

# ISAG . 2019

37th International Society for  
Animal Genetics Conference

July 7 - 12, 2019 - Lleida, Spain



## CONFERENCE PROGRAM

**@isag2019 #ISAG2019**  
**<https://www.isag.us/2019/>**



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José Luis Noguera, Agrifood and Technology Research Institute (IRTA-Lleida)  
Joan Fibla, Biomedic Research Institute (IRB-Lleida)  
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Carmina Nogareda, University of Lleida  
Marta Iglesias, UdL Foundation

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Joan Estany, University of Lleida – Agrotecnio Center,, UdL Foundation  
Romi Pena i Subirà, University of Lleida – Agrotecnio Center,  
Marcel Amills, Center for Research in Agricultural Genomics – CRAG, Universitat Autònoma de Barcelona  
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Roderic Guigó, Center for Genomic Regulation – CRG – Barcelona  
Juanjo Arranz, University of Leon  
Noelia Ibáñez, Polytechnic University of Valencia  
Jorge H Calvo, Agrifood Research and Technology Centre of Aragón – CITA-ARAID

### ISAG 2019 Workshop Chairs

#### Animal epigenetics

Stephanie McKay, University of Vermont

#### Animal forensic genetics

Guillermo Giovambattista, Universidad Nacional De La Plata

#### Applied genetics and genomics in other species of economic importance

Leanne Van de Goor, Dr. van Haeringen Laboratorium B.V.



**Applied genetics in sheep and goats**

Gesine Luehken, University of Giessen

**Applied genetics of companion animals**

Leslie Lyons, University of Missouri, and Jiansheng Qiu, Neogen GeneSeek

**Avian genetics and genomics**

Richard Crooijmans, Wageningen University & Research

**Cattle molecular markers and parentage testing**

Rikke Vingborg, GenoScan A/S

**Companion animal genetics and genomics**

Nuket Bilgen, Ankara University, and Heather Huson, Cornell University

**Comparative and functional genomics**

Fiona McCarthy, The University of Arizona

**Comparative MHC genetics: populations and polymorphism**

Keith Ballingall, Moredun Research Institute

**Domestic animal sequencing and annotation**

James Reecy, Iowa State University

**Equine genetics and Thoroughbred parentage testing**

Cecilia Penedo, University of California, Davis

**Genetics and genomics of aquaculture species**

Francesca Bertolini, National Institute of Aquatic Resources, Technical University of Denmark, and Ross Houston, The Roslin Institute

**Genetics of immune response and disease resistance**

Huaijun Zhou, University of California, Davis

**Genome edited animals**

Bruce Whitelaw, University of Edinburgh

**Horse genetics and genomics**

Tomas Bergström, Swedish University of Agricultural Sciences, and Ted Kalbfleisch, University of Kentucky

**ISAG-FAO genetic diversity**

Catarina Ginja, CIBIO-InBIO, Universidade do Porto

**Livestock genomics for developing countries**

Ntanganedzeni Mapholi, University of South Africa

**Microbiomes**

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

**Pig genetics and genomics**

Romi Pena i Subirà, University of Lleida, and Kyle Schachtschneider, University of Illinois at Chicago

**Ruminant genetics and genomics**

Laercio Porto-Neto, CSIRO Agriculture



## ISAG 2019 Sponsors and Exhibitors

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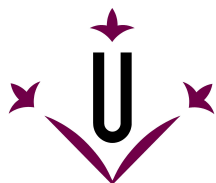


### Exhibitors





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## Schedule of Events

### Sunday, July 7

10:00 – 18:00	Exhibition and Poster Board Setup	Foyer/Poster Room
10:00 – 17:00	ISAG Executive Committee Meeting (Private Invitation)	Boardroom 1
14:00 – 18:00	Registration Desk Open	Hall

### Monday, July 8

08:00 – 18:00	Exhibition and Posters Open	Poster Room
08:00 – 18:00	Registration Desk Open	Hall
09:00 – 09:15	Welcome and Opening	Auditorium 1
09:30	<b>Plenary Presentation:</b> Trans-acting gene regulation drives omnigenic patterns of trait inheritance. (Y. Li)	Auditorium 1
10:30	Coffee/Tea Break	Foyer/Hall
11:00	<b>Plenary Presentation:</b> Can molecular genetics help improve breeding for complex traits? (H. Simianer)	Auditorium 1
12:00	<b>Plenary Presentation:</b> Genome editing tools—Update and novel applications. (L. Montoliu)	Auditorium 1
13:00 – 14:30	Lunch	Foyer/Hall
13:00 – 14:30	Meeting of Board with Chairs (private invitation)	Boardroom 1
13:30 – 14:15	ThermoFisher Vendor Seminar: Generations and Genetics: Advancements in Genetic Tools for Animal Genotyping	Auditorium 2
13:30 – 14:30	Poster Session (authors present)	Poster Room
14:30	Animal Epigenetics	Auditorium 1
14:30	Animal Forensic Genetics	Room 3
14:30	Applied Genetics and Genomics in Other Species of Economic Importance	Room 5
14:30	Genetics of Immune Response and Disease Resistance	Auditorium 2
14:30	Horse Genetics and Genomics	Room 4
16:00 – 16:30	Coffee/Tea Break	Foyer/Hall
18:30 – 21:00	Welcome Reception	Hall/La Llotja Square (outside)

### Tuesday, July 9

08:00 – 18:00	Exhibition and Posters Open	Poster Room
08:00 – 18:00	Registration Desk Open	Hall
09:00	Applied Genetics of Companion Animals	Room 5
09:00	Avian Genetics and Genomics	Auditorium 2
09:00	Genetics and Genomics of Aquaculture Species	Room 3
09:00	Pig Genetics and Genomics	Room 4
09:00	Ruminant Genetics and Genomics	Auditorium 1
10:30 – 11:00	Coffee/Tea Break	Foyer/Hall
12:30 – 14:30	Lunch	Foyer/Hall
13:30 – 14:30	Animal Genetics Editorial Board Meeting (private invitation)	Boardroom 1
13:30 – 14:15	Introduction to FAANG Seminar	Auditorium 2
13:30 – 14:15	Illumina Vendor Presentation	Room 4
13:30 – 14:30	Poster Session (authors present)	Poster Room
14:30	Cattle Molecular Markers and Parentage Testing	Room 3
14:30	Comparative MHC Genetics: Populations and Polymorphism	Room 5
14:30	Domestic Animal Sequencing and Annotation	Auditorium 2
14:30	Genome Edited Animals	Auditorium 1
14:30	ISAG-FAO Genetic Diversity	Room 4
16:00 – 16:30	Coffee/Tea Break	Foyer/Hall
18:30 – 20:30	Product tasting and visit to La Seu Vella (buses provided)	Hall/Foyer



### Wednesday, July 10

08:00 – 13:00	Exhibition and Posters Open	Poster Room
08:00 – 13:00	Registration Desk Open	Hall
08:30	<b>Plenary Presentation:</b> EMBL-EBI, changes in the reference genomes sequence and archive (A. Frankish)	Auditorium 1
09:30	<b>Plenary Presentation:</b> Evolutionary changes in sequence, regulation, and gene expression between <i>Bos taurus</i> and <i>Bos indicus</i> . (M. Naval-Sanchez)	Auditorium 1
10:30	Coffee/Tea Break	Foyer/Hall
11:00	<b>Plenary Presentation:</b> Integrative genomics and network biology in livestock species: New knowledge from existing (and elderly!) data sets. (D. E. MacHugh)	Auditorium 1
12:00 – 13:00	Packed Lunch	Hall
12:30 – 19:00	Tour 4—Land of History	Mid-Conference Tours
12:30 – 20:30	Tour 7—Barcelona on Your Own	Mid-Conference Tours
12:30 – 20:30	Tour 8—Modernist Barcelona	Mid-Conference Tours
13:00 – 18:00	Tour 2—Romanesque Lleida	Mid-Conference Tours
13:00 – 19:00	Tour 3—Land of Olives and Wine	Mid-Conference Tours
13:00 – 18:00	Tour 5—Land of Character	Mid-Conference Tours
13:00 – 19:00	Tour 6—Land of Nature	Mid-Conference Tours
18:30 – 20:00	Tour 1—Musical Lleida	Mid-Conference Tours

### Thursday, July 11

08:00 – 18:00	Exhibition and Posters Open	Poster Room
08:00 – 18:00	Registration Desk Open	Hall
09:00	<b>Plenary Presentation:</b> Transgenerational epigenetic inheritance: How strong is the evidence? (H. Khatib)	Auditorium 1
09:45	<b>Plenary Presentation:</b> Whole-genome sequencing of 722 canids reveals novel genomic regions under selection and variants influencing morphology and longevity (E. A. Ostrander)	Auditorium 1
10:30 – 11:00	Coffee/Tea Break	Foyer/Hall
11:00	<b>Plenary Presentation:</b> Update on the analysis and applications of microbiome information (C. Rogel-Gaillard)	Auditorium 1
11:45	<b>Plenary Presentation:</b> Making the best of large datasets when sequence analysis methods do not scale (C. Notredame)	Auditorium 1
12:30 – 14:30	Lunch	Foyer
13:30 – 14:15	Neogen Vendor Presentation	Room 4
13:30 – 14:30	Poster Session (authors present)	Poster Room
14:30	Applied Sheep and Goat Genetics	Room 3
14:30	Companion Animal Genetics and Genomics	Room 5
14:30	Comparative and Functional Genomics	Auditorium 1
14:30	Equine Genetics and Thoroughbred Parentage Testing	Room 4
14:30	Livestock Genomics for Developing Countries	Room 6
14:30	Microbiomes	Auditorium 2
16:00 – 16:30	Coffee/Tea Break	Foyer/Hall
20:00 – 24:00	Gala Dinner	La Seu Vella

### Friday, July 12

08:00 – 13:00	Registration Desk Open	Hall
09:00	<b>Plenary Presentation:</b> Analysis of the world's sheep reveals contribution of frequent genomic introgressions from congeneric wild species to local climatic adaptation in domestic breeds. (M.-H. Li)	Auditorium 1
10:00	<b>Plenary Presentation:</b> Application of genomics to resolve livestock production and adaptation issues in developing countries. (F. C. Muchadeyi)	Auditorium 1
11:00	Coffee/Tea Break	Foyer/Hall
11:30 – 13:30	Business Meeting and Awards	Auditorium 1
14:00 – 18:00	FAANG: Hands-on metadata validation and data submission training workshop (by invitation)	Room 3



## Social Programme

### **Welcome Reception—Monday, July 8**

The Welcome Reception will take place in La Llotja (conference venue) immediately after the last afternoon session. The event will be organized in the outside square and will include drinks and snacks along with a short exhibition of Catalan culture—for instance, *Castellers* (human towers).

### **Food Tasting and Castle Visit—Tuesday, July 9**

A tasting of local products will be offered to participants in La Llotja immediately after the afternoon session. Tastings will include freshly cut dry-cured ham and locally produced wine (PDO Costers dels Segre). After the tasting, buses will be organized to visit the monumental complex on the top of the Seu Vella mound, where the Old Cathedral, the remains of an older Arabic palace or the former ice cave of the city, are located.

### **Mid-Conference Tours—Wednesday, July 10**

Start times for all tours, except tour 1, indicate the departure time of buses from Lleida; end times indicate the time of return to Lleida.

#### **Tour 1—Musical Lleida (18:30 – 20:00)**

Classical guitar concert featuring popular pieces in the traditional style of several Spanish composers. The concert will be performed by the well-known local singer Montserrat Seró (vocals) and musician Carles Herraiz (Spanish guitar). The concert will take place in Lleida. At the end of the concert, participants will be offered a light snack of cava and canapés.

#### **Tour 2—Romanesque Lleida (13:00 – 18:00)**

Guided visit to Diocesan Museum of Lleida, the city's flagship museum, where archaeological remains, paintings, and sculptures from centenarian collections are conserved. After the visit to the museum, a bus will take participants to Raimat winery (15 km from Lleida), where they will have the chance to discover the details of the modernist winery and savor the quality of their wines.

#### **Tour 3—Land of Olives and Wine (13:00 – 19:00)**

The Artists' Vineyard (Vinya dels Artistes) at La Pobla de Cérvoles (50 km from Lleida) merges art and wine. Participants will visit a vineyard that hosts sculptures and large-scale installations made by different artists. A guided visit of the cellar and a wine and extra-virgin olive oil tasting will also be offered.

#### **Tour 4—Land of History (12:30 – 19:00)**

Travel back in time to the 12th century by visiting the Royal Monastery of Santa Maria de Poblet (60 km from Lleida). It is the most populated monastic enclosure in Europe. After the visit, a taste of wine will be offered in a renowned winery in the vicinity of Poblet.

#### **Tour 5—Land of Character (13:00 – 18:00)**

On the threshold of the Pyrenees, Barbastro (65 km from Lleida) is the capital of Somontano County in the neighbouring region of Aragon. The tour will stop at Sommos cellar, a project of architecture, design, and modernity, with 355 hectares of vines in Denomination of Origin Somontano. The tour will include a 90-minute guided tour for beginners and amateurs in wine.

#### **Tour 6—Land of Nature (13:00 – 19:00)**

The Mont-Rebei Gorge (95 km from Lleida), over the Noguera Ribagorçana River, is the largest gorge in Catalonia. It is a wildlife refuge for great birds of prey, which are typical of the cliffs, particularly hawks, vultures, and eagles. The gorge can be reached on foot but can also be visited by boat or kayak. Given the high temperatures in July, this tour includes a visit to the riverside.

**Tour 7—Barcelona on Your Own (12:30 – 20:30)**

Barcelona (150 km from Lleida) offers many options to visit in a day, from modernist buildings to Boqueria Food Market or a walk through the Gothic Quarter or Barceloneta Beach. In this tour, you will have the chance to stroll freely through Barcelona all afternoon.

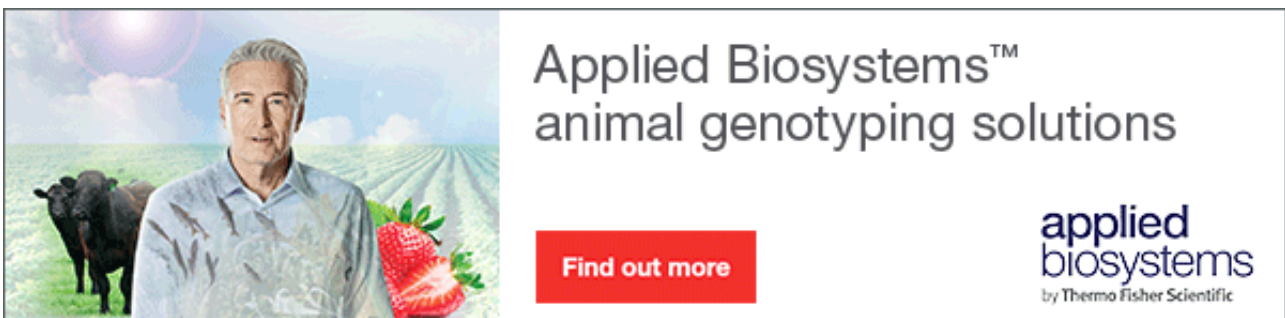
**Tour 8—Modernist Barcelona (12:30 – 20:30; \$30 fee payable at registration)**

Tour 8 is a guided visit to Barcelona (150 km from Lleida) that includes a panoramic view of the city and a visit to Sagrada Familia, an unfinished modernist basilica designed by architect Antoni Gaudí. At the end, a typical tapas tasting will be offered to participants before returning to Lleida.

**Gala Dinner—Thursday, July 11**

The conference Gala Dinner will be served in the complex of the Old Cathedral, on top of the Seu Vella mound. The site oversees the plains and the Pyrenees Mountains to the north. At nightfall, the mound is one of the coolest places in Lleida as it gets the breeze from the river. The sit-down, three-course dinner will be accompanied by light entertainment!

Tickets for the Gala Dinner are included in the registration fee but must be reserved if you wish to attend. You can purchase additional Gala Dinner tickets at the registration desk.



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## POSTER SCHEDULE

### POSTER SESSIONS

All posters will be available for viewing on Monday, Tuesday, Wednesday, and Thursday in the Poster Room.

Posters should be mounted on their boards on Sunday between 10:00 and 18:00 or on Monday between 8:00 and 9:00; posters should be removed on Thursday at 18:00.

Poster presenters must be available to discuss their posters from 13:30 to 14:30 on their designated poster presenting day (Monday, Tuesday, or Thursday, as indicated below). All accepted abstracts, whether selected for oral presentation or not, will be presented as posters.

#### Poster presentations arranged by section:

Section	Poster numbers	Oral numbers	Presenting day
Animal Epigenetics	P1–P14	OP4–OP13	Thursday
Animal Forensic Genetics		OP14–OP20	Tuesday
Applied Genetics and Genomics in Other Species of Economic Importance	P15–P33	OP21–OP24	Tuesday
Applied Sheep and Goat Genetics	P34–P75	OP157–OP165	Tuesday
Avian Genetics and Genomics	P76–P101	OP59–OP72	Monday
Cattle Molecular Markers and Parentage Testing	P102–P121	OP107–OP109	Tuesday
Companion Animal Genetics and Genomics	P122–P135	OP166–OP173	Monday
Comparative and Functional Genomics	P136–P158	OP174–OP184	Tuesday
Comparative MHC Genetics: Populations and Polymorphism	P159–P160	OP110–OP117	Thursday
Domestic Animal Sequencing and Annotation	P161–P167, P451	OP118–OP126	Monday
Equine Genetics and Thoroughbred Parentage Testing	P168–P172	OP185–OP187	Tuesday
Gene Function (jointly with FAANG)	P173–P184		Monday
Genetics and Genomics of Aquaculture Species	P185–P204, P452, P453	OP73–OP82	Monday
Genetics of Immune Response and Disease Resistance	P205–P231, P450	OP25–OP38	Thursday
Genome Edited Animals	P232	OP128–OP138	Thursday
Horse Genetics and Genomics	P233–P249	OP40–OP49	Thursday
ISAG-FAO Genetic Diversity	P250–P267	OP139–OP149	Thursday
Livestock Genomics for Developing Countries	P268–P288	OP188–OP198	Tuesday
Microbiomes	P289–P293	OP199–OP211	Tuesday
Pig Genetics and Genomics	P294–P365	OP83–OP94	Thursday
Ruminant Genetics and Genomics	P366–P449	OP95–OP106	Monday
Applied Genetics of Companion Animals		OP50–OP58	Monday

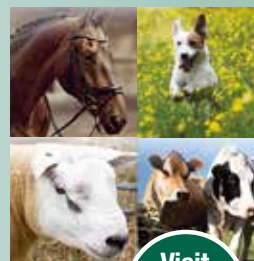
Poster presentations arranged by presenting day:

Presenting day	Section	Poster numbers	Oral numbers
Monday	Applied Genetics of Companion Animals		OP50–OP58
Monday	Avian Genetics and Genomics	P76–P101	OP59–OP72
Monday	Companion Animal Genetics and Genomics	P122–P135	OP166–OP173
Monday	Domestic Animal Sequencing and Annotation	P161–P167, P451	OP118–OP126
Monday	Gene Function (jointly with FAANG)	P173–P184	
Monday	Genetics and Genomics of Aquaculture Species	P185–P204, P452, P453	OP73–OP82
Monday	Ruminant Genetics and Genomics	P366–P449	OP95–OP106
Tuesday	Animal Forensic Genetics		OP14–OP20
Tuesday	Applied Genetics and Genomics in Other Species of Economic Importance	P15–P33	OP21–OP24
Tuesday	Applied Sheep and Goat Genetics	P34–P75	OP157–OP165
Tuesday	Cattle Molecular Markers and Parentage Testing	P102–P121	OP107–OP109
Tuesday	Comparative and Functional Genomics	P136–P158	OP174–OP184
Tuesday	Equine Genetics and Thoroughbred Parentage Testing	P168–P172	OP185–OP187
Tuesday	Livestock Genomics for Developing Countries	P268–P288	OP188–OP198
Tuesday	Microbiomes	P289–P293	OP199–OP211
Thursday	Animal Epigenetics	P1–P14	OP4–OP13
Thursday	Comparative MHC Genetics: Populations and Polymorphism	P159–P160	OP110–OP117
Thursday	Genetics of Immune Response and Disease Resistance	P205–P231, P450	OP25–OP38
Thursday	Genome Edited Animals	P232	OP128–OP138
Thursday	Horse Genetics and Genomics	P233–P249	OP40–OP49
Thursday	ISAG-FAO Genetic Diversity	P250–P267	OP139–OP149
Thursday	Pig Genetics and Genomics	P294–P365	OP83–OP94

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## Sunday, July 7

Exhibition and Poster Board Setup	Foyer/Poster Room	10:00 – 18:00
ISAG Executive Committee Meeting (Private Invitation)	Boardroom 1	10:00 – 17:00
Registration Desk Open	Hall	14:00 – 18:00

## Monday, July 8

Exhibition and Posters Open	Poster Room	08:00 – 18:00
Registration Desk Open	Hall	08:00 – 18:00
Welcome and Opening	Auditorium 1	09:00 – 09:15

Get-together for accompanying people	Room 3	09:30 – 10:30
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This is an opportunity for accompanying people to get together and get to know each other early in the conference. We will provide tourist information, activities to do around Lleida, and how to get around, and help you with any other information you might require.

## ORAL SESSIONS

### Plenary Session I

Chairs: **Romi Pena i Subirà, University of Lleida, and Este van Marle-Köster, University of Pretoria, South Africa**  
**Auditorium 1**

09:30	OP1	<b>Trans-acting gene regulation drives the omnigenic patterns of trait inheritance.</b> <i>Y. Li*, Department of Human Genetics, University of Chicago, Chicago, IL, USA.</i>
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Coffee/Tea break	Foyer/Hall	10:30 – 11:00
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11:00	OP2	<b>Can molecular genetics help improve breeding for complex traits?</b> <i>H. Simianer*, Animal Breeding and Genetics Group, Center for Integrated Breeding Research, University of Goettingen, Goettingen, Germany.</i>
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12:00	OP3	<b>Genome editing tools—Update and novel applications.</b> <i>L. Montoliu*, CNB-CSIC and CIBERER-ISCI, Madrid, Spain.</i>
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Lunch	Foyer/Hall	13:00 – 14:30
Meeting of Board with Chairs (Private Invitation)	Boardroom 1	13:00 – 14:30
ThermoFisher Vendor Seminar	Auditorium 2	13:30 – 14:15

**ThermoFisher Vendor Seminar: Generations and Genetics: Advancements in Genetic Tools for Animal Genotyping**

Genomic technology continues to evolve and significantly impact animal genotyping and parentage verification. During the workshop, industry leaders will discuss the applications of advancements in next-generation sequencing, content curation, and software analysis tools applied to genomics selection and trait verification in ovine and parentage verification in equine. As a partner committed to advancing and serving animal genotyping, Thermo Fisher Scientific provides innovative tools, flexible and economical solutions to laboratories and breeders to accelerate animal genotyping.

- 13:30 **Cost effective and informative genotyping by sequencing using AgriSeq targeted sequencing for genotyping in the livestock industry.**  
Brenda Mae Murdoch, Animal and Veterinary Science, University of Idaho.
- 13:45 **Development of an AgriSeq targeted GBS panel for equine SNP parentage verification and sire/dam allocation.**  
Paul Flynn, Head of R&D, Weatherbys Scientific.

## ORAL SESSIONS

### Animal Epigenetics

Chair: **Stephanie McKay, University of Vermont**  
**Auditorium 1**

- 14:30 OP4 **Comparative analyses of cattle DNA methylome provide insights into tissue specific patterns, epigenomic evolution, and complex traits.**  
G. Liu\*, *Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, USA.*
- 14:50 OP5 **Identification of orthologous tissue-specific enhancer-gene pairs across chicken, pig and cattle.**  
M. M. Halstead\*<sup>1</sup>, C. Kern<sup>1</sup>, Y. Wang<sup>1</sup>, X. Xu<sup>1</sup>, G. Chanthavixay<sup>1</sup>, P. Saelao<sup>1</sup>, S. M. Waters<sup>1</sup>, J. F. Medrano<sup>1</sup>, A. L. Van Eenennaam<sup>1</sup>, M. E. Delany<sup>1</sup>, H. H. Cheng<sup>2</sup>, C. K. Tuggle<sup>3</sup>, C. W. Ernst<sup>4</sup>, H. Zhou<sup>1</sup>, P. J. Ross<sup>1</sup>, <sup>1</sup>*University of California Davis, Davis, CA, USA*, <sup>2</sup>*USDA, ARS, ADOL, East Lansing, MI, USA*, <sup>3</sup>*Iowa State University, Ames, IA, USA*, <sup>4</sup>*Michigan State University, East Lansing, MI, USA.*
- 15:08 OP6 **Whole genome DNA methylation profiles in the central nervous system of sheep naturally infected with scrapie.**  
A. Hernaiz\*<sup>1</sup>, S. Sentre<sup>1</sup>, R. Bolea<sup>2</sup>, O. López-Pérez<sup>1,2</sup>, A. Sanz<sup>1</sup>, P. Zaragoza<sup>1</sup>, J. J. Badiola<sup>2</sup>, J. M. Toivonen<sup>1</sup>, H. Filali<sup>2</sup>, and I. Martín-Burriel<sup>1,2</sup>, <sup>1</sup>*LAGENGIO, Faculty of Veterinary, IA2, University of Zaragoza, Zaragoza, Spain*, <sup>2</sup>*CIEETE, Faculty of Veterinary, IA2, University of Zaragoza, Zaragoza, Spain.*
- 15:26 OP8 **The genome-wide RNA-chromatin interactions revealed by GRID-seq in skeletal muscle of three pig breeds.**  
L. Fu, J. Li\*, Y. Liao, P. Zhou, X. Li, and S. Zhao, *Key Laboratory of Pig Genetics and Breeding, MOA China, Huazhong Agricultural University, Wuhan, Hubei Province, China.*
- 15:44 OP9 **Tissue-specific characterization of the ovine methylome.**  
A. J. Caulton\*<sup>1,2</sup>, R. Brauning<sup>2</sup>, B. M. Murdoch<sup>3</sup>, and S. M. Clarke<sup>2</sup>, <sup>1</sup>*University of Otago, Dunedin, New Zealand*, <sup>2</sup>*AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand*, <sup>3</sup>*University of Idaho, Moscow, ID, USA.*

Coffee/Tea break

Foyer/Hall

16:02 – 16:32

- 16:32 OP10 **Regulatory polymorphisms associated with allele-specific expression (aseQTL) in Nelore (*Bos indicus*) muscle.**  
J. J. Bruscardin<sup>1,2</sup>, M. M. de Souza<sup>3</sup>, K. S. de Oliveira<sup>1</sup>, A. Zerlotini Neto<sup>4</sup>, and L. C. A. Regitano\*<sup>1</sup>, <sup>1</sup>*Embrapa Southeast Livestock, São Carlos, São Paulo, Brazil*, <sup>2</sup>*Graduate Program on Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, São Carlos, São Paulo, Brazil*, <sup>3</sup>*Department of Animal Science, Iowa State University, Ames, IA, USA*, <sup>4</sup>*Embrapa Informatics Agriculture, Campinas, SP, Brazil*, <sup>5</sup>*Department of Animal Science, University of São Paulo, Piracicaba, São Paulo, Brazil.*



- 16:52 OP11 **Can we predict an animal's biological age: A study on DNA methylation from bovine tail hair and liver tissues?**  
L. T. Nguyen\*, E. M. Ross, and B. Hayes, *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, QLD, Australia.*
- 17:11 OP12 **Allele-specific chromatin accessibility and histone modifications in an F<sub>1</sub> cross of MD resistant and susceptible chicken lines.**  
C. Kern\*<sup>1</sup>, Y. Wang<sup>1</sup>, P. Saelao<sup>1</sup>, K. Chanthavixay<sup>1</sup>, M. E. Delany<sup>1</sup>, H. H. Cheng<sup>2</sup>, P. Ross<sup>1</sup>, and H. Zhou<sup>1</sup>, <sup>1</sup>*Department of Animal Science, University of California, Davis, Davis, CA, USA*, <sup>2</sup>*USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA.*
- 17:30 OP13 **Epigenome-wide skeletal muscle DNA methylation profiles at the background of distinct metabolic types and ryano-dine receptor variation.**  
S. Ponsuksili\*<sup>1,2</sup>, N. Trakooljul<sup>1,2</sup>, S. Basavaraj<sup>1,2</sup>, F. Hadlich<sup>1,2</sup>, E. Murani<sup>1,2</sup>, and K. Wimmers<sup>1,2</sup>, <sup>1</sup>*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, <sup>2</sup>*Institute for Genome Biology, Dummerstorf, Germany.*

### Animal Forensic Genetics

Chair: **Guillermo Giovambattista, Universidad Nacional De La Plata**  
**Room 3**

- 14:30 OP7 **Comparing two commercial domestic dog (*Canis familiaris*) STR genotyping kits for forensic identity calculations in a mixed breed dog population sample.**  
S. Kanthaswamy\*, *Evolutionary and Forensic Genetics Laboratory, Arizona State University, Glendale, AZ, USA.*
- 14:45 OP14 **Application of mtDNA for determining species of forensic traces.**  
M. Natonek-Wisniewska\* and A. Radko, *National Institute of Animal Production, Balice, Poland.*
- 15:00 OP15 **Multiplex PCR assay for identification and quantification of bovine and equine in minced meats using species-specific nuclear DNA sequences.**  
X. Zhou\*, W. Wang, and B. Liu, *Huazhong Agricultural University, Wuhan, Hubei, China.*
- 15:15 OP16 **Patterns of SP-InDels for mammalian species identification in forensic casework.**  
M. L. López Díaz, E. J. Santillana, and D. Parra\*, *Departamento de Medio Ambiente, Servicio de Criminalística, Dirección General de la Guardia Civil, Madrid, Madrid, Spain.*
- 15:30 OP17 **Analysis of the cross-reactivity of the canine ISAG 2.0 kit.**  
M. L. López Díaz\*, E. J. Santillana, and D. Parra, *Departamento de Medio Ambiente, Servicio de Criminalística, Dirección General de la Guardia Civil, Madrid, Madrid, Spain.*
- 15:45 OP18 **A robust and in-depth analysis and validation provides multiple metrics supporting use of the proposed Neogen canine parentage and profiling SNP set.**  
O. Forman\*<sup>1</sup>, K. Lytle<sup>2</sup>, R. Mouridsen<sup>4</sup>, E. Laurell<sup>3</sup>, and J. Donner<sup>3</sup>, <sup>1</sup>*Wisdom Health, Waltham on the Wolds, Leicestershire, UK*, <sup>2</sup>*Wisdom Health, Vancouver, WA, USA*, <sup>3</sup>*Wisdom Health, Helsinki, Finland*, <sup>4</sup>*Eurofins, Galten, Denmark.*

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 OP19 **Canine-specific STR typing of traces on the attacked cat.**  
J. Zabavnik Piano\*<sup>1</sup>, M. Gombac<sup>2</sup>, and M. Cotman<sup>1</sup>, <sup>1</sup>*Institute of Preclinical Sciences, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia*, <sup>2</sup>*Institute of Pathology, Game, Fish and Bees, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia.*
- 16:45 OP20 **Investigation of SNP marker combination for new Korean native chicken breeding stocks identification using high-density SNP chip data.**  
S. H. Cho\*<sup>1</sup>, D. Seo<sup>1</sup>, H. Kim<sup>2</sup>, S. H. Lee<sup>1</sup>, and J. H. Lee<sup>1</sup>, <sup>1</sup>*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*, <sup>2</sup>*Insilicogen Inc, Yongin-si, Gyeonggi-do, Republic of Korea.*

- 17:00 Results of the 2018–2019 Comparison Test.
- 17:15 Election of committee members.
- 17:30 Other business.

### Applied Genetics and Genomics in Other Species of Economic Importance

Chair: **Leanne Van de Goor, Dr. van Haeringen Laboratorium B.V.**  
**Room 5**

- 14:30 Welcoming remarks.
- 14:45 **Pig CT Discussion.**  
Emiliano Lasagna.
- 15:00 **Dromedary CT Discussion.**  
Hanaa A. Ahmed.
- 15:15 **Alpaca/Llama CT Discussion.**  
Cecilia Penedo.
- 15:30 **Pigeon CT Discussion.**  
Leanne van de Goor.
- 15:45 Election of committee and any other business.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 OP21 **Invited Workshop Presentation: American mink genome sequencing project.**  
Y. Miar\*<sup>1</sup>, G. Plastow<sup>2</sup>, Z. Wang<sup>2</sup>, and M. Sargolzaei<sup>3,4</sup>, <sup>1</sup>Dalhousie University, Truro, Nova Scotia, Canada, <sup>2</sup>University of Alberta, Edmonton, Alberta, Canada, <sup>3</sup>University of Guelph, Guelph, Ontario, Canada, <sup>4</sup>Select Sires Inc, Plain City, OH, USA.
- 17:00 OP22 **Development of a new multiplex system for analysis of 16 microsatellite markers of reindeer (*Rangifer tarandus*).**  
O. V. Babayan<sup>1</sup>, Y. A. Stolpovsky<sup>2</sup>, M. V. Kholodova<sup>3</sup>, and V. A. Orekhov\*<sup>1</sup>, <sup>1</sup>GORDIZ Ltd, Moscow, Russia, <sup>2</sup>Vavilov Institute of General Genetics Russian Academy of Sciences, Moscow, Russia, <sup>3</sup>A.N.Sevrtsov Institute of Ecology and Evolution Russian Academy of Sciences, Moscow, Russia.
- 17:15 OP23 **Association analysis of coat color in blue wildebeest.**  
R. Van Deventer\*<sup>1,2</sup>, R. Roodt-Wilding<sup>2</sup>, and C. Rhode<sup>2</sup>, <sup>1</sup>Unistel Medical Laboratories, Tygerberg, Western Cape, South Africa, <sup>2</sup>Stellenbosch University, Stellenbosch, Western Cape, South Africa.
- 17:30 OP24 **Estimation of genomic breed composition of individual animals in composite beef cattle.**  
Z. Li<sup>1,2</sup>, X.-L. Wu\*<sup>1,3</sup>, W. Guo<sup>2</sup>, J. He<sup>1,4</sup>, H. Li<sup>1,3</sup>, G. Rosa<sup>3</sup>, D. Gianola<sup>3</sup>, R. Tait Jr<sup>1</sup>, J. Parham<sup>1</sup>, J. Genho<sup>1</sup>, T. Schultz<sup>1</sup>, and S. Bauck<sup>1</sup>, <sup>1</sup>Biostatistics and Bioinformatics, Neogen GeneSeek, Lincoln, NE, USA, <sup>2</sup>Department of Animal Science, University of Wyoming, Laramie, WY, USA, <sup>3</sup>Department of Animal Sciences, University of Wisconsin, Madison, WI, USA, <sup>4</sup>College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China.

