibáñez-Escriche[1], [1]*Instituto de Ciencia y Tecnología Animal. Universitat Politècnica de Valencia, Valencia, Spain*, [2]*Instituto Agroalimentario de Aragón (IA2). Universidad de Zaragoza*, *Zaragoza, Spain*, [3]*Universitat Autònoma de Barcelona*, *Barcelona, Spain*, [4]*INGA FOOD S.A*, *Almendralejo, Spain*.

P424 **Whole genome-based analysis of stage-specific dynamics of *Prevotella* during piglet weaning.**
Jae-Gwon Kim*, Seona Kwon, Jung-Woo Choi, and Won-Hyong Chung, *Kangwon National University*, *Chuncheon, Kangwon, Republic of Korea*.

Pig Genetics and Genomics II

Exhibition Hall 109 + 110 + 111 + 112
11:30 AM - 12:30 PM

P468 **Genome-wide association study and biological network analysis of hematological traits in Yorkshire pigs using imputed whole-genome sequence variants.**
T. H. Kim*[1], Y. J. Lee[2], M. H. Jeong[1], D. B. Hwang[1], J. M. Kim[3], S. H. Lee[3], C. Gondro[4], and H. B. Park[1], [1]*Kongju National University*, *Yesan, Chungcheongnam-do, Republic of Korea*, [2]*National Institute of Animal Science*, *Cheonan, Chungcheongnam-do, Republic of Korea*, [3]*Chung-Ang University*, *Anseong, Gyeonggi-do, Republic of Korea*, [4]*Michigan State University*, *East Lansing, MI, USA*.

P469 **Association analysis of IGFBP-2 genotypes with reproductive traits in pigs.**
Yong-Jun Kang*, Hyeon-Ah Kim, Sang-Geum Kim, Su-Yeon Kim, Jae-Young Choi, Miyoung Won, Sang-Min Shin, and In-Cheol Cho, *Subtropical Livestock Research Center, National Institute of Animal Science, RDA*, *Jeju-si, Jeju-do, Republic of Korea*.

P470 **Estimation of genetic parameters for intramuscular fat using ultrasound in Woori Heukdon pigs.**
Yeon-Ho Kim*[1], Young-Sin Kim[1], Soo-Hyun Back[1], Sun-young Baek[1], Joon-Ki Hong[1], and Jun-Heon Lee[2], [1]*Swine Science Division, National Institute of Animal Science, Rural Development Administration*, *Cheonan-si, Chungcheongnam-do, Republic of Korea*, [2]*Department of Animal Science, Chungnam National University*, *Daejeon, Republic of Korea*.

P471 **Unraveling gene switches for the regulation of litter size through the study of swine with high and low prolificacy.**
E. Varela Martínez*[1], B. Tadeu-Querido[2,3], F. Teixeira[4,5], G. Ferreira-Dias[2,3], J. Lopes[4], E. Bettencourt[4], P. Valente[2,3], M. S. Gonçalves[2,3], L. Telo da Gama[2,3], C. Bettencourt[6,7], S. Branco[4], S. VanHarten[7], K. Sebastino[2,3], H. Chiaia[2,3], M. C. Bressan[7], [1]*Department of Genetics, Physical Anthropology and Animal Physiology, Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Biscay, Spain*, [2]*CIISA - Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Lisbon District, Portugal*, [3]*Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Lisbon, Lisbon District, Portugal*, [4]*MED–Mediterranean Institute for Agriculture, Environment and Development and CHANGE–Global Change and Sustainability Institute, University of Évora*, *Évora, Évora District, Portugal*, [5]*Faculty of Veterinary Medicine, University José Eduardo dos Santos*, *Huambo, Angola*, [6]*Baixo Alentejo Experimentation Center, Herdade da Abóbada, Vila Nova de São Bento, Portugal*, [7]*Faculty of Veterinarian Medicine, Lusófona University*, *Lisbon, Lisbon District, Portugal*.

P472 **ISAG Bursary Award: Genomic prediction of feed efficiency in boars by deep learning.**
Olumide Onabanjo*[1], Theo Meuwissen[1], Hans Magnus Gjøen[1], Fadi Al Machot[2], and Peer Berg[1], [1]*Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences*, *Ås, Norway*, [2]*Department of Data Science, Norwegian University of Life Sciences*, *Ås, Norway*.

P473 **Development of haplotype maps for a Korean native pig composite breed, Woori-Heukdon, using whole-genome sequences.**
B. Ahn*[1], M. Kang[1], J. Shin[1], J. Sim[1], J. Lee[2], E. Cho[2], W. Park[2], and C. Park[1], [1]*Department of Stem Cell and Regenerative Biotechnology, Konkuk University*, *Seoul, Republic of Korea*, [2]*Animal Genomics and Bioinformatics Division, National Institute of Animal Science*, *Wanju, Republic of Korea*.

P474 **A graph-based variome uncovers the genetic architecture and breeding potential of commercial pigs.**
L. Liu*[1], Y. Qiu[1], S. Deng[1], Y. Liu[1], Z. Yao[1], S. Wang[1], F. Zhou[1], Z. Wu[3], H. Zhang[4], D. Martijn[2], E. Zheng[1], Z. Zhang[1], M. Groenen[2], J. Yang[1], Z. Wu[1], [1]*South China Agricultural University*, *China*, [2]*Wageningen University and Research*, *The Netherlands*, [3]*The University of Edinburgh*, *UK*, [4]*Anhui Medical University*, *China*.

P475 **Genetic parameters and genomic investigation of nitrogen use efficiency and its relationship with performance traits in Swiss Large White pigs under a protein-restricted diet.**
E. O. Ewaoluwagbemiga[1], G. Bee[1], A. Lloret-Villas[2,3], A. Poublan-Couzardot[2], H. Pausch[2], and C. Kasper*[1], [1]*Animal GenoPhenomics, Agroscope*, *Posieux, Switzerland*, [2]*Animal Genomics, Department of Environmental Systems Science, ETH Zurich*, *Zurich, Switzerland*, [3]*Center for Evolution and Medicine, School of Life Sciences, Arizona State University*, *Tempe, AZ, USA*.

P476 **Incorporating genomic and transcriptomic effects in linear and structural models for predicting complex traits in pigs.**
I. T. Vourlaki, M. Ballester, T. Jove, Y. Ramayo-Caldas, and M. Piles*, *IRTA, Institute of Agrifood Research and Technology*, *Barcelona, Spain*.

P477 **A comprehensive graph-based pangenome of Large White pigs.**
J. Y. Chu*, Y. Zhou, B. D. P. Soewandi, W. J. Li, W. J. Dong, M. Han, S. Q. Jin, Y. L. Ma, and S. H. 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*.

P478 **Genome-wide characterization of population structure, genetic diversity, and inbreeding in Korean native pigs.**
Soo-Hyun Back*, Young-Sin Kim, Sun-Young Baek, and Joon-Ki Hong, *Swine Science Division, National Institute of Animal Science, Rural Development Administration*, *Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P479 **High-throughput GWAS for more than 250,000 metabolomic features provides novel insights on the genetic mechanisms influencing pig metabolism.**
M. Bolner*[1], S. Bovo[1], G. Schiavo[1], G. Galimberti[2], F. Bertolini[1], A. Ribani[1], S. Dall'Olio[1], P. Zambonelli[1], M. Gallo[3], and L. Fontanesi[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna*, *Bologna, Italy*, [2]*Department of Statistical Sciences "Paolo Fortunati," University of Bologna*, *Bologna, Italy*, [3]*Associazione Nazionale Allevatori Suini*, *Rome, Italy*.

P480 **Numbers of teats in pigs are affected by non-additive variants.**
C. A. Sevillano*[1], B. Harlizius[1], and M. van Son[2], [1]*Topigs Norsvin Research Center*, *'s-Hertogenbosch, the Netherlands*, [2]*Norsvin SA*, *Hamar, Norway*.

P481 **Construction of *de novo* Japanese wild boar (*Sus scrofa leucomystax*) genome assembly.**
D. Gamarra*[1], K. Naito[2], and M. Taniguchi[1], [1]*Institute of Agrobiological Science, National Agriculture and Food Research Organization*, *Tsukuba, Ibaraki, Japan*, [2]*Research Center of Genetic Resources, National Agriculture and Food Research Organization*, *Tsukuba, Ibaraki, Japan*.

P482 **IFAM: Improving genomic prediction accuracy of complex traits by integrating massive types of functional annotation information.**
Zhenshuang Tang[1,2], Haohao Zhang[3], Dong Yin[2], Yuhua Fu[2], Yunxia Zhao[1,2], Jingjin Li[2], Yuan Quan[4], Xiang Zhou[5,6], Xinyun Li[2], Lilin Yin[2], Shuhong Zhao[1,2], Xiaolei Liu[2], and Jingwen Dou*[1], [1]*Yazhouwan National Laboratory*, *Sanya, PR China*, [2]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, PR China*, [3]*School of Computer Science and Technology, Wuhan University of Technology*, *Wuhan, PR China*, [4]*Hubei Key Laboratory of Agricultural Bioinformatics, College of Informatics, Huazhong Agricultural University*, *Wuhan, PR China*, [5]*Department of Biostatistics, University of Michigan*, *Ann Arbor, MI, USA*, [6]*Center for Statistical Genetics, University of Michigan*, *Ann Arbor, MI, USA*.

P483 **Single-cell multiome analysis of the pig testicle and identification of DNA variants linked to genomic activity and spermatid survival.**
Yu Lian[1], Soeren Lukassen[2], Claudia P. Cabrera[3], Johannes Liebig[2], Craig R. G. Lewis[4], Eduardo Rodriguez-Sierra[4], Armand Sanchez[1,5], Christian Conrad[2], and Alex Clop*[1,6], [1]*Centre for Research in Agricultural Genomics CRAG*, *Cerdanyola del Valles, Catalonia, Spain*, [2]*Berlin Institute of Health at Charité*, *Berlin, Germany*, [3]*Queen Mary University of London*, *London, UK*, [4]*PIC Europe*, *Sant Cugat del Valles, Catalonia, Spain*, [5]*Universitat Autonoma de Barcelona*, *Cerdanyola del Valles, Catalonia, Spain*, [6]*Consejo Superior de Investigaciones Científicas CSIC*, *Barcelona, Catalonia, Spain*.