**Genetics of Immune Response and Disease Resistance**

**Chair: Huaijun Zhou, University of California, Davis**  
**Auditorium 2**

- 14:30 OP25 **From phenotype to gene discovery: A case study of host genetics influencing porcine circovirus 2 susceptibility.**  
L. Walker<sup>1</sup>, H. Wijesena<sup>1</sup>, K. Sutton<sup>1</sup>, H. Vu<sup>1</sup>, D. Nonneman<sup>2</sup>, T. Smith<sup>2</sup>, G. Plastow<sup>3</sup>, S. Kachman<sup>1</sup>, and D. Ciobanu<sup>\*1</sup>,  
<sup>1</sup>University of Nebraska-Lincoln, Lincoln, NE, USA, <sup>2</sup>USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA,  
<sup>3</sup>University of Alberta, Edmonton, AB, Canada.
- 15:00 OP26 **Genetic markers for improved resilience to PRRSV-induced abortions in sows.**  
R. N. Pena<sup>\*1</sup>, C. Fernández<sup>2</sup>, M. Blasco-Felip<sup>3</sup>, L. J. Fraile<sup>1</sup>, and J. Estany<sup>1</sup>, <sup>1</sup>Departament de Ciència Animal, Universitat de Lleida, Lleida, Spain, <sup>2</sup>INZAR, S.L, Zaragoza, Spain, <sup>3</sup>Veterinarian, Zaragoza, Spain.
- 15:12 OP27 **Genomic factors affecting host resistance to highly pathogenic avian influenza.**  
W. Drobik-Czwarono<sup>\*1,2</sup>, C. Donnelly<sup>3</sup>, A. Wolc<sup>2,4</sup>, J. E. Fulton<sup>4</sup>, J. Arango<sup>4</sup>, J. Smith<sup>3</sup>, and J. Dekkers<sup>2</sup>, <sup>1</sup>Warsaw University of Life Sciences, Warsaw, Poland, <sup>2</sup>Iowa State University, Ames, IA, USA, <sup>3</sup>The Roslin Institute, Easter Bush Campus, Midlothian, UK, <sup>4</sup>Hy-Line International, Dallas Center, IA, USA.
- 15:24 OP28 **Differential H3K27ac peaks within bursa tissue of two inbred chicken lines under NDV infection and heat stress.**  
G. Chanthavixay<sup>\*1</sup>, C. Kern<sup>1</sup>, Y. Wing<sup>1</sup>, P. Saelao<sup>1</sup>, S. Lamont<sup>2</sup>, R. Gallardo<sup>3</sup>, N. Chubb<sup>4</sup>, R. Gonzalo<sup>4</sup>, and H. Zhou<sup>1</sup>, <sup>1</sup>Department of Animal Science, University of California, Davis, CA, USA, <sup>2</sup>Department of Animal Science, Iowa State University, Ames, IA, USA, <sup>3</sup>School of Veterinary Medicine, University of California, Davis, CA, USA, <sup>4</sup>Zoetis Inc., Kalamazoo, MI, USA.
- 15:36 OP29 **ChHIB promotes ubiquitination and degradation of MyD88 to suppress innate immune response.**  
F. Wang, Q. Li<sup>\*</sup>, Q. Wang, and G. Zhao, Institute of Animal Science of Chinese Academy of Agricultural Sciences, Beijing, China.
- 15:48 OP30 **MicroRNA expression in thymus from calves in a coinfection study challenged with bovine viral diarrhea virus and *Mycoplasma bovis*.**  
E. Casas<sup>\*</sup>, S. M. Falkenberg, R. P. Dassanayake, K. B. Register, and J. D. Neill, USDA, ARS, National Animal Disease Center, Ames, IA, USA.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 OP31 **Identification of ovine serum biomarkers during bacterial endotoxin challenge to characterize stress resilience.**  
D. Naylor<sup>1</sup>, A. Sharma<sup>\*1</sup>, A. Canovas<sup>1</sup>, B. Mallard<sup>2</sup>, and N. Karrow<sup>1</sup>, <sup>1</sup>Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Department of Pathobiology, University of Guelph, Guelph, ON, Canada.
- 16:42 OP32 **Whole-blood transcriptomic signatures after intramammary challenge with *Staphylococcus aureus*.**  
U. Thom<sup>\*1</sup>, A. Heimes<sup>1</sup>, J. Brodhagen<sup>1</sup>, R. Weikard<sup>1</sup>, W. Nolte<sup>1</sup>, J. Günther<sup>1</sup>, F. Hadlich<sup>1</sup>, H. Zerbe<sup>2</sup>, W. Petzl<sup>2</sup>, M. M. Meyerholz<sup>2</sup>, M. Hoedemakers<sup>3</sup>, H.-J. Schuberth<sup>4</sup>, S. Engelmann<sup>5,6</sup>, and C. Kühn<sup>1,7</sup>, <sup>1</sup>Leibniz Institute for Farm Animal Biology (FBN), Institute of Genome Biology, Dummerstorf, Germany, <sup>2</sup>Clinic for Ruminants with Ambulatory and Herd Health Services, Centre for Clinical Veterinary Medicine, Ludwig-Maximilians-University Munich, Oberschleissheim, Germany, <sup>3</sup>Clinic for Cattle, University of Veterinary Medicine Foundation, Hannover, Germany, <sup>4</sup>Immunology Unit, University of Veterinary Medicine Foundation, Hannover, Germany, <sup>5</sup>Institute for Microbiology, Technical University Braunschweig, Braunschweig, Germany, <sup>6</sup>Microbial Proteomics, Helmholtz Centre for Infection Research, Braunschweig, Germany, <sup>7</sup>Agricultural and Environmental Faculty, University Rostock, Rostock, Germany.
- 16:54 OP33 **MicroRNA alterations in circulating blood plasma, cerebrospinal fluid, and isolated exosomes of sheep naturally infected with classical scrapie.**  
O. López-Pérez<sup>1,2</sup>, D. Sanz-Rubio<sup>1</sup>, S. Gómez-Redrado<sup>1</sup>, A. Sanz<sup>1</sup>, A. Hernaiz-Martorell<sup>1</sup>, P. Zaragoza<sup>1</sup>, J. Badiola<sup>2</sup>, R. Bolea<sup>2</sup>, JM Toivonen<sup>1</sup>, and I. Martín-Burriel<sup>\*1,2</sup>, <sup>1</sup>Laboratorio de Genética Bioquímica (LAGENBIO), Universidad de Zaragoza, IA2, IIS Aragón, Zaragoza, Spain, <sup>2</sup>Centro de Encefalopatías y Enfermedades Transmisibles Emergentes, Universidad de Zaragoza, IA2, IIS Aragón, Zaragoza, Spain.
- 17:06 OP34 **Single-cell RNA-seq (scRNA-seq) analysis of porcine peripheral blood mononuclear cells identifies replicating B,  $\alpha\beta$ -T, and  $\gamma\delta$ -T cells, as well as all major known circulating cell types.**  
H. Liu<sup>1</sup>, K. Byrne<sup>2</sup>, C. Loving<sup>2</sup>, and C. Tuggle<sup>\*1</sup>, <sup>1</sup>Department of Animal Science, Iowa State University, Ames, IA, USA, <sup>2</sup>USDA-ARS-National Animal Disease Center, Ames, IA, USA.



- 17:18 OP36 **Lightning Talk: Use of genetic and epigenetic tools to refine a genetic marker of host resilience to ovine lentivirus infection.**  
A. T. Massa\*<sup>1</sup>, M. R. Mouse<sup>2,3</sup>, B. M. Murdoch<sup>4</sup>, J. B. Taylor<sup>5</sup>, D. P. Knowles<sup>1</sup>, and S. N. White<sup>1,2</sup>, <sup>1</sup>Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, <sup>2</sup>Animal Disease Research Unit, Agricultural Research Service, USDA, Pullman, WA, USA, <sup>3</sup>Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA, <sup>4</sup>Department of Animal and Veterinary Science, University of Idaho, Moscow, ID, USA, <sup>5</sup>Range Sheep Production Efficiency Research, Agricultural Research Service, USDA, Dubois, ID, USA.
- 17:26 OP37 **Lightning Talk: Integrative functional genomics of the bovine host response to infection with *Mycobacterium bovis*.**  
T. Hall\*<sup>1</sup>, M. Mullen<sup>2</sup>, C. Correia<sup>1</sup>, G. McHugo<sup>1</sup>, K. Killick<sup>1</sup>, J. Browne<sup>1</sup>, N. Nalpas<sup>4</sup>, S. Gordon<sup>2,5</sup>, and D. MacHugh<sup>1,2</sup>, <sup>1</sup>Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland, <sup>2</sup>Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland, <sup>3</sup>Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany, <sup>4</sup>UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, <sup>5</sup>UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.
- 17:34 OP38 **Lightning Talk: Whole genome re-sequence analysis reveals tick resistance and heat tolerance genes in Iraqi cattle breeds.**  
A. Alshawi\*<sup>1,2</sup>, A. Essa<sup>3</sup>, S. Al-Bayatti<sup>3</sup>, A. Tijjani<sup>1,4</sup>, S. Salman<sup>3</sup>, and O. Hanotte<sup>1,4</sup>, <sup>1</sup>School of Life Sciences, Faculty of Medicine and Health Sciences, University of Nottingham, UK, <sup>2</sup>Department of Internal and Preventive Medicine, College of Veterinary Medicine, University of Baghdad, Iraqi Ministry of Higher Education and Scientific Research, Baghdad, Iraq, <sup>3</sup>Animal Genetics Resources Department, the Ministry of Iraqi Agriculture, Baghdad, Iraq, <sup>4</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.
- 17:42 **Workshop Business Meeting.**

### Horse Genetics and Genomics

Chairs: **Tomas Bergström, Swedish University of Agricultural Sciences,**  
**and Ted Kalbfleisch, University of Kentucky**  
**Room 4**

- OP39 **Withdrawn**
- 14:30 OP40 **The horse X chromosome: Old tricks, new insights.**  
T. Raudsepp\*<sup>1</sup>, C. Castaneda<sup>1</sup>, A. Hillhouse<sup>1</sup>, A. Dubrow<sup>1</sup>, M. Jevit<sup>1</sup>, R. Juras<sup>1</sup>, R. Bellone<sup>2</sup>, and B. W. Davis<sup>1</sup>, <sup>1</sup>Texas A&M University, College Station, TX, USA, <sup>2</sup>University of California Davis, Davis, CA, USA.
- 14:45 OP41 **Whole-genome sequencing reveals the genetic mechanisms underlying the high-altitude adaptation in Tibetan horses.**  
X. Liu\*, Y. Ma, and L. Jiang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China.*
- 15:00 OP42 **Upstream regulators of gene and protein expression influencing glycogen repletion in horses.**  
D. Vélez-Irizarry\*<sup>1</sup>, K. Aldrich<sup>1</sup>, V. Mesquita<sup>2</sup>, J. Pagan<sup>2</sup>, and S. Valberg<sup>1</sup>, <sup>1</sup>Department of Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA, <sup>2</sup>Kentucky Equine Research, Versailles, KY, USA.
- 15:15 OP43 **Neocentromere formation and karyotype evolution in equids.**  
F. M. Piras, E. Cappelletti, M. Corbo, S. Faravelli, E. Raimondi, S. G. Nergadze, and E. Giulotto\*, *Department of Biology and Biotechnology, University of Pavia, Pavia, Italy.*
- 15:30 OP44 **Methylome sequencing of tissues and cell-lines of Polish Coldblood horses.**  
T. Zabek\*<sup>1</sup>, T. Szmatoła<sup>1</sup>, W. WitarSKI<sup>1</sup>, E. Semik-Gurgul<sup>1</sup>, A. Gurgul<sup>1</sup>, and M. Bugno-Poniewierska<sup>2</sup>, <sup>1</sup>National Research Institute of Animal Production, Krakow, Poland, <sup>2</sup>Institute of Veterinary Sciences, University of Agriculture, Krakow, Poland.

15:45 OP45 **Identification of shared and species-specific k-mers in Equids and Caballines to characterize adaptive introgression events.**  
K. de Silva\*<sup>1</sup>, E. Bailey<sup>2</sup>, and T. S. Kalbfleisch<sup>2</sup>, <sup>1</sup>University of Louisville, Louisville, KY, USA, <sup>2</sup>University of Kentucky, Lexington, KY, USA.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

16:30 OP46 **An ancient mutation at TBX3 enhancer contributes to the small body size in Chinese ponies.**  
X. Liu, Y. Zhang, Y. Li, Y. Ma, and L. Jiang\*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China.*

16:45 OP47 **Genetic diversity and relationships among native Japanese horse breeds and horses outside of Japan using genome-wide SNP data.**  
T. Tozaki\*<sup>1,3,6</sup>, M. Kikuchi<sup>1</sup>, H. Kakoi<sup>1</sup>, K.-I. Hirota<sup>1</sup>, S.-I. Nagata<sup>1</sup>, D. Yamashita<sup>2</sup>, T. Ohnuma<sup>2</sup>, M. Takasu<sup>3</sup>, I. Kobayashi<sup>4</sup>, S. Hobo<sup>5</sup>, D. Manglai<sup>6</sup>, and J. Petersen<sup>7</sup>, <sup>1</sup>Genetic Analysis Department, Utsunomiya, Tochigi, Japan, <sup>2</sup>Japan Equine Affairs Association, Chuo-ku, Tokyo, Japan, <sup>3</sup>Department of Veterinary Medicine, Faculty of Applied Biological Sciences, Gifu University, Gifu, Gifu, Japan, <sup>4</sup>Sumiyoshi Livestock Science Station, Field Science Center, University of Miyazaki, Miyazaki, Miyazaki, Japan, <sup>5</sup>Joint Faculty of Veterinary Medicine, Kagoshima University, Kagoshima, Kagoshima, Japan, <sup>6</sup>College of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, <sup>7</sup>Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA.

17:00 OP48 **Genomic studies of stallion fertility: Comparing fertility records with FKBP6 genotype and copy numbers of Y multi-copy genes.**  
C. Castañeda\*<sup>1</sup>, A. Hillhouse<sup>2</sup>, S. Teague<sup>3</sup>, C. Love<sup>3</sup>, D. Varner<sup>3</sup>, and T. Raudsepp<sup>1</sup>, <sup>1</sup>Texas A&M Department of Veterinary Integrative Biosciences, College Station, Tx, USA, <sup>2</sup>Texas A&M Institute for Genome Sciences and Society, College Station, TX, USA, <sup>3</sup>Texas A&M College of Veterinary Medicine, Large Animal Hospital, College Station, TX, USA.

17:15 OP49 **Population structure analysis of the Persian horse breeds and their comparison to worldwide populations using genome-wide SNP genotypes.**  
N. YousefiMashouf<sup>1,3</sup>, J. L. Petersen<sup>2</sup>, H. Mehrabani Yeganeh<sup>3</sup>, A. Nejati Javaremi<sup>3</sup>, T. S. Kalbfleisch<sup>1</sup>, M. Bagher Zandi<sup>4</sup>, and E. Bailey\*<sup>1</sup>, <sup>1</sup>University of Kentucky, Lexington, KY, USA, <sup>2</sup>University of Nebraska-Lincoln, Lincoln, NE, USA, <sup>3</sup>University of Tehran, Karaj, Alborz, Iran, <sup>4</sup>University of Zanjan, Zanjan, Iran.

17:30 **Business Meeting.**

Welcome Reception

Hall/La Llotja Square (outside)

18:30 – 20:00

## Tuesday, July 9

Exhibition and Posters Open	Poster Room	08:00 – 18:00
Registration Desk Open	Hall	08:00 – 18:00

### ORAL SESSIONS

#### Applied Genetics of Companion Animals

Chairs: **Leslie Lyons, University of Missouri, and Jiansheng Qiu, Neogen GeneSeek Room 5**

09:00		<b>Cat Comparison Test.</b>
09:15	OP50	<b>An evaluation of a 118-SNP marker panel for feline identification and parentage verification.</b> M. de Groot*, T. Ras, and W. van Haeringen, <i>VHLGenetics, Wageningen, the Netherlands.</i>
09:30		<b>Dog Comparison Test.</b>
09:45	OP51	<b>A recommendation for a SNP marker panel for canine identification and parentage verification.</b> M. de Groot*, T. Ras, and W. van Haeringen, <i>VHLGenetics, Wageningen, the Netherlands.</i>
10:00	OP52	<b>Development of targeted GBS panels for breeding and parentage applications in cats.</b> A. Burrell*, P. Siddavatam, M. Swimley, C. Willis, H. Suren, K. Gujjula, and R. Conrad, <i>Thermo Fisher Scientific, Austin, TX, USA.</i>
10:15	OP53	<b>Development of targeted GBS panels for breeding and parentage applications in dogs.</b> A. Burrell*, P. Siddavatam, M. Swimley, C. Willis, H. Suren, K. Gujjula, and R. Conrad, <i>Thermo Fisher Scientific, Austin, TX, USA.</i>
Coffee/Tea break		Foyer/Hall
		10:30 – 11:00
11:00	OP54	<b>Can-ID: A SNP-based genetic Identification system to evaluate canine samples on two platforms: Open Array and AgriSeq targeted GBS.</b> O. Ramirez* <sup>1</sup> , K. R. Gujjula <sup>2</sup> , A. Sánchez <sup>1,3</sup> , H. Suren <sup>2</sup> , O. Francino <sup>1,3</sup> , R. Ramadhar <sup>2</sup> , and L. Altet <sup>1</sup> , <sup>1</sup> <i>Vetgenomics, Barcelona, Spain</i> , <sup>2</sup> <i>Thermo Fisher Scientific, Austin, TX, USA</i> , <sup>3</sup> <i>Molecular Genetics Veterinary Service (SVGGM), Veterinary School, Universitat Autònoma de Barcelona, Barcelona, Spain.</i>
11:15	OP55	<b>End-to-end AgriSeq targeted GBS long indel solution.</b> H. Suren <sup>1</sup> , C. Willis* <sup>1</sup> , K. Reddy Gujjula <sup>1</sup> , P. Siddavatam <sup>1</sup> , J. Wall <sup>1</sup> , C. Carrasco <sup>1</sup> , R. Conrad <sup>1</sup> , and J. Schmidt <sup>2</sup> , <sup>1</sup> <i>Thermo Fisher Scientific, Austin, TX, USA</i> , <sup>2</sup> <i>Thermo Fisher Scientific, Santa Clara, CA, USA.</i>
11:30	OP56	<b>High-resolution melt analysis for detecting the causative point mutation for the prcd-PRA in the Bolognese dog breed.</b> C. Previtali*, S. Arabi, G. Bongioni, R. Capoferri, A. Pozzi, and M. Montedoro, <i>Istituto Spallanzani, Rivolta d'Adda, Cremona, Italy.</i>
11:45	OP57	<b>Analysis of clinical samples from Doberman and Toy Poodle dogs with a targeted next-generation genotyping system.</b> A. Arizmendi <sup>1,2</sup> , L. S. Barrientos <sup>1</sup> , J. A. Crespi <sup>1</sup> , G. R. Garces <sup>1</sup> , G. Giovambattista <sup>1</sup> , and P. P. García* <sup>1</sup> , <sup>1</sup> <i>Instituto de Genética Veterinaria (IGEVEVET), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata (UNLP), La Plata, Buenos Aires, Argentina</i> , <sup>2</sup> <i>Sevicio de Cardiología, Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata (UNLP), La Plata, Buenos Aires, Argentina.</i>

12:00 OP58 **First steps in animal genetic testing in Bulgaria.**  
S. Tincheva\*<sup>1</sup>, S. Ategin<sup>1,2</sup>, R. Toshkov<sup>3</sup>, T. Todorov<sup>1</sup>, and A. Todorova<sup>1,2</sup>, <sup>1</sup>Genetic Medico-Diagnostic Laboratory "Genica," Sofia, Bulgaria, <sup>2</sup>Department of Medical Chemistry and Biochemistry, Medical University, Sofia, Bulgaria, <sup>3</sup>Veterinary clinic "Kakadu," Sofia, Bulgaria.

12:15 **Workshop Business Meeting and Elections.**

## Avian Genetics and Genomics

Chair: Richard Crooijmans, Wageningen University & Research  
Auditorium 2

09:00 **Introduction.**  
Richard Crooijmans, Wageningen University & Research.

09:05 OP59 **Initiative for Global Chicken Genome Project (GCGP).**  
M.-S. Peng\*<sup>1</sup>, J. Han<sup>2,3</sup>, O. Hanotte<sup>4,5</sup>, D.-D. Wu<sup>1</sup>, and Y.-P. Zhang<sup>1</sup>, <sup>1</sup>Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China, <sup>2</sup>International livestock Research Institute, Nairobi, Kenya, <sup>3</sup>Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, <sup>4</sup>International livestock Research Institute, Addis Ababa, Ethiopia, <sup>5</sup>University of Nottingham, University Park, Nottingham, UK.

09:20 OP60 **A new 55K SNP genotyping array for the chicken.**  
R. Liu\*<sup>1</sup>, S. Xing<sup>1,2</sup>, R. P. M. A. Crooijmans<sup>2</sup>, G. Zhao<sup>1</sup>, and J. Wen<sup>1</sup>, <sup>1</sup>Chinese Academy of Agricultural Sciences Institute of Animal Science, Beijing China, <sup>2</sup>Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands.

09:35 OP61 **An open chromatin region on GGA1 has an important effect on regulating chicken growth.**  
X. Cao\*<sup>1,2</sup>, Y. Wang<sup>2,3</sup>, and X. Hu<sup>1,2</sup>, <sup>1</sup>College of Biological Sciences, China Agricultural University, Beijing, China, <sup>2</sup>State Key Laboratory of Agro-biotechnology, China Agricultural University, Beijing, China, <sup>3</sup>College of Animal Science and Technology, China Agricultural University, Beijing, China.

09:50 OP64 **Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens.**  
A. Adetula\*<sup>1</sup>, L. Gu<sup>1</sup>, C. Nwafor<sup>2</sup>, X. Du<sup>3</sup>, S. Zhao<sup>1</sup>, and S. Li<sup>1</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction, Ministry of Education, Key Laboratory of Poultry Genetics and Breeding of the Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei Province, China, <sup>2</sup>Faculty of Agriculture, Benson Idahosa University, Benin, Edo State, Nigeria, <sup>3</sup>College of Informatics, Huazhong Agricultural University, Wuhan, Hubei Province, China.

10:05 OP65 **Sauropsida ribosomal repeat: Deciphering of the intergenic spacer in chicken and terrapin.**  
A. Dyomin<sup>1,2</sup>, S. Galkina\*<sup>1</sup>, V. Fillon<sup>3</sup>, S. Cauet<sup>4</sup>, C. Lopez-Roques<sup>5</sup>, N. Rodde<sup>4</sup>, C. Klopp<sup>6</sup>, A. Vignal<sup>3</sup>, A. Sokolovskaya<sup>1</sup>, A. Saifitdinova<sup>1,7</sup>, and E. Gaginskaya<sup>1</sup>, <sup>1</sup>Saint Petersburg State University, Saint Petersburg, Russia, <sup>2</sup>Saratov State Medical University, Saratov, Russia, <sup>3</sup>INRA-GenPhySe, Castanet Tolosan, France, <sup>4</sup>French Plant Genomic Center CNRGV-INRA, Castanet Tolosan, France, <sup>5</sup>INRA-GeT-PlaGe, Castanet Tolosan, France, <sup>6</sup>INRA-Sigenae, Castanet Tolosan, France, <sup>7</sup>Herzen State Pedagogical University, Saint Petersburg, Russia.

10:20 OP66 **Genome-wide association study of dwarf phenotypes in Dutch chicken breeds.**  
Z. Wu\*, C. Bortoluzzi, M. F. L. Derks, M. A. M. Groenen, and R. P. M. A. Crooijmans, Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands.

Coffee/Tea break

Foyer/Hall

10:35 – 11:00

11:00 OP67 **Runting and stunting syndrome in sex-linked dwarf chicken is associated with mitochondrial DNA depletion.**  
H. Li\*, Q. Nie, Q. Luo, W. Luo, and X. Zhang, Department of Animal Genetics, Breeding and Reproduction, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong, China.



- 11:15 OP68 **Discovering lethal alleles across the turkey genome using transmission ratio distortion approach.**  
E. A. Abdalla\*<sup>1</sup>, S. Id-Lahoucine<sup>1,2</sup>, B. J. Wood<sup>1,3</sup>, A. Cánovas<sup>1</sup>, J. Casellas<sup>2</sup>, and F. C. Baes<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>3</sup>Hybrid Turkeys, Kitchener, ON, Canada.
- 11:30 OP69 **Effect of gga-miR-1612 and gga-miR-6701-3p on ALV induced lymphoma cell line DT40 by targeting BCL11B.**  
L. Qiu\*<sup>1</sup>, L. Zhao<sup>1</sup>, X. Liu<sup>2</sup>, and G. Chang<sup>1</sup>, <sup>1</sup>Yangzhou University, Yangzhou, Jiangsu, China, <sup>2</sup>Poultry Institute, Chinese Academy of Agricultural Science, Yangzhou, Jiangsu, China.
- 11:45 OP71 **Integrated metabolomic and transcriptomic analysis evaluating heat and feed stress in layer chickens.**  
D. Laloë<sup>1</sup>, F. Jehl<sup>2</sup>, C. Desert<sup>2</sup>, M. Boutin<sup>2</sup>, S. Leroux<sup>3</sup>, D. Esquerre<sup>4</sup>, C. Klopp<sup>5</sup>, D. Gourichon<sup>6</sup>, F. Pitel<sup>3</sup>, S. Lagarrigue<sup>2</sup>, and T. Zerjal\*<sup>1</sup>, <sup>1</sup>INRA, GABI, Jouy-en-Josas, France, <sup>2</sup>INRA-AGROCAMPUS OUEST, Saint Gilles, France, <sup>3</sup>INRA, GenPhySE, Castanet Tolosan, France, <sup>4</sup>INRA, Plateforme GENOTOUL, Castanet-Tolosan, France, <sup>5</sup>INRA, SIGENAE, Castanet-Tolosan, France, <sup>6</sup>INRA, PEAT, \$Nouzilly, France.
- 12:00 OP72 **Candidate signatures of positive selection in Ethiopian chicken.**  
A. Kebede\*<sup>1,2</sup>, K. Tesfaye<sup>1</sup>, G. Belay<sup>1</sup>, A. Vallejo<sup>5</sup>, T. Dessie<sup>3</sup>, N. Spark<sup>4</sup>, O. Hanotte<sup>3,5</sup>, L. Raman<sup>5</sup>, and A. Gheyas<sup>4,5</sup>, <sup>1</sup>Addis Ababa University (AAU), Addis Ababa, Ethiopia, <sup>2</sup>Amhara Regional Agricultural Research Institute (ARARI), Bahir Dar, Ethiopia, <sup>3</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>4</sup>Center for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>5</sup>School of Life Sciences, University of Nottingham, Nottingham, UK.
- 12:15 **Workshop Business Meeting.**

## Genetics and Genomics of Aquaculture Species

Chairs: Francesca Bertolini, National Institute of Aquatic Resources,  
Technical University of Denmark, and Ross Houston, The Roslin Institute  
Room 3

- 09:00 OP73 **Invited Workshop Presentation: Characterization of the putative host-parasite interactome in the salmon-louse relationship.**  
L. Braden\*<sup>1,2</sup>, J. Poley<sup>3</sup>, W. Cai<sup>2</sup>, and M. Fast<sup>2</sup>, <sup>1</sup>AquaBounty Canada, Souris, PE, Canada, <sup>2</sup>Hoplite Lab, Department of Pathology and Microbiology, Atlantic Veterinary College-UPEI, Charlottetown, PE, Canada, <sup>3</sup>Centre for Aquaculture Technologies, Souris, PE, Canada.
- 09:30 OP74 **The molecular basis of salmon sexual maturation: An integrative multi-omics approach.**  
A. Mohamed\*<sup>1</sup>, M. Sanchez<sup>1</sup>, M. Menzies<sup>1</sup>, A. Reverter<sup>1</sup>, B. Evans<sup>2</sup>, H. King<sup>3</sup>, and J. Kijas<sup>1</sup>, <sup>1</sup>CSIRO Agriculture, St Lucia, QLD, Australia, <sup>2</sup>Tassal Group Ltd., Hobart, Tasmania, Australia, <sup>3</sup>CSIRO Agriculture, Hobart, Tasmania, Australia.
- 09:45 OP75 **Different transcriptional response of susceptible and resistant fish hints at the mechanism of KHV disease resistance in carp.**  
R. Tadmor-Levi<sup>1</sup>, A. Doron-Faigenbaum<sup>2</sup>, G. Hulata<sup>2</sup>, and L. David\*<sup>1</sup>, <sup>1</sup>Department of Animal Sciences, R.H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Rehovot, Israel, <sup>2</sup>Agricultural Research Organization, Bet Dagan, Israel.
- 10:00 OP76 **Analysis of adaptive plasticity of pikeperch (*Sander lucioperca* L., 1758) after temperature change based on gene expression data.**  
T. Goldammer\*<sup>1</sup>, F. Swirplies<sup>1</sup>, S. Wuertz<sup>2</sup>, B. Baßmann<sup>3</sup>, A. Orban<sup>2,4</sup>, N. Schäfer<sup>1</sup>, R. M. Brunner<sup>1</sup>, F. Hadlich<sup>1</sup>, A. Rebl<sup>1</sup>, and M. Verleih<sup>1</sup>, <sup>1</sup>Fish Genetics Unit, Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>2</sup>Department of Ecophysiology and Aquaculture, Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin, Germany, <sup>3</sup>Aquaculture & Sea-Ranching, Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany, <sup>4</sup>Food Chemistry and Food Biotechnology, Justus Liebig University Giessen, Gießen, Germany.
- 10:15 OP77 **Optimizing genotype imputation strategies for genomic selection in farmed Atlantic salmon.**  
S. Tsairidou\*<sup>1</sup>, A. Hamilton<sup>1</sup>, D. Robledo<sup>1</sup>, J. Bron<sup>3</sup>, and R. Houston<sup>1</sup>, <sup>1</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK, <sup>2</sup>Hendrix Genetics Aquaculture BV/ Netherlands Villa 'de Körver', Boxmeer, The Netherlands, <sup>3</sup>Institute of Aquaculture, University of Stirling, Stirling, UK.



Coffee/Tea break

Foyer/Hall

10:30 – 11:00

- 11:00 OP78 **Genomic tools for an efficient management of genetic resources in Atlantic salmon.**  
M. Saura\*<sup>1</sup>, A. Chtioui<sup>1,5</sup>, M. Gabián<sup>2</sup>, P. Morán<sup>2</sup>, A. Caballero<sup>2</sup>, E. Santiago<sup>3</sup>, Al Fernández<sup>1,6</sup>, M. P. Kent<sup>4</sup>, L. Covelo-Soto<sup>2</sup>, A. Fernández<sup>1</sup>, and B. Villanueva<sup>1</sup>, <sup>1</sup>INIA, Madrid, Spain, <sup>2</sup>Universidad de Vigo, Vigo, Spain, <sup>3</sup>Universidad de Oviedo, Oviedo, Spain, <sup>4</sup>Center for Integrative Genetics, Norwegian University of Life Sciences, Ås, Norway, <sup>5</sup>Georg-August-Universität Göttingen, Göttingen, Germany, <sup>6</sup>Red CIBER, Madrid, Spain.
- 11:15 OP79 **Determination of genetic structure and selection signatures in Coho salmon (*Oncorhynchus kisutch*) populations by genome-wide SNP analyses.**  
M. E. López\*<sup>1,2</sup>, A. Barría<sup>2</sup>, E. Rondeau<sup>3</sup>, B. Koop<sup>3</sup>, and J. M. Yáñez<sup>2</sup>, <sup>1</sup>Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>Universidad de Chile, Santiago, RM, Chile, <sup>3</sup>University of Victoria, Victoria, BC, Canada.
- 11:30 OP80 **Identification of a major locus determining a coloration defect in gilthead seabream (*Sparus aurata*).**  
F. Bertolini<sup>1,2</sup>, A. Ribani<sup>3</sup>, F. Capoccioni<sup>4</sup>, L. Buttazoni<sup>4</sup>, V. J. Utzeri<sup>3</sup>, S. Bovo<sup>3</sup>, M. Caggiano<sup>4</sup>, L. Fontanesi\*<sup>3</sup>, and M. F. Rothschild<sup>2</sup>, <sup>1</sup>National Institute of Aquatic Resources, Technical University of Denmark, Lyngby, Denmark, <sup>2</sup>Department of Animal Science, Iowa State University, Ames, IA, USA, <sup>3</sup>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, <sup>4</sup>Centro di ricerca di Zootecnia e Acquacoltura, Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA), Roma, Italy, <sup>5</sup>Panittica Italia Società Agricola Srl, Brindisi, Italy.
- 11:45 OP81 **From sea to plate: Genomically enabling the Australasian snapper (*Chrysophrys auratus*) for aquaculture.**  
M. Wellenreuther\*<sup>1,2</sup>, D. Ashton<sup>1</sup>, E. Hilario<sup>3</sup>, R. Crowhurst<sup>3</sup>, P. M. Whittle<sup>1</sup>, A. Catanach<sup>4</sup>, J. Le Luyer<sup>5</sup>, C. Deng<sup>4</sup>, C. David<sup>4</sup>, P. Ritchie<sup>6</sup>, and L. Bernatchez<sup>7</sup>, <sup>1</sup>The New Zealand Institute for Plant & Food Research Ltd, Nelson, New Zealand, <sup>2</sup>School of Biological Sciences, University of Auckland, Auckland, New Zealand, <sup>3</sup>The New Zealand Institute for Plant & Food Research Ltd, Auckland, New Zealand, <sup>4</sup>The New Zealand Institute for Plant & Food Research Ltd, Lincoln, New Zealand, <sup>5</sup>Ifremer, UMR 241 Ecosystèmes Insulaires Océaniques, Centre Ifremer, Tahiti, French Polynesia, <sup>6</sup>School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand, <sup>7</sup>Institut de Biologie Intégrative et des Systèmes (IBIS), Pavillon Charles-Eugène Marchand, Université Laval, Québec, Canada.
- 12:00 OP82 **Challenges and opportunities for genomics in selective breeding programs for marine mass-spawning fish species.**  
J. M. Yáñez\*<sup>1</sup>, M. E. López<sup>2</sup>, P. Cáceres<sup>1</sup>, and G. M. Yoshida<sup>1</sup>, <sup>1</sup>Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile, <sup>2</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- 12:15 **Workshop Business Meeting.**

### Pig Genetics and Genomics

Chairs: **Romi Pena i Subirà, University of Lleida, and  
Kyle Schachtschneider, University of Illinois at Chicago  
Room 4**

- 09:00 OP83 **Suina genomes and phylogenomics.**  
L. Eory<sup>1</sup>, A. Warr<sup>1</sup>, H. A. Finlayson<sup>1</sup>, S. J. Girling<sup>3</sup>, K. Gharbi<sup>2</sup>, T. Watson<sup>1</sup>, T. Burdon<sup>1</sup>, A. A. MacDonald<sup>1</sup>, E. Okoth<sup>5</sup>, A. Djikeng<sup>4,1</sup>, M. Watson<sup>1</sup>, and A. L. Archibald\*<sup>1</sup>, <sup>1</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, UK, <sup>2</sup>Edinburgh Genomics, University of Edinburgh, Edinburgh, UK, <sup>3</sup>The Royal Zoological Society of Scotland, Edinburgh, UK, <sup>4</sup>Centre for Tropical Livestock Genetics and Health, Nairobi, Kenya, <sup>5</sup>International Livestock Research Institute, Nairobi, Kenya.
- 09:15 OP84 **Loss of function mutations in the pig causing embryonic lethality.**  
M. F. L. Derks<sup>1</sup>, A. B. Gjuvsland<sup>2</sup>, M. Bosse<sup>1</sup>, M. S. Lopes<sup>3,4</sup>, M. van Son<sup>2</sup>, B. Harlizius<sup>3</sup>, E. Grindflek<sup>2</sup>, H. J. Megens<sup>1</sup>, and M. A. M. Groenen\*<sup>1</sup>, <sup>1</sup>Wageningen University & Research, Animal Breeding and Genomics, Wageningen University & Research, Animal Breeding Wageningen, the Netherlands, <sup>2</sup>Norsvin, Hamar, Norway, <sup>3</sup>Topigs Norsvin Research Center, Beuningen, the Netherlands, <sup>4</sup>Topigs Norsvin, Curitiba, Brazil.

- 09:30 OP85 **Pig transcriptome analysis suggests a global regulation mechanism enabling temporary bursts of circular RNAs.**  
A. Robic\*<sup>1</sup>, K. Feve<sup>1</sup>, T. Faraut<sup>1</sup>, S. Djebali<sup>1</sup>, R. Weikard<sup>2</sup>, and C. Kuehn<sup>2,3</sup>, <sup>1</sup>GenPhySE, University of Toulouse, INRA, ENVT, Castanet Tolosan, France, <sup>2</sup>Institute Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>3</sup>Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany.
- 09:45 OP86 **Characterization of A-to-I editing events in fetal pig tissues.**  
R. J. Corbett\*<sup>1</sup>, S. A. Funkhouser<sup>1</sup>, D. J. Nonneman<sup>2</sup>, T. P. L. Smith<sup>2</sup>, and C. W. Ernst<sup>1</sup>, <sup>1</sup>Michigan State University, East Lansing, MI, USA, <sup>2</sup>U.S. Meat Animal Research Center, Clay Center, NE, USA.
- 10:00 OP87 **Whole-genome sequencing reveals population structure and diversity of Nigerian indigenous pigs.**  
A. C. Adeola\*<sup>1,2</sup>, S. Khederzadeh<sup>1,3</sup>, D. H. Mauki<sup>1,2</sup>, C.-P. Huang<sup>1,3</sup>, C. Yan<sup>1,3</sup>, O. O. Oluwole<sup>4</sup>, S. C. Olaogun<sup>5</sup>, L. M. Nneji<sup>1,2</sup>, P. M. Dawuda<sup>6</sup>, O. G. Omitogun<sup>7</sup>, L. Frantz<sup>8</sup>, R. W. Murphy<sup>9</sup>, M.-S. Peng<sup>1,2</sup>, H.-B. Xie<sup>1,2</sup>, Y.-P. Zhang<sup>1,10</sup>, <sup>1</sup>State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China, <sup>2</sup>Sino-Africa Joint Research Center, Chinese Academy of Sciences, Nairobi, Kenya, <sup>3</sup>Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan, China, <sup>4</sup>Institute of Agricultural Research and Training, Obafemi Awolowo University, Ibadan, Oyo State, Nigeria, <sup>5</sup>Department of Veterinary Medicine, University of Ibadan, Ibadan, Oyo State, Nigeria, <sup>6</sup>Department of Veterinary Surgery and Theriogenology, College of Veterinary Medicine, University of Agriculture Makurdi, Makurdi, Benue State, Nigeria, <sup>7</sup>Department of Animal Sciences, Obafemi Awolowo University, Ile-Ife, Osun State, Nigeria, <sup>8</sup>The Palaeogenomics and Bio-Archaeology Research Network, Research Laboratory for Archaeology, University of Oxford, Oxford, UK, <sup>9</sup>Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, Canada, <sup>10</sup>State Key Laboratory for Conservation and Utilization of Bio-Resources, Yunnan University, Kunming, Yunnan, China.
- 10:15 OP88 **Genetic heterogeneity of wattles in sheep and pigs.**  
J. Paris\*<sup>1</sup>, A. Grahofer<sup>2</sup>, A. Letko<sup>1</sup>, I. Haefliger<sup>1</sup>, N. Hirter<sup>1</sup>, P. Ciaramella<sup>3</sup>, G. Leuhken<sup>4</sup>, and C. Droegemueller<sup>1</sup>, <sup>1</sup>Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>2</sup>Clinic for Swine, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>3</sup>University of Naples Federico II, Department of Veterinary Medicine and Animal Production Veterinary, Napoli, Italy, <sup>4</sup>Institute of Animal Breeding and Genetics, Justus Liebig University, Gießen, Germany.
- Coffee/Tea break Foyer/Hall 10:30 – 11:00
- 11:00 OP89 **The little Pygmy hog (*Porcula salvania*), a big piece in resolving fascinating history of the complex speciation of the Suidae.**  
L. Liu\*<sup>1</sup>, M. Bosse<sup>1</sup>, H.-J. Megens<sup>1</sup>, L. Frantz<sup>2,3</sup>, Y. Lee<sup>1</sup>, E. Irving-Pease<sup>3</sup>, G. Narayan<sup>4,5</sup>, M. Groenen<sup>1</sup>, and O. Madsen<sup>1</sup>, <sup>1</sup>Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands, <sup>2</sup>School of Biological and Chemical Sciences, Queen Mary University of London, London, UK, <sup>3</sup>Palaeogenomics and Bioarchaeology Research Network, Research Laboratory for Archeology and History of Art, University of Oxford, Oxford, UK, <sup>4</sup>Durrell Wildlife Conservation Trust, Jersey, Channel Islands, UK, <sup>5</sup>Pygmy Hog Conservation Programme, Guwahati, Assam, India.
- 11:15 OP90 **Sexing in pigs by using gene editing.**  
S. Kurtz\*<sup>1</sup>, A. Frenzel<sup>1</sup>, A. Lucas-Hahn<sup>1</sup>, P. Hassel<sup>1</sup>, R. Becker<sup>1</sup>, H. Niemann<sup>1</sup>, and B. Petersen<sup>1</sup>, Institute of Farm Animal Genetics, Friedrich-Loeffler-Institute, Mariensee, Neustadt am Rübenberge, Germany.
- 11:30 OP91 **Integrative genomics analysis of blood and microbiota data suggests a NAFLD-related disorder in SLAdd minipigs.**  
M. Moroldo\*<sup>1</sup>, P. Munyaka<sup>2</sup>, J. Lecardonnel<sup>1</sup>, G. Lemonnier<sup>1</sup>, E. Venturi<sup>3</sup>, C. Chevalyre<sup>3</sup>, J. Estellé<sup>1</sup>, and C. Rogel-Gailard<sup>1</sup>, <sup>1</sup>GABI, INRA, Jouy-en-Josas, France, <sup>2</sup>University of Alberta, Edmonton, AB, Canada, <sup>3</sup>ISP, INRA, Nouzilly, France.
- 11:45 OP93 **A first insight into the boar sperm microbiome.**  
M. Gòdia<sup>1</sup>, S. Lopez<sup>5</sup>, J. E. Rodríguez-Gil<sup>2</sup>, S. Balasch<sup>3</sup>, C. Lewis<sup>4</sup>, A. Castelló<sup>1</sup>, A. Clop\*<sup>1,6</sup>, and A. Sanchez<sup>1,2</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Valles, Catalonia, Spain, <sup>2</sup>Universitat Autònoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain, <sup>3</sup>Grup Gepork S.A, Masies de Roda, Catalonia, Spain, <sup>4</sup>PIC Europe, Sant Cugat del Vallés, Catalonia, Spain, <sup>5</sup>University of Barcelona, Barcelona, Catalonia, Spain, <sup>6</sup>Consejo Superior de Investigaciones Científicas (CSIC), Barcelona, Catalonia, Spain.
- 12:00 OP94 **Gene editing for resistance against diseases in pigs—What are the consequences of alternative strategies?**  
E. Jonas\*<sup>1</sup>, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- 12:15 **Committee business and new elections.**

**Ruminant Genetics and Genomics**

**Chair: Laercio Porto-Neto, CSIRO Agriculture  
Auditorium 1**

- 09:00 OP95 **Local ancestry and functional genomics of trypanotolerant and trypanosusceptible admixed African cattle breeds.**  
G. P. McHugo<sup>1</sup>, G. M. O’Gorman<sup>2</sup>, E. W. Hill<sup>1</sup>, and D. E. MacHugh<sup>\*1,3</sup>, <sup>1</sup>UCD School of Agriculture and Food Science, University College Dublin, Belfield, Ireland, <sup>2</sup>National Office of Animal Health Ltd, Enfield, UK, <sup>3</sup>UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Ireland.
- 09:15 OP96 **Resequencing the most Northern cattle breeds provides insight into their history and adaptation to cold.**  
L. Buggiotti<sup>1</sup>, A. Yurchenko<sup>2</sup>, H. D. Daetwyler<sup>3,4</sup>, C. J. Vander Jagt<sup>3</sup>, and D. M. Larkin<sup>\*1,2</sup>, <sup>1</sup>Royal Veterinary College, London, UK, <sup>2</sup>Institute of Cytology and Genetics, Novosibirsk, Russia, <sup>3</sup>Agriculture Victoria, Bundoora, Victoria, Australia, <sup>4</sup>La Trobe University, Bundoora, Victoria, Australia.
- 09:30 OP97 **Trends of CNV research in ruminants.**  
G. Liu<sup>\*</sup>, Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, USA.
- 09:45 OP98 **Multi-level conservation of chromosome conformation across livestock species reveals evolutionary links between genome structure and function.**  
S. Foissac<sup>\*1</sup>, S. Djebali<sup>1</sup>, N. Vialaneix<sup>2</sup>, M. Zytnicki<sup>2</sup>, A. Rau<sup>4</sup>, S. Lagarrigue<sup>3</sup>, H. Acloque<sup>4</sup>, and E. Giuffra<sup>4</sup>, <sup>1</sup>GenPhySE, INRA, Toulouse Auzeville, France, <sup>2</sup>MIAT, INRA, Toulouse Auzeville, France, <sup>3</sup>PEGASE, INRA, Rennes, France, <sup>4</sup>GABI, INRA, Paris Jouy-en-Josas, France.
- 10:00 OP99 **Epigenetic factors to face environmental variations in small ruminants.**  
L. Denoyelle<sup>\*1,3</sup>, P. de Villemereuil<sup>1</sup>, F. Boyer<sup>1</sup>, M. Khelifi<sup>1</sup>, C. Gaffe<sup>1</sup>, F. Alberto<sup>1</sup>, B. Benjelloun<sup>2,1</sup>, and F. Pompanon<sup>1</sup>, <sup>1</sup>Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, CNRS, LECA, Grenoble, France, <sup>2</sup>Institut National de la Recherche Agronomique Maroc (INRA-Maroc), Centre Régional de Beni Mellal, Beni Mellal, Morocco, <sup>3</sup>GenPhySE, INRA, INPT, ENVT, Université de Toulouse, Castanet-Tolosan, France.
- 10:15 OP100 **A scalable pipeline to scan for selective sweeps in whole-genome sequences: Application to bovine.**  
D. F. Cardoso<sup>\*1,2</sup>, L. R. Porto-Neto<sup>2</sup>, M. Naval-Sánchez<sup>2</sup>, H. Tonhati<sup>1</sup>, and A. Reverter<sup>2</sup>, <sup>1</sup>Department of Animal Science, School of Agricultural and Veterinarian Sciences, Sao Paulo State University (UNESP), Jaboticabal, SP, Brazil, <sup>2</sup>CSIRO Agriculture & Food, St. Lucia, Brisbane, Australia.

Coffee/Tea break

Foyer/Hall

10:30 – 11:00

- 11:00 OP101 **Identification of novel haplotypes and recessive lethal alleles affecting reproduction and its pleiotropic effects in cattle.**  
A. Cánovas<sup>\*1</sup>, S. Id-Lahoucine<sup>1</sup>, A. Suarez-Vega<sup>1</sup>, P. Fonseca<sup>1</sup>, S. P. Miller<sup>2</sup>, M. Lohuis<sup>3</sup>, F. Schenkel<sup>1</sup>, M. Sargolzaei<sup>1,4</sup>, F. Miglior<sup>1</sup>, J. F. Medrano<sup>5</sup>, and J. Casellas<sup>6</sup>, <sup>1</sup>University of Guelph, Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, Guelph, ON, Canada, <sup>2</sup>Angus Genetics Inc, Saint Joseph, MO, USA, <sup>3</sup>Semex Alliance, Guelph, ON, Canada, <sup>4</sup>Select Sires Inc, Plain City, Ohio, USA, <sup>5</sup>University of California-Davis, Department of Animal Science, Davis, CA, USA, <sup>6</sup>Universitat Autònoma de Barcelona, Bellaterra, Spain.
- 11:15 OP102 **Involvement of PRAMEY in the bovine sperm development and maturation.**  
W. Liu<sup>\*</sup>, C. Kern, and W. Feotosa, Department of Animal Science, Center for Reproductive Biology and Health (CRBH), College of Agricultural Sciences, The Pennsylvania State University, University Park, PA, USA.
- 11:30 OP103 **Investigating emerging inherited diseases in Australian livestock: A snapshot.**  
S. A. Woolley<sup>\*1</sup>, E. R. Tsimnadis<sup>1</sup>, R. L. Tulloch<sup>1</sup>, P. Hughes<sup>1</sup>, B. Hopkins<sup>1</sup>, S. E. Hayes<sup>1</sup>, M. R. Shariflou<sup>1</sup>, A. Bauer<sup>2</sup>, V. Jagannathan<sup>2</sup>, C. Drögemüller<sup>2</sup>, T. Leeb<sup>2</sup>, M. S. Khatkar<sup>1</sup>, C. E. Willet<sup>3</sup>, B. A. O’Rourke<sup>4</sup>, I. Tammen<sup>1</sup>, <sup>1</sup>The University of Sydney, Faculty of Science, Sydney School of Veterinary Science, Camden, NSW, Australia, <sup>2</sup>The University of Bern, Institute of Genetics, Vetsuisse Faculty, Bern, Switzerland, <sup>3</sup>The University of Sydney, Sydney Informatics Hub, Core Research Facilities, Sydney, NSW, Australia, <sup>4</sup>The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, NSW, Australia.
- 11:45 OP104 **A de novo mutation causes polledness and a modified shape of the skull in Fleckvieh cattle.**  
L. Gehrke<sup>1</sup>, M. Upadhyay<sup>\*2</sup>, K. Heidrich<sup>2</sup>, E. Kunz<sup>2</sup>, D. Seichter<sup>3</sup>, A. Graf<sup>2</sup>, S. Krebs<sup>2</sup>, A. Capitan<sup>4</sup>, G. Thaller<sup>1</sup>, and I. Medugorac<sup>2</sup>, <sup>1</sup>Christian-Albrechts-University Kiel, Kiel, Schleswig-Holstein, Germany, <sup>2</sup>Ludwig Maximilians University Munich, Munich, Bavaria, Germany, <sup>3</sup>Tierzuchforschung e.V. München, Grub, Bavaria, Germany, <sup>4</sup>GABI, INRA, AgroParisTech, Paris, France.



- 12:00 OP105 **Graph-based variant genotyping reveals natural sequence variants (NSVs) for targeted genome editing to enhance genetic resistance to *Mycobacterium bovis* infection in cattle.**  
 C. N. Correia\*<sup>1</sup>, D. Crysanto<sup>2</sup>, T. S. Sonstegard<sup>3</sup>, S. V. Gordon<sup>4,5</sup>, T. J. Hall<sup>1</sup>, J. Bostrom<sup>3</sup>, D. F. Carlson<sup>3</sup>, D. A. Simpson<sup>6</sup>, A. Margariti<sup>6</sup>, S. Kelaini<sup>6</sup>, H. Pausch<sup>2</sup>, and D. E. MacHugh<sup>1,5</sup>, <sup>1</sup>UCD School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, <sup>2</sup>Animal Genomics, Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland, <sup>3</sup>Recombinetics Inc, St Paul, MN, USA, <sup>4</sup>UCD School of Veterinary Medicine, University College Dublin, Dublin, Ireland, <sup>5</sup>UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland, <sup>6</sup>Centre for Experimental Medicine, Queen's University Belfast, Belfast, UK.
- 12:15 OP106 **Variants in the bovine X chromosome are relevant to predict bull fertility.**  
 M. R. S. Fortes\*<sup>1,2</sup>, L. R. Porto-Neto<sup>3</sup>, N. Satake<sup>4</sup>, L. T. Nguyen<sup>2</sup>, A. C. Freitas<sup>5</sup>, T. P. Melo<sup>5</sup>, B. Hayes<sup>2</sup>, F. S. Raidan<sup>3</sup>, A. Reverter<sup>3</sup>, and G. B. Boe-Hansen<sup>4</sup>, <sup>1</sup>School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Qld, Australia, <sup>2</sup>Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Brisbane, Qld, Australia, <sup>3</sup>CSIRO Agriculture and Food, Brisbane, Qld, Australia, <sup>4</sup>School of Veterinary Science, The University of Queensland, Gatton, Qld, Australia, <sup>5</sup>Universidade Estadual de Sao Paulo, Jaboticabal, SP, Brazil.
- 12:30 **Workshop Business Meeting.**

Lunch	Foyer/Hall	12:30 – 14:30
Animal Genetics Editorial Board Meeting (private invitation)	Boardroom 1	13:30 – 14:30
Introduction to FAANG (see below)	Auditorium 2	13:30 – 14:15
Illumina Vendor Presentation (see below)	Room 4	13:30 – 14:15

**Introduction to FAANG—Goals and Opportunities**

This presentation will introduce the goals and current activities of the global Functional Annotation of Animal Genomics (FAANG) Consortium, including the objectives of funded projects in several countries, as well as how newcomers can participate in FAANG. Two presentations will provide basic information to set the stage and substantial time has been set aside for audience participation in a Q&A session to follow.

- 13:30 Christopher Tuggle, Iowa State University
- 13:50 Elisabetta Giuffra, INRA.
- 14:10 Q&A

**Illumina Vendor Presentation: Accelerating Animal Genomic Breakthroughs**

- 13:30 Paul Flynn, head of Research and Development at Weatherbys Scientific, will give details on their latest collaboration with Illumina, their findings, and their new method of working with a high-throughput, low-turnaround time workflow to meet industry needs.
- 13:50 Jason Cruz, product manager for Array Market Development at Illumina, will introduce the genomic tools of today and the enhancements being made to help support the agriculture community in the future.

## ORAL SESSIONS

### Cattle Molecular Markers and Parentage Testing

Chair: **Rikke Vingborg, GenoScan A/S**  
**Room 3**

14:30	Welcoming remarks.
14:35	Cattle STR/SNP Comparison Test 2018-2019.
14:40	Presentation by Duty Lab.
14:55	Presentation of STR results.
15:10	Presentation of SNP results.
15:25	Evaluation of the results by the chair.
15:40	Next Comparison Test (2020-2021).

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

16:30	OP107	<b>Development of targeted GBS panels for breeding and parentage applications in cattle and swine.</b> A. Burrell <sup>1</sup> , P. Siddavatam <sup>1</sup> , M. Swimley <sup>1</sup> , C. Willis* <sup>1</sup> , M. de Groot <sup>2</sup> , R. Ferretti <sup>3</sup> , and R. Conrad <sup>1</sup> , <sup>1</sup> Thermo Fisher Scientific, Austin, TX, USA, <sup>2</sup> VHL Genetics, Wageningen, Netherlands, <sup>3</sup> Neogen GeneSeek, Lincoln, NE, USA.
16:50	OP108	<b>Poll diagnostics, scur genetics, and production concurrence in naturally hornless cattle.</b> I. A. S. Randhawa* <sup>1</sup> , M. R. McGowan <sup>1</sup> , L. R. Porto-Neto <sup>2</sup> , B. J. Hayes <sup>3</sup> , and R. E. Lyons <sup>1</sup> , <sup>1</sup> School of Veterinary Science, University of Queensland, Gatton, QLD, Australia, <sup>2</sup> Agriculture and Food, CSIRO, St Lucia, QLD, Australia, <sup>3</sup> Centre for Animal Science, Queensland Alliance for Agriculture and Food Innovation, University of Queensland, St Lucia, QLD, Australia.
17:10	OP109	<b>Validation of the OpenArray SNP assays for cattle parentage control.</b> A. Piestrzynska-Kajtoch*, D. Rubis, A. Fornal, A. Gurgul, I. Jasielczuk, and A. Radko, National Research Institute of Animal Production, Balice, Poland.
17:30		Election of committee.
17:40		Any other business.

### Comparative MHC Genetics: Populations and Polymorphism

Chair: **Sabine Hammer, Moredun Research Institute**  
**Room 5**

14:30		Welcoming remarks.
14:35	OP110	<b>Invited Workshop Presentation: IPD-MHC Database: Improving analysis tools to promote MHC research.</b> G. Maccari <sup>1,2</sup> , J. Robinson <sup>2,3</sup> , S. G. E. Marsh <sup>2,3</sup> , and J. A. Hammond* <sup>1</sup> , <sup>1</sup> The Pirbright Institute, Pirbright, Woking, UK, <sup>2</sup> Anthony Nolan Research Institute (ANRI), Royal Free Hospital, London, UK, <sup>3</sup> UCL Cancer Institute, Royal Free Campus, London, UK.



- 15:15 OP111 **Nomenclature for factors of the Swine Leukocyte Antigen (SLA) system: Update 2019.**  
S. E. Hammer<sup>\*1</sup>, J. K. Lunney<sup>2</sup>, A. Ando<sup>3</sup>, C. Rogel-Gaillard<sup>4</sup>, J.-H. Lee<sup>5</sup>, L. B. Schook<sup>6</sup>, and S. Ho<sup>7</sup>, <sup>1</sup>*Institute of Immunology, University of Veterinary Medicine Vienna, Vienna, Austria*, <sup>2</sup>*USDA, Beltsville, MD, USA*, <sup>3</sup>*Tokai University School of Medicine, Isehara, Japan*, <sup>4</sup>*GABI, INRA, Jouy-en-Josas, France*, <sup>5</sup>*Chungnam National University, Daejeon, Republic of Korea*, <sup>6</sup>*University of Illinois, Urbana, IL, USA*, <sup>7</sup>*Gift of Life Michigan, Ann Arbor, MI, USA*.
- 15:30 OP112 **Target resequencing for bovine major histocompatibility complex region.**  
S.-N. Takeshima<sup>\*1,2</sup>, A. Kawamura<sup>1</sup>, A. Ishida<sup>1</sup>, Y. Murakawa<sup>1</sup>, G. Giovambattista<sup>3</sup>, and Y. Aida<sup>2</sup>, <sup>1</sup>*Jumonji university, Niiza, Saitama, Japan*, <sup>2</sup>*Nakamura Laboratory, Baton Zone Program, RIKEN Cluster for Science, Technology and Innovation Hub, Wako, Saitama, Japan*, <sup>3</sup>*UNLP, La Plata, Argentina*.
- 15:45 OP113 **Bovine leukemia virus proviral load were associated with bovine MHC DRB3 and DQA1 alleles in Japanese Holstein population from 2011 to 2014.**  
Y. Aida<sup>\*1,2</sup>, S.-N. Takeshima<sup>1,3</sup>, A. Ohno<sup>2</sup>, and L. Borjigin<sup>1</sup>, <sup>1</sup>*Nakamura Laboratory, Baton Zone Program, RIKEN Cluster for Science, Technology and Innovation Hub, Wako, Saitama, Japan*, <sup>2</sup>*Viral Infectious Diseases Unit, RIKEN, Wako, Saitama, Japan*, <sup>3</sup>*Department of Food and Nutrition, Faculty of Human Life, Jumonji University, Niiza, Saitama, Japan*.
- Coffee/Tea break Foyer/Hall 16:00 – 16:30
- 16:30 OP114 **Assessing the genetic diversity of MHC-linked and non-MHC linked microsatellite markers in local chickens from four geographical regions.**  
P. Manjula<sup>\*</sup>, S. H. Cho, D. Seo, and J. H. Lee, *Division of Animal and Dairy Science, Chungnam National University, Daejeon, Republic of Korea*.
- 16:45 OP115 **Effectiveness of bovine leukemia virus (BLV) infection control strategies using cattle carrying resistant and susceptible bovine MHC DRB3 alleles.**  
L. Borjigin<sup>\*1</sup>, L. Bai<sup>2</sup>, T. Hirose<sup>1</sup>, H. Sato<sup>1</sup>, S. Watanuki<sup>1</sup>, S. Yoneyama<sup>3</sup>, M. Inokuma<sup>4</sup>, K. Fujita<sup>4</sup>, Y. Shinozaki<sup>5</sup>, R. Yamana-ka<sup>6</sup>, A. Yasui<sup>6</sup>, Y. Sohei<sup>6</sup>, M. Baba<sup>6</sup>, S.-N. Takeshima<sup>1,7</sup>, Y. Aida<sup>1</sup>, <sup>1</sup>*Nakamura Laboratory, Baton Zone Program, RIKEN Cluster for Science, Technology and Innovation Hub, Wako, Saitama, Japan*, <sup>2</sup>*Photonics Control Technology Team, RIKEN Center for Advanced Photonics, Wako, Saitama, Japan*, <sup>3</sup>*Kenou Livestock Hygiene Service Center, Utsunomiya, Tochigi, Japan*, <sup>4</sup>*Chuo Livestock Hygiene Service Center, Chiba, Japan*, <sup>5</sup>*Nanbu Livestock Hygiene Service Center, Chiba, Kamogawa, Japan*, <sup>6</sup>*Kumagaya Livestock Hygiene Service Center, Kumagaya, Saitama, Japan*, <sup>7</sup>*Department of Food and Nutrition, Jumonji University, Niiza, Saitama, Japan*.
- 17:00 OP116 **Characterization of bovine MHC DRB3 diversity in worldwide cattle breeds focusing on Myanmar cattle.**  
G. Giovambattista<sup>\*1,2</sup>, K. K. Moe<sup>1,3</sup>, M. Palati<sup>1</sup>, L. Borjigin<sup>1</sup>, H. H. Moe<sup>3</sup>, S.-N. Takeshima<sup>4</sup>, and Y. Aida<sup>1</sup>, <sup>1</sup>*Nakamura Laboratory, RIKEN Baton Zone Program, RIKEN Industrial Co-creation Program, Wako, Saitama, Japan*, <sup>2</sup>*IGEVET (UNLP-CON-ICET LA PLATA), Facultad de Ciencias Veterinarias UNLP, La Plata, Buenos Aires, Argentina*, <sup>3</sup>*University of Veterinary Science, Yezin, Nay Pyi Taw, Myanmar*, <sup>4</sup>*Department of Food and Nutrition, Faculty of Human Life, Jumonji University, Niiza-shi, Saitama, Japan*.
- 17:15 OP117 **Determination of MHC haplotypes in pure-breed Spanish horses using microsatellites.**  
L. Barrachina<sup>\*1,2</sup>, A. Cequier<sup>1</sup>, A. Vitoria<sup>1,2</sup>, C. Cons<sup>1</sup>, A. Sanz<sup>1</sup>, P. Zaragoza<sup>1</sup>, A. Romero<sup>1,2</sup>, FJ Vázquez<sup>1,2</sup>, and C. Rodellar<sup>1</sup>, <sup>1</sup>*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza), Instituto Agroalimentario de Aragón (Universidad de Zaragoza-CITA), Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, <sup>2</sup>*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.
- 17:30 **Workshop Business Meeting.**

**Domestic Animal Sequencing and Annotation**

**Chair: Jim Reecy, Iowa State University**  
**Auditorium 2**

- 14:30 OP118 **Invited Workshop Presentation: Navigating the genome with epigenome maps: Profiling *cis* regulatory elements at high-throughput and single-cell resolution.**  
J. Chiou<sup>1</sup>, J. Y. Han<sup>2</sup>, C. Zheng<sup>3</sup>, F. Cheng<sup>2</sup>, M. Schlichting<sup>3,4</sup>, S. Huang<sup>3,4</sup>, J. Wang<sup>3,4</sup>, Y. Sui<sup>3,4</sup>, A. Deogaygay<sup>3</sup>, M.-L. Okino<sup>3</sup>, Y. S. Sun<sup>3</sup>, P. Kudtarkar<sup>3</sup>, R. Fan<sup>3</sup>, M. Sander<sup>3,4</sup>, K. Galton<sup>3,5</sup>, S. Preissl<sup>2,4</sup>, and D. Gorkin<sup>\*2,4</sup>, <sup>1</sup>Biomedical Graduate Studies Program, University of California San Diego, La Jolla, CA, <sup>2</sup>Center for Epigenomics, University of California San Diego, La Jolla, CA, <sup>3</sup>Department of Pediatrics, University of California San Diego, La Jolla, CA, <sup>4</sup>Department of Cellular and Molecular Medicine, University of California San Diego, La Jolla, CA, <sup>5</sup>Institute for Genomic Medicine, University of California San Diego, La Jolla, CA.
- 15:15 OP119 **Update on the functional annotation of the equine genome project with a focus on histone modifications across tissues.**  
R. R. Bellone<sup>\*1,2</sup>, J. L. Petersen<sup>3</sup>, N. B. Kingsley<sup>2</sup>, C. Creppe<sup>4</sup>, S. Peng<sup>1</sup>, E. N. Burns<sup>1</sup>, T. Kalbfleisch<sup>5</sup>, C. Kern<sup>6</sup>, H. Zhou<sup>6</sup>, J.N. MacLeod<sup>5</sup>, and C. J. Finno<sup>1</sup>, <sup>1</sup>University of California-Davis, School of Veterinary Medicine, Department of Population Health and Reproduction, Davis, CA, USA, <sup>2</sup>University of California-Davis, School of Veterinary Medicine, Veterinary Genetics Laboratory, Davis, CA, USA, <sup>3</sup>University of Nebraska-Lincoln, Department of Animal Science, Lincoln, NE, USA, <sup>4</sup>Diagneode, Liège, Belgium, <sup>5</sup>University of Kentucky, Gluck Equine Research Center, Lexington, KY, USA, <sup>6</sup>University of California-Davis, Department of Animal Science, Davis, CA, USA.
- 15:30 OP120 **The Ovine FAANG Project: A high-resolution atlas of transcription start sites in the new Rambouillet sheep genome.**  
E. L. Clark<sup>\*1</sup>, M. Salavati<sup>1</sup>, I. Gazova<sup>1</sup>, R. Clark<sup>2</sup>, T. P. Smith<sup>3</sup>, K. C. Worley<sup>4</sup>, N. E. Cockett<sup>5</sup>, A. L. Archibald<sup>1</sup>, and B. Murdoch<sup>6</sup>, <sup>1</sup>The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>2</sup>Clinical Research Facility, University of Edinburgh, Edinburgh, UK, <sup>3</sup>USDA, ARS, USMARC, Clay Center, NE, USA, <sup>4</sup>Baylor College of Medicine, Houston, TX, USA, <sup>5</sup>Utah State University, Logan, UT, USA, <sup>6</sup>University of Idaho, Moscow, ID, USA.
- 15:45 OP121 **Genome-wide identification of functional DNA elements in the pig genome.**  
Z. Yunxia<sup>1</sup>, H. Mingyang<sup>1</sup>, H. Ye<sup>1</sup>, X. Yueyuan<sup>1</sup>, Z. Huanhuan<sup>1</sup>, F. Yuhua<sup>1</sup>, Y. Hongbo<sup>2</sup>, Y. Feng<sup>2</sup>, L. Xinyun<sup>1</sup>, and Z. Shuhong<sup>\*1</sup>, <sup>1</sup>Key Lab of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, China, <sup>2</sup>Department of Biochemistry and Molecular Biology, College of Medicine, The Pennsylvania State University, University Park, PA, USA.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 OP122 **The impact of the 1000 Bull Genomes Project and its future.**  
A. J. Chamberlain<sup>\*1</sup>, C. J. Vander Jagt<sup>1</sup>, R. Xiang<sup>2</sup>, M. E. Goddard<sup>1,2</sup>, I. M. MacLeod<sup>1</sup>, R. D. Schnabel<sup>3</sup>, B. J. Hayes<sup>4</sup>, and H. D. Daetwyler<sup>1,5</sup>, <sup>1</sup>Agriculture Victoria, Centre for AgriBiosciences, Bundoora, Victoria, Australia, <sup>2</sup>Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville, Victoria, Australia, <sup>3</sup>Division of Animal Sciences, Informatics Institute, University of Missouri, Columbia, MO, USA, <sup>4</sup>Centre for Animal Science, The University of Queensland, St Lucia, Queensland, Australia, <sup>5</sup>School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia.
- 16:45 OP123 **Analysis of alternative splicing events across cattle tissues by genome-wide integration of PacBio Iso-seq and RNA-Seq data.**  
H. Beiki, J. Koltjes, Z.-L. Hu, and J. Reecy\*, Iowa State University, Ames, IA, USA.
- 17:00 OP124 **BovReg: An international consortium for functional annotation of the bovine genome.**  
C. Kühn<sup>\*1</sup>, J. Vanselow<sup>1</sup>, C. Notredame<sup>2</sup>, D. Rocha<sup>3</sup>, D. Boichard<sup>3</sup>, D. Allaer<sup>4</sup>, C. Charlier<sup>5</sup>, H. Pausch<sup>6</sup>, Y. deHaas<sup>7</sup>, M. Lund<sup>8</sup>, J. Vilkki<sup>9</sup>, H. Taniguchi<sup>10</sup>, F. Meijboom<sup>11</sup>, D. Zerbino<sup>12</sup>, A. Rosati<sup>13</sup>, G. Plastow<sup>14</sup>, E. Clark<sup>15</sup>, J. Prendergast<sup>15</sup>, A. Bruce<sup>15</sup>, M. Schmicke<sup>16</sup>, A. Chamberlain<sup>17</sup>, H. Daetwyler<sup>17</sup>, V. Blanquet<sup>18</sup>, A. J. Amaral<sup>19</sup>, and D. Bruce<sup>20</sup>, <sup>1</sup>Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>2</sup>Centre for Genomic Regulation (CRG), Barcelona, Spain, <sup>3</sup>Institut National de Recherche Agronomique (INRA), Jouy-en-Josas, France, <sup>4</sup>DIAGENODE, Liege, Belgium, <sup>5</sup>GIGA, Université de Liège, Liege, Belgium, <sup>6</sup>Eidgenössische Technische Hochschule, Zuerich, Switzerland, <sup>7</sup>Stichting Wageningen Research, Wageningen, Netherlands, <sup>8</sup>Aarhus University, Foulum, Denmark, <sup>9</sup>Natural Resources Institute Finland (LUKE), Jokioinen, Finland, <sup>10</sup>Institute of Genetics and Breeding, Jastrebic, Poland, <sup>11</sup>University Utrecht, Utrecht, Netherlands, <sup>12</sup>European Molecular Biology Laboratory (EMBL-EBI), Hinxton, UK, <sup>13</sup>European Association for Animal Production, Rome, Italy, <sup>14</sup>University of Alberta, Edmonton, Canada, <sup>15</sup>The University of Edinburgh, Edinburgh, UK, <sup>16</sup>Stiftung Tierärztliche Hochschule Hannover, Hannover, Germany, <sup>17</sup>Agriculture Victoria, Centre for AgriBiosciences, Bundoora, Australia, <sup>18</sup>University of Limoges, Limoges, France, <sup>19</sup>Centre for Interdisciplinary in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, <sup>20</sup>Edinethics Ltd., Edinburgh, UK.

- 17:15 OP125 **Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks.**  
M. Farré<sup>1</sup>, J. Kim<sup>2</sup>, A. A. Proskuryakova<sup>3,4</sup>, Y. Zhang<sup>5</sup>, A. I. Kulemzina<sup>3</sup>, Q. Li<sup>6</sup>, Y. Zhou<sup>6</sup>, Y. Xiong<sup>6</sup>, J. L. Johnson<sup>7</sup>, P. L. Perelman<sup>3,4</sup>, W. E. Johnson<sup>8,9</sup>, W. Warren<sup>10</sup>, A. V. Kukekova<sup>7</sup>, G. Zhang<sup>6,11,12</sup>, S. J. O'Brien<sup>13</sup>, O. A. Ryder<sup>14</sup>, A. S. Graphodatsky<sup>3,4</sup>, J. Ma<sup>5</sup>, H. A. Lewin<sup>15</sup>, D. M. Larkin<sup>\*1,16</sup>, <sup>1</sup>Royal Veterinary College, University of London, London, UK, <sup>2</sup>Konkuk University, Seoul, Korea, <sup>3</sup>Institute of Molecular and Cellular Biology, Novosibirsk, Russia, <sup>4</sup>Novosibirsk State University, Novosibirsk, Russia, <sup>5</sup>Carnegie Mellon University, Pittsburgh, PA, USA, <sup>6</sup>BGI-Shenzhen, Shenzhen, China, <sup>7</sup>University of Illinois at Urbana-Champaign, Urbana, IL, USA, <sup>8</sup>Smithsonian Conservation Biology Institute, Front Royal, VA, USA, <sup>9</sup>Smithsonian Institution, Suitland, MD, USA, <sup>10</sup>Washington University School of Medicine, St. Louis, MO, USA, <sup>11</sup>Kunming Institute of Zoology, Kunming, China, <sup>12</sup>University of Copenhagen, Copenhagen, Denmark, <sup>13</sup>St. Petersburg State University, St. Petersburg, Russian Federation, <sup>14</sup>San Diego Zoo, Escondido, CA, USA, <sup>15</sup>University of California, Davis, Davis, CA, USA, <sup>16</sup>The Federal Research Center Institute of Cytology and Genetics, Novosibirsk, Russia.
- 17:30 OP126 **eMIRNA: A comprehensive pipeline for discovery and annotation of microRNAs in multiple species.**  
E. Mármol-Sánchez<sup>\*1</sup>, S. Cirera<sup>2</sup>, R. Quintanilla<sup>3</sup>, A. Pla<sup>4</sup>, and M. Amills<sup>1,5</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>2</sup>Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark, <sup>3</sup>Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimón, Caldes de Montbui, Spain, <sup>4</sup>Department of Medical Genetics, University of Oslo, Oslo, Norway, <sup>5</sup>Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.
- 17:45 **Workshop Business Meeting.**

## Genome Edited Animals

Chair: **Bruce Whitelaw, University of Edinburgh**  
**Auditorium 1**

- 14:30 **Introduction.**  
Bruce Whitelaw, University of Edinburgh.
- 14:45 OP128 **A genome-wide CRISPR library for high-throughput genetic screening in pig cells.**  
S. Xie<sup>\*</sup>, C. Zhao, H. Liu, T. Xiao, X. Cheng, X. Nie, X. Han, C. Li, X. Li, D. Zhang, and S. Zhao, *Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Lab of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, China.*
- 15:00 OP129 **Precision editing for IAV resistance in pig cells.**  
Y. Du<sup>\*1,2</sup>, S. Lilloco<sup>1</sup>, C. Proudfoot<sup>1</sup>, and B. Whitelaw<sup>1</sup>, <sup>1</sup>The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>2</sup>Radcliffe Department of Medicine, University of Oxford, Oxford, UK.
- 15:15 OP130 **Programmable base editing of the goat and sheep genomes for genetic improvement.**  
S. Zhou<sup>1</sup>, G. Li<sup>1</sup>, B. Cai<sup>1</sup>, C. Li<sup>1</sup>, B. Ma<sup>1</sup>, H. Yu<sup>2</sup>, B. Petersen<sup>3</sup>, T. Sonstegard<sup>4</sup>, X. Huang<sup>5</sup>, Y. Chen<sup>1</sup>, and X. Wang<sup>\*1</sup>, <sup>1</sup>Northwest A&F University, Yangling, Xianyang, China, <sup>2</sup>Guilin Medical University, Guilin, China, <sup>3</sup>Institute of Farm Animal Genetics, Friedrich-Loeffler-Institut, Neustadt, Germany, <sup>4</sup>Recombinetics, Saint Paul, MN, USA, <sup>5</sup>School of Life Science and Technology, ShanghaiTech University, Shanghai, China.
- 15:30 OP131 **Trio-based deep sequencing reveals rare off-target mutations in Cas9-edited animals and their offspring.**  
C. Li<sup>1</sup>, S. Zhou<sup>1</sup>, Y. Jiang<sup>1</sup>, B. Ma<sup>1</sup>, T. Sonstegard<sup>2</sup>, X. Huang<sup>3</sup>, B. Petersen<sup>4</sup>, Y. Chen<sup>1</sup>, and X. Wang<sup>\*1</sup>, <sup>1</sup>Northwest A&F University, Yangling, China, <sup>2</sup>Recombinetics, Saint Paul, MN, USA, <sup>3</sup>School of Life Science and Technology, ShanghaiTech University, Shanghai, China, <sup>4</sup>Institute of Farm Animal Genetics, FLI, Neustadt, Germany.
- 15:45 OP132 **Efforts to produce genetically edited goats that carry the ovine callipyge mutation.**  
T. Hadfield<sup>\*1</sup>, M. Regouski<sup>1</sup>, C. Reichhardt<sup>1</sup>, C. Bidwell<sup>3</sup>, K. Thornton<sup>1</sup>, S. Fahrenkrug<sup>2</sup>, D. Webster<sup>2</sup>, D. F. Carlson<sup>2</sup>, I. A. Polejaeva<sup>1</sup>, and N. Cockett<sup>1</sup>, <sup>1</sup>Utah State University, Logan, UT, USA, <sup>2</sup>Recombinetics Inc, St. Paul, MN, USA, <sup>3</sup>Purdue University, West Lafayette, IN, USA.