P484 **Genome-wide association studies for residual feed intake and feed conversion ratio in Canadian pigs.**
B. Kim*[1], D. N. Do[1], M. Jafarikia[2,3], D. Tulpan[3], D. Adewole[4], B. Sullivan[2], J. Holl[5], and Y. Miar[1], [1]*Dalhousie University*, *Truro, NS, Canada*, [2]*Canadian Centre for Swine Improvement*, *Ottawa, ON, Canada*, [3]*University of Guelph*, *Guelph, ON, Canada*, [4]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [5]*Pig Improvement Company*, *Hendersonville, TN, USA*.

P485 **ISAG Bursary Award: Insights into genomic regulation of serum metabolite levels in 3-way cross-bred pigs.**
E. Ibragimov*, J. P. Nielsen, M. K. Morsing, M. P. Rydal, M. Fredholm, and P. Karlskov-Mortensen, *Department of Veterinary and Animal Sciences, University of Copenhagen*, *Frederiksberg, Denmark*.

P486 **Recombination suppression and natural selection against female heterozygotes drive the faster-X evolution in pigs.**
Qing-Long Li[2], Li-Gang Wang[3], Long-Chao Zhang[3], Nalini Hirimuthugoda[4], Hai-Bing Xie*[1], and Ya-Ping Zhang[1], [1]*Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, Yunnan, China*, [2]*State Key Laboratory for Conservation and Utilization of Bio-resource in Yunnan, School of Ecology and Environmental Science, Yunnan University*, *Kunming, Yunnan, China*, [3]*Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [4]*Department of Animal Science, Faculty of Agriculture, University of Ruhuna*, *Matara, Sri Lanka*.

P487 **Tissue-specific responses to dietary lipid levels in pigs revealed by gene co-expression analysis.**
S. L. Fanalli*[1,2], R. P. M. A. Crooijmans[2], I. C. Gervasio[3], J. D. Gomes[3], B. P. M. Silva[3], C. T. Moncau-Gadbem[1], V. V. Almeida[4], and A. S. M. Cesar[1,3], [1]*School of Animal Science and Food Engineering, (FZEA), University of São Paulo*, *Pirassununga, São Paulo, Brazil*, [2]*Wageningen University and Research, Animal Breeding and Genomics*, *Wageningen, Gelderland, the Netherlands*, [3]*Luiz de Queiroz College of Agriculture (ESALQ), University of São Paulo*, *Piracicaba, São Paulo, Brazil*, [4]*Federal University of Goiás*, *Goiânia, Goiás, Brazil*.

OTHER EVENTS

Lunch
Exhibition Hall 109 + 110 + 111 + 112
12:30 PM - 1:30 PM

SYMPOSIA AND ORAL SESSIONS

Animal Genetic Testing Standardization (AGTS)

Chair: **Leslie Lyons, University of Missouri**
Room 105 + 106
1:30 PM - 6:00 PM

Agenda
Animal Genetic Testing Standardization (AGTS) Committee

The Animal Genetic Testing Standardization (AGTS) Committee looks forward to your participation at the ISAG Conference in Daejong, South Korea on Thursday, July 24, 2025 from 13:30 – 18:00 in Rooms 105 - 106. Below is a draft agenda for the workshop, which includes the organization and establishment of goals for each of the four working groups. This committee will be working in tandem with the Online Mendelian Inheritance in Animals resource to present decisions and outcomes of the four working groups. The committee will also interact with the World Small Animal Veterinary Association's Hereditary Disease Committee, which will help provide both genetic and veterinary input for the decisions of the working groups and further endorse the recommendations. This year the committee is hosting Dr. Steven Harrison from the Clinical Genome Resource (ClinGen) program. Within ClinGen, Dr. Harrison co-chairs the Sequence Variant Interpretation Working Group. The four working groups include:

1) Nomenclature Committee (13:30 – 14:30)
   Leslie Lyons, PhD, University of Missouri, will lead this working group and present the initial efforts to define and adopt the nomenclature for DNA variants in the cat that affect traits and diseases. Using nomenclature standards defined in human and murine genetic communities, the preliminary nomenclature for the cat regarding breed names and trait and disease alleles will the presented and discussed. Team leader can be switched for the next species of interest.

2) Variant Pathogenicity of Animal DNA Variants (14:30 – 15:30)
Bart Broeckx, PhD, University of Ghent, will lead this sub-committee and present the initial efforts to define criteria in animals to determine variant pathogenicity, which has been adapted from the standards developed in human medicine. His team has worked to define the pathogenicity of the DNA variants for the domestic cat and dog as their preliminary efforts. See also published works as examples:
Boeykens F, Abitbol M, Anderson H, Casselman I, de Citres CD, Hayward JJ, Häggström J, Kittleson MD, Lepri E, Ljungvall I, Longeri M, Lyons LA, Ohlsson Å, Peelman L, Smets P, Vezzosi T, van Steenbeek FG, Broeckx BJG. Development and validation of animal variant classification guidelines to objectively evaluate genetic variant pathogenicity in domestic animals. Front Vet Sci. 2024 Dec 5;11:1497817. doi: 10.3389/fvets.2024.1497817. PMID: 39703406; PMCID: PMC11656590.
Boeykens F, Abitbol M, Anderson H, Dargar T, Ferrari P, Fox PR, Hayward JJ, Häggström J, Davison S, Kittleson MD, van Steenbeek F, Ljungvall I, Lyons LA, Longeri M, Ohlsson Å, Peelman L, Dufaure de Citres C, Smets P, Turba ME, Broeckx BJG. Classification of feline hypertrophic cardiomyopathy-associated gene variants according to the American College of Medical Genetics and Genomics guidelines. Front Vet Sci. 2024 Feb 2;11:1327081. doi: 10.3389/fvets.2024.1327081. Erratum in: Front Vet Sci. 2024 Aug 12;11:1458433. doi: 10.3389/fvets.2024.1458433. PMID: 38371598; PMCID: PMC10873919.

Break - (15:30 – 16:00)

3) Genetic Test Reporting (16:00 – 17:00)
Leslie Lyons, PhD, University of Missouri, will lead this working group while work continues for the domestic cat. Presented will be preliminary verbiage to be considered for the reporting of several of the 45 disease traits that have been identified in domestic cat breeds. The DNA variants for these diseases are recommended to be part of breed management plans and need to be properly considered when breeding to avoid the production of animals with heritable maladies. These reports should reflect information provided by the Pathogenicity working group. The committee will work closely with the WSAVA HDC to provide reporting that is appropriate as part of veterinary health care decisions. Translation of the reporting verbiage into different languages will be sought so that worldwide commercial testing services can adopt the same verbiage. Leslie Lyons, PhD, University of Missouri, will lead this working group while work continues for the domestic cat.
Considerations:
1) Do we want to extend to the rare diseases that have been identified in only random bred cats?
2) What is the advice to a breed when a commercial service finds the variant in a new breed, but of only one or a few individuals?
    a. Should commercial companies be expected to confirm these findings by variant validation using another technique, ideally Sanger sequencing?
    b. Should OMIA list these findings?

4) Health & Phenotypic Variant Comparison testing (17:00 – 18:00)
Team leader needs to be identified. Recommendations relating to comparison testing for causal variants is the main focus of this group. This working group will interact with the Comparison Test workshops for each species to decide which variants should be included in a given Comparison Test. Outcomes from the Variant Pathogenicity working group will be supportive. Standardizing data sharing between genetic testing laboratories will also be a focus of the working group.

1:30 PM **Nomenclature Committee.**
Leslie Lyons.

2:30 PM **Variant Pathogenicity of Animal DNA Variants.**
Bart Broeckx.

3:30 PM **Coffee Break.**

4:00 PM **Genetic Test Reporting.**
Leslie Lyons.

5:00 PM **Health & Phenotypic Variant Comparison Testing.**
TBD.

Comparative and Functional Genomics

Chair: Christa Kühn, Friedrich-Loeffler-Institute (FLI) Riems, Greifswald - Insel Riems, Germany

Room 101 + 102
1:30 PM - 6:00 PM

1:30 PM OP197 **Decoding the bovine regulatory landscape: Genome-wide high-resolution mapping of regulatory elements in cattle.**
R. Zhao*[1], R. Owen[1], L. Pagie[2], M. Marr[1], K. Jensen[1], V. Bisht[2], T. Connelley[1], L. Morrison[1], J. van Arensbergen[2], M. Hassan[1], and J. Prendergast[1], [1]*Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, United Kingdom*, [2]*Annogen B.V., Science Park 406, 1098XH, Amsterdam, The Netherlands*.

2:00 PM OP198 **An atlas of gene expression in goats.**
M. J. Wang*[1,2], A. Noce[1], M. Luigi Sierra[1], D. Vargas[1], E. Mármol-Sánchez[1], K. Wang[1], E. Petretto[1], S. Olvera Maneu[3,4], P. Serres[4], J. Gardela[4], M. López Béjar[4], and M. Amills[1,2], [1]*Centre de Recerca Agrigenòmica (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [3]*Department of Veterinary Medicine, University of Nicosia, School of Veterinary Medicine, Nicosia, Cyprus*, [4]*Department of Animal Health and Anatomy, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*.

2:18 PM OP199 **Cross-species integration of single-cell RNA sequencing reveals conserved mechanisms in bovine and ovine placentation.**
M. L. Leavitt[1], W. C. Warren[2,3], T. E. Spencer[2,4], and K. M. Davenport*[1], [1]*Department of Animal Sciences, Washington State University, Pullman, WA, USA*, [2]*Division of Animal Sciences, University of Missouri, Columbia, MO, USA*, [3]*Institute for Data Science and Informatics, University of Missouri, Columbia, MO, USA*, [4]*Department of Obstetrics, Gynecology, and Women's Health, University of Missouri, Columbia, MO, USA*.

2:36 PM OP200 **ISAG Bursary Award: RNA-editing, a potential mechanism to influence gene expression, is regulated by genomic variation in *Bos taurus* and *Bos indicus* cattle.**
M. S. Tahir*[1], M. Goddard[1,4], B. Hayes[2], C. Van der Jagt[1], R. Xiang[1], B. Mason[1], M. Forutan[2], E. Ross[2], L. T. Nguyen[2], I. van den Berg[1], S. Meier[3], C. Phyn[3], C. Burke[3], and A. Chamberlain[1,5], [1]*AgriBio Center, Agriculture Victoria Research, Bundoora, Victoria, Australia*, [2]*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Queensland, Australia*, [3]*DairyNZ, Newstead, Hamilton, New Zealand*, [4]*University of Melbourne, Parkville, Victoria, Australia*, [5]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia*.