- 16:30 OP133 **Generation of pigs with a Belgian Blue mutation in *MSTN* using CRISPR/Cpf1-assisted ssODN-mediated homologous recombination.**  
Y. Zou<sup>1,2</sup>, Z. Li<sup>2</sup>, Y. Zou<sup>3</sup>, H. Hao<sup>2</sup>, J. Hu<sup>2</sup>, N. Li<sup>2</sup>, and Q. Li<sup>\*2</sup>, <sup>1</sup>State Key Laboratory of Silkworm Genome Biology, Key Laboratory of Sericultural Biology and Genetic Breeding, Ministry of Agriculture, College of Biotechnology, Southwest University, Chongqing China, <sup>2</sup>State Key Laboratory for Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing China, <sup>3</sup>College of Veterinary Medicine, China Agricultural University, Beijing China.
- 16:45 OP134 **Transgene insertion site mapping in a goat TGF- $\beta$  biomedical model of atrial fibrillation.**  
A. J. Thomas<sup>1,2</sup>, K. P. Morgado<sup>1,2</sup>, M. Regouski<sup>2</sup>, R. Ranjan<sup>3</sup>, I. A. Polejaeva<sup>2</sup>, and C. J. Davies<sup>\*1,2</sup>, <sup>1</sup>Center for Integrated BioSystems, Utah State University, Logan, UT, USA, <sup>2</sup>Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, UT, USA, <sup>3</sup>Department of Internal Medicine, Division of Cardiovascular Medicine, University of Utah, Salt Lake City, UT, USA.
- 17:00 OP135 **Loss of GHR in GHR knockout pig model leads to hepatic steatosis via PPAR $\alpha$  signaling.**  
Q. Han, H. Chen, and R. Zhang<sup>\*</sup>, China Agricultural University, Beijing, China.
- 17:15 OP136 **Transgenic chickens generating through targeting PGC with antibody-directed lentiviral.**  
Z. Jiang<sup>\*1,2</sup>, H. Wu<sup>1,2</sup>, J. Tian<sup>1,2</sup>, and X. Hu<sup>1,2</sup>, <sup>1</sup>College of Biological Sciences, China Agricultural University, Beijing, China, <sup>2</sup>State Key Laboratory of Agro-biotechnology, China Agricultural University, Beijing, China.
- 17:30 OP137 **In vitro transfection of chicken primordial germ cells and generation of cell-chimeric chicken using the Sleeping Beauty transposon system.**  
S. Altgilbers<sup>\*</sup>, S. Klein, W. A. Kues, and S. Weigend, Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Mariensee, Neustadt, Germany.
- 17:45 OP138 **Genome modification in chicken for therapeutic protein production.**  
Y. M. Kim<sup>\*</sup>, Y. H. Park, J. M. Kim, J. S. Park, H. J. Lee, K. Y. Lee, and J. Y. Han, Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.

## ISAG-FAO Genetic Diversity

Chair: Catarina Ginja, CIBIO-InBIO, Universidade do Porto  
Room 4

- 14:30 OP139 **Invited Workshop Presentation: Towards a sustainable management of farm animal genetic diversity in the era of whole-genome data: The case of sheep and goats.**  
F. Pampanon<sup>\*1</sup> and B. Benjelloun<sup>2</sup>, <sup>1</sup>Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, CNRS, LECA, Grenoble, France, <sup>2</sup>Institut National de la Recherche Agronomique Maroc (INRA-Maroc), Morocco.
- 15:00 OP140 **Genetic characterization of cattle populations for optimized performance in African ecosystems.**  
R. Crooijmans<sup>\*1</sup>, N. Ghanem<sup>2</sup>, C. Ginja<sup>3</sup>, D. Kugonza<sup>4</sup>, L. Makgahlela<sup>5</sup>, and J. Kantanen<sup>6</sup>, <sup>1</sup>Animal Breeding and Genomics, Wageningen University and Research, Wageningen, the Netherlands, <sup>2</sup>Animal Production Department, Faculty of Agriculture, Cairo University, Giza, Egypt, <sup>3</sup>Centro de Investigação em Biodiversidade e Recursos Genéticos, University of Porto, Porto, Portugal, <sup>4</sup>Animal breeding and Genetics, Makerere University, Kampala, Uganda, <sup>5</sup>Animal breeding and Genetics, Agricultural Research Council, Pretoria, South Africa, <sup>6</sup>Natural Resources Institute Finland, Jokioinen, Finland.
- 15:15 OP141 **Towards a complete genomic characterization of African indigenous cattle.**  
A. Tijjani<sup>\*1,3</sup>, K. Marshal<sup>2,3</sup>, H. Kim<sup>4,5</sup>, H. Jianlin<sup>2,6</sup>, and O. Hanotte<sup>7,8</sup>, <sup>1</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>2</sup>International livestock Research Institute (ILRI), Nairobi, Kenya, <sup>3</sup>Center for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>4</sup>Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea, <sup>5</sup>C&K genomics, Seoul National University Research Park, Seoul, Republic of Korea, <sup>6</sup>ILRI-CAAS Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China, <sup>7</sup>LiveGene-CTLGH, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>8</sup>Cells, Organism and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, UK.

- 15:30 OP142 **Genomic diversity and differentiation of Iberian native cattle.**  
R. da Fonseca<sup>1,2</sup>, I. Ureña<sup>3</sup>, S. Alfonso<sup>3</sup>, A. E. Pires<sup>3,4</sup>, E. Jørsboe<sup>2</sup>, L. Chikhi<sup>5,6</sup>, and C. Ginja<sup>3</sup>, <sup>1</sup>Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark, <sup>2</sup>The Bioinformatics Centre, Department of Biology, University of Copenhagen, Copenhagen, Denmark, <sup>3</sup>CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal, <sup>4</sup>LARC, Laboratório de Arqueociências, Direcção Geral do Património Cultural, Lisboa, Portugal, <sup>5</sup>Laboratoire Évolution et Diversité Biologique, Université de Toulouse Midi-Pyrénées, CNRS, Toulouse, France, <sup>6</sup>Instituto Gulbenkian de Ciência, Oeiras, Portugal.
- 15:45 OP143 **Integrating in situ and ex situ genomic data of domestic chicken breeds for conservation in China.**  
M. Zhang\* and K. Wu, China Agricultural University, Beijing, China.
- Coffee/Tea break Foyer/Hall 16:00 – 16:30
- 16:30 OP144 **Investigating introgression of river-buffalo loci in the genome of Brazilian Carabao swamp buffaloes.**  
M. Barbato<sup>1</sup>, L. Colli<sup>1</sup>, M. Milanese<sup>2,3</sup>, Y. T. Utsunomiya<sup>2,3</sup>, J. R. V. Herrera<sup>4</sup>, L. Cruz<sup>4</sup>, P. Baruselli<sup>5</sup>, M. M. J. Amaral<sup>6</sup>, M. G. Drummond<sup>7</sup>, J. F. Garcia<sup>2,3</sup>, J. L. W. Williams<sup>8</sup>, International Buffalo Consortium<sup>8</sup>, and P. Ajmone-Marsan\*<sup>1</sup>, <sup>1</sup>Department of Animal Science, Food and Nutrition - DIANA, Università Cattolica del S. Cuore, Piacenza, Italy, <sup>2</sup>Universidade Estadual Paulista "Júlio de Mesquita Filho," Faculdade de Medicina Veterinária de Araçatuba, Araçatuba, Brazil, <sup>3</sup>International Atomic Energy Agency (IAEA), Collaborating Centre on Animal Genomics and Bioinformatics, Araçatuba, Brazil, <sup>4</sup>Philippine Carabao Centre, Nueva Ecija, Philippines, <sup>5</sup>Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, Brazil, <sup>6</sup>Instituto de Biociências, Letras e Ciências Exatas, Universidade Estadual Paulista, São José do Rio Preto, Brazil, <sup>7</sup>R&D Department, Myleus, Belo Horizonte, Brazil, <sup>8</sup>The Davies Research Centre, School of Animal and Veterinary Science, University of Adelaide, Roseworthy, SA, Australia.
- 16:45 OP145 **Y-chromosomal haplotyping in horses—New achievements and future potentials.**  
S. Felkel, V. Dobretberger, D. Rigler, C. Vogl, G. Brem, and B. Wallner\*, University of Veterinary Medicine Vienna, Vienna, Austria.
- 17:00 OP146 **Introgression with domestic goats has expanded the genetic variability of the Spanish ibex.**  
T. Figueiredo-Cardoso<sup>1</sup>, R. Tonda<sup>2</sup>, M. G. Luigi-Sierra<sup>1</sup>, A. Castelló<sup>1,3</sup>, B. Cabrera<sup>1,3</sup>, A. Noce<sup>1</sup>, S. Beltrán<sup>2</sup>, R. García-González<sup>4</sup>, A. Fernández-Arias<sup>5</sup>, J. Folch<sup>6</sup>, A. Sánchez<sup>1,3</sup>, A. Clop<sup>1</sup>, and M. Amills\*<sup>1,3</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>2</sup>Centre Nacional d'Anàlisi Genòmica-Centre for Genomic Regulation (CRG), Barcelona, Barcelona, Spain, <sup>3</sup>Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>4</sup>Instituto Pirenaico de Ecología (IPE-CSIC), Spain, <sup>5</sup>Servicio de Investigación Agroalimentaria, Spain, <sup>6</sup>Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Zaragoza, Spain.
- 17:15 OP147 **Unraveling the genomic diversity and population structure of 20 autochthonous European pig breeds.**  
M. Muñoz\*<sup>1</sup>, R. Bozzi<sup>2</sup>, J. M. García-Casco<sup>1</sup>, Y. Núñez<sup>1</sup>, A. Ribani<sup>3</sup>, M. Škrlep<sup>4</sup>, R. Quintanilla<sup>5</sup>, M. J. Mercat<sup>6</sup>, J. Riquet<sup>7</sup>, J. Estellé<sup>8</sup>, M. Candek-Potokar<sup>4</sup>, A. I. Fernández<sup>1</sup>, L. Fontanesi<sup>3</sup>, and C. Óvilo<sup>1</sup>, <sup>1</sup>Departamento Mejora Genética Animal, INIA, Madrid, Spain, <sup>2</sup>DAGRI, Animal Science Section, Università degli Studi di Firenze, Firenze, Italy, <sup>3</sup>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, <sup>4</sup>Kmetijski inštitut Slovenije, Ljubljana, Slovenia, <sup>5</sup>IRTA, Programa de Genética y Mejora Animal, Barcelona, Spain, <sup>6</sup>IFIP – Institut du Porc, Le Rheu, France, <sup>7</sup>INRA, Génétique Physiologie et Système d'Élevage, Castanet-Tolosan, France, <sup>8</sup>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France.
- 17:30 OP148 **IMAGE: Innovative Management of Animal Genetic Resources.**  
O. Cortes\*<sup>1</sup>, L. T. Gama<sup>2</sup>, S. Dunner<sup>1</sup>, IMAGE Consortium<sup>3</sup>, and M. Tixier-Boichard<sup>3</sup>, <sup>1</sup>Veterinary Faculty, University Complutense of Madrid, Madrid, Spain, <sup>2</sup>CIISA, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal, <sup>3</sup>INRA, France.
- 17:45 OP149 **Sequencing of reindeer (*Rangifer tarandus*) genomes: Insights into evolution, domestication, and adaptation.**  
M. Weldenogdguad<sup>1,2</sup>, K. Pokharel<sup>1</sup>, Y. Ming<sup>3</sup>, M. Honkatukia<sup>1,4</sup>, J. Peippo<sup>1</sup>, T. Reilas<sup>1</sup>, K. H. Røed<sup>5</sup>, and J. Kantanen\*<sup>1</sup>, <sup>1</sup>Natural Resources Institute Finland, Jokioinen, Finland, <sup>2</sup>Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland, <sup>3</sup>BGI-Tech, Guangdong, China, <sup>4</sup>NordGen Nordic Genetic Resources Centre, Ås, Norway, <sup>5</sup>Norwegian University of Life Sciences, Oslo, Norway.
- 18:00 **Workshop Committee Business Meeting.**

## Wednesday, July 10

Exhibition and Posters Open	Poster Room	08:00 – 13:00
Registration Desk Open	Hall	08:00 – 13:00

### ORAL SESSIONS

#### Plenary Session II

Chairs: **Cristina Óvilo, INIA - Instituto Nacional Investigación y Tecnología Agraria y Alimentaria, and Jordi Estellé, INRA (Institut National de la Recherche Agronomique)**  
**Auditorium 1**

08:30	OP150	<b>EMBL-EBI, changes in the reference genomes sequence and archive.</b> A. Frankish*, <i>EMBL-EBI, United Kingdom.</i>
09:30	OP151	<b>Evolutionary changes in sequence, regulation, and gene expression between <i>Bos taurus</i> and <i>Bos indicus</i>.</b> M. Naval-Sánchez* <sup>1</sup> , M. Menzies <sup>1</sup> , L. R. Porto-Neto <sup>1</sup> , D. F. Cardoso <sup>1,2</sup> , C. Kern <sup>3</sup> , M. Halstead <sup>3</sup> , M. R. S. Fortes <sup>4</sup> , A. Cánovas <sup>5</sup> , B. J. Hayes <sup>6</sup> , H. D. Daetwyler <sup>7,8</sup> , P. J. Ross <sup>3</sup> , H. Zhou <sup>3</sup> , J. Kijas <sup>1</sup> , and A. Reverter <sup>1</sup> , <sup>1</sup> <i>CSIRO Agriculture &amp; Food, St. Lucia, QLD, Australia</i> , <sup>2</sup> <i>Department of Animal Science, School of Agricultural and Veterinarian Sciences, Sao Paulo State University (UNESP), Jaboticabal, SP, Brazil</i> , <sup>3</sup> <i>Department of Animal Science, University of California Davis, Davis, CA, USA</i> , <sup>4</sup> <i>School of Chemistry and Molecular Biosciences, The University of Queensland, Queensland, Australia</i> , <sup>5</sup> <i>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada</i> , <sup>6</sup> <i>Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Queensland, Australia</i> , <sup>7</sup> <i>Agriculture Victoria, AgriBio, Centre for AgriBioscience, Centre for, Bundoora, Victoria, Australia</i> , <sup>8</sup> <i>School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia.</i>

Coffee/Tea break	Foyer/Hall	10:30 – 11:00
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11:00	OP152	<b>Integrative genomics and network biology in livestock species: New knowledge from existing (and elderly!) data sets.</b> D. E. MacHugh*, <i>UCD School of Agriculture and Food Science, University College Dublin, Belfield, Ireland.</i>
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Packed Lunch	Hall	12:00 – 13:00
Tour 4—Land of History	Mid-Conference Tours	12:30 – 19:00
Tour 7—Barcelona on Your Own	Mid-Conference Tours	12:30 – 20:30
Tour 8—Modernist Barcelona	Mid-Conference Tours	12:30 – 20:30
Tour 2—Romanesque Lleida	Mid-Conference Tours	13:00 – 18:00
Tour 3—Land of Olives and Wine	Mid-Conference Tours	13:00 – 19:00
Tour 5—Land of Character	Mid-Conference Tours	13:00 – 18:00
Tour 6—Land of Nature	Mid-Conference Tours	13:00 – 19:00
Tour 1—Musical Lleida	Mid-Conference Tours	18:30 – 20:00

## Thursday, July 11

Exhibition and Posters Open	Poster Room	08:00 – 18:00
Registration Desk Open	Hall	08:00 – 18:00

### ORAL SESSIONS

#### Plenary Session III

Chairs: **Masaaki Taniguchi, NIAS, National Institute of Agrobiological Sciences,**  
**and Marcel Amills, Center for Research in Agricultural Genomics (CRAG), Universitat Autònoma**  
**de Barcelona**  
**Auditorium 1**

09:00	OP153	<b>Transgenerational epigenetic inheritance: How strong is the evidence?</b> H. Khatib*, <i>Department of Animal Sciences, University of Wisconsin-Madison, Madison, WI, USA.</i>
09:45	OP154	<b>Whole-genome sequencing of 722 canids reveals novel genomic regions under selection and variants influencing morphology and longevity.</b> J. Plassais <sup>1</sup> , J. Kim <sup>1</sup> , B. W. Davis <sup>1,2</sup> , D. M. Karyadi <sup>1</sup> , A. N. Hogan <sup>1</sup> , A. C. Harris <sup>1</sup> , B. Decker <sup>1,2</sup> , H. G. Parker <sup>1</sup> , and E. A. Ostrander* <sup>1</sup> , <sup>1</sup> <i>National Institutes of Health, Bethesda, MD, USA</i> , <sup>2</sup> <i>Texas A&amp;M University, College Station, TX, USA</i> , <sup>3</sup> <i>Brigham and Women's Hospital, Boston, MA, USA.</i>

Coffee/Tea break	Foyer/Hall	10:30 – 11:00
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11:00	OP155	<b>Update on the analysis and applications of microbiome information.</b> C. Rogel-Gaillard*, <i>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France.</i>
11:45	OP156	<b>Making the best of large datasets when sequence analysis methods do not scale.</b> C. Notredame*, <i>Centre for Genomic Regulation (CRG), Barcelona Institute for Science and Technology, Barcelona, Spain.</i>

Lunch	Foyer	12:30 – 14:30
Neogen Vendor Presentation (title and speakers to be announced)	Room 4	13:30 – 14:15
ION-BRU and IBER-ION, a presentation of Nanopore users associations Amanda Warr, The Roslin Institute, and Oscar González-Recio, INIA	Room 3	13:30 – 14:30

## ORAL SESSIONS

### Applied Sheep and Goat Genetics

Chair: **Gesine Luhken, University of Giessen**  
**Room 3**

- 14:30 OP157 **Invited Workshop Presentation: AdaptMap project: Exploring worldwide goat diversity and adaptation.**  
L. Colli\*<sup>1</sup>, E. L. Nicolazzi<sup>1</sup>, F. Bertolini<sup>3,4</sup>, C. P. Van Tassell<sup>5</sup>, M. F. Rothschild<sup>3</sup>, B. D. Rosen<sup>5</sup>, T. S. Sonstegard<sup>6</sup>, B. Sayre<sup>7</sup>, P. Ajmone-Marsan<sup>1</sup>, P. Crepaldi<sup>8</sup>, G. Tosser-Klopp<sup>9</sup>, S. Joost<sup>10</sup>, A. Stella<sup>11</sup>, and AdaptMap Consortium<sup>12</sup>, <sup>1</sup>DIANA Department of Animal Science, Food and Nutrition & BioDNA Research Centre on Biodiversity and Ancient DNA, Università Cattolica del S. Cuore, Piacenza, Italy, <sup>2</sup>Fondazione Parco Tecnologico Padano, Lodi, Italy, <sup>3</sup>Department of Animal Science, Iowa State University, Ames, IA, USA, <sup>4</sup>National center of aquatic resources, Technical University of Denmark, Lyngby, Denmark, <sup>5</sup>Animal Genomics and Improvement Laboratory, USDA, Agricultural Research Service, Beltsville, MD, USA, <sup>6</sup>Acceligen Inc, St. Paul, MN, USA, <sup>7</sup>Department of Biology, Virginia State University, Petersburg, VA, USA, <sup>8</sup>Dipartimento di Medicina Veterinaria, University of Milan, Milan, Italy, <sup>9</sup>GenPhySE, INRA, Université de Toulouse, INPT, ENVT, Castanet Tolosan, France, <sup>10</sup>Laboratory of Geographic Information Systems (LASIG), School of Architecture, Civil and Environmental Engineering (ENAC), École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland, <sup>11</sup>Istituto di Biologia e Biotecnologia Agraria, Consiglio Nazionale delle Ricerche, Milan, Italy, <sup>12</sup>www.goatadaptmap.org.
- 15:00 OP158 **Flock54: A new targeted marker panel for the sheep industry.**  
L. Eidman<sup>1</sup>, J. Thorne<sup>2,3</sup>, M. Duan<sup>2,4</sup>, S. Hunter<sup>5</sup>, K. Davenport<sup>2</sup>, G. Becker<sup>2</sup>, and B. Murdoch\*<sup>2</sup>, <sup>1</sup>Superior Farms, Dixon, CA, USA, <sup>2</sup>Animal and Veterinary Science, University of Idaho, Moscow, ID, USA, <sup>3</sup>Texas A&M, ArgLife Research and Extension Center, San Angelo, TX, USA, <sup>4</sup>School of Molecular Biosciences, Washington State University, Pullman, WA, USA, <sup>5</sup>IBEST Genomics Resource Core, University of Idaho, Moscow, ID, USA.
- 15:15 OP159 **Effect of genotyping strategies in the sustained genetic gain across multiple generations of selection using ssGBLUP.**  
M. Sánchez-Mayor\*<sup>1</sup>, V. Riggio<sup>2</sup>, L. F. de la Fuente<sup>1</sup>, B. Gutiérrez-Gil<sup>1</sup>, J. J. Arranz<sup>1</sup>, and R. Pong-Wong<sup>2</sup>, <sup>1</sup>Dpto. Producción Animal, Universidad de León, León, Spain, <sup>2</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Roslin, Midlothian, UK.
- 15:30 OP160 **Genome-wide association with footrot in hair and wool sheep.**  
M. U. Cinar<sup>1,2</sup>, R. D. Oliveira<sup>1</sup>, T. S. Hadfield<sup>3</sup>, A. Lichtenwalner<sup>4,5</sup>, R. J. Brzozowski<sup>5</sup>, C. T. Settlemire<sup>6</sup>, S. B. Schoenian<sup>7</sup>, C. Parke<sup>8</sup>, H. L. Neibergs<sup>9,10</sup>, N. Cockett<sup>3</sup>, and S. N. White\*<sup>11,1</sup>, <sup>1</sup>Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, <sup>2</sup>Faculty of Agriculture, Erciyes University, Kayseri, Turkey, <sup>3</sup>Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, UT, USA, <sup>4</sup>Department of Animal and Veterinary Science, University of Maine, Orono, ME, USA, <sup>5</sup>Cooperative Extension, University of Maine, Falmouth, ME, USA, <sup>6</sup>Departments of Biology and Chemistry, Bowdoin College, Brunswick, ME, USA, <sup>7</sup>Western Maryland Research & Education Center, University of Maryland, Keedysville, MD, USA, <sup>8</sup>Retired, Ohio, USA, <sup>9</sup>Department of Animal Science, Washington State University, Pullman, WA, USA, <sup>10</sup>Center for Reproductive Biology, Washington State University, Pullman, WA, USA, <sup>11</sup>USDA-ARS Animal Disease Research, Pullman, WA, USA.
- 15:45 OP161 **Genomic background of heat stress in Assaf sheep.**  
M. J. Carabaño\*<sup>1</sup>, I. Ureña<sup>1</sup>, J. H. Calvo<sup>2</sup>, M. A. Jiménez<sup>3</sup>, M. Ramon<sup>4</sup>, C. Díaz<sup>1</sup>, F. Freire<sup>3</sup>, and M. Serrano<sup>1</sup>, <sup>1</sup>INIA, Madrid, Spain, <sup>2</sup>CITA-ARAID, Zaragoza, Spain, <sup>3</sup>ASSAFE, Toro, Spain, <sup>4</sup>IRIAF, Valdepeñas, Spain.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 OP162 **Functional fertility genomics in sheep (*Ovis aries*).**  
K. Pokharel\*<sup>1</sup>, J. Peippo<sup>1</sup>, M. Honkatukia<sup>2</sup>, M.-H. Li<sup>3</sup>, and J. Kantanen<sup>1</sup>, <sup>1</sup>Natural Resources Institute Finland, Jokioinen, Finland, <sup>2</sup>Nordgen – The Nordic Genetic Resources Center, Ås, Norway, <sup>3</sup>Chinese Academy of Sciences (CAS), Beijing, China.
- 16:45 OP163 **Genetic diagnosis of sex chromosome aberrations in sheep based on parentage test by microsatellite DNA and analysis of X- and Y-linked markers.**  
J. A. Bouzada\*<sup>1</sup>, J. M. Lozano, M. R. Maya, A. Trigo, L. B. Pitarch, T. Mayoral, and E. Anadón, Laboratorio Central de Veterinaria, Algete (Madrid) Spain.



- 17:00 OP164 **Selection signatures in goat breeds reveal the molecular basis for six different coat color phenotypes.**  
J. Henkel\*<sup>1</sup>, R. Saif<sup>1,2</sup>, V. Jagannathan<sup>1</sup>, C. Drögemüller<sup>1</sup>, C. Flury<sup>3</sup>, and T. Leeb<sup>1</sup>, <sup>1</sup>*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, <sup>2</sup>*Institute of Biotechnology, Gulab Devi Educational Complex, Lahore, Pakistan*, <sup>3</sup>*School of Agricultural, Forest and Food Sciences HAFL, Bern University of Applied Sciences, Zollikofen, Switzerland*.
- 17:15 OP165 **Polled intersex syndrome (PIS) in goats—Nanopore sequencing revealed a complex structural variant and made it possible to devise a simple genetic test for identification of intersexual goats.**  
R. Simon\*<sup>1</sup>, H. Tschanz-Lischer<sup>2</sup>, I. Keller<sup>2</sup>, I. Häfliger<sup>3</sup>, A. Pienkowska-Schelling<sup>3</sup>, C. Schelling<sup>4</sup>, C. Drögemüller<sup>3</sup>, and G. Lühken<sup>1</sup>, <sup>1</sup>*Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Germany*, <sup>2</sup>*Interfaculty Bioinformatics Unit, University of Bern, Bern, Switzerland*, <sup>3</sup>*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, <sup>4</sup>*Clinic for Reproductive Medicine, Vetsuisse Faculty, University of Zürich, Zürich, Switzerland*.
- 17:30 PM **Sheep CT Discussion.**
- 17:40 PM **Goat CT Discussion.**
- 17:50 PM **Election of new committee.**

### Companion Animal Genetics and Genomics

Chairs: **Nuket Bilgen, Ankara University, Heather Huson, Cornell University, and Leslie Lyons, University of Missouri**  
**Room 5**

- 14:30 OP166 **A comparative review of the deleterious variants burden in the domestic cat.**  
W. C. Warren\*<sup>1</sup>, R. Buckley<sup>1</sup>, F. H. G. Farias<sup>2</sup>, R. Middelton<sup>3</sup>, W. J. Murphy<sup>4</sup>, and L. A. Lyons<sup>1</sup>, <sup>1</sup>*University of Missouri, Columbia, MO, USA*, <sup>2</sup>*Washington University School of Medicine, St Louis, MO, USA*, <sup>3</sup>*Nestlé Purina Research, St Louis, MO, USA*, <sup>4</sup>*Texas A&M University, College Station, TX, USA*.
- 15:00 OP168 **Mining the 99 Lives cat genome sequencing initiative database.**  
L. A. Lyons\*, R. M. Buckley, and 99 Lives Consortium, *College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*.
- 15:15 OP214 **Precision medicine in dogs: Some new causative variants for inherited diseases.**  
Tosso Leeb\*<sup>1</sup> and Dog Biomedical Variant Database Consortium (DBVDC)<sup>2</sup>, <sup>1</sup>*Institute of Genetics, Vetsuisse Faculty, University of Bern, Switzerland*, <sup>2</sup>*DBVDC (Gus Aguirre, Catherine André, Danika Bannasch, Doreen Becker, Brian Davis, Cord Drögemüller, Kari Ekenstedt, Kiterie Faller, Oliver Forman, Steve Friedenber, Eva Furrow, Urs Giger, Christophe Hitte, Marjo Hytönen, Vidhya Jagannathan, Tosso Leeb, Hannes Lohi, Cathryn Mellersh, Jim Mickelson, Leonardo Murgiano, Anita Oberbauer, Sheila Schmutz, Jeffrey Schoenebeck, Kim Summers, Frank van Steenbeek, Claire Wade)*.
- 15:30 OP171 **Multi-breed comparison of canine lymphoma susceptibility.**  
S. A. Mortlock, M. M.-J. Chen, P. Soh, V. W. T. Hsu, M.-S. Khatkar, P. F. Bennett, R. M. Taylor, and P. Williamson\*, *The University of Sydney, Sydney, NSW, Australia*.
- 15:45 OP172 **Assessing the genetic contribution to complex behavioural traits in German Shepherd dogs.**  
J. Friedrich\*<sup>1</sup>, P. Arvelius<sup>2</sup>, E. Strandberg<sup>3</sup>, A. Talenti<sup>1</sup>, E. Sánchez-Molano<sup>1</sup>, R. Pong-Wong<sup>1</sup>, J. Hickey<sup>1</sup>, M. Haskell<sup>4</sup>, and P. Wiener<sup>1</sup>, <sup>1</sup>*Division of Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, UK*, <sup>2</sup>*Swedish Armed Forces Dog Training Center, MÅRSTA, Sweden*, <sup>3</sup>*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*, <sup>4</sup>*Scotland's Rural College, Edinburgh, UK*.

- 16:30 OP170 **An early onset retinopathy in Golden retriever dogs.**  
S. Mäkeläinen\*<sup>1</sup>, K. Narfström<sup>2</sup>, B. Ekestén<sup>3</sup>, G. Andersson<sup>1</sup>, and TF Bergström<sup>1</sup>, <sup>1</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>Section for Comparative Ophthalmology, College of Veterinary Medicine, University of Missouri-Columbia, Columbia, Missouri, USA, <sup>3</sup>Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- 17:00 OP173 **A haplotype view of cystinuria in dog.**  
S. Frattini\*<sup>1</sup>, M. Cortellari<sup>1</sup>, A. Talenti<sup>2</sup>, A. Negro<sup>1</sup>, C. Biagini<sup>1</sup>, M. Polli<sup>1</sup>, and P. Crepaldi<sup>1</sup>, <sup>1</sup>Department of Veterinary Medicine, University of Milan, Milan, Italy, <sup>2</sup>The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK.
- 17:15 **Update: Conference on Canine and Feline Genetics and Genomics.**
- 17:30 **Business meeting.**

### Comparative and Functional Genomics

Chair: **Fiona McCarthy, The University of Arizona**  
**Auditorium 1**

- 14:30 OP174 **FAANGMine: A genomic data mining warehouse for domesticated animal species.**  
C. G. Elsik\*, M. Shamimuzzaman, D. A. Triant, J. J. Le Tourneau, and A. T. Walsh, *University of Missouri, Columbia, MO, USA.*
- 14:45 OP175 **High-order gene-by-gene and gene-by-environment interactions: Is there a need to consider them when dissecting the genetic basis of complex traits?**  
Ö. Carlborg\* and Y. Zan, *Department of Medical Biochemistry and Microbiology, Uppsala, Sweden.*
- 15:00 OP176 **Evaluation of RNA-Sequencing pipelines for optimized power and accuracy of SNP and INDEL identification.**  
S. Lam\*<sup>1</sup>, F. Miglior<sup>1</sup>, J. Zeidan<sup>1</sup>, I. Gómez-Redondo<sup>1,2</sup>, A. Suárez-Vega<sup>1</sup>, P. A. S. Fonseca<sup>1</sup>, and F. Schenkel<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Spanish National Institute for Agriculture and Food Research and Technology, Madrid, Spain.
- 15:15 OP177 **Genetic control of temperament traits across species: association of autism spectrum disorder genes with cattle temperament.**  
R. Costilla\*<sup>1,2</sup>, K. Kemper<sup>1</sup>, E. Byrne<sup>1</sup>, L. Porto-Neto<sup>4</sup>, R. Carvalheiro<sup>5</sup>, D. Berry<sup>6</sup>, D. Purfield<sup>6</sup>, J. Doyle<sup>6</sup>, S. Moore<sup>2</sup>, N. Wray<sup>1</sup>, and B. Hayes<sup>2</sup>, <sup>1</sup>Institute for Molecular Bioscience, The University of Queensland, Brisbane, Australia, <sup>2</sup>Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Australia, <sup>3</sup>Queensland Brain Institute, The University of Queensland, Brisbane, Australia, <sup>4</sup>Commonwealth Scientific and Industrial Research Organization (CSIRO), Agriculture and Food, Brisbane, Australia, <sup>5</sup>School of Agricultural and Veterinary Sciences, Sao Paulo State University, Sao Paulo, Brazil, <sup>6</sup>Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland.
- 15:30 OP178 **Copy number variants reveal traces of recent selection in two dairy cattle breeds.**  
Y. L. Lee\*<sup>1</sup>, A. Bouwman<sup>1</sup>, M. A. M. Groenen<sup>1</sup>, E. Mullaart<sup>2</sup>, R. F. Veerkamp<sup>1</sup>, and M. Bosse<sup>1</sup>, <sup>1</sup>Wageningen University & Research, Animal Breeding and Genomics, Wageningen, the Netherlands, <sup>2</sup>CRV B.V, Arnhem, the Netherlands.
- 15:45 OP179 **Chromatin accessibility conservation across four livestock species.**  
S. Djebali\*<sup>1</sup>, S. Foissac<sup>1</sup>, N. Vialaneix<sup>2</sup>, K. Munyard<sup>3</sup>, A. Rau<sup>4</sup>, T. Faraut<sup>1</sup>, S. Lagarrigue<sup>5</sup>, H. Acloque<sup>4</sup>, E. Giuffra<sup>4</sup>, and FR-AgENCODE Consortium<sup>1,4</sup>, <sup>1</sup>GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France, <sup>2</sup>MIAT, INRA, Castanet Tolosan, France, <sup>3</sup>Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia, <sup>4</sup>GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France, <sup>5</sup>UMR PEGASE, INRA, Rennes, France and UMR PEGASE, Agrocampus Ouest, Rennes, France.

- 16:30 OP180 **Meta-analysis of differentially co-expressed gene modules for high- and sub-fertile beef cows.**  
P. A. de Souza Fonseca\*, A. Suárez-Vega, S. Lam, F. S. Schenkel, S. Id-Lahoucine, and A. Canovas, *University of Guelph, Guelph, ON, Canada.*
- 16:45 OP181 **Broadening the miRNA catalogue in livestock species: A contribution to the functional annotation of animal genomes.**  
A. J. Amaral\*<sup>1</sup>, C. Anthon<sup>2</sup>, G. Corsi<sup>2</sup>, A. Vasconcelos<sup>1</sup>, S. Marthey<sup>3</sup>, A. Hoffman<sup>4</sup>, J. Lagnel<sup>5</sup>, F. Haack<sup>6</sup>, K. Pokharel<sup>7</sup>, O. Palasca<sup>2</sup>, S. Seemann<sup>2</sup>, L. T. Gama<sup>1</sup>, M. A. M. Groenen<sup>8</sup>, J. Kantanen<sup>7</sup>, R. P. M. A. Crooijmans<sup>9</sup>, M. Rijnkels<sup>9</sup>, T. Kalbfleisch<sup>10</sup>, E. Giuffra<sup>3</sup>, P. F. Stadler<sup>4</sup>, O. Madsen<sup>8</sup>, and J. Gorodkin<sup>2</sup>, <sup>1</sup>Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, <sup>2</sup>Center for noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark, <sup>3</sup>GABI, AgroParis-Tech, INRA, Université Paris Saclay, Jouy-en-Josas, France, <sup>4</sup>Bioinformatics Group, Department of Computer Science University of Leipzig, Leipzig, Germany, <sup>5</sup>INRA PACA, Montfavet Cedex, France, <sup>6</sup>Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, <sup>7</sup>Natural Resources Institute Finland, Jokioinen, Finland, <sup>8</sup>Wageningen University, Wageningen, Netherlands, <sup>9</sup>Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA, <sup>10</sup>Department of Biochemistry and Molecular Genetics, School of Medicine, University of Louisville, Louisville, KY, USA.
- 17:00 OP182 **Detection of long non-coding RNAs from the differential transcriptomic analysis of abomasal lymph node from resistant and susceptible sheep to the infection by *Teladorsagia circumcincta*.**  
P. K. Chitneedi<sup>1</sup>, C. Kühn<sup>2</sup>, R. Weikard<sup>2</sup>, J. J. Arranz<sup>1</sup>, M. Martínez-Valladares<sup>3,4</sup>, and B. Gutiérrez-Gil\*<sup>1</sup>, <sup>1</sup>Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, Spain, <sup>2</sup>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>3</sup>Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, León, Spain, <sup>4</sup>Instituto de Ganadería de Montaña, CSIC-Universidad de León, Grulleros (León), Spain.
- 17:15 OP183 **Circular RNA expression in turkey skeletal muscle and response to thermal challenge.**  
K. M. Reed\*<sup>1</sup>, K. M. Mendoza<sup>1</sup>, and J. E. Abrahamte<sup>2</sup>, <sup>1</sup>Department of Veterinary and Biomedical Sciences, University of Minnesota, St. Paul, MN, USA, <sup>2</sup>University of Minnesota Informatics Institute, University of Minnesota, Minneapolis, MN, USA.
- 17:30 OP184 **Functional analysis of G-protein-coupled receptors during porcine subcutaneous preadipocytes differentiation.**  
M. Taniguchi\*<sup>1</sup>, A. Arakawa<sup>1</sup>, I. Nakajima<sup>1</sup>, H. Uenishi<sup>2</sup>, and S. Mikawa<sup>1</sup>, <sup>1</sup>Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan, <sup>2</sup>Institute of Agrobiological Sciences, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan.
- 17:45 **Business meeting.**

## Equine Genetics and Thoroughbred Parentage Testing

Chair: Cecilia Penedo, University of California, Davis  
Room 4

- 14:30 Welcoming remarks.
- 14:40 Horse Comparison Test.
- 15:20 Donkey Comparison Test.
- 15:40 Horse SNP Comparison Test.