2:54 PM OP201 **Chromosome-level genome assembly of Korean long-tailed chicken and pangenome of 40 *Gallus gallus* assemblies.**
H. D. Shin*[1], W. Park[2], H. Chai[2], Y. Lee[1], J. Jung[1], BJ Ko[3], and H. Kim[1,3], [1]*Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea*, [2]*Animal Genomics & Bioinformatics Division, National Institute of Animal Science, RDA 1500, Wanju, Republic of Korea*, [3]*Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea*.

3:12 PM OP202 **Identification of goat molQTL based on large-scale transcriptome data.**
Min Tian[1], Meiwen Song[1], Zhen Zhang[1], Yifan Li[1], Xueqing Han[1], Jun Luo[1], Lingzhao Fang[2], and Cong Li*[1], [1]*College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China*, [2]*Center for Quantitative Genetics and Genomics, Aarhus University, Aarhus, Denmark*.

3:30 PM **Coffee Break.**

4:00 PM OP203 **A comprehensive miRNA resource for livestock genomics.**
K. Pokharel*[1], A. J. Amaral[2], B. Liang[3], C. Anthon[3], G. Corsi[3], S. Marthey[4], A. Hoffman[5], J. Lagnel[6], F. Haack[7], O. Palasca[3], S. Seemann[3], L. T. Gama[2], M. A. M. Groenen[8], J. Kantanen[1], R. P. M. A. Crooijmans[8], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal*, [3]*Center for Noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark*, [4]*GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France*, [5]*Bioinformatics Group, Department of Computer Science, University of Leipzig, Leipzig, Germany*, [6]*INRA PACA, Montfavet Cedex, France*, [7]*Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany*, [8]*Wageningen University & Research, Wageningen, the Netherlands*, [9]*Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [10]*Veterinary Science Department, Martin-Gatton College of Agriculture, Food, and Environment, Lexington, KY, USA*.

4:18 PM OP204 **Deep learning deciphers the regulatory grammar of transcription initiation in non-model immune cells.**
C. Zhu*, R. Owen, T. Connelley, L. Morrison, M. Hassan, D. Macqueen, R. Zhao, and J. Prendergast, *Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, Scotland, UK*.

4:36 PM OP205 **Chromatin activation direct asymmetrical gonadal development in female but not male chickens.**
Z. L. Peng*, Y. Q. Jiang, Y. L. Liao, X. Y. Li, and H. Wang, *Huazhong Agricultural University, Wuhan, Hubei, China*.

4:54 PM OP206 **Comparison of pig, human, and mouse transcriptomes: Implications for complex traits and disease modeling.**
Jingwen Dou*[1], Xin Huang[1], Jingjin Li[1], Hong Liu[1], Yong Liao[1], Yue Wang[1], Jingya Xu[1], Zhengshuang Tang[1], Xinyun Li[1,2], Shuhong Zhao[1,2], Xiaolei Liu[1,2], and Yuhua Fu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei 430070, PR China;*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei 430070, PR China*, [3]*Hubei Hongshan Laboratory, Wuhan, Hubei 430070, PR China*.

5:12 PM OP207 **European Network on Livestock Phenomics: An international initiative to enhance genome to phenome integration in all livestock species for applications in animal breeding.**
Luca Fontanesi*[1], Tomas Norton[2], and EU-LI-PHE Consortium1[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy*, [2]*M3-BIORES Research Group, Division of Animal and Human Health Engineering, De-partment of Biosystems, KU Leuven, Leuven, Belgium*.

5:30 PM OP208 **Enrichment of fertility-related quantitative trait loci in regulatory regions of the bovine placenta.**
M. D. Wagle*[1], H. L. Neibergs[1], T. E. Spencer[2,3], and K. M. Davenport[1], [1]*Department of Animal Sciences, Washington State University, Pullman, Washington, United States of America*, [2]*Division of Animal Sciences, University of Missouri, Columbia, Missouri, United States of America*, [3]*Department of Obstetrics, Gynecology, and Women's Health, University of Missouri, Columbia, Missouri, United States of America*.

5:48 PM **Business meeting.**

Horse Genetics and Genomics

Chair: **(1) Robin Everts, (2) Sebastian Peyrás, (1) Etalon Dx, San Diego, CA, USA, (2) Departamento de Genética, Universidad de Cordoba, España, Cordoba, Spain**
Room 107
1:30 PM - 3:30 PM

1:30 PM OP209 **ISAG Bursary Award: A telomere-to-telomere assembly of the horse Y chromosome reveals its complete repeat structure.**
K. Li[1], J. L. Ciosek[1], E. D. Robyn*[1], N. Hussien AbouEl Ela[1], L. C. Johnson[1], J. N. Cullen[2], S. C. Stroupe[3], S.A. Durward-Akhurst[2], M. E. McCue[2], B. W. Davis[3], S. C. Loux[4], J. L. Petersen[5], T.S. Kalbfleisch[1], and T. Raudsepp[3], [1]*University of Kentucky, Lexington, KY, USA*, [2]*University of Minnesota, St. Paul, MN, USA*, [3]*Texas A&M University, College Station, TX, USA*, [4]*Louisiana State University, Baton Rouge, LA, USA*, [5]*University of Nebraska–Lincoln, Lincoln, NE, USA*.

1:45 PM OP210 **Changing references: How breed-specific genomes impact measures of diversity in the horse.**
J. L. Petersen*[1], J. Ciosek[2], K. Li[2], N. P. Balasubramaniam[1,2], E. Bailey[2], and T. Kalbfleisch[2], [1]*University of Nebraska-Lincoln, Lincoln, NE, USA*, [2]*University of Kentucky, Lexington, KY, USA*.

2:00 PM OP211 **Transcriptome-wide association studies for performance traits in Thoroughbred horses identify functionally relevant genes for exercise.**
M. Feng*[1], T. J. Hall[1], J. Francis O. Grady[1], D. E. MacHugh[1,2], L. M. Katz[3], and E. W. Hill[1,4], [1]*UCD School of Agriculture and Food Science, Belfield, Dublin, D04 V1W8, Ireland*, [2]*UCD Conway Institute of Biomolecular and Biomedical Research, Belfield, Dublin, D04 V1W8, Ireland*, [3]*UCD School of Veterinary Medicine, Belfield, Dublin, D04 V1W8, Ireland*, [4]*Zinto Labs Ltd., The Highline, Pottery Rd, Dun Laoghaire, Co. Dublin, Ireland*.

2:15 PM OP212 **ISAG Bursary Award: Galloping towards an equid pangenome.**
J. L. Ciosek*[1], L. C. Johnson[1], K. Li[1], E. D. Robyn[1], N. Hussien AbouEl Ela[1], N. Subramaniam[1], J. Cullen[2], S. Stroupe[3], J. L. Petersen[4], S. A. Durward-Akhurst[2], M. E. McCue[2], B. W. Davis[3], and T. S. Kalbfleisch[1], [1]*University of Kentucky, Lexington, Kentucky, USA*, [2]*University of Minnesota, St. Paul, Minnesota, USA*, [3]*Texas A&M University, College Station, Texas, USA*, [4]*University of Nebraska-Lincoln, Lincoln, Nebraska, USA*.

2:30 PM OP213 **Further insight into the genetics behind hypermobility in horses.**
M. Ablondi[1,2], Å Gelinder-Viklund[2], S. Eriksson[2], and S. Mikko*[2], [1]*Parma University, Parma, Italy*, [2]*Swedish University of Agricultural Sciences, Uppsala, Sweden*.

2:45 PM OP214 **Germline mutations identified by whole-genome sequencing in Thoroughbreds.**
Teruaki Tozaki*[1], Risako Furukawa[1], Koki Kawate[1], Mio Kikuchi[1], Taichiro Ishige[1], Yukihide Momozawa[2], and Hironaga Kakoi[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [2]*Laboratory for Genotyping Development, RIKEN Center for Integrative Medical Sciences, Yokohama, Kanagawa, Japan*.

3:00 PM OP215 **A combination of spectrophotometric and genotypic data with a machine learning approach as a potential tool for effective prediction of coat colour in horses.**
Jelena Kotišcak*[1], Minja Zorc[2], Matjaž Mesaric[3], and Marko Cotman[1], [1]*University of Ljubljana, Veterinary Faculty, Institute for Preclinical Sciences, Gerbiceva 60, 1000 Ljubljana, Slovenia*, [2]*University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Jamnikarjeva 101, 1000, Ljubljana, Slovenia*, [3]*University of Ljubljana, Veterinary Faculty, Clinic for Reproduction and Large Animals, Cesta v Mestni log 47, 1000 Ljubljana, Slovenia*.

3:15 PM OP216 **mtDNA variability in SNCT produced cloned horses: Are they so identical genomically?**
Ayelén Karlau[1], Gabriel Anaya[1], Pablo Trigo[2], Florencia Azcona[2], Maria Yuzhi Arjona[1], Juan Pablo Sanchez Serrano[1], Antonio Molina[1], and Sebastián Demyda Peyrás*[1], [1]*Department of Genetics, Veterinary School, University of Córdoba, Spain*, [2]*Veterinary School, National University of La Plata, La Plata, Buenos Aires, Argentina*.

Microbiomes

Chair: **Oscar Gonzalez-Recio (1), Jordi Estelle (2), (1) The Roslin Institute and Royal (Dick) School of Veterinary Studies R(D)SVS, The University of Edinburgh, Scotland (UK), (2) INRAE, Jouy-en-Josas, France**
Room 103 + 104
1:30 PM - 6:00 PM

1:30 PM OP217 **Invited Workshop Presentation: Metagenomes, methylation, and methane: Using quantitative microbiology to tackle livestock emissions.**
E. M. Ross*, L. T. Nguyen, Z. Chen, Y. lI, and C. T. Ong, *University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Queensland, Australia*.

2:00 PM OP218 **Microbiomes and holobionts as genetic resources for agroecology.**
Gwendal Restoux[1], Jordi Estellé[1], Catherine Larzul[2], Paul Cotter[3], Nichole Ginnan[4], Kelly Eversole[5], and Claire Rogel-Gaillard*[1], [1]*Université Paris Saclay, INRAE, AgroParisTech, GABI, 78350, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, 31320, Castanet-Tolosan, France*, [3]*Teagasc Food Research Centre, Moorepark, Cork; APC Microbiome Ireland, Ireland; VistaMilk, Ireland*, [4]*One Health Microbiome Center, Huck Institute of the Life Sciences, Pennsylvania State University, University Park, PA, USA*, [5]*Animal Microbiome Working Group, International Alliance for Phytobiomes Research, Eau Claire, WI, USA*.

2:15 PM OP219 **Effects of multigenerational early-life metabolic disruption in the intestinal microbiome of mouse.**
V. de Anca Prado*[1], J. C. Jiménez-Chillarón[2], M. Gódia Perello[3], and C. Guerrero Bosagna[1], [1]*Uppsala University, Uppsala, Uppsala, Sweden*, [2]*University of Barcelona, Barcelona, Catalunya, Spain*, [3]*Wageningen University and Research, Wageningen, The Netherlands*.

2:30 PM OP220 **HolomiRA: Insights into the regulatory influence of host-derived miRNAs on human and bovine gut microbiota.**
T. F. Cardoso[1], J. J. Bruscadin[2,1], L. C. Conteville[1], J. V. da Silva[2,1], A. M. G. Ibelli[1], G. A. C. Pena[1], T. Porto[2,1], P. S. N. de Oliveira[2,1], B. G. N. Andrade[3], A. Zerlotini[4], and L. C. de A. Regitano*[1], [1]*Embrapa Southeastern Livestock, São Carlos, São Paulo, Brazil*, [2]*Center of Biological and Health Sciences - Federal University of São Carlos, São Carlos, São Paulo, Brazil*, [3]*Munster Technological University, Bishopstown Cork, Ireland*, [4]*Embrapa Digital Agriculture, Campinas, São Paulo, Brazil*.

2:45 PM OP221 **Differential response to an *in vivo* infectious challenge in pigs genetically selected for contrasting enterotypes.**
A. Ucero-Carretón[1], H. Argüello[1], G. Lemonnier[2], A. Carvajal[1], C. Niort[3], C. Rogel-Gaillard[2], C. Larzul[4], F. Blanc[2], and J. Estellé*[2], [1]*Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, 24071 León, Spain*, [2]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350, Jouy-en-Josas, France*, [3]*INRAE, GenESI, 17700, Surgères, France*, [4]*Université de Toulouse, INRAE, ENVT, GenPhySE, 31320 Castanet-Tolosan, France*.

3:00 PM OP222 **ISAG Bursary Award: Microbial signatures as predictors of fatty acid composition in Iberian pigs.**
L. Azouggagh*[1], C. Casto-Rebollo[1], P. Hernández[1], L. Varona[2], J. Casellas[3], S. Negro[4], and N. Ibáñez-Escriche[1], [1]*Instituto de Ciencia y Tecnología Animal. Universitat Politècnica de Valencia, Valencia, Spain*, [2]*Instituto Agroalimentario de Aragón (IA2). Universidad de Zaragoza, Zaragoza, Spain*, [3]*Universitat Autònoma de Barcelona, Barcelona, Spain*, [4]*INGA FOOD S.A, Almendralejo, Spain*.

3:15 PM OP223 **Influence of the leptin receptor gene on the gut microbiota in pigs.**
R. Suárez-Mesa[1,2], H. Laghouaouta[1,2], R. Ros-Freixedes[1,2], R. N. Pena[1,2], and J. Estany*[1,2], [1]*University of Lleida*, *Spain*, [2]*Agrotecnio-CERCA Center*, *Spain*.

3:30 PM **Coffee Break.**

4:00 PM OP224 **Impact of host inbreeding on vaginal microbiota diversity and pregnancy rate in sheep.**
E. L. Reinoso-Peláez[1,2], M. Serrano[1], A. Fernández[1], B. Villanueva[1], and M. Saura*[3], [1]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA-CSIC), Madrid, Spain*, [2]*Universidad Politécnica de Madrid (UPM), Madrid, Spain*, [3]*Instituto de Investigacións Mariñas (IIM-CSIC), Vigo, Spain*.

4:15 PM OP225 **Microbiome-metabolome interactions under prolonged social stress in a porcine model.**
R. Río-López*[1], I. T. Voularki[2], A. Clavell-Sansalvador[2], A. Valdés[3], L. Padilla[1], J. García-Gil[4], X. Xifró[5], F. X. Prenafeta-Boldú[6], M. Ballester[2], R. Quintanilla[2], A. Dalmau[1], and Y. Ramayo-Caldas[2], [1]*Animal Welfare Program, Institute of Agrifood Research and Technology (IRTA), Monells, Girona, Spain*, [2]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*, [3]*Department of Bioactivity and Food Analysis, Food Science Research Institute (CIAL) and Spanish National Research Council (CSIC), Madrid, Madrid, Spain*, [4]*Digestive Diseases and Microbiota Group, Biomedical Research Institute of Girona (IDIBGI), Girona, Girona, Spain*, [5]*New Therapeutic Targets Laboratory Research Group, Medical Sciences Department, Faculty of Medicine, University of Girona (UdG), Girona, Girona, Spain*, [6]*Sustainability in Biosystems, Institute of Agrifood Research and Technology (IRTA), Caldes de Montbui, Barcelona, Spain*.

4:30 PM OP226 **A comprehensive view of the rumen microbiome and virome to accelerate reduction of enteric methane production through selective breeding.**
O. González-Recio*[1], C. N. Marcos[2], B. J. Sepulveda[3], M. Gutierrez-Rivas[1], J. E. Pryce[3], and A. J. Chamberlain[3], [1]*INIA-CSIC, Madrid 28040, Spain*, [2]*Facultad de Veterinaria. Universidad Complutense de Madrid, Madrid 28040, Spain*, [3]*Agriculture Victoria Research, AgriBio, Centre for AgriBioscience*, *Victoria 3083, Australia*.

4:45 PM OP227 **Microbiome as boosters of the genetic potential of beef cattle.**
P. A. Alexandre*[1], A. Wilson[2], T. P. R. A. Legrand[1], R. J. Farr[2], S. E. Denman[1], and A. Reverter[1], [1]*CSIRO Agriculture & Food*, *St Lucia, Queensland, Australia*, [2]*CSIRO Health & Biosecurity*, *Geelong, Victoria, Australia*.

5:00 PM OP228 **The gut microbiome influences the porcine hepatosomatic index by regulating hepatic lipid metabolism.**
P. Zhou*[1], J. Yuan[1], Y. Wang[1], T. Wang[1], Z. Liu[1], M. Fu[1], X. Zhou[1,2], and B. Liu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, China*, [2]*Hubei Hongshan Laboratory*, *Wuhan, China*.

5:15 PM OP229 **Integrative analysis between the gene expression of liver and fecal microbiota profile reveals hub genes in response to different diets.**
C. Oliveira[1], S. Fanalli[1], T. dos Santos[1], A. Felício-Ament[1], B. Silva-Vignato[1], L. Brito[2], V. de Almeida[3], and A. Cesar*[1], [1]*University of São Paulo*, *Piracicaba, São Paulo, Brazil*, [2]*Purdue University*, *West Lafayette, Indiana, USA*, [3]*Federal University of Goiás*, *Goiânia, Goiás, Brazil*.

5:30 PM OP230 **Whole genome-based analysis of stage-specific dynamics of prevotella during piglet weaning.**
Jae-Gwon Kim*, Seona Kwon, Jung-Woo Choi, and Won-Hyong Chung, *Kangwon National University*, *Chuncheon, Kangwon, Republic of Korea*.

5:45 PM **Meeting of Microbiomes Committee.**

Early Career Scientist Workshop

Chair: **Josué Chinchilla-Vargas, Cornell University, Ithaca, New York, USA**
Room 108
4:00 PM - 6:00 PM

4:00 PM OP231 **ISAG Bursary Award: De novo assembly of a Mozambique tilapia (*Oreochromis mossambicus*): an update using high-accuracy technology.**
T. S. Tshilate*[1], L. T. Nesengani[1], S. Mdyongolo[2], A. H. Smith[2], T. Molotsi[1], C. Masebe[2], N. Rhode[3], and N. Mapholi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, UNISA Science Campus, Johannesburg, GAuteng, South Africa*, [2]*Department of Life and Consumer Sciences, College of Agriculture and Environmental Sciences, UNISA Science Campus, Johannesburg, GAuteng, South Africa*, [3]*Department of Genetics, Stellenbosch University, Stellenbosch, Western Cape, South Africa*.

4:20 PM OP232 **ISAG Bursary Award: Structural variation and breed evolution in the equine pangenome.**
J. N. Cullen*[1], S. Stroupe[2], S. A. Durward-Akhurst[1], M. Paini[3], M. Delledonne[3], J. L. Petersen[4], T. Kalbfleisch[5], B. W. Davis[2], and M. E. McCue[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, Minneapolis, MN, USA*, [2]*College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA*, [3]*Department of Biotechnology, University of Verona, Verona, Italy*, [4]*Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln, Lincoln, NE, USA*, [5]*Department of Veterinary Science, Martin Gatton-College of Agriculture, Food and Environment, University of Kentucky, Lexington, KY, USA*.

4:40 PM **Break.**

4:45 PM **AnGen Talk.**

5:15 PM **Break.**

5:20 PM OP233 **ISAG Bursary Award: Insights into genomic regulation of serum metabolite levels in three-way cross-bred pigs.**
E. Ibragimov*, J. P. Nielsen, M. K. Morsing, M. P. Rydal, M. Fredholm, and P. Karlskov-Mortensen, *Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark*.