Coffee/Tea break

Foyer/Hall

16:00 – 16:30

- 16:30 **ISBC Requirements Update.**
- 16:50 OP185 **Development of an AgriSeq targeted GBS panel for equine SNP parentage verification and sire/dam allocation.**  
P. Flynn\*<sup>1,3</sup>, R. Morrin-O'Donnell<sup>1</sup>, J. Carlsson<sup>3</sup>, P. Siddavatam<sup>2</sup>, S. Chadaram<sup>2</sup>, H. Suren<sup>2</sup>, C. Carrasco<sup>2</sup>, and R. Conrad<sup>2</sup>, <sup>1</sup>Weatherbys Scientific, Naas, Ireland, <sup>2</sup>Thermo Fisher Scientific, Austin, TX, USA, <sup>3</sup>University College Dublin, School of Biology & Environmental Science, UCD, Belfield, Dublin, Ireland.



- 17:05 OP186 **Development of an equine SNP parentage panel which complements historic and current high-density genotyping resources.**  
R. G. Tait Jr.\*<sup>1</sup>, D. J. G. Arts<sup>2</sup>, R. Ferretti<sup>1</sup>, H. Hofeneder-Barclay<sup>3</sup>, B. Simpson<sup>1</sup>, L. Kock<sup>1</sup>, and J. Qiu<sup>1</sup>, <sup>1</sup>Neogen GeneSeek Operations, Lincoln, NE, USA, <sup>2</sup>KWPN Royal Dutch Sport Horse Studbook, Ermelo, Netherlands, <sup>3</sup>Neogen Europe, Ayr, UK.
- 17:20 OP187 **Potential methods of detecting indiscriminate genetic manipulation in thoroughbred racehorses.**  
T. Tozaki\*<sup>1</sup>, A. Ohnuma<sup>1</sup>, M. Kikuchi<sup>1</sup>, H. Kakoi<sup>2</sup>, K.-I. Hirota<sup>1</sup>, K. Kusano<sup>2</sup>, and S.-I. Nagata<sup>1</sup>, <sup>1</sup>Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan, <sup>2</sup>Ritto Training Center Racehorse Hospital, Japan Racing Association, Ritto, Shiga, Japan.
- 17:35 **Election of committee members and any other business.**

### Livestock Genomics for Developing Countries

Chair: **Ntanganedzeni Mapholi, University of South Africa**  
**Room 6**

- 14:30 OP188 **Investigating large structural variants in African cattle using long-read sequencing and optical mapping.**  
A. Talenti\*<sup>1</sup>, H. Hemmink<sup>2</sup>, E. A. J. Cook<sup>2</sup>, D. Wragg<sup>1</sup>, J. Powell<sup>1</sup>, C. Ezeasor<sup>3</sup>, E. Obishakin<sup>4</sup>, A. Fisch<sup>5</sup>, R. Kelly<sup>6</sup>, I. K. Silwamba<sup>7</sup>, W. Amanyre<sup>8</sup>, D. Muhanguzi<sup>8</sup>, M. Watson<sup>1</sup>, P. Wiener<sup>1</sup>, P. Toye<sup>2</sup>, L. Morrison<sup>1</sup>, T. Connelley<sup>1</sup>, and J. Prendergast<sup>1</sup>, <sup>1</sup>The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK, <sup>2</sup>The International Livestock Research Institute, Nairobi, Kenya, <sup>3</sup>University of Nigeria, Nsukka, Enugu State, Nigeria, <sup>4</sup>National Veterinary Research Institute, Vom-Jos, Nigeria, <sup>5</sup>University of São Paulo, São Paulo, Brazil, <sup>6</sup>Royal (Dick) School of Veterinary Medicine, University of Edinburgh, Edinburgh, UK, <sup>7</sup>School of Veterinary Medicine, University of Zambia, Lusaka, Zambia, <sup>8</sup>College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala, Uganda.
- 14:45 OP189 **The effect of allele ancestry on production traits of tropical composite cattle.**  
L. R. Porto-Neto\*<sup>1</sup>, S. M. McWilliam<sup>1</sup>, M. Naval-Sanchez<sup>1</sup>, B. J. Hayes<sup>2</sup>, and A. Reverter<sup>1</sup>, <sup>1</sup>Commonwealth Scientific and Industrial Research Organization (CSIRO), St Lucia, QLD, Australia, <sup>2</sup>Queensland Alliance for Agriculture and Food Innovation (QAAFI), St Lucia, QLD, Australia.
- 15:00 OP190 **Autosomal genome evidence for introgression from other Gallus species into African and Middle East indigenous chicken.**  
A. S. Al-Jumaili\*<sup>1,2</sup>, A. Gheyas<sup>3,4</sup>, A. Kebede<sup>5,6</sup>, J. Smith<sup>3,4</sup>, and O. Hanotte<sup>1,5</sup>, <sup>1</sup>School of Life Sciences, the University of Nottingham, University Park, Nottingham, United Kingdom, <sup>2</sup>University of Anbar, Anbar, Iraq, <sup>3</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, UK, <sup>4</sup>Centre for Tropical Livestock Genetics and Health, The Roslin Institute, Edinburgh, UK, <sup>5</sup>LiveGene, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>6</sup>Addis Ababa University (AAU), Addis Ababa, Ethiopia.
- 15:15 OP191 **Single nucleotide polymorphism selection methods to optimize imputation accuracy for South African Drakensberg beef cattle.**  
S. F. Lashmar<sup>1,2</sup>, D. P. Berry<sup>3,1</sup>, R. Pierneef<sup>2</sup>, F. C. Muchadeyi<sup>2</sup>, and C. Visser\*<sup>1</sup>, <sup>1</sup>University of Pretoria, Department of Animal & Wildlife Science, Pretoria, Gauteng, South Africa, <sup>2</sup>Agricultural Research Council, Biotechnology Platform, Pretoria, Gauteng, South Africa, <sup>3</sup>Teagasc, Animal and Grassland Research and Innovation Center, Fermoy, Cork, Ireland.
- 15:30 OP192 **Accuracy of imputation from SNP array data to whole-genome sequence data in cattle.**  
Y. Jiang\*<sup>1</sup>, Z. Zhang<sup>2</sup>, L. S. Huang<sup>2</sup>, Q. Zhang<sup>3,1</sup>, and X. Ding<sup>1</sup>, <sup>1</sup>China Agricultural University, Beijing, China, <sup>2</sup>Jiangxi Agricultural University, Nanchang, China, <sup>3</sup>Shandong Agricultural University, Taian, China.
- 15:45 OP193 **Genome-wide identification and characterization of InDels and SNPs in Black Bengal goat for breed identification.**  
M. B. R. Mollah\*<sup>1</sup>, M. S. A. Bhuiyan<sup>1</sup>, M. A. M. Y. Khandoker<sup>1</sup>, M. A. Jalil<sup>2</sup>, and G. K. Deb<sup>2</sup>, <sup>1</sup>Bangladesh Agricultural University, Mymensingh, Bangladesh, <sup>2</sup>Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh.

- 16:30 OP194 **Whole-genome sequencing unveils helmeted guinea fowl (*Numida meleagris*) domestication in West Africa.**  
M.-S. Peng<sup>1,2,3,27</sup>, A. C. Adeola<sup>1,2,27</sup>, Q.-K. Shen<sup>1,2,3,27</sup>, S. Duan<sup>4,27</sup>, Y.-W. Miao<sup>5</sup>, Y. Du<sup>4</sup>, M.-S. Wang<sup>1,25,26</sup>, J. K. Lichotti<sup>6</sup>, O. S. Charles<sup>7</sup>, O. J. Sanke<sup>8</sup>, P. M. Dawuda<sup>9</sup>, A. O. Okeyoyin<sup>10</sup>, J. Musina<sup>11</sup>, P. Njoroge<sup>11</sup>, B. Agwanda<sup>11</sup>, M. G. Strillacci<sup>12</sup>, E. Gorla<sup>12</sup>, A. Bagnato<sup>12</sup>, S. Kusza<sup>13</sup>, H. A. Nanaei<sup>14</sup>, R. Pedar<sup>14</sup>, N. T. Abdulloevich<sup>15</sup>, M. E. Afanasevna<sup>15</sup>, K. B. Ibrohimovich<sup>15</sup>, S.-F. Wu<sup>1</sup>, X. Chen<sup>16,17</sup>, W.-K. Yang<sup>16,17</sup>, N. O. Otecko<sup>1,2,3</sup>, R. W. Murphy<sup>18</sup>, L. M. Nneji<sup>1,2</sup>, A. Esmailzadeh<sup>1,14</sup>, Y. Dong<sup>19,20,21</sup>, S. C. Ommeh<sup>\*11,22</sup>, and Y.-P. Zhang<sup>1,2,3,23,24</sup>, <sup>1</sup>State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China, <sup>2</sup>Sino-Africa Joint Research Center, Chinese Academy of Sciences, Nairobi, Kenya, <sup>3</sup>Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China, <sup>4</sup>Nowbio Biotechnology Company, Kunming, China, <sup>5</sup>Faculty of Animal Science and Technology, Yunnan Agricultural University, Kunming, China, <sup>6</sup>State Department of Livestock, Ministry of Agriculture Livestock Fisheries and Irrigation, Nairobi, Kenya, <sup>7</sup>Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria, <sup>8</sup>Taraba State Ministry of Agriculture and Natural Resources, Jalingo, Nigeria, <sup>9</sup>Department of Veterinary Surgery and Theriogenology, College of Veterinary Medicine, University of Agriculture, Makurdi, Nigeria, <sup>10</sup>National Park Service Headquarter, Federal Capital Territory, Abuja, Nigeria, <sup>11</sup>Department of Zoology, National Museums of Kenya, Nairobi, Kenya, <sup>12</sup>Department of Veterinary Medicine, University of Milan, Milan, Italy, <sup>13</sup>Animal Genetics Laboratory, Institute of Animal Husbandry, Biotechnology and Nature Conservation, University of Debrecen, Debrecen, Hungary, <sup>14</sup>Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, Kerman, Iran, <sup>15</sup>E.N. Pavlovsky Institute of Zoology and Parasitology, Academy of Sciences of Republic of Tajikistan, Dushanbe, Tajikistan, <sup>16</sup>Research Center for Ecology and Environment of Central Asia, Chinese Academy of Sciences, Urumqi, China, <sup>17</sup>Key Laboratory of Biogeography and Bioresource in Arid Land, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, Urumqi, China, <sup>18</sup>Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, Canada, <sup>19</sup>College of Biological Big Data, Yunnan Agriculture University, Kunming, China, <sup>20</sup>State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Kunming, China, <sup>21</sup>Key Laboratory for Agro-biodiversity and Pest Control of Ministry of Education, Yunnan Agricultural University, Kunming, China, <sup>22</sup>Institute of Biotechnology Research, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya, <sup>23</sup>State Key Laboratory for Conservation and Utilization of Bio-resource in Yunnan, Yunnan University, Kunming, China, <sup>24</sup>Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China, <sup>25</sup>Howard Hughes Medical Institute, University of California Santa Cruz, Santa Cruz, CA, USA, <sup>26</sup>Department of Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, CA, USA.
- 16:45 OP195 **Genetic diversity of the HSP70 gene in the native chicken (*Gallus gallus domesticus* L.) breeds of the Philippines.**  
M. B. Valdez Jr.\*<sup>1</sup>, R. V. F. Castillo<sup>1</sup>, R. G. T. Romero<sup>1</sup>, C. S. Daljog<sup>1</sup>, R. C. Thomas Jr.<sup>1</sup>, and R. C. Santiago<sup>2</sup>, <sup>1</sup>Department of Biological Sciences, Institute of Arts and Sciences, Far Eastern University, Manila, Philippines, <sup>2</sup>National Swine and Poultry Research Center, Bureau of Animal Industry, Department of Agriculture, Quezon, Philippines.
- 17:00 OP196 **Indigenous African sheep genomes reveal insights on fat-tail deposition and morphology.**  
A. Ahbara\*<sup>1,2</sup>, H. Musa<sup>3</sup>, E. Clark<sup>4</sup>, C. Robert<sup>4</sup>, M. Watson<sup>4</sup>, A. Abeba<sup>5</sup>, S. Latairish<sup>6</sup>, O. Hanotte<sup>7</sup>, and J. Mwacharo<sup>8</sup>, <sup>1</sup>School of Life Sciences, University of Nottingham, Nottingham, UK, <sup>2</sup>Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya, <sup>3</sup>Faculty of Medical Laboratory Sciences, Khartoum, Sudan, <sup>4</sup>The Centre for Tropical Livestock Genetics and Health, The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>5</sup>Debre Berhan Research Centre, Debre Berhan, Ethiopia, <sup>6</sup>Department of Animal Production, Faculty of Agriculture, Misurata, Libya, <sup>7</sup>LiveGene, International Livestock Research Institute, Addis Ababa, Ethiopia, <sup>8</sup>Small Ruminant Genomics, International Center for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia.
- 17:15 OP197 **Genomic selection: A pretentious paradigm needs implementation for river buffalo production in developing countries.**  
M. Javed\*, A. Nadeem, A. S. Hashmi, and W. Shehzad, Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan.
- 17:30 OP198 **Advancing livestock genomics education and research in developing countries using strategies from the Virginia Tech PREP and IMSD training programs.**  
E. Smith\*, Virginia Tech, Blacksburg, VA, USA.
- 17:45 **Business meeting and election of committee.**

**Microbiomes**

Chair: **Claire Rogel-Gaillard, GABI, INRA, AgroParisTech, Université Paris-Saclay**  
**Auditorium 2**

- 14:30 OP199 **A comprehensive strategy to assemble the rumen metagenome with long reads and detect high methane emitters.**  
O. González-Recio<sup>\*1,2</sup>, M. Gutiérrez-Rivas<sup>1</sup>, R. Atxaerandio<sup>3</sup>, I. Goiri<sup>3</sup>, J. Rey<sup>3</sup>, J. Tamames<sup>4</sup>, F. Puente-Sánchez<sup>4</sup>, C. González<sup>1</sup>, J. A. Jiménez-Montero<sup>5</sup>, and A. García-Rodríguez<sup>3</sup>, <sup>1</sup>INIA, Madrid, Spain, <sup>2</sup>Departamento de Producciones Agrarias, Escuela Técnica Superior de Ingeniería Agronómica, Alimentaria y de Biosistemas, Universidad Politécnica de Madrid, Madrid, Spain, <sup>3</sup>NEIKER-Tecnalia, Vitoria-Gasteiz, Spain, <sup>4</sup>Spanish Center for Biotechnology, CSIC, Madrid, Spain, <sup>5</sup>CON-AFE, Valdemoro, Spain.
- 14:55 OP200 **Going full circle: Assembly of high-quality, single-contig microbial genomes from the rumen microbiome using long-read sequencing.**  
A. Warr<sup>\*1</sup>, R. Stewart<sup>1</sup>, M. Aufrett<sup>2</sup>, A. Walker<sup>3</sup>, R. Roehe<sup>2</sup>, and M. Watson<sup>1</sup>, <sup>1</sup>The Roslin Institute, Edinburgh, UK, <sup>2</sup>SRUC, Edinburgh, UK, <sup>3</sup>The Rowett Institute, Aberdeen, UK.
- 15:10 OP201 **High-throughput metagenome sequencing for prediction of quantitative traits.**  
M. Hess<sup>\*1</sup>, L. Zetouni<sup>1</sup>, J. Budel<sup>1</sup>, T. Van Stijn<sup>1</sup>, H. Henry<sup>1</sup>, R. Brauning<sup>1</sup>, A. McCulloch<sup>1</sup>, S. Hickey<sup>2</sup>, A. Hess<sup>1</sup>, M. Kirk<sup>3</sup>, S. Kumar<sup>3</sup>, N. Morton<sup>4</sup>, H. Flay<sup>5</sup>, S. Kittelmann<sup>3</sup>, G. Henderson<sup>3</sup>, S. Hendy<sup>4</sup>, G. Wood<sup>1</sup>, G. Attwood<sup>3</sup>, J. McEwan<sup>1</sup>, and S. Rowe<sup>1</sup>, <sup>1</sup>AgResearch Ltd, Mosgiel, New Zealand, <sup>2</sup>AgResearch Ltd, Ruakura, New Zealand, <sup>3</sup>AgResearch Ltd, Palmerston North, New Zealand, <sup>4</sup>Te Pūnaha Matatini, University of Auckland, Auckland, New Zealand, <sup>5</sup>DairyNZ, Hamilton, New Zealand.
- 15:25 OP202 **Link-HD: A versatile integrative approach applied to across-kingdom microbial communities.**  
M. L. Zingaretti<sup>\*1</sup>, G. Renand<sup>2</sup>, D. Morgavi<sup>3</sup>, and Y. Ramayo-Caldas<sup>2,4</sup>, <sup>1</sup>CRAG, Bellaterra, Barcelona, Spain, <sup>2</sup>INRA, Jouy-en-Josas, Paris, France, <sup>3</sup>INRA, Saint Genès-Champanelle, France, <sup>4</sup>IRTA, Caldes de Montbui, Barcelona, Spain.
- 15:40 OP203 **Metagenomic de novo assembly of *Corynebacterium bovis* in lactating Assaf sheep: A preliminary study.**  
C. Esteban-Blanco<sup>\*1</sup>, F. Puente-Sánchez<sup>2</sup>, B. Gutiérrez-Gil<sup>1</sup>, H. Marina<sup>1</sup>, J. Tamames<sup>2</sup>, and J. J. Arranz<sup>1</sup>, <sup>1</sup>University of Leon, León, Castilla y León, Spain, <sup>2</sup>CNB-CSIC, Madrid, Madrid, Spain.

Coffee/Tea break

Foyer/Hall

15:55 – 16:30

- 16:30 OP204 **Genomic surveillance of gut microbiome of Dohne merino sheep by Minlon sequencing.**  
P. Soma<sup>\*1</sup>, R. Pierneef<sup>2</sup>, B. Kooverjee<sup>1</sup>, and F. Muchadeyi<sup>2</sup>, <sup>1</sup>Agricultural Research Council, Animal Production, Irene, Pretoria, South Africa, <sup>2</sup>Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, South Africa.
- 16:45 OP205 **Correlated responses to selection for intramuscular fat in the metagenomic profile on three gut sites in rabbits.**  
M. Martínez-Álvaro, A. Zubiri-Gaitán<sup>\*</sup>, A. Blasco, and P. Hernández, Instituto de Ciencia y Tecnología Animal, Universitat Politècnica de València, Valencia, Spain.
- 17:00 OP206 **Unraveling the effects of the gut microbiota composition and function on horse endurance physiology.**  
S. Plancade<sup>1</sup>, A. Clark<sup>2</sup>, C. Philippe<sup>3</sup>, J.-C. Helbling<sup>4</sup>, M.-P. Moisan<sup>4</sup>, D. Esquerre<sup>5</sup>, L. Le Moyec<sup>6</sup>, C. Robert<sup>7,8</sup>, E. Barrey<sup>7</sup>, and N. Mach<sup>\*7</sup>, <sup>1</sup>MaIAGE, INRA, Université Paris-Saclay, Jouy en Josas, France, <sup>2</sup>Gastroenterology Department, Vall d'Hebron Institut de Reserca, Barcelona, Spain, <sup>3</sup>UMR 1319, INRA, AgroParisTech, Université Paris-Saclay, Jouy en Josas, France, <sup>4</sup>UMR 1286, INRA, Université Bordeaux, Nutrition et neurobiologie intégrée, Bordeaux, France, <sup>5</sup>UMR 444, INRA, Plateforme GET, Castanet-Tolosan, France, <sup>6</sup>Unité de Biologie Intégrative et Adaptation à l'Exercice, UBIAE, EA7362, Université d'Evry, Evry, France, <sup>7</sup>UMR 1313, INRA, AgroParisTech, Université Paris-Saclay, Jouy en Josas, France, <sup>8</sup>Ecole Nationale Vétérinaire d'Alfort, Maisons-Alfort, France.
- 17:15 OP207 **Microbiome and metabolome changes occurring in early *Salmonella* Typhimurium infection in pigs.**  
H. Arguello<sup>\*1</sup>, S. Zaldívar-López<sup>1</sup>, N. Bellido<sup>1</sup>, F. Priego-Capote<sup>2,3</sup>, Á. Jiménez-Marín<sup>1</sup>, L. Morera<sup>1</sup>, and J. J. Garrido<sup>1</sup>, <sup>1</sup>Animal Breeding and Genomics Group, Department of Genetics, University of Córdoba, Córdoba, Spain, <sup>2</sup>Department of Analytical Chemistry, Annex Marie Curie Building, Campus of Rabanales, University of Córdoba, Córdoba, Spain, <sup>3</sup>Institute of Biomedical Research Maimónides (IMIBIC), Reina Sofía University Hospital, University of Córdoba, Córdoba, Spain.
- 17:30 OP208 **Gut microbiome, birth weight, and productive traits in pigs in Iberian × Duroc crossbred pigs.**  
M. Vázquez-Gómez<sup>\*1</sup>, J. Estellé<sup>2</sup>, C. García-Contreras<sup>3</sup>, R. Benitez<sup>3</sup>, S. Astiz<sup>4</sup>, J. L. Pesantez-Pacheco<sup>5</sup>, C. López-Bote<sup>1</sup>, A. Gonzalez-Bulnes<sup>4</sup>, B. Isabel<sup>1</sup>, and C. Ovilo<sup>3</sup>, <sup>1</sup>Faculty of Veterinary Medicine, UCM, Madrid, Spain, <sup>2</sup>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, <sup>3</sup>Department of Animal Breeding, INIA, Madrid, Spain, <sup>4</sup>Department of Animal Reproduction, Madrid, Spain, <sup>5</sup>School of Veterinary Medicine and Zootechnics, UCuenca, Cuenca, Ecuador.

- 17:45 OP209 **The gut microbiota composition at slaughter as a potential certification tool for the Iberian pig traditional farming system.**  
J. M. García-Casco<sup>1</sup>, M. Muñoz<sup>1</sup>, G. Lemonnier<sup>2</sup>, J. M. Babilliot<sup>2</sup>, O. Bouchez<sup>3</sup>, A. I. Fernández<sup>1</sup>, F. R. Massacci<sup>2</sup>, M. A. Fernández-Barroso<sup>1</sup>, A. López-García<sup>1</sup>, C. Caraballo<sup>1</sup>, C. Óvilo<sup>1</sup>, and J. Estellé\*<sup>2</sup>, <sup>1</sup>INIA, Centro de I+D en Cerdo Ibérico, Dpto. Mejora Genética Animal, Zafra, Badajoz, Spain, <sup>2</sup>INRA, UMR1313 GABI, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, <sup>3</sup>INRA, US 1426 GeT-PlaGe, Genotoul, Castanet-Tolosan, France.
- 18:00 OP210 **Lightning Talk: Identification of microbial profiles that promote honeybee colony health.**  
J. Gorrochategui\*<sup>1</sup>, A. Fernandez<sup>1</sup>, M. Muñoz-Colmenero<sup>1,2</sup>, M. Parejo<sup>1,3</sup>, M. Kovacic<sup>4</sup>, J. Filipi<sup>5</sup>, R. Buechler<sup>6</sup>, A. Estonba<sup>1</sup>, and I. Zarraonaindia<sup>1</sup>, <sup>1</sup>Department of Genetics, Physical Anthropology and Animal Physiology, University of the Basque Country (UPV/EHU), Leioa, Spain, <sup>2</sup>Institute of Marine Research, Vigo, Spain, <sup>3</sup>Swiss Bee Research Center, Agroscope, Bern, Switzerland, <sup>4</sup>Josip Juraj Strossmayer University of Osijek, Osijek, Croatia, <sup>5</sup>University of Zadar, Zadar, Croatia, <sup>6</sup>Landesbetrieb Landwirtschaft Hessen, Kirchhain, Germany.
- 18:03 OP211 **Lightning Talk: Holofood: A holo'omic solution towards sustainable animal food production.**  
S. Marcos\*<sup>1</sup>, I. Zarraonaindia<sup>1</sup>, D. Sandvang<sup>4</sup>, M. Limborg<sup>2</sup>, J. Zentek<sup>5</sup>, D. Jozefiak<sup>6</sup>, E. Johansen<sup>4</sup>, J. Tarradas<sup>3</sup>, A. Estonba<sup>1</sup>, T. Gilbert<sup>2</sup>, and A. Alberdi<sup>2</sup>, <sup>1</sup>Department of Genetics, Physical Anthropology and Animal Physiology, University of the Basque Country (UPV/EHU), Leioa, Spain, <sup>2</sup>Department for Evolutionary Genomics at University of Copenhagen's (UCPH) Natural History Museum of Denmark (SNM), Copenhagen, Denmark, <sup>3</sup>Institute for Food and Agricultural Research and Technology (IRTA), Tarragona, Spain, <sup>4</sup>Chr Hansen A/S, Hoersholm, Denmark, <sup>5</sup>Department of Veterinary Medicine Free University of Berlin (FUB), Berlin, Germany, <sup>6</sup>Piast Pasze Sp. z o.o. (Piast Group Ilc.), Poland.
- 18:06 PM **Business Meeting.**

Gala Dinner

La Seu Vella

20:00 – 24:00

## Friday, July 12

Registration Desk Open

Hall

08:00 – 13:00

### ORAL SESSIONS

#### Plenary Session IV

Chairs: **Juan José Arranz, University of León,**  
**and Max F. Rothschild, Iowa State University**  
**Auditorium 1**

- 09:00 OP212 **Analysis of the world's sheep reveals contribution of frequent genomic introgressions from congeneric wild species to local climatic adaptation in domestic breeds.**  
M.-H. Li\*<sup>1</sup>, Presentation given by Jian lin Han<sup>2</sup>, <sup>1</sup>*Institute of Zoology, Chinese Academy of Sciences, Beijing, China*, <sup>2</sup>*International Livestock Research Institute (ILRI), Kenya*.
- 10:00 OP213 **Application of genomics to resolve livestock production and adaptation issues in developing countries.**  
F. C. Muchadeyi\*, *Agricultural Research Council-Biotechnology Platform, Onderstepoort, South Africa*.

Coffee/Tea break

Foyer/Hall

11:00 – 11:30

Business Meeting and Awards

Auditorium 1

11:30 – 13:30

FAANG: Hands-on metadata validation and data submission training workshop  
(invitation only)

Room 3

14:00 – 18:00



## POSTER PRESENTATIONS

### Animal Epigenetics

- P1 **Identification of epigenetic related genes associated with carcass traits in Nguni cattle using Illumina BovineSNP50 BeadChip.**  
K. T. E. Makua<sup>1,2</sup>, A. A. Zwane<sup>2</sup>, K. A. Nephawe<sup>1</sup>, and B. Mtsheni<sup>1\*</sup>, <sup>1</sup>Department of Animal Sciences, Tshwane University of Technology, Pretoria, Gauteng, South Africa, <sup>2</sup>Animal Production Institute, Agricultural Research Council, Pretoria, Gauteng, South Africa.
- P2 **Unpredictable light schedule causes sex-specific epigenetic and transcriptional changes in the chicken's pineal gland.**  
F. Pértile<sup>\*1,2</sup>, N. Mitheiss<sup>2</sup>, P. Løtvedt<sup>2</sup>, L. L. Coutinho<sup>1</sup>, P. Jensen<sup>2</sup>, and C. Guerrero-Bosagna<sup>2</sup>, <sup>1</sup>Luiz de Queiroz College of Agriculture from University of São Paulo (ESALQ/USP), Piracicaba, São Paulo, Brazil, <sup>2</sup>Linköping University, Linköping, Ostergötland, Sweden.
- P3 **Genetics of epigenetics in sheep.**  
L. Drouilhet<sup>\*1</sup>, F. Plisson-Petit<sup>1</sup>, D. Marcon<sup>2</sup>, F. Bouvier<sup>2</sup>, C. Moreno-Romieux<sup>1</sup>, S. Fabre<sup>1</sup>, and D. Hazard<sup>1</sup>, <sup>1</sup>Institut National de la Recherche Agronomique, UMR1388 GenPhySE, Castanet Tolosan, France, <sup>2</sup>Institut National de la Recherche Agronomique, UE0332 Domaine de la Sapinière, Osmoy, France.
- P4 **Epigenetic state of genes of immune responsiveness relevant to bovine mastitis.**  
T. Zabek<sup>\*1</sup>, E. Semik-Gurgul<sup>1</sup>, T. Szmatoła<sup>1</sup>, E. Kawecka<sup>2</sup>, E. Kosciuk<sup>2</sup>, and E. Bagnicka<sup>2</sup>, <sup>1</sup>National Research Institute of Animal Production, Krakow, Poland, <sup>2</sup>Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland.
- P5 **Monocytes methylome in dairy cattle and genetic diversity.**  
H. Jammes<sup>\*1</sup>, A. Chaulot-Talmon<sup>1</sup>, C. Pontlevoiy<sup>1</sup>, L. Jouneau<sup>1</sup>, C. Richard<sup>1</sup>, G. Foucras<sup>2</sup>, and H. Kiefer<sup>1</sup>, <sup>1</sup>UMR1198 BDR, INRA, ENVA, Université Paris Saclay, Jouy en Josas, France, <sup>2</sup>UMR1225 IHAP, Université de Toulouse, ENVT, INRA, Toulouse, France.
- P6 **Epigenetic and transcriptomic characterization of pure adipocyte fractions from obese pigs identifies candidate pathways controlling metabolism.**  
M. J. Jacobsen<sup>1</sup>, J. H. Havgaard<sup>1</sup>, C. Anthon<sup>1</sup>, C. M. Junker<sup>1</sup>, S. Cirera<sup>1</sup>, P. M. Sørensen<sup>1</sup>, S. Pundhir<sup>1</sup>, P. Karlskov-Mortensen<sup>\*1</sup>, C. S. Bruun<sup>1</sup>, P. Lesnik<sup>2</sup>, M. Guerin<sup>2</sup>, J. Gorodkin<sup>1</sup>, C. B. Jørgensen<sup>1</sup>, M. Fredholm<sup>1</sup>, R. Barrès<sup>3</sup>, <sup>1</sup>Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark, <sup>2</sup>INSERM UMS 1166, Team A, Institute of Cardiometabolism and Nutrition (ICAN), Pierre and Marie Curie University, Pitié-Salpêtrière Hospital, Paris, France, <sup>3</sup>Novo Nordisk Foundation Centre for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark.
- P7 **Investigation of genetic variation in global DNA methylation in bull semen and its relationship with semen quality and fertility parameters.**  
Y. He<sup>1</sup>, C. Maltecca<sup>1</sup>, F. Tiezzi<sup>1</sup>, A. Canovas<sup>2</sup>, S. Bhattarai<sup>3</sup>, and S. McKay<sup>\*3</sup>, <sup>1</sup>Department of Animal Science, North Carolina State University, Raleigh, NC, USA, <sup>2</sup>Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>3</sup>Department of Animal and Veterinary Sciences, University of Vermont, Burlington, VT, USA.
- P8 **DNA methylation dynamics across the bovine genome.**  
B. Cantrell<sup>1</sup>, S. Bhattarai<sup>1</sup>, E. Stassen<sup>1</sup>, S. Liu<sup>2,3</sup>, T. Buttolph<sup>1</sup>, H. Lachance<sup>1</sup>, J. O'Neil<sup>1</sup>, J. F. Garcia<sup>4</sup>, B. Murdoch<sup>5</sup>, R. Schnabel<sup>6</sup>, J. Taylor<sup>6</sup>, R. Funston<sup>7</sup>, R. Weaber<sup>8</sup>, G. Liu<sup>2</sup>, S. McKay<sup>\*1</sup>, <sup>1</sup>University of Vermont, Burlington, VT, USA, <sup>2</sup>United States Department of Agriculture-ARS, Beltsville, MD, USA, <sup>3</sup>China Agricultural University, Beijing, China, <sup>4</sup>Universidade Estadual Paulista, Araçatuba, Brasil, <sup>5</sup>University of Idaho, Moscow, ID, USA, <sup>6</sup>University of Missouri, Columbia, MO, USA, <sup>7</sup>University of Nebraska, North Platte, NE, USA, <sup>8</sup>Kansas State University, Manhattan, KS, USA.
- P9 **Differential H3K27ac peaks within bursa tissue of two inbred chicken lines under NDV infection and heat stress.**  
G. Chanthavixay<sup>\*1</sup>, C. Kern<sup>1</sup>, Y. Wing<sup>1</sup>, P. Saelao<sup>1</sup>, S. Lamont<sup>2</sup>, R. Gallardo<sup>3</sup>, N. Chubb<sup>4</sup>, R. Gonzalo<sup>4</sup>, and H. Zhou<sup>1</sup>, <sup>1</sup>Department of Animal Science, University of California, Davis, CA, USA, <sup>2</sup>Department of Animal Science, Iowa State University, Ames, IA, USA, <sup>3</sup>School of Veterinary Medicine, University of Califo, Davis, CA, USA, <sup>4</sup>Zoetis Inc, Kalamazoo, MI, USA.
- P10 **Regulation mechanism of DNA methylation on hair morphogenesis in cashmere goat (*Capra hircus*).**  
S. Wang<sup>\*</sup> and X. Wang, College of Animal Science & Technology, Northwest A&F University, Yangling, Shaanxi, China.
- P11 **Inter-generational epigenetic inheritance patterns associated with growth traits in chickens.**  
J. A. P. Marchesi<sup>\*1</sup>, C. G. Verruma<sup>1</sup>, J. Peixoto<sup>2</sup>, M. C. Ledur<sup>2</sup>, and E. S. Ramos<sup>1</sup>, <sup>1</sup>Universidade de São Paulo, Ribeirão Preto, São Paulo, Brazil, <sup>2</sup>Embrapa Suínos e Aves, Concórdia, São Paulo, Brazil.