5:40 PM OP234 **ISAG Bursary Award: Enhancing genomic prediction accuracy through molecular phenotyping in ducks.**
Wentao Cai*, Zhengkui Zhou, and Shuisheng Hou, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

Small Ruminant Genetics and Genomics

Chair: **Michelle Mousel, USDA/ARS/ADRU, Pullman, WA, USA**
Room 107
4:00 PM - 6:00 PM

4:00 PM OP235 **GWAS analysis of coccidiosis resistance in Portuguese Merino sheep.**
E. Varela Martínez*[1], A. Afonso[2,3], D. Mainou[4], F. Teixeira[5,6], T. Nunes[7,8], P. Vieira[9], I. Sarraguça[7,8], C. Martins[2], N. Campbell[2,5], R. Cordeiro da Silva[10], T. Perloiro[10], L. Madeira de Carvalho[7,8], A. C. Ferreira[2,9], L. Telo da Gama[7,8], H. Waap[2,7], [1]*Department of Genetics, Physical Anthropology and Animal Physiology, Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Biscay, Spain*, [2]*Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Oeiras, Lisbon District, Portugal*, [3]*Global Health and Tropical Medicine (GHTM), Associate Laboratory in Translation and Innovation Towards Global Health, LA-REAL, Instituto de Higiene e Medicina Tropical (IHMT), Universidade NOVA de Lisboa (UNL), Lisbon, Lisbon District, Portugal*, [4]*Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Central Macedonia, Greece*, [5]*MED—Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute, University of Évora, Évora, Évora District, Portugal*, [6]*School of Science and Technology, University of Evora, Évora, Évora District, Portugal*, [7]*CIISA - Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Lisbon District, Portugal*, [8]*Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Lisbon, Lisbon District, Portugal*, [9]*Faculdade de Medicina Veterinária, Universidade Lusófona de Humanidades e Tecnologias, Centro Universitário de Lisboa, Lisbon, Lisbon District, Portugal*, [10]*Associação Nacional de Criadores de Ovinos de Raça Merina (ANCORME), Évora, Évora District, Portugal*.

4:20 PM	OP236	**Rumen microbiome profiling of indigenous goats in North West and Limpopo for optimal health and production.** S. Mani*, *Agricultural Research Council - Animal Production*, *Irene, Gauteng, South Africa*.
4:34 PM	OP237	**Genetic diversity, selection signatures, and genome-wide association studies identify candidate genes related to functional longevity in Cyprus Chios sheep.** Theodoulakis Christofi* and Georgia Hadjipavlou, *Agricultural Research Institute*, *Nicosia, Cyprus*.
4:48 PM	OP238	**Identification of genes related to fitness and robustness traits using CNVs in South African sheep breeds.** T. Rapudi[1], F. Mudau*[1], and AH Molotsi[1,2], [1]*Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*, [2]*University of South Africa*, *Johannesburg, Gauteng, South Africa*.
5:02 PM	OP239	**Landscape genomics reveal signatures of environmental adaptation in goats.** Y. Li*[1,2], P. Su[1], Y. Gong[1], L. Tang[2], Z. Zhang[3], Q. Ren[1], Z. Wang[1,4], Y. Pu[1], Y. Ma[1], and L. Jiang[1], [1]*National Germplasm Center of Domestic Animal Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS)*, *Beijing, P. R. China*, [2]*GIGA & Faculty of Veterinary Medicine, University of Liège*, *Liège, Belgium*, [3]*Wageningen University and Research, Animal Breeding and Genomics*, *WG Wageningen, The Netherlands*, [4]*College of Animal Science, Shanxi Agricultural University*, *Taigu, Shanxi, P. R. China*.
5:16 PM	OP240	**Spatio-temporal expression of the *KRT86* gene and the effect of its genetic variation on wool traits.** Zhanzhao Chen* and Hongxian Sun, *Gansu Agricultural University, College of Animal Science and Technology*, *Lanzhou, Gansu, China*.
5:30 PM	OP241	**Worldwide analysis of the variability of microRNA genes in domestic goats.** E. Marmol Sanchez[1], P. Bardou[2], L. Colli[3,4], The VarGoats Consortium2[2], M. Luigi-Sierra[5], G. Tosser-Klopp[2], and M. Amills*[5,6], [1]*Center for Evolutionary Hologenomics*, *Copenhagen, Denmark*, [2]*GenPhySE, Université de Toulouse, INRAE, ENVT*, *Castanet Tolosan, France*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Univ. Cattolica del S. Cuore di Piacenza*, *Piacenza, Italy*, [4]*Centro di Ricerca sulla Biodiversità e sul DNA antico BioDNA, Univ. Cattolica del S. Cuore di Piacenza*, *Piacenza, Italy*, [5]*Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB*, *Bellaterra, Spain*, [6]*Departament de Ciència Animal i dels Aliments, Universitat Autonoma de Barcelona*, *Bellaterra, Spain*.
5:44 PM		**Standing Committee Meeting.**

OTHER EVENTS

Gala Dinner
Grand Ballroom 201 + 202
7:20 PM - 8:00 PM

Friday, July 25

SYMPOSIA AND ORAL SESSIONS

Avian Genetics and Genomics

Chair: **(1) Huaijun Zhou, (2) Min-Sheng Peng, (1) University of California, Davis, (2) Kunming Institute of Zoology, CAS, Kunming, China**
Room 107 + Room 108
8:00 AM - 11:50 AM

8:00 AM OP242 **Invited Workshop Presentation: The Duck 1000 Genomes Project.**
Zhengkui Zhou*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

8:30 AM OP243 **Beyond traditional GWAS: Machine learning uncovers novel genetic variants of flavor compounds in Korean native chickens.**
E. Cho*, M. Kim, and JH. Lee, *Chungnam National University, Daejeon, Republic of Korea*.

8:45 AM OP244 **CRISPR-based insights into chicken antiviral defense.**
E. A. Weaver*, G. E. Schmidt, J. H. Han, and T. H. Kim, *Pennsylvania State University, Pennsylvania, USA*.

9:00 AM OP245 **Functional characterization of noncoding SNP regions identified by GWAS for taste-related nucleotide compounds in chicken meat using the CRISPRa toolkit.**
J. Kim*[1], JH. Han[2], M. Kim[1], G. Schmidt[2], E. Cho[1], Y. Kim[1], TH. Kim[2], and JH. Lee[1], [1]*Chungnam National University, Daejeon, South Korea*, [2]*The Pennsylvania State University, University Park, PA, United States*.

9:15 AM OP246 **A multiomics characterisation of chicken resistance to avian influenza infection.**
A. Hinsu[1], T. Bremmer[1], C. Cuffe[1], M. A. Hoque[2], M. A. Samad[3], H. T. T. Pham[4], P. T. Ngoc[5], S. Butt[1], G. Fournié[1], D. Blake[1], F. Tomley[1], and A. Psifidi*[1], [1]*Royal Veterinary College, Hatfield, UK*, [2]*Chattogram Veterinary and Animal Sciences University, Chattogram, Bangladesh*, [3]*Bangladesh Livestock Research Institute, Ashulia, Bangladesh*, [4]*CIRAD, Hanoi, Vietnam*, [5]*National Institute of Veterinary Research, Hanoi, Vietnam*, [6]*French National Institute for Agricultural Research INRAE, Paris, France*.

9:30 AM OP247 **Functional analysis of chicken *IRF9* in the innate anti-viral immune response.**
G. E. Schmidt*, E. A. Weaver, J. H. Han, and T. H. Kim, *Penn State University, University Park, PA, United States*.

9:45 AM OP248 **Single-cell cross-species perspective reveals the synergistic mechanism of muscle tissue development in chickens.**
Y. Wang, H. Cui, Y. Chen, J. Zhuang, H. Yang, G. Zhao, and J. Wen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*.

10:00 AM **Coffee Break.**

10:20 AM OP249 **Telomere-to-telomere genome assembly of eight chicken breeds and its application.**
R. Liu*[1], Y. Zhang[1], X. Yang[1], L. Bai[1], K. Li[2], G. Zhao[1], and J. Wen[1], [1]*State Key Laboratory of Animal Biotech Breeding, State Key Laboratory of Animal Nutrition and Feeding, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [2]*Huazhi Biotechnol Co Ltd, Changsha, China*.

10:35 AM OP250 **Meta-analysis and metabolite-based genome-wide studies reveal the genetic basis of lipid accumulation in chickens.**
Na Luo[1,2], Peihao Liu[1], Limin Wei[3,4], Jie Wen[1], Bingxing An[1], and Guiping Zhao*[1,3], [1]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*College of Animal Science and Technology, Henan University of Animal Husbandry and Economy, Zhengzhou, China*, [3]*Sanya Research Institute of Hainan Academy of Agricultural Sciences (Hainan Provincial Laboratory Animal Research Center), Sanya, China*, [4]*Institute of Animal Husbandry and Veterinary Medicine, Hainan Academy of Agricultural Sciences, Haikou, China*.

10:50 AM OP251 **Meta GWAS reveal novel growth trait loci in chicken using Global Chicken Reference Panel V2.0.**
Chenghao Zhai*[1,2] and Yuzhe Wang[1,2], [1]*State Key Laboratory of Animal Biotech Breeding, College of Biological Sciences, China Agricultural University, Beijing, China*, [2]*National Research Facility for Phenotypic and Genotypic Analysis of Model Animals (Beijing), China Agricultural University, Beijing, China*.

11:05 AM OP252 **Metabolome genome-wide association analyses identify a splice mutation in *AADAT* affects lysine degradation in duck skeletal muscle.**
Dapeng Liu*, Wenlei Fan, Youyou Yang, Shuisheng Hou, and Zhengkui Zhou, *State Key Laboratory of Animal Biotech Breeding, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P.R. China*.

11:20 AM OP253 **Structural variations highlight selection for environmental adaptability and productivity in indigenous chickens.**
A. Vallejo-Trujillo*[1], O. Hanotte[2,3], and J. Smith[1], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Easter Bush Campus, Edinburgh, Midlothian, EH25 9RG, UK*, [2]*International Livestock Research Institute (ILRI), P.O. Box - 5689, Addis Ababa, Ethiopia*, [3]*School of Life Sciences, University of Nottingham, Nottingham, NG7 2RD, UK*.