- P12 **Tissue-specific characterisation of the ovine methylome.**  
A. J. Caulton<sup>\*1,2</sup>, R. Brauning<sup>2</sup>, B. M. Murdoch<sup>3</sup>, and S. M. Clarke<sup>2</sup>, <sup>1</sup>University of Otago, Dunedin, New Zealand, <sup>2</sup>AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand, <sup>3</sup>University of Idaho, Moscow, ID, USA.
- P13 **The genome-wide RNA-chromatin interactions revealed by GRID-seq in skeletal muscle of three pig breeds.**  
L. Fu, J. Li<sup>\*</sup>, Y. Liao, P. Zhou, X. Li, and S. Zhao, Key Laboratory of Pig Genetics and Breeding, MOA China, Huazhong Agricultural University, Wuhan, Hubei Province, China.
- P14 **Identification of orthologous tissue-specific enhancer-gene pairs across chicken, pig and cattle.**  
M. M. Halstead<sup>\*1</sup>, C. Kern<sup>1</sup>, Y. Wang<sup>1</sup>, X. Xu<sup>1</sup>, G. Chanthavixay<sup>1</sup>, P. Saelao<sup>1</sup>, S. M. Waters<sup>1</sup>, J. F. Medrano<sup>1</sup>, A. L. Van Eenennaam<sup>1</sup>, M. E. Delany<sup>1</sup>, H. H. Cheng<sup>2</sup>, C. K. Tuggle<sup>3</sup>, C. W. Ernst<sup>4</sup>, H. Zhou<sup>1</sup>, P. J. Ross<sup>1</sup>, <sup>1</sup>University of California Davis, Davis, CA, USA, <sup>2</sup>USDA, ARS, ADOL, East Lansing, MI, USA, <sup>3</sup>Iowa State University, Ames, IA, USA, <sup>4</sup>Michigan State University, East Lansing, MI, USA.
- Applied Genetics and Genomics in Other Species of Economic Importance**
- P15 **Genetic profiling of lactation curve in Murrah buffaloes using leptin gene polymorphism.**  
V. Jamuna<sup>\*1</sup>, A. K. Gupta<sup>2</sup>, and A. K. Chakravarty<sup>2</sup>, <sup>1</sup>Kerala Veterinary and Animal Sciences University, Thrissur, Kerala, India, <sup>2</sup>National Dairy Research Institute, Karnal, Haryana, India.
- P16 **Genome sequencing-based genetic diversity in Pakistani *Camelus dromedarius*.**  
S. Sabahat<sup>1</sup>, P. Thomson<sup>2</sup>, and A. Nadeem<sup>\*1</sup>, <sup>1</sup>Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan, <sup>2</sup>University of Sydney, Camden, The University of Sydney, Australia.
- P17 **Application of best linear unbiased predictor (BLUP) in estimation of breeding value for rabbit bucks raised in humid tropics.**  
A. I. Adeolu<sup>\*1</sup>, V. U. Oleforuh-Okoleh<sup>2</sup>, S. N. Ibe<sup>3</sup>, R. U. Onyeneke<sup>1</sup>, and K. P. Ogbuagu<sup>3</sup>, <sup>1</sup>Alex Ekwueme Federal University, Ndufu-Alike, Abakaliki, Ebonyi State, Nigeria, <sup>2</sup>Rivers State University of Science and Technology, Nkpolu-Oroworukwo, Port Harcourt, Rivers State, Nigeria, <sup>3</sup>Michael Okpara University of Agriculture Umudike, Umuahia, Abia State, Nigeria.
- P18 **Systematic analysis of non-coding RNAs Involved in the Angora rabbit (*Oryctolagus cuniculus*) hair follicle cycle by RNA sequencing.**  
B. Zhao<sup>\*1</sup>, Y. Chen<sup>1,2</sup>, S. Hu<sup>1</sup>, N. Yang<sup>1</sup>, M. Wang<sup>2</sup>, M. Liu<sup>1</sup>, J. Li<sup>1</sup>, and X. Wu<sup>1,2</sup>, <sup>1</sup>College of Animal Science and Technology, Yangzhou University, Yangzhou, Jiangsu, China, <sup>2</sup>Joint International Research Laboratory of Agriculture & Agri-Product Safety, Yangzhou University, Yangzhou, Jiangsu, China.
- P19 **Analysis of candidate genes for the hygienic behaviour regulation in honey bees (*Apis mellifera*).**  
P. Modesto<sup>\*1</sup>, C. Biolatti<sup>1</sup>, M. G. Maniaci<sup>1</sup>, D. Laurino<sup>2</sup>, P. Mogliotti<sup>1</sup>, F. Mutinelli<sup>3</sup>, A. Manino<sup>2</sup>, P. Barzanti<sup>1</sup>, F. Ingravalle<sup>1</sup>, M. Caramelli<sup>1</sup>, M. Porporato<sup>2</sup>, and P. L. Acutis<sup>1</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy, <sup>2</sup>Dipartimento di Scienze Agrarie, Forestali e Alimentari, Turin, Italy, <sup>3</sup>Istituto Zooprofilattico Sperimentale delle Venezie, Laboratorio nazionale di riferimento per le malattie delle api, Legnaro (PD), Italy.
- P20 **Genetic variability of Russian reindeer populations (*Rangifer tarandus* L., 1758) revealed by high-density SNP array.**  
V. Kharzinova<sup>\*1</sup>, A. Dotsev<sup>1</sup>, T. Deniskova<sup>1</sup>, K. Layshev<sup>2</sup>, T. Romanenko<sup>3</sup>, I. Okhlopov<sup>4</sup>, K. Wimmers<sup>5</sup>, H. Reyer<sup>5</sup>, and G. Brem<sup>1,6</sup>, <sup>1</sup>L.K. Ernst Federal Science Center for Animal Husbandry, Dubrovitzky, Moscow, Russia, <sup>2</sup>North-West Center for Interdisciplinary Researches of Food Maintenance Problems, Federal Agency of Scientific Organizations, St. Petersburg, Russia, <sup>3</sup>Federal Center for Integrated Arctic Research (FCIARctic) Nenets Division, Agro-Experimental Station, Federal Agency of Scientific Organizations, Naryan-Mar, Nenets AO, Russia, <sup>4</sup>Institute for Biological Problems of Cryolithozone Siberian Branch of RAS, Yakutsk, Russia, <sup>5</sup>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology [FBN], Dummerstorf, Germany, <sup>6</sup>Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.
- P21 **Microsatellite markers based on next-generation DNA sequencing for parentage of Asiatic black bear population reintroduced in South Korea.**  
S.-H. Han<sup>\*</sup>, J.-Y. Moon, S.-J. Jeong, T.-W. Kim, J.-J. Kim, D.-H. Jeong, and D.-J. Song, Species Restoration Technology Institute, Korea National Park Service.
- P22 **Genetic association between residual feed intake and subcutaneous fat thickness in Nelore cattle.**  
A. M. Maiorano<sup>\*1</sup>, R. A. S. Faria<sup>1</sup>, M. E. Mercadante<sup>2</sup>, L. G. Albuquerque<sup>1</sup>, and J. A. V. Silva<sup>3</sup>, <sup>1</sup>Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil, <sup>2</sup>Instituto de Zootecnia, Sertaozinho, Sao Paulo, Brazil, <sup>3</sup>Universidade Estadual Paulista, Botucatu, Sao Paulo, Brazil.



- P23 **Genome-wide association study on fatty liver weight and body weight in geese using 2b-RAD.**  
Y. Yang<sup>\*1,3</sup>, H. Wang<sup>1</sup>, C. Wang<sup>1</sup>, S. Gong<sup>1</sup>, Y. Liu<sup>1</sup>, G. Li<sup>1</sup>, G. Cheng<sup>2</sup>, and D. He<sup>1</sup>, <sup>1</sup>*Institute of Animal Husbandry & Veterinary Science, Shanghai Academy of Agricultural Sciences, Shanghai, China*, <sup>2</sup>*Nanfeng Administration of Husbandry and Veterinary, Nanfeng, Jiangxi Province*, <sup>3</sup>*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*.
- P24 **Assessing inbreeding networks from partial correlations and information theory in rabbits.**  
S. T. Rodríguez-Ramilo<sup>\*1</sup>, A. Reverter<sup>2</sup>, J. P. Sánchez<sup>3</sup>, M. Velasco-Galilea<sup>3</sup>, O. González<sup>3</sup>, and M. Piles<sup>3</sup>, <sup>1</sup>*INRA, Castanet-Tolosan, France*, <sup>2</sup>*CSIRO Agriculture & Food, Brisbane, QLD, Australia*, <sup>3</sup>*IRTA, Caldes de Montbui, Spain*.
- P25 **Valuation of polymorphism 22 STR markers used for parentage control in pigeons in Poland.**  
A. Radko<sup>\*</sup>, A. Podbielska, and A. Szumiec, *National Research Institute of Animal Production, Krakowska, Balice, Poland*.
- P26 **Investigation of  $\alpha$ -LA and  $\beta$ -LG gene polymorphism and association with milk production trait in Azarbayjan native buffalo by PCR-SSCP technique.**  
R. Salehi<sup>\*</sup>, A. Hashemi, M. Ghaffari, and G. Elyasi, *Animal Science, West Azarbaijan, Iran*.
- P27 **Phenotypic biodiversity of Carniolan honeybee (*Apis mellifera carnica*) in Croatia.**  
N. Raguz, B. Lukic<sup>\*</sup>, M. Kovacic, P. Margeta, and Z. Puskadija, *Department for Animal Production and Biotechnology, Faculty of Agrobiotechnical Sciences, J.J. Strossmayer University of Osijek, Osijek, Croatia*.
- P28 **Identification of genomic signatures of divergent selection for birth weight environmental variance in a mice experiment. Preliminary analysis.**  
I. Cervantes<sup>\*1</sup>, N. Formoso-Rafferty<sup>1</sup>, J. P. Gutiérrez<sup>1</sup>, and F. Goyache<sup>2</sup>, <sup>1</sup>*Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid, Madrid, Spain*, <sup>2</sup>*Área de Genética y Reproducción Animal, SERIDA-Deva, Gijón, Spain*.
- P29 **Evaluation of GEBV for milk production traits in Korean Holstein dairy cattle using Illumina bovine 54K SNP chips.**  
J. J. Kim<sup>\*1</sup>, Y. M. Lee<sup>1</sup>, C. K. Dang<sup>2</sup>, K. D. Park<sup>3</sup>, K. H. Cho<sup>4</sup>, and Y. S. Kim<sup>1</sup>, <sup>1</sup>*Yeungnam University, Gyeongsan, Gyeongbuk, Korea*, <sup>2</sup>*National Institute of Animal Science, RDA, Jeonju, Jeonbuk, Korea*, <sup>3</sup>*Chonbuk National University, Jeonju, Jeonbuk, Korea*, <sup>4</sup>*Korea National College of Agriculture and Fisheries, Jeongju, Jeonbuk, Korea*.
- P30 **Genomic regions associated with individual growth and cage feed efficiency in rabbits under two feeding regimes.**  
J. P. Sánchez<sup>\*1</sup>, A. Legarra<sup>2</sup>, M. Velasco-Galilea<sup>1</sup>, M. Piles<sup>1</sup>, O. Rafel<sup>1</sup>, O. González<sup>1</sup>, and M. Ballester<sup>1</sup>, <sup>1</sup>*Animal Breeding and Genetics Program, IRTA, Caldes de Montbui, Spain*, <sup>2</sup>*UMR 1388 GenPhySE, INRA, Castanet-Tolosan, France*.
- P32 **Disentangling the genetic background of environmental variance of litter size using whole-genome sequencing data in rabbits.**  
C. Casto-Rebollo<sup>\*1</sup>, M. J. Argente<sup>2</sup>, M. L. García<sup>2</sup>, A. Blasco<sup>1</sup>, and N. Ibáñez-Escriche<sup>1</sup>, <sup>1</sup>*Institute for Animal Science and Technology, Universitat Politècnica de València, València, Spain*, <sup>2</sup>*Departamento de Tecnología Agroalimentaria, Universidad Miguel Hernández de Elche, Orihuela, Spain*.
- P33 **Identification and analysis of differential expressed microRNAs in subcutaneous of yak under nutrition pressure.**  
M. Chu<sup>\*1,2</sup>, P. Yan<sup>1,2</sup>, C. N. Liang<sup>1,2</sup>, X. Y. Wu<sup>1,2</sup>, X. Z. Ding<sup>1,2</sup>, X. Guo<sup>1,2</sup>, L. Xiong<sup>1,2</sup>, and J. Pei<sup>1,2</sup>, <sup>1</sup>*Key Laboratory of Yak Breeding Engineering, Gansu Province, China*, <sup>2</sup>*Lanzhou Institute of Husbandry and Pharmaceutical Sciences, Chinese Academy of Agricultural Sciences, Lanzhou, China*.

### Applied Sheep and Goat Genetics

- P34 **Variations in ovine leptin gene of Cholistani and Sipli sheep in Punjab, Pakistan.**  
M. Safdar<sup>\*1</sup> and Y. Junejo<sup>2</sup>, <sup>1</sup>*Cholistan University of Veterinary & Animal Sciences, Bahawalpur, Punjab, Pakistan*, <sup>2</sup>*Virtual University of Pakistan-Multan, Multan, Punjab, Pakistan*.
- P36 **Deciphering climatic conditions effect on the ovine sperm transcription by RNA-seq.**  
I. Ureña<sup>\*1</sup>, C. González<sup>1</sup>, M. Ramón<sup>2</sup>, M. Godia<sup>3</sup>, A. Clop<sup>3,4</sup>, J. H. Calvo<sup>5</sup>, M. J. Carabaño<sup>1</sup>, and M. Serrano<sup>1</sup>, <sup>1</sup>*Department of Animal Breeding and Genetics, INIA, Madrid, Spain*, <sup>2</sup>*IRIAF-CERSYRA, Valdepeñas, Ciudad Real, Spain*, <sup>3</sup>*Animal Genomics Group, Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Vallès, Barcelona, Spain*, <sup>4</sup>*Consejo Superior de Investigaciones Científicas (CSIC), Barcelona, Spain*, <sup>5</sup>*CITA-ARAID-IA2, Zaragoza, Spain*.
- P37 **Comparative analysis of *FABP4* variations found in ten ovine populations from China and New Zealand.**  
W. Yan<sup>\*</sup>, *School of Animal Science and Technology, Jiangsu Agri-animal Husbandry Vocational College, Taizhou, Jiangsu, China*.



- P38 **Association between callipyge mutation and *DLK2* gene with muscle quality in Hampshire sheep from Mexico.**  
L. Lopez-Echeverria<sup>1</sup>, N. Rivero-Perez<sup>1</sup>, D. Ojeda-Ramirez<sup>1</sup>, A. Pelaez-Acero<sup>1</sup>, and C. G. Sosa-Gutierrez<sup>\*1,2</sup>, <sup>1</sup>Instituto de Ciencias Agropecuarias, Universidad Autónoma del Estado de Hidalgo, Tulancingo de Bravo, Hidalgo, Mexico, <sup>2</sup>Laboratorio Nacional de Genómica y Salud, Tulancingo de Bravo, Hidalgo, Mexico.
- P39 **Genome-wide association study of sperm traits in Assaf rams.**  
M. M. Serrano<sup>\*1</sup>, M. Ramón<sup>2</sup>, J. H. Calvo<sup>3</sup>, F. Freire<sup>4</sup>, J. M. Vazquez<sup>5</sup>, M. A. Jiménez<sup>1</sup>, and J. J. Arranz<sup>5</sup>, <sup>1</sup>Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria INIA, Madrid, Spain, <sup>2</sup>Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal IRIAF-CERSYRA, Valepeñas, Ciudad Real, Spain, <sup>3</sup>Centro de Investigación y Tecnología Agroalimentaria de Aragón CI-TA-Fundación Agencia Aragonesa para la Investigación y el Desarrollo ARAID-IAZ, Zaragoza, Spain, <sup>4</sup>ASSAFE Asociación Nacional de Criadores de la Raza Ovina Assaf, Toro, Zamora, Spain, <sup>5</sup>OVIGEN Centro de selección y mejora genética del ganado Ovino y Caprino, Toro, Zamora, Spain, <sup>6</sup>Dpto. Producción Animal Universidad de León ULE, León, Spain.
- P40 **Identification of variation in the growth differentiation growth factor 9 (*GDF9*) gene associated with litter size in New Zealand sheep (*Ovis aries*) breeds.**  
H. A. Najafabadi<sup>\*1</sup>, J. Hickford<sup>1</sup>, H. Zhou<sup>1</sup>, and M. Khansefid<sup>2</sup>, <sup>1</sup>Lincoln University, Christchurch, Selwyn, New Zealand, <sup>2</sup>AgriBio Centre for AgriBioscience, Bundoora, VIC, Australia.
- P41 **Differential selection patterns between sexes could be revealed by ROH analysis in dairy goats.**  
S. Demyda-Peyrás<sup>1,2</sup>, Y. Pirovano<sup>1,2</sup>, M. Ramón<sup>3</sup>, T. Ziegler<sup>1,2</sup>, M. Sanchez<sup>4</sup>, M. E. Fernandez<sup>1,2</sup>, M. E. Muñoz<sup>4</sup>, M. Solé<sup>\*5</sup>, and A. Molina<sup>6</sup>, <sup>1</sup>Departamento de Producción Animal, Facultad de Veterinaria, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina, <sup>2</sup>IGEVEV (CONICET, UNLP), La Plata, Buenos Aires, Argentina, <sup>3</sup>CERSYRA-IRIAF, Valdepeñas, España, <sup>4</sup>Departamento de Producción Animal, Universidad de Córdoba, Córdoba, Spain, <sup>5</sup>Department of Animal Breeding and Genetics Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>6</sup>Departamento de Genética, Universidad de Córdoba, Córdoba, Spain.
- P42 **Comparison of DNA extraction methods to genotype Kazakh sheep breeds using the 50K SNP (OvineSNP50) BeadChip.**  
A. Khamzina<sup>\*</sup>, S. Kassymbekova, A. Kantay, Z. Khamzina, and N. Karimov, Kazakh Scientific Research Institute of Livestock and Forage production, Almaty, Kazakhstan.
- P43 **Genetic diversity of Nubian ibex in comparison to other ibex and domesticated goat species.**  
L. Hassan<sup>\*1,2</sup>, D. Arends<sup>3</sup>, S. Rahmatalla<sup>3,4</sup>, M. Reissmann<sup>3</sup>, H. Reyer<sup>5</sup>, K. Wimmers<sup>5</sup>, S. Abukashawa<sup>2</sup>, and G. Brockmann<sup>3</sup>, <sup>1</sup>Wildlife Research Center, Animal Resource Research Corporation, Federal Ministry of Livestock, Fisheries and Rangelands, Khartoum, Sudan, <sup>2</sup>Faculty of Sciences, Department of Zoology, University of Khartoum, Khartoum, Sudan, <sup>3</sup>Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Humboldt-Universität, Berlin, Germany, <sup>4</sup>Faculty of Animal Production, Department of Dairy Production, University of Khartoum, Khartoum North, Sudan, <sup>5</sup>Institute for Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.
- P44 **Entropion in Swiss White Alpine sheep is associated with the *CTNND1* region on chromosome 15.**  
N. Hirter<sup>\*1</sup>, A. Letko<sup>1</sup>, I. Häfliger<sup>1</sup>, D. Greber<sup>2</sup>, and C. Drögemüller<sup>1</sup>, <sup>1</sup>Institute of Genetics, University Berne, Berne, Switzerland, <sup>2</sup>Clinic for Ruminants, University Berne, Berne, Switzerland.
- P45 **Novel variants of growth differentiation factor 9 (*GDF9*) gene affect promoter activity and their relationship with litter size in Mongolia sheep (*Ovis aries*).**  
B. Tong<sup>\*1,2</sup>, Y. Yang<sup>1,2</sup>, J. Wang<sup>1,2</sup>, and G. Li<sup>1,2</sup>, <sup>1</sup>State Key Laboratory of Reproductive Regulation & Breeding of Grassland Livestock, Inner Mongolia University, Hohhot City, Inner Mongolia Autonomous Region, China, <sup>2</sup>School of Life Sciences, Inner Mongolia University, Hohhot City, Inner Mongolia Autonomous Region, China.
- P46 **Study on muscle- and fat-related lncRNA of Bashibai sheep regress to F<sub>2</sub> generation.**  
A. Sulayman, Y. Sulaiman<sup>\*</sup>, L. Wujun, and J. Aniwashi, College of Animal Science, Xinjiang Agricultural University, Urumqi, Xinjiang, China.
- P47 **Complete mitochondrial genome sequencing reveals new extinct group of snow sheep (*Ovis nivicola*).**  
A. V. Dotsev<sup>\*1</sup>, E. Kunz<sup>2</sup>, A. V. Protopopov<sup>3</sup>, I. M. Okhlopkov<sup>4</sup>, A. V. Shakhin<sup>1</sup>, V. R. Kharzinova<sup>1</sup>, M. S. Fornara<sup>1</sup>, S. Krebs<sup>5</sup>, J. Peters<sup>6</sup>, D. G. Medvedev<sup>7</sup>, T. P. Sipko<sup>8</sup>, V. A. Bagirov<sup>1</sup>, G. Brem<sup>1,9</sup>, I. Medugorac<sup>2</sup>, N. A. Zinovieva<sup>1</sup>, <sup>1</sup>L.K. Ernst Federal Science Center for Animal Husbandry, Podolsk, Moscow Region, Russia, <sup>2</sup>Department of Veterinary Sciences, Ludwig-Maximilians-University, Munich, Germany, <sup>3</sup>Mammoth Fauna Study Department, Academy of Sciences of the Republic of Sakha (Yakutia), Yakutsk, Russia, <sup>4</sup>Institute for Biological Problems of Cryolithozone, Yakutsk, Russia, <sup>5</sup>Laboratory for Functional Genome Analysis (LAFUGA), Gene Center, Ludwig-Maximilians-University, Munich, Germany, <sup>6</sup>Department of Veterinary Sciences, Institute of Palaeoanatomy, Ludwig-Maximilians-University, Munich, Germany, <sup>7</sup>Department of Game Management and Bioecology, Irkutsk State University of Agriculture, Molodetny Settlement, Irkutsk region, Russia, <sup>8</sup>Sevrtsov Institute of Ecology and Evolution, Moscow, Russia, <sup>9</sup>Institute of Animal Breeding and Genetics, University of Veterinary Medicine, Vienna, Austria.



- P48 **Effects of aluminium hydroxide adjuvant in ovine encephalon assessed by high-throughput RNA sequencing (RNA-seq).**  
E. Varela-Martínez<sup>\*1</sup>, M. Bilbao-Arribas<sup>1</sup>, N. Abendaño<sup>1</sup>, J. Asín<sup>2</sup>, M. Pérez<sup>2</sup>, L. Luján<sup>2</sup>, and B. M. Jugo<sup>1</sup>, <sup>1</sup>Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Bizkaia, Spain, <sup>2</sup>Veterinary Faculty, University of Zaragoza, Zaragoza, Aragón, Spain.
- P49 **Detection of SNP in the stearyl-CoA desaturase (SCD) gene in Suffolk Down sheep breed.**  
S. Bravo<sup>\*1</sup>, G. Larama<sup>2</sup>, N. Sepúlveda<sup>2</sup>, and M. Díaz<sup>1</sup>, <sup>1</sup>Institute of Animal Production, Faculty of Agricultural Sciences, Universidad Austral de Chile, Valdivia, Chile, <sup>2</sup>Meat Technology and Innovation Center, Faculty of Agricultural and Forestry Sciences, Universidad de La Frontera, Temuco, Chile.
- P50 **Inferring the population structure of six North African sheep breeds using a medium-density SNP chip.**  
S. Ben Jemaa<sup>\*1</sup>, S. Kdidi<sup>2</sup>, A. M. Gdura<sup>3</sup>, A. S. Dayhum<sup>4</sup>, and M. Boussaha<sup>5</sup>, <sup>1</sup>Institut National de la Recherche Agronomique de Tunisie, Ariana, Ariana, Tunisia, <sup>2</sup>Arid Lands Institute, Médenine, Médenine, Tunisia, <sup>3</sup>Ministry of Agriculture, Tripoli, Libya, <sup>4</sup>Faculty of Veterinary Medicine, Tripoli, Libya, <sup>5</sup>GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy en Josas, Ile de France, France.
- P51 **Associations of single nucleotide polymorphisms in the ovine prolactin and prolactin receptor genes with milk traits in Assaf dairy sheep.**  
M. R. Marques<sup>\*1,2</sup>, D. S. Ribeiro<sup>3</sup>, S. Gomes<sup>4</sup>, A. T. Belo<sup>1</sup>, J. R. Ribeiro<sup>1</sup>, A. P. Martins<sup>4,5</sup>, and C. C. Belo<sup>1</sup>, <sup>1</sup>UEISPSA, INIAV Instituto Nacional de Investigação Agrária e Veterinária I.P, Vale de Santarém, Portugal, <sup>2</sup>CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Lisboa, Portugal, <sup>3</sup>ESAC, Escola Superior Agrária de Coimbra, Coimbra, Portugal, <sup>4</sup>UTI, INIAV, Instituto Nacional de Investigação Agrária e Veterinária I.P, Oeiras, Portugal, <sup>5</sup>LEAF, Linking Landscape, Environment, Agriculture and Food, ISA, Lisboa, Portugal.
- P52 **Effects of prolactin and prolactin receptor polymorphism upon milk composition and milk coagulation properties in Assaf ewes.**  
M. R. Marques<sup>\*1,2</sup>, S. Gomes<sup>3</sup>, D. S. Ribeiro<sup>4</sup>, J. R. Ribeiro<sup>1</sup>, A. T. Belo<sup>1</sup>, A. P. Martins<sup>3,5</sup>, and C. C. Belo<sup>1</sup>, <sup>1</sup>UEISPSA, INIAV, Instituto Nacional de Investigação Agrária e Veterinária I.P, Vale de Santarém, Portugal, <sup>2</sup>CIISA, Centro de Investigação Interdisciplinar em Sanidade Animal, Lisboa, Portugal, <sup>3</sup>UTI, INIAV, Instituto Nacional de Investigação Agrária e Veterinária I.P, Oeiras, Portugal, <sup>4</sup>ESAC, Escola Superior Agrária de Coimbra, Coimbra, Portugal, Coimbra, Portugal, <sup>5</sup>LEAF, Linking Landscape, Environment, Agriculture and Food, ISA, Lisboa, Portugal.
- P53 **Genome-wide association studies for somatic cell count in Assaf breed.**  
Y. Öner<sup>\*1</sup>, M. Serrano<sup>2</sup>, M. Ramón<sup>3</sup>, M. P. Sarto<sup>4</sup>, L. P. Iguacel<sup>4</sup>, M. Joy<sup>4</sup>, M. Blanco<sup>4</sup>, O. Estrada<sup>4</sup>, T. Juan<sup>4</sup>, and J. H. Calvo<sup>4</sup>, <sup>1</sup>Bursa Uludag University, Bursa, Turkey, <sup>2</sup>INIA (Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain, <sup>3</sup>Centro Regional de Selección y Reproducción Animal (CERSYRA)- Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal de Castilla-La Mancha (IRIAF-JCCM), Valdepeñas, Spain, <sup>4</sup>Centro De Investigación Y Tecnología Agroalimentaria De Aragón (CITA), Zaragoza, Zaragoza, Spain.
- P54 **Identification of a new mutation responsible for epidermolysis bullosa in Mouton Vendéen sheep.**  
L. Chantepie<sup>\*</sup>, L. Drouilhet, C. Genêt, F. Plisson-Petit, J. Sarry, G. Tosser-Klopp, F. Woloszyn, and S. Fabre, *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France.*
- P55 **Differential gene expression and identification of growth-related genes in pituitary gland of South African goats.**  
K. T. Ncube<sup>1,2</sup>, B. Rosen<sup>3</sup>, E. F. Dzomba<sup>2</sup>, C. P. Van Tassell<sup>3</sup>, and F. C. Muchadeyi<sup>\*1</sup>, <sup>1</sup>Agricultural Research Council, Biotechnology Platform, Onderstepoort, Gauteng, South Africa, <sup>2</sup>University of Kwa-Zulu Natal, Discipline of Genetics, School of Life Sciences, Pietermaritzburg, Kwa-Zulu Natal, South Africa, <sup>3</sup>Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD, USA.
- P56 **Identification of polymorphism in MC4R gene and its association with dry matter and crude protein intake in post-weaned Bligon goats.**  
L. Latifah<sup>\*1</sup>, A. Kustantiah<sup>2</sup>, D. Maharani<sup>1</sup>, and T. Hartatik<sup>1</sup>, <sup>1</sup>Department of Animal Breeding and Reproduction, Faculty of Animal Science, Universitas Gadjja Mada, Yogyakarta, Indonesia, <sup>2</sup>Department of Animal Nutrition and Feed Science, Faculty of Animal Science, Universitas Gadjja Mada, Yogyakarta, Indonesia.
- P57 **Haplotype diversity and maternal origin of Swedish goat landraces.**  
G. M. Tarekegn<sup>\*1,2</sup>, E. Jonas<sup>1</sup>, and A. Johansson<sup>1</sup>, <sup>1</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala Sweden, <sup>2</sup>Department of Animal Production and Technology, Bahir Dar University, Bahir Dar Ethiopia.
- P58 **Unravelling ovine lncRNA expression in the presence of aluminium hydroxide adjuvants.**  
M. Bilbao-Arribas<sup>\*1</sup>, E. Varela-Martínez<sup>1</sup>, N. Abendaño<sup>1</sup>, J. Asín<sup>2</sup>, M. M. Pérez<sup>2</sup>, R. Reina<sup>3</sup>, D. de Andrés<sup>3</sup>, L. Luján<sup>2</sup>, and B. M. Jugo<sup>1</sup>, <sup>1</sup>Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Basque Country, Spain, <sup>2</sup>Veterinary Faculty, University of Zaragoza, Zaragoza, Aragón, Spain, <sup>3</sup>Institute of Agrobiotechnology, CSIC-UPNA, Pamplona, Navarra, Spain.

- P59 **The use of an animal linear model to predict genotypes at a single locus of ungenotyped animals.**  
M. N. Boareki\*<sup>1</sup>, D. Kennedy<sup>2</sup>, L. R. Schaeffer<sup>1</sup>, A. Suarez-Vega<sup>1</sup>, F. S. Schenkel<sup>1</sup>, and A. Cánovas<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, ON, Canada.
- P60 **Identification of genes associated with variation in thoracic vertebral number in Mongolian sheep using whole-genome resequencing.**  
Q. Liu\*<sup>1</sup>, X. Wang<sup>1</sup>, Q. Sun<sup>1</sup>, R. Di<sup>1</sup>, W. Hu<sup>1</sup>, X. Zhang<sup>2</sup>, J. Zhang<sup>2</sup>, and M. Chu<sup>1</sup>, <sup>1</sup>Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, <sup>2</sup>Tianjin Institute of Animal Sciences, Tianjin, China.
- P61 **Association studies for the age at first lambing in Rasa Aragonesa ewes.**  
L. P. Iguacel\*<sup>1</sup>, K. Lakhssassi<sup>1</sup>, M. P. Sarto<sup>1</sup>, B. Lahoz<sup>1</sup>, J. Folch<sup>1</sup>, M. A. Jiménez<sup>2</sup>, M. Serrano<sup>2</sup>, J. L. Alabart<sup>1</sup>, and J. H. Calvo<sup>3</sup>, <sup>1</sup>CITA-IA2, Zaragoza, Spain, <sup>2</sup>Department of Animal Breeding and Genetics, INIA, Madrid, Spain, <sup>3</sup>CITA-ARAID-IA2, Zaragoza, Spain.
- P62 **Genome-wide association study (GWAS) identifies the FecX<sup>Gr</sup> allele in BMP15 segregating in Rasa Aragonesa sheep breed.**  
L. Chantepie<sup>1</sup>, M. Serrano<sup>2</sup>, M. P. Sarto<sup>3</sup>, L. P. Iguacel<sup>3</sup>, M. A. Jiménez<sup>2</sup>, J. L. Alabart<sup>3</sup>, J. Folch<sup>3</sup>, B. Lahoz<sup>3</sup>, S. Fabre<sup>1</sup>, and J. H. Calvo\*<sup>4</sup>, <sup>1</sup>Université de Toulouse, INRA, Toulouse, France, <sup>2</sup>INIA, Madrid, Spain, <sup>3</sup>CITA-IA2, Zaragoza, Spain, <sup>4</sup>CITA-ARAID-IA2, Zaragoza, Spain.
- P63 **Differential gene expression in pars tuberalis and hypothalamus tissue from Rasa Aragonesa sheep with different oestrous and anoestrous phases using RNA-Seq.**  
K. Lakhssassi\*<sup>1</sup>, I. Ureña<sup>2</sup>, B. Marín<sup>3</sup>, M.P. Sarto<sup>1</sup>, B. Lahoz<sup>1</sup>, J.L. Alabart<sup>1</sup>, J. Folch<sup>1</sup>, J.H. Calvo<sup>1,4</sup>, and M. Serrano<sup>2</sup>, <sup>1</sup>CITA-IA2, Zaragoza, Spain, <sup>2</sup>INIA, Madrid, Spain, <sup>3</sup>Centro de Encefalopatías y Enfermedades Transmisibles Emergentes, Zaragoza, Spain, <sup>4</sup>CITA-ARAID-IA2, Zaragoza, Spain.
- P64 **Analysis of the allelic sequences in the DNA microsatellite loci used in parentage control in sheep: Preliminary studies.**  
A. Szumiec, A. Radko, A. Piestrzynska-Kajtoch, A. Koseniuk\*, A. Podbielska, and D. Rubis, National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland.
- P65 **Association of a nucleotide variant in Tenascin X with objective milk production traits in US dairy sheep.**  
K. M. Hemmerling<sup>1</sup>, T. W. Murphy<sup>2</sup>, M. K. Herndon<sup>1</sup>, A. T. Massa<sup>1</sup>, M. U. Cinar<sup>3,1</sup>, D. L. Thomas<sup>4</sup>, S. N. White<sup>5,6</sup>, and M. R. Mousel\*<sup>5,7</sup>, <sup>1</sup>Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, <sup>2</sup>USDA, ARS, Meat Animal Research Center, Clay Center, NE, USA, <sup>3</sup>Animal Science Erciyes University, Kayseri, Turkey, <sup>4</sup>Animal Sciences, University of Wisconsin, Madison, WI, USA, <sup>5</sup>USDA, ARS, Animal Disease Research, Pullman, WA, USA, <sup>6</sup>Center for Reproductive Biology, Washington State University, Pullman, WA, USA, <sup>7</sup>School for Global Animal Health, Washington State University, Pullman, WA, USA.
- P66 **Framework for successful implementation of community-based breeding programs in small ruminants in Ethiopia.**  
A. Haile\*<sup>1</sup>, T. Getachew<sup>1</sup>, M. Reki<sup>2</sup>, A. Abebe<sup>3</sup>, and B. Rischkowsky<sup>1</sup>, <sup>1</sup>International Center for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia, <sup>2</sup>ICARDA, Amman, Jordan, <sup>3</sup>Debre Berhan Agricultural Research Center, Debre Berhan, Ethiopia.
- P67 **Use of whole-genome sequencing datasets to study the genetic variability of the LALBA gene across different sheep breeds.**  
H. Marina, B. Gutierrez-Gil, C. Esteban-Blanco, R. Pelayo, and J.-J. Arranz\*, Departamento de Producción Animal, Facultad de Veterinaria, Universidad de Leon, Leon, Spain.
- P68 **A follow-up study on the genome-wide relationships among Merino and Merino-derived sheep breeds.**  
S. Ceccobelli<sup>1</sup>, E. Ciani<sup>2</sup>, E. Lasagna\*<sup>1</sup>, F. S. Silva<sup>3</sup>, G. Lühken<sup>4</sup>, S. Kusza<sup>5</sup>, M. Spehar<sup>6</sup>, R. Niznikowski<sup>7</sup>, M. Swiatek<sup>7</sup>, V. A. Balteanu<sup>8</sup>, G. Ciappesoni<sup>9</sup>, T. Karsli<sup>10</sup>, N. W. Kunene<sup>11</sup>, F. Pilla<sup>12</sup>, F. M. Sarti<sup>1</sup>, <sup>1</sup>Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy, <sup>2</sup>Department of Biosciences, Biotechnologies and Biopharmaceutics, University of Bari "Aldo Moro," Bari, Italy, <sup>3</sup>Instituto Nacional de Investigação Agrária e Veterinária, I.P., Santarém, Portugal, <sup>4</sup>Institut für Tierzucht und Haustiergenetik, Justus-Liebig-Universität, Liebig, Germany, <sup>5</sup>Animal Genetics Laboratory, Institute of Animal Husbandry, Biotechnology and Nature Conservation, University of Debrecen, Debrecen, Hungary, <sup>6</sup>Croatian Agricultural Agency, Croatia, <sup>7</sup>Department of Animal Breeding and Production, Warsaw University of Life Sciences, Warsaw, Poland, <sup>8</sup>Institute of Life Sciences, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania, <sup>9</sup>Instituto Nacional de Investigación Agropecuaria, Las Brujas, Uruguay, <sup>10</sup>Department of Animal Science, Agriculture Faculty, Akdeniz University, Antalya, Turkey, <sup>11</sup>Department of Agriculture, University of Zululand, Richards Bay, South Africa, <sup>12</sup>Dipartimento Agricoltura Ambiente e Alimenti, Università degli Studi del Molise, Campobasso, Italy.
- P69 **Identifying genetic structure and admixture in sheep from terminal breeds in the United States.**  
K. M. Davenport\*<sup>1</sup>, C. Hiemke<sup>2</sup>, S. McKay<sup>3</sup>, J. W. Thorne<sup>4,1</sup>, R. M. Lewis<sup>5</sup>, T. Taylor<sup>6</sup>, and B. M. Murdoch<sup>1</sup>, <sup>1</sup>University of Idaho, Moscow, ID, USA, <sup>2</sup>Niman Ranch & Mapleton Mynd Shropshires, Stoughton, WI, USA, <sup>3</sup>University of Vermont, Burlington, VT, USA, <sup>4</sup>Texas A&M AgriLife Research and Extension Center, San Angelo, TX, USA, <sup>5</sup>University of Nebraska-Lincoln, Lincoln, NE, USA, <sup>6</sup>University of Wisconsin-Madison Arlington Research Center, Arlington, WI, USA.



- P70 **Seasonal gene expression differences in hair follicle development in Angora goats.**  
B. C. Kul\*, N. Bilgen, M. Y. Akkurt, O. Ozmen, and O. S. Cildir, *Ankara University, Faculty of Veterinary Medicine, Department of Genetics, Ankara, Turkey.*
- P71 **Runs of homozygosity patterns of distribution and level of inbreeding in South African sheep breeds.**  
E. F. Dzomba\*<sup>1</sup> and F. C. Muchadeyi<sup>2</sup>, <sup>1</sup>*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*, <sup>2</sup>*Biotechnology Platform, Agriculture Research Council, Pretoria, Gauteng, South Africa.*
- P72 **Genetic structure of the Canary goat using genome-wide SNPs profiling.**  
J. A. Bouzada\*<sup>1</sup>, V. Landi<sup>2</sup>, A. M. Martínez<sup>2</sup>, M. E. Camacho<sup>3</sup>, J. Capote<sup>4</sup>, N. Darmanin<sup>4</sup>, M. M. Gómez<sup>2</sup>, A. Torres<sup>4</sup>, J. V. Delgado<sup>5</sup>, and M. Fresno<sup>4</sup>, <sup>1</sup>*Laboratorio Central de Veterinaria, Algete. Madrid. Spain*, <sup>2</sup>*Animal Breeding Consulting S.L, Córdoba, Spain*, <sup>3</sup>*Instituto de Investigación y Formación Agraria y Pesquera (IFAPA), Córdoba, Spain*, <sup>4</sup>*Instituto Canario de Investigaciones Agrarias (ICIA), Tenerife, Spain*, <sup>5</sup>*Dpto. de Genética, Universidad de Córdoba, Campus Universitario de Rabanales, Córdoba, Spain.*
- P73 **Polled intersex syndrome (PIS) in goats—Nanopore sequencing revealed a complex structural variant and made it possible to devise a simple genetic test for identification of intersexual goats.**  
R. Simon\*<sup>1</sup>, H. Tschanz-Lischer<sup>2</sup>, I. Keller<sup>2</sup>, I. Häfliger<sup>3</sup>, A. Pienkowska-Schelling<sup>3</sup>, C. Schelling<sup>4</sup>, C. Drögemüller<sup>3</sup>, and G. Lühken<sup>1</sup>, <sup>1</sup>*Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Germany*, <sup>2</sup>*Interfaculty Bioinformatics Unit, University of Bern, Bern, Switzerland*, <sup>3</sup>*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, <sup>4</sup>*Clinic for Reproductive Medicine, Vetsuisse Faculty, University of Zürich, Zürich, Switzerland.*
- P74 **Selection signatures in goat breeds reveal the molecular basis for six different coat color phenotypes.**  
J. Henkel\*<sup>1</sup>, R. Saif<sup>1,2</sup>, V. Jagannathan<sup>1</sup>, C. Drögemüller<sup>1</sup>, C. Flury<sup>3</sup>, and T. Leeb<sup>1</sup>, <sup>1</sup>*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, <sup>2</sup>*Institute of Biotechnology, Gulab Devi Educational Complex, Lahore, Pakistan*, <sup>3</sup>*School of Agricultural, Forest and Food Sciences HAFL, Bern University of Applied Sciences, Zollikofen, Switzerland.*
- P75 **Use of genetic and epigenetic tools to refine a genetic marker of host resilience to ovine lentivirus infection.**  
A. T. Massa\*<sup>1</sup>, M. R. Mousel<sup>2,3</sup>, B. M. Murdoch<sup>4</sup>, J. B. Taylor<sup>5</sup>, D. P. Knowles<sup>1</sup>, and S. N. White<sup>1,2</sup>, <sup>1</sup>*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA*, <sup>2</sup>*Animal Disease Research Unit, Agricultural Research Service, USDA, Pullman, WA, USA*, <sup>3</sup>*Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA*, <sup>4</sup>*Department of Animal and Veterinary Science, University of Idaho, Moscow, ID, USA*, <sup>5</sup>*Range Sheep Production Efficiency Research, Agricultural Research Service, USDA, Dubois, ID, USA.*

## Avian Genetics and Genomics

- P76 **Identification of positional candidate genes in the reduced interval of a major growth QTL on chicken chromosome 4.**  
M. K. Nassar\*<sup>1</sup>, S. Lyu<sup>2,3</sup>, D. Arends<sup>2</sup>, A. Weigend<sup>4</sup>, S. Weigend<sup>4</sup>, R. Preisinger<sup>5</sup>, and G. A. Brockmann<sup>2</sup>, <sup>1</sup>*Cairo University, Faculty of Agriculture, Giza, Egypt*, <sup>2</sup>*Humboldt-Universität zu Berlin, Albrecht Daniel Thaer-Institut für Agricultural and Horticultural Sciences, Berlin, Germany*, <sup>3</sup>*Henan Academy of Agricultural Sciences, Institute of Animal Science and Veterinary Medicine, Zhengzhou, China*, <sup>4</sup>*Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt-Mariensee, Germany*, <sup>5</sup>*Lohmann Tierzucht GmbH, Cuxhaven, Germany.*
- P78 **GWAS using imputed exonic SNPs revealed novel QTLs associated with heart weight in chickens.**  
G. C. M. Moreira\*<sup>1</sup>, M. Salvian<sup>1</sup>, C. Boschiero<sup>1</sup>, A. S. M. Cesar<sup>1</sup>, J. M. Reecy<sup>2</sup>, D. Garrick<sup>3</sup>, T. F. Godoy<sup>1</sup>, M. E. Cantão<sup>4</sup>, M. C. Ledur<sup>4</sup>, A. M. G. Ibelli<sup>4</sup>, J. O. Peixoto<sup>4</sup>, and L. L. Coutinho<sup>1</sup>, <sup>1</sup>*University of São Paulo (USP), Luiz de Queiroz College of Agriculture (ESALQ), Piracicaba, São Paulo, Brazil*, <sup>2</sup>*Iowa State University (ISU), Department of Animal Science, Ames, IA, USA*, <sup>3</sup>*School of Agriculture, Massey University, Ruakura, Hamilton, New Zealand*, <sup>4</sup>*Embrapa Suínos e Aves, Concórdia, Santa Catarina, Brazil.*
- P79 **Fine-mapping of ancestral haplotype undergoing mosaic positive selection for body weight in the domestic chicken.**  
Y. Wang\*<sup>1,2</sup>, X. Cao<sup>2,3</sup>, and X. Hu<sup>2,3</sup>, <sup>1</sup>*College of Animal Science and Technology, China Agricultural University, Beijing, China*, <sup>2</sup>*State Key Laboratory of Agrobiotechnology, China Agricultural University, Beijing, China*, <sup>3</sup>*College of Biological Sciences, China Agricultural University, Beijing, China.*
- P81 **A genomic inference of the White Plymouth Rock genealogy.**  
Y. Guo\*<sup>1</sup>, M. Lillie<sup>1</sup>, Y. Zan<sup>1</sup>, J. Beranger<sup>3</sup>, A. Martin<sup>3</sup>, C. Honaker<sup>2</sup>, P. Siegel<sup>2</sup>, and Ö. Carlborg<sup>1</sup>, <sup>1</sup>*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*, <sup>2</sup>*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA, USA*, <sup>3</sup>*The Livestock Conservancy, Pittsboro, NC, USA.*

- P82 **Genome-wide detection of selection signatures in Ogye in comparison to the white leghorn chickens.**  
Y.-S. Lee\*, D. Shin, H.-K. Lee, and K.-D. Song, *Department of Animal Biotechnology, Chonbuk National University, Jeonju, Republic of Korea.*
- P83 **Deciphering genome-wide selective signatures between Cornish and Korean native chicken (KNC) based on XP-EHH.**  
G. Kim, Y.-S. Lee\*, H.-K. Lee, D. Shin, and K.-D. Song, *Department of Animal Biotechnology, Chonbuk National University, Jeonju, Republic of Korea.*
- P84 **Additional molecular evidence that the Royal Palm is probably a turkey breed and not a strain.**  
E. Smith\*, J. Xu, J. Adikari, and K. Russell, *Virginia Tech, Blacksburg Virginia, US.*
- P85 **Marek's disease virus infection induced mitochondria changes in two genetically divergent lines of chickens.**  
Q. Chu\*<sup>1</sup>, Y. Ding<sup>2</sup>, and J. Song<sup>2</sup>, <sup>1</sup>*Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China,* <sup>2</sup>*Department of Animal and Avian Sciences, University of Maryland, College Park, MD, USA.*
- P86 **Genome-wide association studies for colour traits in Chinese Crested duck using whole-genome sequencing.**  
X. Yuan\*, Q. Guo, H. Bai, Q. Xu, G. Chang, and G. Chen, *Key Laboratory of Animal Genetics and Breeding and Molecular Design of Jiangsu Province, Yangzhou University, Yangzhou, Jiangsu, China.*
- P87 **Unravelling kinship in a captive colony of greater flamingos (*Phoenicopterus roseus*) without a studbook.**  
C. Biolatti\*<sup>1</sup>, C. Beltramo<sup>1</sup>, A. Dogliero<sup>2</sup>, V. Campia<sup>1</sup>, S. Peletto<sup>1</sup>, S. Colussi<sup>1</sup>, P. Modesto<sup>1</sup>, and P. L. Acutis<sup>1</sup>, <sup>1</sup>*Regional Reference Centre for Exotic Animals, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino, Italy,* <sup>2</sup>*International Foundation for Wildlife Research - Rawdat Al Faras Houbara Breeding Center (Ministry of Municipality&Environment), Doha, State of Qatar.*
- P88 **First preliminary overview of genetic diversity and conservation status of Ecuadorian creole chicken.**  
P. Toalombo\*<sup>1,2</sup>, V. Landi<sup>2</sup>, A. M. Martínez<sup>2</sup>, M. M. Gómez<sup>2</sup>, C. A. Camacho<sup>1</sup>, M. E. Camacho<sup>3</sup>, J. M. León<sup>2</sup>, and J. V. Delgado<sup>2</sup>, <sup>1</sup>*Escuela Superior de Chimborazo, Riobamba, Ecuador,* <sup>2</sup>*Universidad de Córdoba, Córdoba, Spain,* <sup>3</sup>*IFAPA Alameda del Obispo, Córdoba, Spain.*
- P89 **Desmin and vimentin gene expression study in pectoralis major muscle of broilers affected by muscular abnormalities.**  
M. Zappaterra\*<sup>1</sup>, F. Soglia<sup>2</sup>, M. Mazzoni<sup>3</sup>, M. Bordini<sup>1</sup>, M. Di Nunzio<sup>2</sup>, M. Petracci<sup>2</sup>, and R. Davoli<sup>1</sup>, <sup>1</sup>*Department of Agricultural and Food Sciences (DISTAL), Alma Mater Studiorum-University of Bologna, Bologna, Italy,* <sup>2</sup>*Department of Agricultural and Food Sciences (DISTAL), Alma Mater Studiorum-University of Bologna, Cesena, Italy,* <sup>3</sup>*Department of Veterinary Medical Sciences (DI-MEVET), Alma Mater Studiorum-University of Bologna, Bologna, Italy.*
- P90 **Discriminant and factor analysis of four strains of starter broiler chickens.**  
F. E. Sola-Ojo and D. I. Ibiwoye\*, *University of Ilorin, Kwara State, Nigeria.*
- P92 **Analysis of the brain transcriptome in lines of laying hens divergently selected for feather pecking before and after light stimulation.**  
J. Beier<sup>1</sup>, C. Falker-Gieske<sup>1</sup>, H. Iffland<sup>2</sup>, S. Preuß<sup>2</sup>, W. Bessei<sup>2</sup>, J. Bennewitz<sup>2</sup>, and J. Tetens\*<sup>1,3</sup>, <sup>1</sup>*Department of Animal Sciences, Georg-August-University, Göttingen, Germany,* <sup>2</sup>*Institute of Animal Science, University of Hohenheim, Stuttgart, Germany,* <sup>3</sup>*Center for Integrated Breeding Research, Georg-August-University, Göttingen, Germany.*
- P93 **Discovery and detection of associated loci plumage and shank color in chicken.**  
G. Hua\*, Y. Zhang, X. Dong, J. Chen, and X. Deng, *China Agricultural University, Beijing, China.*
- P94 **Marker-assisted introgression of blue eggshell color into a white egg layer line.**  
C. Dierks\*<sup>1</sup>, N. T. Ha<sup>2</sup>, D. Cavero<sup>3</sup>, H. Simianer<sup>2</sup>, R. Preisinger<sup>4</sup>, and S. Weigend<sup>1,2</sup>, <sup>1</sup>*Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt, Germany,* <sup>2</sup>*University of Goettingen, Department of Animal Sciences, Goettingen, Germany,* <sup>3</sup>*H&N International, Cuxhaven, Germany,* <sup>4</sup>*EW GROUP GmbH, Visbek, Germany.*
- P95 **Development of a SNP-based parentage verification panel for lovebirds.**  
H. Van der Zwan<sup>1</sup>, C. Visser<sup>2</sup>, M. Schoonen\*<sup>1</sup>, and R. Van der Sluis<sup>1</sup>, <sup>1</sup>*Focus Area for of Human Metabolomics, North-West University, Potchefstroom, South Africa,* <sup>2</sup>*Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, South Africa.*
- P96 **Transcriptome analysis reveals the effect of melanogenesis on shank color conversion in chickens.**  
Z. Xin\*, L. Shijun, C. Guoting, M. Changhuan, and R. Hongji, *Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei Province, China.*
- P97 **Integrating the transcriptome and metabolome of the post-hatch chicken liver and serum.**  
C. Schmidt\*, H. Van Every, and A. Singh, *University of Delaware, Newark, DE, USA.*



- P98 **Single-step methodology for genomic evaluation in turkeys (*Meleagris gallopavo*).**  
E. A. Abdalla\*<sup>1</sup>, B. J. Wood<sup>1,2</sup>, H. E. Begli<sup>1</sup>, K. Pieters<sup>3</sup>, P. van As<sup>3</sup>, M. Bink<sup>3</sup>, O. W. Willems<sup>2</sup>, R. Vanderhout<sup>1</sup>, F. S. Schenkel<sup>1</sup>, and C. F. Baes<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Hybrid Turkeys, Kitchener, ON, Canada, <sup>3</sup>Hendrix Genetics, Boxmeer, Netherlands.
- P99 **Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens.**  
A. Adetula\*<sup>1</sup>, L. Gu<sup>1</sup>, C. Nwafor<sup>2</sup>, X. Du<sup>3</sup>, S. Zhao<sup>1</sup>, and S. Li<sup>1</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction, Ministry of Education, Key Laboratory of Poultry Genetics and Breeding of the Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei Province, China, <sup>2</sup>Faculty of Agriculture, Benson Idahosa University, Benin, Edo State, Nigeria, <sup>3</sup>College of Informatics, Huazhong Agricultural University, Wuhan, Hubei Province, China.
- P100 **An open chromatin region on GGA1 has an important effect on regulating chicken growth.**  
X. Cao\*<sup>1,2</sup>, Y. Wang<sup>2,3</sup>, and X. Hu<sup>1,2</sup>, <sup>1</sup>College of Biological Sciences, China Agricultural University, Beijing, China, <sup>2</sup>State Key Laboratory of Agro-biotechnology, China Agricultural University, Beijing, China, <sup>3</sup>College of Animal Science and Technology, China Agricultural University, Beijing, China.
- P101 **Candidate signatures of positive selection in Ethiopian chicken.**  
A. Kebede\*<sup>1,2</sup>, K. Tesfaye<sup>1</sup>, G. Belay<sup>1</sup>, A. Vallejo<sup>5</sup>, T. Dessie<sup>3</sup>, N. Spark<sup>4</sup>, O. Hanotte<sup>3,5</sup>, L. Raman<sup>5</sup>, and A. Gheyas<sup>4,5</sup>, <sup>1</sup>Addis Ababa University (AAU), Addis Ababa, Ethiopia, <sup>2</sup>Amhara Regional Agricultural Research Institute (ARARI), Bahir Dar, Ethiopia, <sup>3</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>4</sup>Center for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, UK, <sup>5</sup>School of Life Sciences, University of Nottingham, Nottingham, UK.

### Cattle Molecular Markers and Parentage Testing

- P102 **Roles of bta-miR-23a and bta-miR-24-3p in the myogenic differentiation of bovine PDGFR $\alpha$  progenitor cells.**  
X. Hu\*, Y. Xing, L. Ren, Y. Wang, Q. Li, J. Li, and L. Zhang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*
- P103 **Evaluation of genotyping concordance for commercial bovine SNP chips using quality-assurance samples.**  
J. Qiu\*<sup>1</sup>, X.-L. Wu<sup>1</sup>, J. Xu<sup>2</sup>, H. Li<sup>1</sup>, J. He<sup>3</sup>, Q. Xiao<sup>3</sup>, R. Ferretti<sup>1</sup>, B. Simpson<sup>1</sup>, T. Mitchell<sup>1</sup>, S. Kachman<sup>2</sup>, and S. Bauck<sup>1</sup>, <sup>1</sup>Neogen GeneSeek, Lincoln, NE, USA, <sup>2</sup>Department of Statistics, University of Nebraska, Lincoln, NE, USA, <sup>3</sup>College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China.
- P104 **Birth size and birth weight in Brahman Cattle offspring and association with a PvuII polymorphism in the IGFBP-3 gene.**  
T. Hartatik\*<sup>1</sup>, D. A. Priyadi<sup>1</sup>, R. Y. Rahmawati<sup>1</sup>, P. Panjono<sup>2</sup>, S. Bintara<sup>1</sup>, I. Ismaya<sup>1</sup>, I. G. S. Budisatria<sup>2</sup>, B. P. Widyobroto<sup>2</sup>, A. Agus<sup>3</sup>, and P. Leroy<sup>4</sup>, <sup>1</sup>Department of Animal Breeding and Reproduction, FAS, UGM, Indonesia, <sup>2</sup>Departemen of Animal Production, FAS, UGM, Indonesia, <sup>3</sup>Departemen of Animal Nutrition and Feed Science, FAS, UGM, Indonesia, <sup>4</sup>Faculty of Veterinary Medicine, University of Liege, Belgium.
- P105 **Average daily gain and single nucleotide polymorphism analysis of 211-bp growth hormone gene in crossbred cattle.**  
T. Hartatik\*<sup>1</sup>, S. Bintara<sup>1</sup>, I. Ismaya<sup>1</sup>, P. Panjono<sup>2</sup>, B. P. Widyobroto<sup>2</sup>, A. Agus<sup>3</sup>, I. G. S. Budisatria<sup>2</sup>, and P. Leroy<sup>4</sup>, <sup>1</sup>Department of Animal Breeding and Reproduction, Faculty of Animal Science, UGM, Indonesia, <sup>2</sup>Departemen of Animal Production, Faculty of Animal Science, UGM, Indonesia, <sup>3</sup>Departemen of Animal Nutrition and Feed Science, Faculty of Animal Science, UGM, Indonesia, <sup>4</sup>Faculty of Veterinary Medicine, University of Liege, Belgium.
- P106 **Associations between MSTN variants and milk fatty acid composition in New Zealand cross-bred Holstein-Friesian  $\times$  Jersey cows.**  
I.L. Haruna\*, U.J. Ekegbu, Y. Li, H. Amirpour-Najafabadi, H. Zhou, and J. G.H. Hickford, *Faculty of Agriculture and Life Sciences, Lincoln University, Christchurch, Canterbury, New Zealand.*
- P107 **Developing a traceability system in Nguni cattle population using Illumina BovineSNP50 BeadChip.**  
LS Modise<sup>1</sup>, AA Zwane<sup>2</sup>, B. Mtileni<sup>1</sup>, and KA Nephawe\*<sup>1</sup>, <sup>1</sup>Department of Animal Sciences, Tshwane University of Technology, Pretoria, Gauteng, South Africa, <sup>2</sup>Animal Production Institute, Agricultural Research Council, Pretoria, Gauteng, South Africa.
- P109 **The allele and genotype distribution in SNP g.408 C>G of the FABP4 gene in Kebumen Ongole grade cattle.**  
A. Fathoni\*, D. Maharani, S. Sumadi, and T. Hartatik, *Universitas Gadjah Mada, Yogyakarta, Indonesia.*
- P110 **Strong signatures of selection in three Korean cattle breeds exposed to different selective pressures.**  
K.-S. Kim\* and Z. Edea, *Chungbuk National University, Cheongju, Chungbuk, South Korea.*

- P111 **Identification and validation of suitable reference genes for qRT-PCR analysis in yak testis development.**  
X. L. Zhou<sup>1,2</sup>, X. Y. Wu<sup>2</sup>, M. Chu<sup>2</sup>, X. Guo<sup>2</sup>, and P. Yan<sup>\*2</sup>, <sup>1</sup>State Key Laboratory of Grassland Agro-ecosystems, College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, Gansu, China, <sup>2</sup>Key Laboratory of Yak Breeding Engineering Gansu Province, Lanzhou Institute of Husbandry and Pharmaceutical Sciences, Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China.
- P112 **Molecular genetic analysis of male infertility in Holstein Friesian cattle.**  
S. Shan<sup>\*1</sup>, F. Xu<sup>1</sup>, M. Bleyer<sup>2</sup>, T. Melbaum<sup>1</sup>, S. Becker<sup>1</sup>, W. Wemheuer<sup>1</sup>, M. Hirschfeld<sup>1</sup>, M. Hölker<sup>3</sup>, C. Wacker<sup>1</sup>, E. Schütz<sup>1</sup>, S. Zhao<sup>4</sup>, and B. Brenig<sup>1</sup>, <sup>1</sup>University of Goettingen, Institute of Veterinary Medicine, Göttingen, Niedersachsen, Germany, <sup>2</sup>Pathology Unit, German Primate Center, Leibniz-Institute for Primate Research Göttingen, Göttingen, Niedersachsen, Germany, <sup>3</sup>University of Bonn, Institute for Animal Sciences, Königswinter, Nordrhein-Westfalen, Germany, <sup>4</sup>Key Lab of Animal Genetics, Breeding and Reproduction, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China.
- P113 **Validation of microsatellite markers for parentage verification in Indian HF cattle.**  
A. S. Khade<sup>\*</sup>, M. P. Sawane, and V. D. Pawar, *Department of Animal Genetics and Breeding, Bombay Veterinary College, Mumbai, Maharashtra, India.*
- P114 **Association of gonadotropin releasing hormone receptor (GnRHR) and Luteinizing hormone receptor (LHR) genes polymorphism with sperm quality and quantity traits in Iranian Holstein bulls.**  
M. Zarrinnia<sup>\*</sup> and A. Gorbani, *Shabestar University.*
- P116 **Molecular characterization of indigenous Zambian cattle breeds.**  
D. Zulu<sup>\*</sup>, K. Gyenai, J. Xu, and E. Smith, *Virginia Tech, Blacksburg, VA, USA.*
- P117 **Genetic diversity and structure of four zebu cattle breeds raised in Colombia.**  
L. M. Romero<sup>\*1</sup>, J. F. Borbon<sup>1</sup>, A. Arenas<sup>2</sup>, G. Gómez<sup>2</sup>, and Y. M. Gómez<sup>1</sup>, <sup>1</sup>Biotecnología y Genética S.A, Biotecgen, Bogotá, Colombia, <sup>2</sup>Asociación Colombiana de Criadores de Ganado Cebú Asocebu, Bogotá, Colombia.
- P118 **Identification of SNP in the LMNA gene in a heifer with suspected progeria.**  
G. Smolucha, A. Koseniuk<sup>\*</sup>, A. Kozubska-Sobocinska, A. Majewska, and B. Danielak-Czech, *The National Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland.*
- P120 **Comparison of results of mandatory ISAG bovine SNPs obtained by assays using microarray and NGS (GBS).**  
K. T. Souza<sup>\*1</sup>, C. T. F. S. Diniz<sup>2</sup>, R. M. G. Lima<sup>1</sup>, and C. L. P. Meneses<sup>1</sup>, <sup>1</sup>Linhagen Biotecnologia, Belo Horizonte, MG, Brazil, <sup>2</sup>Pontifícia Universidade Católica (PUC), Belo Horizonte, MG, Brazil.
- P121 **Genome-wide CNV identification and CNVR association with carcass and meat quality traits.**  
M. A. Andrade<sup>1</sup>, A. C. Fernandes<sup>2</sup>, A. S. Carmo<sup>3</sup>, T. C. S. Chud<sup>4</sup>, M. S. Carvalho<sup>5</sup>, M. N. Bonin<sup>6</sup>, E. C. Mattos<sup>5</sup>, J. B. S. Ferraz<sup>5</sup>, and F. M. Rezende<sup>\*1,2</sup>, <sup>1</sup>Instituto de Biotecnologia - UFU, Patos de Minas, MG, Brazil, <sup>2</sup>Faculdade de Medicina Veterinária - UFU, Uberlândia, MG, Brazil, <sup>3</sup>Universidade Federal de Goiás, G, Brazil, <sup>4</sup>University of Guelph, Guelph, Guelph, ON, Canada, <sup>5</sup>Universidade de São Paulo, Pirassununga, SP, Brazil, <sup>6</sup>Universidade Federal do Mato Grosso do Sul, Campo Grande, MS, Brazil.

### Companion Animal Genetics and Genomics

- P122 **DNA polymorphisms in the APC gene in dogs with intestinal adenomatous polyposis.**  
F. Rofes, G. Ramírez, and R. Pena<sup>\*</sup>, *Departament de Ciència Animal, Universitat de Lleida, Lleida, Spain.*
- P123 **Optimized fragment analysis kit to determine canine parentage with ISAG-recommended STR markers.**  
D. Meza, R. Tebbs, S. Chadaram<sup>\*</sup>, and R. Conrad, *Thermo Fisher Scientific, Austin, TX, USA.*
- P124 **A cell line model for mammary gland tumors: Immunological characterization of CF33.**  
P. Modesto<sup>\*1</sup>, B. Chirullo<sup>2</sup>, P. Petrucci<sup>2</sup>, C. Campanella<sup>1</sup>, C. Pistoia<sup>2</sup>, P. Pasquali<sup>2</sup>, A. Ferrari<sup>1</sup>, and E. Razzuoli<sup>1</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy, <sup>2</sup>Istituto Superiore di Sanità, Rome, Italy.
- P125 **Evaluation of alternative treatment for canine mammary tumors using CF33 cell line.**  
P. Modesto<sup>\*1</sup>, B. Chirullo<sup>2</sup>, P. Petrucci<sup>2</sup>, C. Campanella<sup>1</sup>, C. Pistoia<sup>2</sup>, P. Pasquali<sup>2</sup>, A. Ferrari<sup>1</sup>, and E. Razzuoli<sup>1</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy, <sup>2</sup>Istituto Superiore di Sanità, Rome, Italy.



- P126 **Investigation of canine APOA5 gene polymorphisms in some breeds.**  
M. Takeda<sup>\*1</sup>, M. Hattori<sup>1</sup>, H. Yasuda<sup>2</sup>, and Y. Mizoguchi<sup>1</sup>, <sup>1</sup>Meiji University, Kawasaki, Kanagawa, Japan, <sup>2</sup>Yasuda Veterinary Clinic, Meguro, Tokyo, Japan.
- P127 **Analysis of ocular diseases in Shetland Sheepdog population and evaluation of candidate genes for oculocutaneous albinism.**  
J. Bíla<sup>\*</sup>, M. Bieliková, and A. Dudáš, *Department of Molecular Biology, Faculty of Natural Sciences, Comenius University, Bratislava, Slovak Republic.*
- P128 **Proteins and miRNAs in feline renal amyloid deposits.**  
F. Genova<sup>\*1</sup>, S. Nonnis<sup>1</sup>, E. Maffioli<sup>1</sup>, F. Grassi Scalvini<sup>1</sup>, N. Di Nanni<sup>3</sup>, F. Cupaioli<sup>3</sup>, E. Mosca<sup>3</sup>, A. Mezzelani<sup>3</sup>, G. Sironi<sup>1</sup>, LA Lyons<sup>2</sup>, G. Tedeschi<sup>1</sup>, and M. Longeri<sup>1</sup>, <sup>1</sup>Department of Veterinary Medicine, University of Milan, Milan, Italy, <sup>2</sup>Department of Veterinary Medicine and Surgery, University of Missouri, Columbia, MO, USA, <sup>3</sup>Bioinformatics Group, Institute of Biomedical Technologies, National Research Council of Italy, Segrate, Italy.
- P129 **Genomic origin of Balkan livestock guardian dogs.**  
M. Janeš<sup>1</sup>, M. Zorc<sup>2</sup>, M. Ferencakovic<sup>1</sup>, I. Curik<sup>1</sup>, P. Dovc<sup>2</sup>, and V. Cubric-Curik<sup>\*1</sup>, <sup>1</sup>University of Zagreb, Faculty of Agriculture, Department of Animal Science, Zagreb, Croatia, <sup>2</sup>University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Ljubljana, Slovenia.
- P130 **Candidate gene search for canine hip dysplasia expression using genome-wide association study (GWAS) in Korean army dogs.**  
J. M. Kang<sup>\*1</sup>, C. J. Gajaweera<sup>1</sup>, S. B. Jang<sup>1</sup>, Y. K. Kim<sup>1</sup>, Y. J. Chung<sup>1</sup>, S. H. Lee<sup>1</sup>, D. H. Lee<sup>1</sup>, Y. H. Ju<sup>3</sup>, C. K. Lee<sup>4</sup>, B. H. Choi<sup>2</sup>, and S. H. Lee<sup>1</sup>, <sup>1</sup>Division of Animal and Dairy Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon, South Korea, <sup>2</sup>Animal Genome and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju, South Korea, <sup>3</sup>Department of Defense Military Observer Corps, South Korea, <sup>4</sup>Division of Biotechnology, Korea University, Seoul, South Korea.
- P131 **An R-based methodology for remapping SNPs to nascent genome assemblies.**  
W. Zhang<sup>\*1</sup>, J. McGrath<sup>1</sup>, J. Brockman<sup>2</sup>, D. Gunn-Moore<sup>1</sup>, R. Mellanby<sup>1</sup>, and J. Schoenebeck<sup>1</sup>, <sup>1</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, UK, <sup>2</sup>Hill's Pet Nutrition, Pet Nutrition Center, Topeka, KS, USA.
- P132 **cDNA cloning and variant analysis of the canine CMAH gene.**  
Y. Uno<sup>\*</sup>, S. Kawakami, K. Ochiai, and T. Omi, *Faculty of Veterinary Science, Nippon Veterinary and Life Science University, Musashino, Tokyo, Japan.*
- P133 **Genetic population study of STR loci (Finnzymes Canine Genotypes Panel 1.1) in Slovenian dog population.**  
M. Cotman<sup>\*</sup> and J. Zabavnik Piano, *University of Ljubljana, Veterinary Faculty, Institute of Preclinical Sciences, Ljubljana, Slovenia.*
- P134 **Genetic background of aortic stenosis in Slovenian population of Boxer dogs.**  
A. Perovic<sup>1,2</sup>, A. D. Petric<sup>1</sup>, I. D. Kusec<sup>3</sup>, M. Zorc<sup>4</sup>, and P. Dovc<sup>\*4</sup>, <sup>1</sup>University of Ljubljana, Veterinary Faculty, Ljubljana, Slovenia, <sup>2</sup>Sonar d.o.o, Ljubljana, Slovenia, <sup>3</sup>University of Osijek, Faculty of Agrobiotechnical Sciences, Osijek, Croatia, <sup>4</sup>University of Ljubljana, Biotechnical Faculty, Ljubljana, Slovenia.
- P135 **An early onset retinopathy in Golden retriever dogs.**  
S. Mäkeläinen<sup>\*1</sup>, K. Narfström<sup>2</sup>, B. Ekestén<sup>3</sup>, G. Andersson<sup>1</sup>, and TF Bergström<sup>1</sup>, <sup>1</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>Section for Comparative Ophthalmology, College of Veterinary Medicine, University of Missouri-Columbia, Columbia, MO, USA, <sup>3</sup>Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden.

### Comparative and Functional Genomics

- P136 **Discovery and characterization of lncRNA involved in lipogenesis and lipid composition in different types of adipose tissues of Wagyu cattle.**  
J. Mi<sup>1</sup>, Z. Zhao<sup>1</sup>, X. Fang<sup>1</sup>, A. Elke<sup>2</sup>, S. Maak<sup>2</sup>, and R. Yang<sup>\*1</sup>, <sup>1</sup>Jilin University, Changchun, Jilin, China, <sup>2</sup>Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.
- P138 **Optimizing the number of SNP required to differentiate cows and somatic cell count in a bulk tank milk: The case of Geno-Cells.**  
F. Perrin<sup>\*1</sup>, P. Lenormand<sup>2</sup>, N. Taupin<sup>1</sup>, M. Collet<sup>1</sup>, M.-F. Quesnel<sup>1</sup>, M. Foucher<sup>1</sup>, and J.-B. Davière<sup>2</sup>, <sup>1</sup>AGRANIS Laboratory, Genomic department, Saint Berthevin, France, <sup>2</sup>SEENOVIA, Research and Development department, Saint Berthevin, France.



- P139 **Data visualization toolkit for targeted genotyping-by-sequencing (GBS).**  
P. Siddavatam, H. Suren, K. Gujjula, R. Willis\*, and J. Schmidt, *Thermo Fisher Scientific, Austin, TX, USA.*
- P140 **An intercross population study among domestic and wild sheep reveals genes associated with morphological and body conformation traits using a hybrid genome.**  
X. Li<sup>1,2</sup> and M.H. Li<sup>\*1</sup>, <sup>1</sup>CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences (CAS), Beijing, China, <sup>2</sup>University of Chinese Academy of Sciences (UCAS), Beijing, China.
- P141 **Copy number variations in South African Holstein and Jersey cattle: Prevalence, characterisation and milk trait associations.**  
M. D. Pierce<sup>\*1</sup>, L. H. Pickering<sup>2</sup>, and K. Dzama<sup>1</sup>, <sup>1</sup>University of Stellenbosch, Stellenbosch, Western Cape, South Africa, <sup>2</sup>Unistel Medical Laboratories, Cape Town, Western Cape, South Africa.
- P142 **Interaction effects on adipose tissue transcriptome in Iberian and Duroc pigs fed different energy sources.**  
R. Benítez<sup>\*1</sup>, N. Trakooljul<sup>2</sup>, Y. Núñez<sup>1</sup>, B. Isabel<sup>3</sup>, E. Murani<sup>2</sup>, E. De Mercado<sup>4</sup>, E. Gómez-Izquierdo<sup>4</sup>, J. Garcia-Casco<sup>1</sup>, C. López-Bote<sup>3</sup>, K. Wimmers<sup>2</sup>, and C. Óvilo<sup>1</sup>, <sup>1</sup>INIA, Madrid, Spain, <sup>2</sup>Leibniz-Institute for Farm Animal Biology (FBN) Institute for Genome Biology, Dummerstorf, Germany, <sup>3</sup>Departamento de Producción Animal, Facultad de Veterinaria, UCM, Madrid, Spain, <sup>4</sup>Centro de pruebas de porcino ITACYL, Hontalbilla, Segovia, Spain.
- P143 **The European Variation Archive: Genetic variation archiving and accessioning for all species.**  
C. Y. Gonzalez, J. M. Mut, S. Venkataraman, A. Silva, B. A. Koylass\*, and T. Keane, *The European Bioinformatics Institute, Cambridgeshire, United Kingdom.*
- P144 **Piglet body weight drives functional changes in hypothalamic and muscle transcriptome.**  
R. Benitez<sup>1</sup>, J. Segura<sup>2</sup>, M. Vázquez-Gómez<sup>2</sup>, J. Viguera<sup>3</sup>, L. Calvo<sup>4</sup>, JI Moríñigo<sup>5</sup>, Y. Nuñez<sup>1</sup>, C. López-Bote<sup>2</sup>, and C. Ovilo<sup>\*1</sup>, <sup>1</sup>Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, <sup>2</sup>Universidad Complutense de Madrid (UCM), Madrid, Spain, <sup>3</sup>Imasde Agroalimentaria, Madrid, Spain, <sup>4</sup>Incarlopsa, Cuenca, Spain, <sup>5</sup>Ibercom, Badajoz, Spain.
- P145 **Conjugated linoleic acid promotes bovine intramuscular adipogenesis.**  
N. Mizuta and Y. Mizoguchi\*, *Meiji University, Kawasaki, Kanagawa, Japan.*
- P146 **Transcriptome profiling and heat stress-related genes identification with RNA-seq data in rat model.**  
J. Dou<sup>\*1</sup>, Y. Yu<sup>1</sup>, Y. Wang<sup>2</sup>, and Y. Wang<sup>1</sup>, <sup>1</sup>Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture of China, National Engineering Laboratory of Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China, <sup>2</sup>State Key Laboratory of Animal Nutrition, Beijing Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, China Agricultural University, Beijing, China.
- P147 **Characterization of pregnancy-associated glycoprotein-1 gene in locally adapted Nigerian cattle breeds.**  
J. A. Aderoju<sup>\*1</sup>, M. Ozoje<sup>2</sup>, N. Oyekanmi<sup>1</sup>, A. Tijani<sup>1</sup>, and B. Ilori<sup>2</sup>, <sup>1</sup>National Biotechnology Development Agency, Abuja, Nigeria, <sup>2</sup>Federal University of Agriculture, Abeokuta, Ogun State, Nigeria.
- P148 **Agriseq targeted GBS is a customizable high-throughput genotyping technology that permits fast, easy, and inexpensive alteration of marker content.**  
C. Carrasco, K. Gujjula, H. Suren, P. Siddavatam, and C. Adams\*, *Thermo Fisher Scientific, Austin, TX USA.*
- P149 **Tannin supplementation in Mangalitsa pigs: Effects on muscle transcriptome.**  
Y. Núñez<sup>\*1</sup>, C. Radovic<sup>2</sup>, R. Savic<sup>3</sup>, M. Candek-Potokar<sup>4</sup>, R. Benítez<sup>1</sup>, D. Radojkovic<sup>3</sup>, M. Lukic<sup>2</sup>, M. Gogic<sup>2</sup>, L. Fontanesi<sup>5</sup>, and C. Ovilo<sup>1</sup>, <sup>1</sup>INIA, Madrid, Spain, <sup>2</sup>Institute for Animal Husbandry-Pig, Belgrade-Zemun, Serbia, <sup>3</sup>University of Belgrade, Belgrade-Zemun, Serbia, <sup>4</sup>Kmetijski inštitut Slovenije, Ljubljana, Slovenia, <sup>5</sup>University of Bologna, Bologna, Italy.
- P150 **Galectin encoding genes as indicators of selective susceptibility to endotoxin in ruminants.**  
M. Worku<sup>\*1</sup>, E. Ekwemalor<sup>1</sup>, E. Asiamah<sup>2</sup>, S. Adjei-Fremah<sup>1</sup>, and B. Osei<sup>1</sup>, <sup>1</sup>Department of Animal Sciences, North Carolina A&T State University, Greensboro, NC USA, <sup>2</sup>Department of Animal Sciences, University of Arkansas at Pine Bluff, Pine Bluff, AR USA, <sup>3</sup>Department of Biology, North Carolina A&T State University, Greensboro, NC, USA, <sup>4</sup>Functional and Chemical Genomics, Oklahoma Medical Research Foundation, Oklahoma City, OK, USA.
- P151 **Blood transcriptome analysis in a buck-ewe hybrid (geep) and its parents.**  
C. Falker-Gieske<sup>1</sup>, C. Knorr<sup>1</sup>, and J. Tetens<sup>\*1,2</sup>, <sup>1</sup>Department of Animal Sciences, Georg-August-University, Göttingen, Germany, <sup>2</sup>Center for Integrated Breeding Research, Georg-August-University, Göttingen, Germany.