11:35 AM **Business Meeting.**

11:50 AM **Break.**

Equine Genetics and Thoroughbred Parentage Testing

Chair: **Leanne Van De Goor, VHLGenetics, Wageningen, Netherlands**
Room 101 + 102
8:00 AM - 11:50 AM

8:00 AM **Welcoming Remarks.**

8:10 AM **Horse Comparison Test.**

8:40 AM **Donkey Comparison Test.**

9:00 AM OP254 **Development of a robust across breed equine parentage ISAG SNP panel.**
R.R. Bellone*[1,2], E. Esdaile[1], F. Avila[1], B. J. Till[1], B. Wallner[3], T. Raudsepp[4], S. Hughes[1], J. Hughes[1], R Grahn[1], S. Chadaram[5], S. Shrestha[5], A. S. Grulikowski[1], M. McCue[6], P. Flynn[7], T. Mansour[2], [1]*Veterinary Genetics Laboratory, University California Davis, Davis, CA, USA*, [2]*Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, CA, USA*, [3]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, AT*, [4]*Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, School of Veterinary Medicine and Biomedical Sciences, College Station, TX, USA*, [5]*Thermo Fisher Scientific, Waltham, MA USA*, [6]*Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, MN, USA*, [7]*Weatherbys, Kildaire, IE*.

9:20 AM OP255 **Genetic diversity and the evaluation of the effectiveness of single nucleotide polymorphisms compared to microsatellite markers for parentage verification in horse breeds.**
Daeha Choi[1], Sun-Young Lee[1], Shin-Wook Kang[1], and Giljae Cho*[2], [1]*Racing Laboratory, Korea Racing Authority, Gwacheon-Si, Gyeonggi-Do, Korea*, [2]*College of Veterinary Medicine, Kyungpook National University, Buk-gu, Daegu, Korea*.

9:40 AM OP256 **Evaluation of SNP markers for parentage testing in Taishu horse population.**
Taichiro Ishige*[1], Tomoko Yoshihara[2], Koki Kawate[1], Mio Kikuchi[1], Risako Furukawa[1], Teruaki Tozaki[1], and Hironaga Kakoi[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya-shi, Tochigi, Japan*, [2]*Joint Faculty of Veterinary Medicine, Kagoshima University, Kagoshima-shi, Kagoshima, Japan*.

10:00 AM **Coffee Break.**

10:20 AM **Challenges and practicalities regarding the transition from STRs to SNPs for parentage verification. Romy Morrin, Weatherbys, Kildaire, IE.**

10:40 AM **Discussion several aspects of SNPs in horses (Nomenclature, Exchange profiles, Next CT, rules parentage verification).**

11:35 AM **Election of CT Duty Labs, Election of Committee and Any Other Business.**

11:50 AM **Break.**

ISAG-FAO Genetic Diversity

Chair: **(1) Juha Kantanen, (2) Catarina Ginja, (1) Natural Resources Institute Finland, Jokioinen, Finland, (2) CIISA, Faculty of Veterinary Medicine, University of Lisbon, Porto, Portugal**

Room 105 + 106

8:00 AM - 10:00 AM

8:00 AM OP257 **Developing novel genetic erosion footprint for livestock in life cycle assessment.**
Ira Bhattarai* and Kirsi Usva, *Natural Resources Institute Finland, Jokioinen, Finland*.

8:13 AM OP258 **REZGEN-IBA: Ibero-American network on zoogenomic resources and their resilience.**
C. Ginja*[1,2], REZGEN-IBA Consortium3[3], and A. Martínez[4], [1]*CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, 1300-477 Lisboa, Portugal,* [2]*BIOPOLIS -Program in Genomics, Biodiversity and Land Planning, Universidade do Porto, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal,* [3]*REZGEN-IBA Consortium, https://www.cyted.org/web_redes.php?id_rede=511,* [4]*Departamento de Genética, Universidad de Córdoba, Córdoba 14071, Spain*.

8:26 AM OP259 **Genomic insights into cattle domestication and aurochs legacy in the Balkans.**
V. Cubric-Curik*[1], R. Sosic-Klindzic[2], G. Tomac[2], I. Drzaic[1], V. Brajkovic[1], I. Kersic[1], I. Curik[1], and P. T. Miracle[3], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia,* [2]*University of Zagreb Faculty of Humanities and Social Sciences, Zagreb, Croatia,* [3]*McDonald Institute for Archaeological Research University of Cambridge, Cambridge, UK*.

8:39 AM OP260 **The VarGoats 1000 genome project dataset: An alternative approach for WGS data filtering for large-scale analysis of livestock diversity.**
L. Colli*[1,2], B. Lazzari[1,3], Y. Li[4], A. Bionda[5], M. Milanesi[6], A. Talenti[7], A. Stella[3], G. Tosser-Klopp[8], P. Crepaldi[5], and The VarGoats Consortium9[9], [1]*DIANA Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del S. Cuore, Piacenza, PC, Italy,* [2]*BioDNA Centro di Ricerca sulla Biodiversità e sul DNA Antico, Università Cattolica del S. Cuore, Piacenza, PC, Italy,* [3]*Istituto di Biologia e Biotecnologia Agraria, CNR National Research Council, Milano, MI, Italy,* [4]*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, P. R. China,* [5]*Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia, Università degli Studi di Milano, Milano, MI, Italy,* [6]*Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo, VT, Italy,* [7]*The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, United Kingdom,* [8]*GenPhySE, Université de Toulouse, INRA, ENVT, Castanet Tolosan, France,* [9]*http://www.goatgenome.org/vargoats.html*.

8:52 AM OP261 **Genomic diversity and selection signatures in Portuguese coarse wool sheep breeds.**
D. Gaspar*[1,2], A. Usié[3,4], C. Bruno de Sousa[2,5], J. Matos[6], C. Matos[7], A. E. Pires[2,8], and C. Ginja[2,5], [1]*Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal,* [2]*BIOPOLIS/CIBIO, Program in Genomics, Biodiversity and Land Planning, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Vairão, Portugal,* [3]*Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo (CEBAL)/ Instituto Politécnico de Beja, Beja, Portugal,* [4]*MED- Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute, CEBAL – Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Beja, Portugal,* [5]*CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal,* [6]*Instituto Nacional de Investigação Agrária E Veterinária, I.P. (INIAV, I.P.), Oeiras, Portugal,* [7]*ACOS-Agricultores do Sul, Beja, Portugal,* [8]*Faculdade de Medicina Veterinária, Universidade Lusófona, Lisboa, Portugal*.

9:05 AM OP262 **ISAG Bursary Award: Population structure and genetic diversity of native African cattle using whole genome sequence data: A case of five breeds from Uganda.**
R. Okwasiimire*[1,2], D. Kugonza[3], M. Weldenegodguad[2], N. Ghanem[4], M. L. Makgahlela[5], C. Ginja[6], R. Crooijmans[7], J. Kantanen[2], P. Uimari[1], and K. Pokharel[2], [1]*University of Helsinki, Department of Agricultural Sciences, Helsinki, Finland*, [2]*Natural Resources Institute Finland, Jokioinen, Finland*, [3]*Makerere University, College of Agricultural and Environmental Sciences, Kampala, Uganda*, [4]*University of Cairo, Department of Animal Reproduction, Cairo, Egypt*, [5]*Agricultural Research Council, Animal Breeding and Genetics, Pretoria, South Africa*, [6]*CIISA, Faculty of Veterinary Medicine, University of Lisbon and BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal*, [7]*Wageningen University and Research, Animal Breeding and Genomics, Wageningen, the Netherlands*.

9:18 AM OP263 **Genetic diversity and population structure of heritage Finnish landrace chickens using whole-genome sequencing data.**
Melak Weldenegodguad*[1], Petra Tuunainen[2], Kisun Pokharel[3], and Juha Kantanen[3], [1]*Natural Resources Institute Finland, Helsinki, Finland*, [2]*Natural Resources Institute Finland, Maaninka, Finland*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*.

9:31 AM OP264 **Estimation of contemporary and historical effective population size in horses.**
I. Curik*[1,2], N. Moravcikova[3], E. Santiago[4], A. Caballero[5], M. Shihabi[1], R. Kasarda[3], H. Vostra-Vydrova[6], V. Cubric-Curik[1], and L. Vostry[6], [1]*University of Zagreb Faculty of Agriculture, Zagreb, Croatia*, [2]*Hungarian University of Agriculture & Life Sciences (MATE), Kaposvár, Hungary*, [3]*Slovak University of Agriculture in Nitra, Institute of Nutrition & Genomics, Nitra, Slovakia*, [4]*Universidad de Oviedo, Facultad de Biología, Oviedo, Spain*, [5]*Universidade de Vigo, Facultade de Bioloxía, Vigo, Spain*, [6]*Czech University of Life Sciences Prague, Prague, Czech Republic*.

9:44 AM **Standing Committee Meeting.**

Pig Genetics and Genomics

Chair: **(1) Catherine Larzul, (2) Shuhong Zhao, (1) INRAE, Castanet-Tolosan, France, (2) Huazhong Agricultural University, Wuhan, China**
Room 103 + 104
8:00 AM - 11:50 AM

8:00 AM OP265 **IFAM: Improving genomic prediction accuracy of complex traits by integrating massive types of functional annotation information.**
Zhenshuang Tang[1,2], Haohao Zhang[3], Dong Yin[2], Yuhua Fu[2], Yunxia Zhao[1,2], Jingjin Li[2], Yuan Quan[4], Xiang Zhou[5,6], Xinyun Li[2], Lilin Yin[2], Shuhong Zhao[1,2], Xiaolei Liu[2], and Jingwen Dou*[1], [1]*Yazhouwan National Laboratory, Sanya 572024, China*, [2]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan 430070, PR China*, [3]*School of Computer Science and Technology, Wuhan University of Technology, Wuhan 430070, PR China*, [4]*Hubei Key Laboratory of Agricultural Bioinformatics, College of Informatics, Huazhong Agricultural University, Wuhan 430070, PR China*, [5]*Department of Biostatistics, University of Michigan, Ann Arbor, MI, USA*, [6]*Center for Statistical Genetics, University of Michigan, Ann Arbor, MI, USA*.

8:15 AM OP266 **Genetic parameters and genomic investigation of nitrogen use efficiency and its relationship with performance traits in Swiss Large White pigs under a protein-restricted diet.**
E. O. Ewaoluwagbemiga[1], G. Bee[1], A. Lloret-Villas[2,3], A. Poublan-Couzardot[2], H. Pausch[2], and C. Kasper*[1], [1]*Animal Geno-Phenomics, Agroscope, Posieux, Switzerland*, [2]*Animal Genomics, Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland*, [3]*Center for Evolution and Medicine, School of Life Sciences, Arizona State University, Tempe, AZ, USA*.

8:30 AM OP267 **A comprehensive graph-based pangenome of Large White Pigs.**
J. Y. Chu*, Y. Zhou, B. D. P. Soewandi, W. J. Li, W. J. Dong, M. Han, S. Q. Jin, Y. L. Ma, and S. H. Zhao, *Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of the Ministry of Education & Key Laboratory of Swine Genetics and Breeding of the Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei, China*.

8:45 AM OP268 **High-throughput GWAS for more than 250,000 metabolomic features provides novel insights on the genetic mechanisms influencing pig metabolism.**
M. Bolner*[1], S. Bovo[1], G. Schiavo[1], G. Galimberti[2], F. Bertolini[1], A. Ribani[1], S. Dall'Olio[1], P. Zambonelli[1], M. Gallo[3], and L. Fontanesi[1], [1]*Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy*, [2]*Dept. of Statistical Sciences "Paolo Fortunati," University of Bologna, Bologna, Italy*, [3]*Associazione Nazionale Allevatori Suini, Roma, Italy*.

9:00 AM OP269 **ISAG Bursary Award: Genomic prediction of feed efficiency in boars by deep learning.**
Olumide Onabanjo*[1], Theo Meuwissen[1], Hans Magnus Gjøen[1], Fadi Al Machot[2], and Peer Berg[1], [1]*Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway*, [2]*Department of Data Science, Norwegian University of Life Sciences, Ås, Norway*.

9:15 AM OP270 **Development of haplotype maps for a Korean Native Pig Composite breed, Woori-heukdon, using Whole Genome Sequences.**
B. Ahn*[1], M. Kang[1], J. Shin[1], J. Sim[1], J. Lee[2], E. Cho[2], W. Park[2], and C. Park[1], [1]*Department of Stem Cell and Regenerative Biotechnology, Konkuk University, Seoul, Republic of Korea*, [2]*Animal Genomics and Bioinformatics Division, National Institute of Animal Science, Wanju, Republic of Korea*.

9:30 AM OP271 **Recombination suppression and natural selection against female heterozygotes drive the faster-X evolution in pigs.**
Qing-Long Li[2], Li-Gang Wang[3], Long-Chao Zhang[3], Nalini Hirimuthugoda[4], Hai-Bing Xie*[1], and Ya-Ping Zhang[1], [1]*Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*State Key Laboratory for Conservation and Utilization of Bio-resource in Yunnan, School of Ecology and Environmental Science, Yunnan University, Kunming, Yunnan, China*, [3]*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [4]*Department of Animal Science, Faculty of Agriculture, University of Ruhuna, Matara, Sri Lanka*.

9:45 AM OP272 **Single-cell multiome analysis of the pig testicle and identification of DNA variants linked to genomic activity and spermatid survival.**
Yu Lian[1], Soeren Lukassen[2], Claudia P. Cabrera[3], Johannes Liebig[2], Craig RG Lewis[4], Eduardo Rodriguez-Sierra[4], Armand Sanchez[1,5], Christian Conrad[2], and Alex Clop*[1,6], [1]*Centre for Research in Agricultural Genomics CRAG, Cerdanyola del Valles, Catalonia, Spain*, [2]*Berlin Institute of Health at Charité, Berlin, Germany*, [3]*Queen Mary University of London, London, UK*, [4]*PIC Europe, Sant Cugat del Valles, Catalonia, Spain*, [5]*Universitat Autonoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain*, [6]*Consejo Superior de Investigaciones Científicas CSIC, Barcelona, Catalonia, Spain*.

10:00 AM **Coffee Break.**

10:20 AM OP273 **Genome-wide association studies for residual feed intake and feed conversion ratio in Canadian pigs.**
B. Kim*[1], D. N. Do[1], M. Jafarikia[2,3], D. Tulpan[3], D. Adewole[4], B. Sullivan[2], J. Holl[5], and Y. Miar[1], [1]*Dalhousie University, Truro, NS, Canada*, [2]*Canadian Centre for Swine Improvement, Ottawa, ON, Canada*, [3]*University of Guelph, Guelph, ON, Canada*, [4]*University of Saskatchewan, Saskatoon, SK, Canada*, [5]*Pig Improvement Company, Hendersonville, TN, USA*.

10:35 AM OP274 **Incorporating genomic and transcriptomic effects in linear and structural models for predicting complex traits in pigs.**
I. T. Vourlaki, M. Ballester, T. Jove, Y. Ramayo-Caldas, and M. Piles*, *IRTA, Institut of Agrifood Research and Tecnology, 08140 Caldes de Montbui, Barcelona, Spain*.

10:50 AM OP275 **Genome-wide characterization of population structure, genetic diversity, and inbreeding in Korean native pigs.**
Soo-Hyun Back*, Young-Sin Kim, Sun-Young Baek, and Joon-Ki Hong, *Swine Science Division, National Institute of Animal Science, Rural Development Administration, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

11:05 AM OP276 **Number of teats in pigs are affected by non-additive variants.**
C. A. Sevillano*[1], B. Harlizius[1], and M. van Son[2], [1]*Topigs Norsvin Research Center, 's-Hertogenbosch, the Netherlands*, [2]*Norsvin SA, Hamar, Norway*.

11:20 AM OP277 **Tissue-specific responses to dietary lipid levels in pigs revealed by gene co-expression analysis.**
S. L. Fanalli*[1,2], R. P. M. A. Crooijmans[2], I. C. Gervasio[3], J. D. Gomes[3], B. P. M. Silva[3], C. T. Moncau-Gadbem[1], V. V. Almeida[4], and A. S. M. Cesar[1,3], [1]*School of Animal Science and Food Engineering, (FZEA), University of São Paulo, Pirassununga, São Paulo, Brazil*, [2]*Wageningen University & Research, Animal Breeding and Genomics, Wageningen, Gelderland, Netherlands*, [3]*Luiz de Queiroz College of Agriculture (ESALQ), University of São Paulo, Piracicaba, São Paulo, Brazil*, [4]*Federal University of Goiás, Goiânia, Goiás, Brazil*.

11:35 AM **Business Meeting.**

11:50 AM **Break.**

OTHER EVENTS

Speaker Ready Room
Room 209
8:00 AM - 12:00 PM

SYMPOSIA AND ORAL SESSIONS

Livestock Genomics for Developing Countries

Chair: **(1) Dr Khanyisile Hadebe, (2) Dr Kwan-Suk Kim , (1) Agricultural Research Council, Centurion, South Africa, (2) Chungbuk National University, Cheongju, Chungbuk, Korea, Republic of**
Room 105 + 106
10:00 AM - 11:30 AM

10:00 AM		**Chairs Opening Remarks.**
10:02 AM	OP278	**Annotation of African indigenous sheep reveals high-quality ovine genome with unique structure.** Lucky Nesengani*[1], Thendo Tshilate[1], Sinebongo Mdyogolo[1], Rae Smith[1], Tracy Masebe[1], Thomas Raphulu[2], Isidore Houaga[1,3], and Ntanganedzeni Mapholi[1], [1]*College of Agriculture and Environmental Sciences, UNISA Science Campus, Florida, Johannesburg, South Africa*, [2]*Limpopo Department of Agriculture, Polokwane, 0700, South Africa*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK*.
10:13 AM	OP279	**Integrative analysis of transcriptome and microRNA profiling in the mammary gland of Indian dairy goats across lactation stages.** A. Kumar*, S. P. Singh, D. Sharma, B. Kumari, Pooja, G. K. Gupta, R. P. Pandey, and M. Anand, *U.P. Pt. Deen Dayal Upadhyay Pashu Chikitsa Vigyan Vishwavidyalaya Evam Go-Ansundhan Sansthan, (DUVASU), Mathura, UP, India*.
10:24 AM	OP280	**Development of an early prediction model for key swine traits using genomic estimated breeding values and weather data.** S. W. Yoon*, Y. S. Kim, H. J. Beak, E. S. Hong, O. C. Kwon, N. R. Choi, Y. M. Jo, and D. W. Seo, *TNT Research Co., Ltd, Jeonju-si, Jeollabuk-do, Korea*.
10:35 AM	OP281	**ISAG Bursary Award: The landscape of genomic structural variation in East Asian cattle.** Xiwen Guan*, Chuzhao Lei, and Ningbo Chen, *Northwest A&F University, Yangling, Shannxi, China*.
10:46 AM	OP282	**Comparative analysis of the indigenous Venda chicken genome versus the reference chicken genome to identify structural variants involved in adaptation.** A. H. Molotsi*, J. Rees, L. Nesengani, S. Mdyogolo, R. Smith, T. S. Tshiliate, and N. O. Mapholi, *University of South Africa, Florida, Gauteng, South Africa*.
10:57 AM	OP283	**Genetic control of DNA methylation in bovine sperm cells.** Y. Tang* and Y. Yu, *Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture and National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*.
11:08 AM	OP284	**Beyond traditional GWAS: Machine learning uncovers novel genetic variants of flavor compounds in Korean native chickens.** E. Cho*, M. Kim, and JH. Lee, *Chungnam National University, Daejeon, Republic of Korea*.
11:19 AM		**Business Meeting and Election of Committee.**
11:30 AM		**Break.**

OTHER EVENTS

Business Meeting & Closing
Grand Ballroom 201
12:10 PM - 1:20 PM

AWARD WINNERS

ISAG/IFAG 2025 Travel Bursary Award Winners

P113 + OP104
ISAG Bursary Award: Epigenetic signatures of early-life stress: Investigating stress-induced epigenetic variation in the chicken brain.
F. Sourani, Department of Organismal Biology, Uppsala University, Uppsala, Sweden

P125
ISAG Bursary Award: DNA metabarcoding approach, a promising tool for disentangling the precise dietary spectrum of pangolins.
Stanislas Zanvo, Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Abomey-Calavi, Benin

P133
ISAG Bursary Award: Advancing hilsa genomics: Refining genome assembly and identifying novel genes with multi-tissue RNA-seq.
M. B. R. Mollah, Bangladesh Agricultural University, Mymensingh, Bangladesh

P149
ISAG Bursary Award: Prevalence and genetic diversity of *Haemoproteus* and *Leucocytozoon* in raptors and other captive birds at the National Zoological Garden, South Africa.
R. M. Gaorekwe, South African National Biodiversity Institute, Pretoria, Gauteng, South Africa

P158 + OP234
ISAG Bursary Award: Enhancing genomic prediction accuracy through molecular phenotyping in ducks.
Wentao Cai, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

P171
ISAG Bursary Award: Exploring expressional and regulative pattern of paternal alleles in *Cairina moschata* using haplotype-resolved assemblies.
Te Li, China Agricultural University, Beijing, China

P172
ISAG Bursary Award: Dynamic embryonic skeletal muscle development atlas and its foundation model at single-cell resolution across different chicken breeds.
Chong Li, China Agricultural University, Beijing, China

P194
ISAG Bursary Award: Genetic diversity, admixture analysis and pedigree validation in South African smallholder dairy cattle populations using genome-wide SNP data.
L. C. Mthethwa, Agricultural Research Council-Animal Production, Pretoria, Irene, 0062, South Africa

P196 + OP118
ISAG Bursary Award: Application of variation graphs for genotyping structural variants in 14 French cattle breeds.
M. M. Naji, Université Paris Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy en Josas, France

P197
ISAG Bursary Award: Utilisation of genomic parentage verification and discovery techniques in the South African Beefmaster cattle breed.
J. J. Reding, University of Pretoria, Pretoria, Gauteng, South Africa

P208 + OP124
ISAG Bursary Award: ZMYND10 frameshift deletion in Eurasier dogs with primary ciliary dyskinesia.
C. Schwarz, Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland

P212 + OP122
ISAG Bursary Award: Beyond the exome: Identifying non-coding driver mutations in canine diffuse large B-cell lymphoma.
A. D. van der Heiden, Uppsala University, Uppsala, Sweden

P213
ISAG Bursary Award: Comparative transcriptome analysis of ovarian tissues from high and low prolific ewes of South African Merino sheep using RNA-seq.
J. Mamutse, Stellenbosch University, Stellenbosch, Western Cape, South Africa

P225
ISAG Bursary Award: Chromosomal divergences between the small red brocket deer *Mazama rufa toba* (Lonnberg, 1919) and *Mazama rufa* (Illiger, 1815): Evidence for a potentially valid species of Neotropical deer.
Eluzai Dinai Pinto Sandoval, Deer Research and Conservation Center (NUPECCE), School of Agricultural and Veterinarian Sciences. São Paulo State University (UNESP), Jaboticabal, São Paulo, Brazil

P239 + OP200
ISAG Bursary Award: RNA-editing, a potential mechanism to influence gene expression, is regulated by genomic variation in *Bos taurus* and *Bos indicus* cattle.
M. S. Tahir, AgriBio Center, Agriculture Victoria Research, Bundoora, Victoria, Australia

P245 + OP129
ISAG Bursary Award: Telomere-to-telomere genome assembly of a male goat reveals variants associated with cashmere traits.
H. Wu, Frontiers Science Center for Molecular Design Breeding (MOE), State Key Laboratory of Animal Biotech Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China

P267 + P268 + OP169 + OP231
ISAG Bursary Award: De novo assembly of a Mozambique Tilapia *Oreochromis mossambicus*: An update using high-accuracy technology.
T. S. Tshilate, Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, UNISA Science Campus, Johannesburg, Gauteng, South Africa

P289
ISAG Bursary Award: Genome-wide CRISPR screening identified TIRAP as a critical host factor facilitating *Brucella* intracellular survival.
Xiaolong Wang, International Joint Agriculture Research Center for Animal Bio-Breeding of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China

P293
ISAG Bursary Award: High-resolution genotyping reveals the crucial role of SLA in PRRSV resistance.
L. Yang, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China

P298
ISAG Bursary Award: Integration of CRISPR screening and proteomic analysis of WDR91 manipulation of endosome-to-cytosol transport of African swine fever virus.
H. L. Liu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei, China

P303 + OP180
ISAG Bursary Award: Development of a blood-based transcriptional biosignature for accurate discrimination of *M. bovis* infected and control non-infected cattle.
J. F. O'Grady, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland

P310 + OP140
ISAG Bursary Award: Fertility following germline transplantation in sterile *NANOS2* knockout surrogate bulls.
B. E. Latham, College of Veterinary Medicine, Washington State University, Pullman, WA, USA

P329
ISAG Bursary Award: Moving towards personalized pangenomic veterinary medicine in equids.
S. C. Stroupe, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, USA

P335 +OP232
ISAG Bursary Award: Structural variation and breed evolution in the equine pangenome.
J. N. Cullen, Department of Veterinary Population Medicine, University of Minnesota, Minneapolis, MN, USA

P337 + OP212
ISAG Bursary Award: Galloping towards an equid pangenome.
J. L. Ciosek, University of Kentucky, Lexington, KY, USA

P340 + OP209
ISAG Bursary Award: A telomere-to-telomere assembly of the horse Y chromosome reveals its complete repeat structure.
E. D. Robyn, University of Kentucky, Lexington, KY, USA

P344
ISAG Bursary Award: Microsatellite marker analysis of Tswana cattle kept under *in situ* conservation at Botswana University of Agriculture and Natural Resources.
T. Bakae, Botswana University of Agriculture and Natural Resources, Gaborone, Botswana

P345
ISAG Bursary Award: Probabilities that 2 alleles between individuals are identity-by-state at unobserved loci can be predicted by observed SNPs in simulated and real cattle populations.
R. Nagai, Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan

P351
ISAG Bursary Award: Why should we care about Portuguese native dog breeds?—A genome-wide perspective.
Ludmilla Blaschikoff, Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal

P368
ISAG Bursary Award: ABC-random forest machine learning estimates admixture and migration timing of indicine cattle into Africa.
Mulusew Kassa Bitew, Department of Agriculture, Environmental and Food Sciences, University of Molise, Campobasso, Italy

P371
ISAG Bursary Award: Detecting signatures of selection to environmental drivers of adaptation in Indigenous cattle in Tigray, Northern Ethiopia.
Tsadkan Zegeye, Mekelle Agricultural Research Center, Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia

P374 + OP281
ISAG Bursary Award: The landscape of genomic structural variation in East Asian cattle.
Xiwen Guan, Northwest A&F University, Yangling, Shannxi, China

P383
ISAG Bursary Award: Genomic diversity, population structure and admixture in native cattle breeds of Benin.
Loukaiya Zorobouragui, Laboratory of Ecology, Health and Animal Production (LESPA), Faculty of Agronomy, University of Parakou, Parakou, Benin

P391 + OP262
ISAG Bursary Award: Population structure and genetic diversity of native African cattle using whole-genome sequence data: A case of five breeds from Uganda.
R. Okwasiimire, University of Helsinki, Department of Agricultural Sciences, Helsinki, Finland

P423 + OP222
ISAG Bursary Award: Microbial signatures as predictors of fatty acid composition in Iberian pigs.
L. Azouggagh, Instituto de Ciencia y Tecnología Animal. Universitat Politècnica de Valencia, Valencia, Spain

P426
ISAG Bursary Award: ZBED6 is a key regulator of lipogenesis in pig and mouse.
Dandan Wang, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

P427
ISAG Bursary Award: A genome-wide association study examining 24 hematological traits at two different ages in production pigs.
J. Sun, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark

P428
ISAG Bursary Award: Exploring genomic regions regulating the liver transcriptome and energy homeostasis in pigs.
F. Llobet-Cabau, Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Barcelona, Spain

P430
ISAG Bursary Award: Genetic architecture of vitamin D metabolism and bone turnover in pigs.
Dipanwita Paul, Research Institute for Farm Animal Biology (FBN), Dummerstorf, Mecklenburg-Vorpommern, Germany

P436
ISAG Bursary Award: Genome-wide association study identified new QTL and candidate genes on SSC2 associated with teat number in Large White × Tongcheng crossed pigs.
Qinghua Yang, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China

P446
ISAG Bursary Award: Enhancing prime editing efficiency through modulation of methylation on the newly synthesized DNA strand and prolonged expression.
X. H. Xu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, P. R. China

P460 + OP191
ISAG Bursary Award: Oxford Nanopore Technologies reveals age-related genes in beef cattle.
Loan T. Nguyen, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia

P472 + OP269
ISAG Bursary Award: Genomic prediction of feed efficiency in boars by deep learning.
Olumide Onabanjo, Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway

P485 + OP233
ISAG Bursary Award: Insights into genomic regulation of serum metabolite levels in 3-way cross-bred pigs.
E. Ibragimov, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark

P500
ISAG Bursary Award: Integrating GWAS, RNA-seq, and functional annotation to identify causal genes for complex traits in dairy cattle.
Mohammad Ghoreishifar, Agriculture Victoria Research, AgriBio Centre for AgriBioscience, Bundoora, VIC 3083, Australia

P524
ISAG Bursary Award: Comparative analysis of whole-genome amplification methods and genotyping strategies for preimplantation embryo genomic selection in cattle.
S. H. Yan, China Agricultural University, Beijing, China

P529
ISAG Bursary Award: Validation of the effects of gene polymorphisms on BTA19 on fatty acid composition revealed a common QTL in 3 Japanese Black populations.
C. Toiguchi, Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Hyogo, Japan

P534
ISAG Bursary Award: Multi-ancestry meta-analysis of genome-wide association studies for udder confirmation traits and stature in 4 cattle breeds.
N. W. Watson, ETH Zurich, Zurich, Switzerland

P538
ISAG Bursary Award: Genome-wide analysis of selection signatures and genetic variants associated with economic traits in Karan Fries cattle.
P. Pal, Animal Genetics and Breeding Division, ICAR-National Dairy Research Institute, Karnal, Haryana, India

P542
ISAG Bursary Award: Nepalese wild and domestic buffaloes: A whole-genome based insight into genetic relationship.
A. Dhakal, National Engineering Laboratory for Animal Breeding, Key Laboratory of Animal Genetics, Breeding and Reproduction of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing, China

P570
ISAG Bursary Award: Uncovering the role of structural variants in genetic selection for New Zealand sheep.
R. M. Clarke, AgResearch, Invermay, Mosgiel, New Zealand

AUTHOR INDEX

Numbers following names refer to abstract numbers. A number preceded by OP indicates an oral presentation, and a number preceded by P indicates a poster. Orals are listed first, followed by posters in session and number order.

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