- P152 **Functional genomics approach to characterize four adipose tissues in Finnish and Yakutian reindeer (*Rangifer tarandus*).**  
M. Weldenegodguad\*<sup>1,2</sup>, K. Pokharel<sup>1</sup>, I. Ammosov<sup>3</sup>, M. Honkatukia<sup>4</sup>, J. Peippo<sup>1</sup>, T. Reilas<sup>1</sup>, P. Soppela<sup>5</sup>, N. Mazzullo<sup>5</sup>, V. Fedorov<sup>6</sup>, and J. Kantanen<sup>1</sup>, <sup>1</sup>Natural Resources Institute Finland (Luke), Jokioinen, Finland, <sup>2</sup>University of Eastern Finland, Kuopio, Finland, <sup>3</sup>Board of Agricultural Office of Eveno-Bytantaj Region, Batagay-Alyta, Russia, <sup>4</sup>The Nordic Genetic Resources Center (Nordgen), Ås, Norway, <sup>5</sup>Arctic Centre, University of Lapland, Rovaniemi, Finland, <sup>6</sup>Yakutian Research Institute of Agriculture (FGBNU Yakutskij NIISH), Yakutsk, Russia.
- P153 **Differentially expressed tRNA fragments in bovine fetuses with assisted-reproduction induced congenital overgrowth syndrome.**  
A. K. Goldkamp\*<sup>1</sup>, Y. Li<sup>2</sup>, Q. Sun<sup>1</sup>, L. Zhu<sup>1</sup>, R. Rivera<sup>2</sup>, and D. Hagen<sup>1</sup>, <sup>1</sup>Oklahoma State University, Stillwater, OK, USA, <sup>2</sup>University of Missouri-Columbia, Columbia, MO, USA.
- P154 **Apoptosis of porcine alveolar macrophages by regulating the expression of the *Streptococcus suis*-induced *PPP1R11* gene.**  
G. Liu\*<sup>1,2</sup>, J. Wu<sup>1,2</sup>, M. Qiao<sup>1,2</sup>, J. Zhou<sup>1,2</sup>, X. Peng<sup>1,2</sup>, and S. Mei<sup>1,2</sup>, <sup>1</sup>Institute of Animal and Veterinary Sciences, Hubei Academy of Agricultural Sciences, Wuhan, Hubei Province, China, <sup>2</sup>Hubei Key Lab for Animal Embryo Engineering and Molecular Breeding, Wuhan, Hubei Province, China.
- P155 **Worldwide geophylogenetic analysis of *Bubalus bubalis* D-loop region from publicly available data.**  
F. Araujo<sup>1,2</sup>, R. Ramos<sup>1</sup>, B. Brenig<sup>2</sup>, and A. Silva\*<sup>1</sup>, <sup>1</sup>Federal University of Para, Belém, PA, Brazil, <sup>2</sup>University of Goettingen, Goettingen, Germany.
- P156 **Prediction and quantitative expression of tRNA genes in bovine tissues.**  
D. Hagen\*<sup>1</sup>, A. Goldkamp<sup>1</sup>, T. Ji<sup>2</sup>, and R. Rivera<sup>2</sup>, <sup>1</sup>Oklahoma State University, Stillwater, OK, USA, <sup>2</sup>University of Missouri, Columbia, MO, USA.
- P157 **Genetic control of temperament traits across species: Association of autism spectrum disorder genes with cattle temperament.**  
R. Costilla\*<sup>1,2</sup>, K. Kemper<sup>1</sup>, E. Byrne<sup>1</sup>, L. Porto-Neto<sup>4</sup>, R. Carvalheiro<sup>5</sup>, D. Berry<sup>6</sup>, D. Purfield<sup>6</sup>, J. Doyle<sup>6</sup>, S. Moore<sup>2</sup>, N. Wray<sup>1</sup>, and B. Hayes<sup>2</sup>, <sup>1</sup>Institute for Molecular Bioscience, The University of Queensland, Brisbane, Australia, <sup>2</sup>Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Australia, <sup>3</sup>Queensland Brain Institute, The University of Queensland, Brisbane, Australia, <sup>4</sup>Commonwealth Scientific and Industrial Research Organization (CSIRO), Agriculture and Food, Brisbane, Australia, <sup>5</sup>School of Agricultural and Veterinarian Sciences, Sao Paulo State University, Sao Paolo, Brasil, <sup>6</sup>Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co, Cork, Ireland.
- P158 **Evaluation of RNA-sequencing pipelines for optimized power and accuracy of SNP and INDEL identification.**  
S. Lam\*<sup>1</sup>, F. Miglior<sup>1</sup>, J. Zeidan<sup>1</sup>, I. Gómez-Redondo<sup>1,2</sup>, A. Suárez-Vega<sup>1</sup>, P. A. S. Fonseca<sup>1</sup>, and F. Schenkel<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Spanish National Institute for Agriculture and Food Research and Technology, Madrid, Spain.

### Comparative MHC Genetics: Populations and Polymorphism

- P159 **Bovine leukemia virus proviral load were associated with bovine MHC DRB3 and DQA1 alleles in Japanese Holstein population from 2011 to 2014.**  
Y. Aida\*<sup>1,2</sup>, S.-N. Takeshima<sup>1,3</sup>, A. Ohno<sup>2</sup>, and L. Borjigin<sup>1</sup>, <sup>1</sup>Nakamura Laboratory, Baton Zone Program, RIKEN Cluster for Science, Technology and Innovation Hub, Wako, Saitama, Japan, <sup>2</sup>Viral Infectious Diseases Unit, RIKEN, Wako, Saitama, Japan, <sup>3</sup>Department of Food and Nutrition, Faculty of Human Life, Jumonji University, Niiza, Saitama, Japan.
- P160 **Effectiveness of bovine leukemia virus (BLV) infection control strategies using cattle carrying resistant and susceptible bovine MHC DRB3 alleles.**  
L. Borjigin\*<sup>1</sup>, L. Bai<sup>2</sup>, T. Hirose<sup>1</sup>, H. Sato<sup>1</sup>, S. Watanuki<sup>1</sup>, S. Yoneyama<sup>3</sup>, M. Inokuma<sup>4</sup>, K. Fujita<sup>4</sup>, Y. Shinozaki<sup>5</sup>, R. Yamanaka<sup>6</sup>, A. Yasui<sup>6</sup>, Y. Sohei<sup>6</sup>, M. Baba<sup>6</sup>, S.-N. Takeshima<sup>1,7</sup>, Y. Aida<sup>1</sup>, <sup>1</sup>Nakamura Laboratory, Baton Zone Program, RIKEN Cluster for Science, Technology and Innovation Hub, Wako, Saitama, Japan, <sup>2</sup>Photonics Control Technology Team, RIKEN Center for Advanced Photonics, Wako, Saitama, Japan, <sup>3</sup>Kenou Livestock Hygiene Service Center, Utsunomiya, Tochigi, Japan, <sup>4</sup>Chuo Livestock Hygiene Service Center, Chiba, Japan, <sup>5</sup>Nanbu Livestock Hygiene Service Center, Chiba, Kamogawa, Japan, <sup>6</sup>Kumagaya Livestock Hygiene Service Center, Kumagaya, Saitama, Japan, <sup>7</sup>Department of Food and Nutrition, Jumonji University, Niiza, Saitama, Japan.

### Domestic Animal Sequencing and Annotation

- P161 **SeqBreed: A python tool to evaluate genomic selection with sequence data.**  
M. Perez-Enciso<sup>1,2</sup>, M. L. Zingaretti<sup>\*2</sup>, and L. Ramirez-Ayala<sup>2</sup>, <sup>1</sup>ICREA, Barcelona, Spain, <sup>2</sup>CRAG, Bellaterra, Spain.
- P163 **Rambouillet sheep transcriptome annotation resources.**  
R. A. Harris<sup>1,2</sup>, X. Qin<sup>1,2</sup>, Y. Han<sup>1</sup>, Q. Meng<sup>1</sup>, T. P. Smith<sup>3</sup>, M. P. Heaton<sup>3</sup>, B. P. Dalrymple<sup>4</sup>, F. Thibaud-Nissen<sup>5</sup>, E. Clark<sup>6</sup>, J. Kijas<sup>7</sup>, N. E. Cockett<sup>8</sup>, B. Murdoch<sup>9</sup>, D. M. Muzny<sup>1</sup>, K. C. Worley<sup>\*1,2</sup>, for the Ovine FAANG Project<sup>9</sup>, <sup>1</sup>Baylor College of Medicine, Human Genome Sequencing Center, Houston, TX, USA, <sup>2</sup>Baylor College of Medicine, Department of Molecular and Human Genetics, Houston, TX, USA, <sup>3</sup>USDA Agricultural Research Service, U.S. Meat Animal Research Center, Clay Center, NE, USA, <sup>4</sup>University of Western Australia, Institute of Agriculture, Perth, Western Australia, Australia, <sup>5</sup>National Center for Bio, Bethesda, MD, USA, <sup>6</sup>The Roslin Institute, The University of Edinburgh, Edinburgh, UK, <sup>7</sup>CSIRO, St. Lucia, Australia, <sup>8</sup>Utah State University, President's Office, Logan, UT, USA, <sup>9</sup>University of Idaho, Animal and Veterinary Science, Moscow, ID, USA.
- P164 **Resolving the polled locus in Brahman (*Bos indicus*) cattle using Nanopore long read sequencing.**  
H. Lamb<sup>\*1,2</sup>, B. Hayes<sup>2</sup>, S. Moore<sup>2</sup>, R. Lyons<sup>3</sup>, and E. Ross<sup>2</sup>, <sup>1</sup>School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, QLD, Australia, <sup>2</sup>Centre for Animal Science, QAAFI, Brisbane, QLD, Australia, <sup>3</sup>School of Veterinary Science, The University of Queensland, Brisbane, QLD, Australia.
- P165 **Preliminary sequence assembly of the alpaca (*Vicugna pacos*) Y chromosome.**  
M. Jevit<sup>\*1</sup>, B. Davis<sup>1</sup>, M. Richardson<sup>2</sup>, M. Ferguson-Smith<sup>3</sup>, A. Hillhouse<sup>1</sup>, R. Juras<sup>1</sup>, A. Tibary<sup>4</sup>, V. Trifinov<sup>5</sup>, and T. Raudsepp<sup>1</sup>, <sup>1</sup>Texas A&M University, College Station, TX, USA, <sup>2</sup>Deakin University, Burwood, Victoria, Australia, <sup>3</sup>University of Cambridge, Cambridge, United Kingdom, <sup>4</sup>Washington State University, Pullman, WA, USA, <sup>5</sup>Institute of Molecular and Cellular Biology, Novosibirsk, Russian Federation.
- P166 **A metadata ruleset solution for the Innovative Management of Animal Genetic Resources (IMAGE) unification of European Gene Bank Data.**  
J. Fan<sup>\*1</sup>, P. Cozzi<sup>1</sup>, A. Sokolov<sup>1</sup>, O. Selmoni<sup>3</sup>, E. Vajana<sup>3</sup>, S. Joost<sup>3</sup>, E. Groeneveld<sup>2</sup>, G. Cochrane<sup>1</sup>, P. Flicek<sup>1</sup>, P. Harrison<sup>1</sup>, and A. Stella<sup>2</sup>, <sup>1</sup>EMBL-European Bioinformatics Institute, Hinxton, UK, <sup>2</sup>National Research Council, Milan, Italy, <sup>3</sup>École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland.
- P167 **Whole-genome sequencing analysis of six Eurasian native cattle breeds.**  
C.-W. Lee<sup>1</sup>, H.-S. Seong<sup>2</sup>, W.-H. Chung<sup>3</sup>, D.-H. Son<sup>2</sup>, N.-H. Hwang<sup>2</sup>, Y.-M. Kim<sup>2,4</sup>, J.-B. Kim<sup>2</sup>, B.-H. Choi<sup>5</sup>, J. A. Lenstra<sup>6</sup>, J. Kantanen<sup>7</sup>, J.-W. Choi<sup>\*2</sup>, and D. Lim<sup>5</sup>, <sup>1</sup>Gangwon Province Livestock Technology Research Institute, Hoengseong, Republic of Korea, <sup>2</sup>College of Animal Life Science, Kangwon National University, Chuncheon, Republic of Korea, <sup>3</sup>Division of Food Functionality Research, Research Group of Healthcare, Wanju, Republic of Korea, <sup>4</sup>Division of Swine Science, National Institute of Animal Science, RDA, Cheonan, Republic of Korea, <sup>5</sup>Division of Animal Genomics and Bioinformatics, National Institute of Animal Science, RDA, Wanju, Republic of Korea, <sup>6</sup>Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands, <sup>7</sup>Department of Production Systems, Natural Resources Institute Finland (Luke), Helsinki, Finland.
- P451 **De novo assembly and analysis of a Banteng (*Bos javanicus*).**  
W.-H. Chung<sup>1</sup>, J.-W. Choi<sup>\*2</sup>, H.-S. Seong<sup>2</sup>, D. Lim<sup>3</sup>, D.-H. Son<sup>2</sup>, Y.-M. Kim<sup>2,4</sup>, J. A. Lenstra<sup>5</sup>, and B.-H. Choi<sup>3</sup>, <sup>1</sup>Division of Food Functionality Research, Research Group of Healthcare, Wanju, Republic of Korea, <sup>2</sup>College of Animal Life Science, Kangwon National University, Chuncheon, Republic of Korea, <sup>3</sup>Division of Animal Genomics and Bioinformatics, National Institute of Animal Science, RDA, Wanju, Republic of Korea, <sup>4</sup>Division of Swine Science, National Institute of Animal Science, RDA, Cheonan, Republic of Korea, <sup>5</sup>Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands.

### Equine Genetics and Thoroughbred Parentage Testing

- P168 **Expression profiling of circulating miRNAs throughout the gestation period in pregnant mares.**  
M. Kikuchi<sup>\*1</sup>, H. Kakoi<sup>1</sup>, T. Tozaki<sup>1</sup>, F. Sato<sup>2</sup>, K. Hirota<sup>1</sup>, and S. Nagata<sup>1</sup>, <sup>1</sup>Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan, <sup>2</sup>Hidaka Training and Research Center, Japan Racing Association, Urakawa, Hokkaido, Japan.
- P170 **A medium-density SNP array for the horse genotyping.**  
A. Fornal<sup>\*</sup>, A. Piestrzynska-Kajtoch, and A. Radko, National Research Institute of Animal Production, Balice, Poland.
- P171 **STR polymorphism in donkey (*Equus asinus*) from Poland.**  
A. Fornal<sup>\*1</sup>, B. Dlugosz<sup>2</sup>, A. Piestrzynska-Kajtoch<sup>1</sup>, and K. Kowalska<sup>1</sup>, <sup>1</sup>National Research Institute of Animal Production, Balice, Poland, <sup>2</sup>Agricultural University, Animal Science Institute, Krakow, Poland.



P172 **Innate effectors of neutrophil homing are increased in peripheral lung tissue during pasture-associated severe equine asthma exacerbation.**

K. A. Thomas, J. E. Bowser, C. A. Mochal, A. L. Eddy, A. Claude, S. Mukherjee, and C. E. Swiderski\*, *Department of Clinical Sciences, College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA.*

### Gene Function (jointly with FAANG)

- P173 **Proteomics recapitulates markers regulating pathways relevant to ovarian activity in pubertal *Bos indicus* heifers.**  
M. S. Tahir<sup>\*1</sup>, L. T. Nguyen<sup>1,2</sup>, B. L. Schulz<sup>1</sup>, G. A. Boe-Hansen<sup>1</sup>, M. G. Thomas<sup>3</sup>, S. S. Moore<sup>1,2</sup>, and M. R. S. Fortes<sup>1,2</sup>, <sup>1</sup>*University of Queensland, Brisbane, Queensland, Australia*, <sup>2</sup>*Queensland Alliance for Agriculture and Food Innovation, Brisbane, Queensland, Australia*, <sup>3</sup>*Colorado State University, Fort Collins, CO, USA.*
- P174 **A microsatellite tandem repeat in the promoter of *Myo5a* causes the gray coat color phenotype in mice.**  
H. Zhang<sup>\*1</sup>, Z. Wu<sup>1</sup>, Z. Zhang<sup>2</sup>, H. Chen<sup>3</sup>, and J. Ren<sup>1</sup>, <sup>1</sup>*College of Animal Science, South China Agricultural University, Guangzhou, China*, <sup>2</sup>*First Affiliated Hospital, Gannan Medical University, Ganzhou, China*, <sup>3</sup>*College of Life Science, Jiangxi Science and Technology Normal University, Nanchang, China.*
- P175 **An extensive evaluation of the contribution of genome-wide regulatory and evolutionary signals to bovine complex traits.**  
R. Xiang<sup>\*1,2</sup>, I. Van Den Berg<sup>1,2</sup>, I. MacLeod<sup>2</sup>, B. Hayes<sup>3</sup>, C. Prowse-Wilkins<sup>1,2</sup>, M. Wang<sup>2,4</sup>, S. Bolormaa<sup>2</sup>, Z. Liu<sup>2</sup>, S. Rochfort<sup>2</sup>, C. Reich<sup>2</sup>, B. Mason<sup>2</sup>, C. Vander Jagt<sup>2</sup>, H. Daetwyler<sup>2,4</sup>, A. Chamberlain<sup>2</sup>, M. Goddard<sup>1,2</sup>, <sup>1</sup>*The University of Melbourne, Melbourne, Victoria, Australia*, <sup>2</sup>*Agriculture Victoria, Bundoora, Victoria, Australia*, <sup>3</sup>*The University of Queensland, St. Lucia, Queensland, Australia*, <sup>4</sup>*La Trobe University, Bundoora, Victoria, Australia.*
- P176 **The FAANG Data Coordination Centre: Infrastructure to enable functional annotation of livestock genomes.**  
A. Sokolov<sup>\*</sup>, J. Fan, G. Cochrane, D. Zerbino, P. Harrison, and P. Flicek, *EMBL-EBI, Hinxton, UK.*
- P177 **Identification of functional elements in dairy cattle.**  
C. P. Prowse-Wilkins<sup>\*1,2</sup>, A. J. Chamberlain<sup>1</sup>, and M. E. Goddard<sup>1,2</sup>, <sup>1</sup>*Agriculture Victoria, Centre for AgriBiosciences, Bundoora, Victoria, Australia*, <sup>2</sup>*Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville, Victoria, Australia.*
- P178 **Functional analysis and association studies of bovine *CDC10* gene with growth-related traits.**  
B. Tong<sup>\*1</sup>, L. Wang<sup>1</sup>, X. Kong<sup>1</sup>, G. Cheng<sup>2,3</sup>, L. Zan<sup>2,3</sup>, T. Yamada<sup>4</sup>, and G. Li<sup>1</sup>, <sup>1</sup>*State Key Laboratory of Reproductive Regulation & Breeding of Grassland Livestock, Inner Mongolia University, Hohhot City, Inner Mongolia Autonomous Region, China*, <sup>2</sup>*College of Animal Science and Technology, Northwest A&F University, Yangling City, Shaanxi Province, China*, <sup>3</sup>*National Beef Cattle Improvement Center, Northwest A&F University, Yangling City, Shaanxi Province, China*, <sup>4</sup>*Department of Agrobiolgy, Faculty of Agriculture, Niigata University, Niigata City, Niigata ken, Japan.*
- P179 **Bovine transcription factor *KLF3* regulates proliferation and differentiation of bovine myoblasts through the *PI3K/AKT* pathway.**  
J. Xu, J. Wang, C. Song, Y. Wen, B. Yue, X. Cao, C. Lei, R. Dang, X. Lan, H. Chen, and Y. Huang<sup>\*</sup>, *Northwest A&F University, Yangling, Shaanxi, China.*
- P180 **The relationship between genetic variation, DNA methylation and expression of *CRABP2* gene in beef cattle.**  
Y. Wen, J. Wang, J. W. Xu, C. Song, B. Yue, X. C. Cao, C. Lei, R. Dang, X. Lan, H. Chen, and Y. Huang<sup>\*</sup>, *Northwest A&F University, Yangling, Shaanxi 712100, China.*
- P181 **Bovine pleomorphic adenoma gene 1 (*PLAG1*) promotes proliferation and inhibits apoptosis of myoblasts.**  
J. Wang, Y. Huang, J. Xu, B. Yue, C. Song, Y. Wen, X. Cao, C. Lei, X. Lan, and H. Chen<sup>\*</sup>, *Northwest A&F University, Yangling, Shaanxi, China.*
- P182 **Function and mechanisms of a novel lncRNA *IGF2 AS* in bovine skeletal muscle development.**  
C. Song, Z. Yang, R. Jiang, J. Cheng, B. Yue, J. Wang, X. Sun, Y. Huang, X. Lan, C. Lei, and H. Chen<sup>\*</sup>, *Northwest A&F University, Yangling, Shaanxi, China.*
- P183 **Genome-wide mapping of alternative polyadenylation sites in cattle.**  
Z. Jiang<sup>\*1</sup>, J. J. Michal<sup>1</sup>, X. Zhou<sup>1</sup>, S. He<sup>1</sup>, M. Stotts<sup>1</sup>, Y. Zhang<sup>1</sup>, X. Zhang<sup>1</sup>, X. Leng<sup>2</sup>, Y. Zhang<sup>1</sup>, H. Wang<sup>1</sup>, H. Jiang<sup>2</sup>, M. Du<sup>1</sup>, M. Maquivar<sup>1</sup>, and L. K. Fox<sup>1</sup>, <sup>1</sup>*Washington State University, Pullman, WA, USA*, <sup>2</sup>*Virginia Polytechnic Institute and State University, Blacksburg, VA, USA.*

- P184 **Gene expression of myogenic factors and its association with sex and growth period in cattle.**  
J. Kyselova\*<sup>1</sup>, D. Rehak<sup>1</sup>, D. Bures<sup>1</sup>, L. Barton<sup>1</sup>, and J. Simunek<sup>2</sup>, <sup>1</sup>Department of Genetics and Animal Breeding, Institute of Animal Science, Prague, Czech Republic, <sup>2</sup>Institute of Animal Physiology and Genetics CAS, Prague, Czech Republic.

### Genetics and Genomics of Aquaculture Species

- P185 **A transcriptomics overview of the biological changes in the liver after induced maturation of female European eel (*Anguilla anguilla*).**  
F. Bertolini\*<sup>1</sup>, M. G. Pinto Jørgensen<sup>1</sup>, C. Henkel<sup>2</sup>, and J. Tomkiewicz<sup>1</sup>, <sup>1</sup>National Institute of Aquatic Resources, Technical University of Denmark, Lyngby, Denmark, <sup>2</sup>Department of Basic Sciences and Aquatic Medicine, Norwegian university of Life Science, Oslo, Norway.
- P186 **Expression analysis in Atlantic salmon (*Salmo salar*) liver tissue reveals miRNAs associated with parr-smolt transformation and seawater transfer.**  
A. Shwe\*<sup>1</sup>, T.-K. Knutsdatter Østbye<sup>2</sup>, and R. Andreassen<sup>1</sup>, <sup>1</sup>Department of Life Sciences and Health, Faculty of Health Sciences, Oslo Metropolitan University, Oslo, Norway, <sup>2</sup>Nofima AS, Ås, Norway.
- P187 **Assessing isomiR-like HTS sequence artifacts and characterization of true isomiRs in Atlantic salmon.**  
N.T. Woldemariam\*<sup>1</sup>, O. Agafonov<sup>2</sup>, B. Høyheim<sup>3</sup>, R.D. Houston<sup>4</sup>, J.B. Taggart<sup>5</sup>, and R. Andreassen<sup>1</sup>, <sup>1</sup>Department of Life Sciences and Health, Faculty of Health Sciences, OsloMet–Oslo Metropolitan University, Oslo, Norway, <sup>2</sup>Bioinformatics Core Facility, Department of Core Facilities, Institute of Cancer Research, Radium Hospital, Oslo University Hospital, Oslo, Norway, <sup>3</sup>Department of Basic Sciences and Aquatic Medicine, Faculty of Veterinary Medicine, Norwegian University of Life Sciences, Oslo, Norway, <sup>4</sup>Division of Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, United Kingdom, <sup>5</sup>Institute of Aquaculture, University of Stirling, Stirling, Scotland, United Kingdom.
- P188 **Transcriptome display sex difference of Chinese soft-shell turtle (*Trionyx sinensis*) in sex differentiation and mature period as revealed by RNA-Seq analysis.**  
X. Wang\*<sup>1,2</sup>, X. Zhou<sup>1,3</sup>, D. Zeng<sup>1,2</sup>, P. Wang<sup>1,2</sup>, Q. Qin<sup>1,2</sup>, and Z.-N. Chen<sup>1,2</sup>, <sup>1</sup>College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China, <sup>2</sup>Collaborative Innovation Center for Efficient and Health Production of Fisheries in Hunan Province, Changde, Hunan, China, <sup>3</sup>Station of aquaculture in Xiangxi, Jishou, Hunan, China.
- P191 **Prediction of miRNA target genes in full-length Atlantic salmon (*Salmo salar*) mRNA transcripts from PacBio Iso-seq sequencing.**  
S. Ramberg\*<sup>1</sup>, B. Høyheim<sup>2</sup>, and R. Andreassen<sup>1</sup>, <sup>1</sup>Oslo Metropolitan University, Oslo, Norway, <sup>2</sup>Norwegian University of Life Sciences, Oslo, Norway.
- P192 **Developing genomic information for *Holothuria polii* (Echinodermata: Holothuroidea), a novel potential aquaculture species.**  
V. J. Utzeri, A. Ribani, S. Bovo, V. Taurisano, and L. Fontanesi\*, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy.
- P193 **Genome and transcriptome assembly of the Florida Pompano: Investigating genetic markers useful for aquaculture.**  
L. E. King\*<sup>1</sup>, G. Ghosh<sup>2</sup>, C. S. Perricone<sup>1</sup>, E. Guisbert<sup>2</sup>, P. S. Wills<sup>1</sup>, R. Turingan<sup>2</sup>, and N. J. Dickens<sup>1</sup>, <sup>1</sup>FAU Harbor Branch Oceanographic Institute, Fort Pierce, FL, USA, <sup>2</sup>Florida Institute of Technology, Melbourne, FL, USA.
- P194 **Analysis on the evolution of AMP repertoires between terrestrial and aquatic mammalian genomes.**  
M. Kang\*, B. Ahn, J. Yum, H. Cho, H. Jeon, N. Soundararajan, and C. Park, Konkuk University, Seoul, Korea.
- P195 **Mapping quantitative trait loci and identifying candidate genes affecting feed conversion ratio based on three linkage maps in common carp (*Cyprinus carpio* L.).**  
C. Lu\*, X. Zhang, X. Zheng, D. Cao, and X. Sun, National Local Joint Engineering Laboratory for Freshwater Fish Breeding, Heilongjiang River Fisheries Research Institute, Chinese Academy of Fishery Sciences, Harbin, China.
- P196 **Genomics of New Zealand trevally: Genomically enabling a new species for aquaculture.**  
N. Valenza-Troubat\*<sup>1,2</sup>, P. Morrison-Whittle<sup>1</sup>, D. Ashton<sup>1</sup>, P. Ritchie<sup>2</sup>, and M. Wellenreuther<sup>1,3</sup>, <sup>1</sup>The New Zealand Institute for Plant and Food Research, Nelson, New Zealand, <sup>2</sup>School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand, <sup>3</sup>Faculty of Science, University of Auckland, Auckland, New Zealand.
- P197 **Genomic solutions for the New Zealand aquaculture industry.**  
S. M. Clarke\*<sup>1</sup>, J. E. Symonds<sup>2</sup>, S. P. Walker<sup>2</sup>, N. King<sup>2</sup>, H. J. Baird<sup>1</sup>, R. M. Anderson<sup>1</sup>, R. Ashby<sup>1</sup>, A. Hess<sup>1</sup>, and K. G. Dodds<sup>1</sup>, <sup>1</sup>AgResearch, Dunedin, New Zealand, <sup>2</sup>Cawthron Institute, Nelson, New Zealand.



- P198 **Detection of recent signatures of selection between three strains of Nile tilapia (*Oreochromis niloticus*) by whole-genome sequencing.**  
M. I. Cádiz<sup>\*1</sup>, M. E. Lopez<sup>2</sup>, D. Díaz-Domínguez<sup>3</sup>, G. Cáceres<sup>1</sup>, G. M. Yoshida<sup>1</sup>, and J. M. Yáñez<sup>1</sup>, <sup>1</sup>Facultad de Ciencias Veterinarias y Pecuarias. Universidad de Chile, Santiago, Chile, <sup>2</sup>Department of Animal Breeding and Genetics. Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>3</sup>Departamento de Ciencias de la Computación. Universidad de Chile, Santiago, Chile.
- P201 **RNA-seq analysis of two critical periods of induced ovarian development in European eel, *Anguilla anguilla*.**  
M. G. Pinto Jørgensen<sup>\*</sup>, F. Bertolini, and J. Tomkiewicz, National Institute of Aquatic Resources, Technical University of Denmark, Kgs. Lyngby, Denmark.
- P202 **Detection of genomic regions involved in sex determination in Nile tilapia (*Oreochromis niloticus* L.) using whole-genome sequencing.**  
C. Giovanna<sup>\*1</sup>, L. M. Eugenia<sup>2</sup>, C. M. Ignacia<sup>1</sup>, Y. Grazyella<sup>1</sup>, and Y. J. Manuel<sup>1</sup>, <sup>1</sup>Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Universidad de Chile, <sup>2</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- P203 **Optimising genotype imputation strategies for genomic selection in farmed Atlantic salmon.**  
S. Tsairidou<sup>\*1</sup>, A. Hamilton<sup>2</sup>, D. Robledo<sup>1</sup>, J. Bron<sup>3</sup>, and R. Houston<sup>1</sup>, <sup>1</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK, <sup>2</sup>Hendrix Genetics Aquaculture BV/ Netherlands Villa 'de Körver', Boxmeer, The Netherlands, <sup>3</sup>Institute of Aquaculture, University of Stirling, Stirling, UK.
- P204 **Determination of genetic structure and selection signatures in Coho salmon (*Oncorhynchus kisutch*) populations by genome-wide SNP analyses.**  
M. E. López<sup>\*1,2</sup>, A. Barriá<sup>2</sup>, E. Rondeau<sup>3</sup>, B. Koop<sup>3</sup>, and J. M. Yáñez<sup>2</sup>, <sup>1</sup>Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>Universidad de Chile, Santiago, RM, Chile, <sup>3</sup>University of Victoria, Victoria, British Columbia, Canada.
- P452 **Breeding technology for aquaculture species in the post-genome era.**  
X. Sun<sup>\*</sup>, National Local Joint Engineering Laboratory for Freshwater Fish Breeding, Heilongjiang River Fisheries Research Institute, Chinese Academy of Fishery Sciences, Harbin, China.
- P453 **First look at patterns of DNA methylation in Atlantic salmon and its involvement in sexual maturation.**  
J. Kijas<sup>\*1</sup>, A. Reverter<sup>1</sup>, B. Evans<sup>2</sup>, H. King<sup>3</sup>, and A. Mohamed<sup>1</sup>, <sup>1</sup>CSIRO Agriculture, St Lucia Brisbane Queensland, Australia, <sup>2</sup>Tassal Group Limited, Hobart, Tasmania, Australia, <sup>3</sup>CSIRO Agriculture, Hobart, Tasmania, Australia.

## Genetics of Immune Response and Disease Resistance

- P205 **Genetic signature of strong recent positive selection at the *DRB-1* gene in goat.**  
A. R. Asif<sup>\*1,2</sup>, A. Muhammad<sup>1</sup>, S. Qadri<sup>3</sup>, J. A. Bhatti<sup>1</sup>, X. Du Du<sup>2</sup>, and A. H. Saleem<sup>1</sup>, <sup>1</sup>University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan, <sup>2</sup>Huazhong Agricultural University, Wuhan, Wuhan, Hubei, China, <sup>3</sup>Livestock and Dairy Development Punjab, Jhang, Punjab, Pakistan.
- P206 **Dynamic transcriptomic changes of goat abomasal mucosa during an experimental *Haemonchus contortus* infection in resistant and susceptible genotypes.**  
H. M. Aboshady<sup>\*1,2</sup>, N. Mandonnet<sup>3</sup>, A. M. Johansson<sup>2</sup>, E. Jonas<sup>2</sup>, and J. C. Bambou<sup>3</sup>, <sup>1</sup>AgroParisTech, Paris, France, <sup>2</sup>Swedish University of Agriculture Science, Uppsala, Sweden, <sup>3</sup>INRA-URZ, Petit-Bourg, Guadeloupe, France.
- P207 **Screening of potential markers in the JAK-STAT pathway related genes for mastitis resistance in dairy cattle at sub tropical conditions of Pakistan.**  
T. Usman<sup>\*1</sup>, N. Ali<sup>1,2</sup>, S. Niaz<sup>1</sup>, Y. Wang<sup>2</sup>, and Y. Yu<sup>2</sup>, <sup>1</sup>Abdul Wali Khan University Mardan, Mardan, Khyber Pakhtunkhwa, Pakistan, <sup>2</sup>China Agricultural University, Haidian, Beijing, China.
- P208 **Host synaptogyrin-2 facilitates replication of PCV2b.**  
L. Walker<sup>\*1</sup>, T. Engle<sup>1</sup>, H. Vu<sup>1</sup>, E. Tosky<sup>1</sup>, D. Nonneman<sup>2</sup>, T. Smith<sup>2</sup>, T. Borza<sup>3</sup>, T. Burkey<sup>1</sup>, G. Plastow<sup>4</sup>, S. Kachman<sup>1</sup>, and D. Ciobanu<sup>1</sup>, <sup>1</sup>University of Nebraska-Lincoln, Lincoln, NE, USA, <sup>2</sup>USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA, <sup>3</sup>Dalhousie University, Truro, Nova Scotia, Canada, <sup>4</sup>University of Alberta, Edmonton, Alberta, Canada.
- P209 **Modulation of innate immune responses in jejunal epithelial cells by *Yersinia enterocolitica*.**  
P. Modesto<sup>\*1</sup>, W. Vencia<sup>1</sup>, E. Parisia<sup>1</sup>, F. Lazzara<sup>1</sup>, M. Amadori<sup>2</sup>, T. Andreoli<sup>1</sup>, C. Ercolini<sup>1</sup>, A. Ferrarì<sup>1</sup>, and E. Razzuoli<sup>1</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy, <sup>2</sup>Istituto Zooprofilattico Sperimentale della Lombardia e Dell'Emilia Romagna, Brescia, Italy.

- P210 **Hepatic transcriptome responses of chicken embryos to ochratoxin A.**  
S. Y. Choi<sup>\*1</sup>, M. W. Hong<sup>1</sup>, H. Lee<sup>1</sup>, T. S. Park<sup>2</sup>, and S. J. Lee<sup>1</sup>, <sup>1</sup>College of Animal Life Sciences, Kangwon National University, Chuncheon, Republic of Korea, <sup>2</sup>Institute of Green-Bio Science and Technology, Seoul National University, Pyeongchang, Republic of Korea.
- P211 **e-PIG-enetics: Porcine miRNA and tRNA expression during highly pathogenic PRRSV infections.**  
D. S. Fleming<sup>\*1,2</sup> and L. C. Miller<sup>2</sup>, <sup>1</sup>ORAU/ORISE, Oak Ridge, TN, USA, <sup>2</sup>Virus and Prion Diseases of Livestock Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, Ames, IA, USA.
- P212 **Transcriptomic analysis of varying immune responses to BRD vaccination in BVDV challenged cattle.**  
D. S. Fleming<sup>\*1,2</sup> and C. A. Gill<sup>3</sup>, <sup>1</sup>ORAU/ORISE, Oak Ridge, TN, USA, <sup>2</sup>Virus and Prion Diseases of Livestock Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, Ames, IA, USA, <sup>3</sup>Texas A&M University, College Station, TX, USA.
- P213 **Hypothalamic transcriptomic perturbations in mice developmentally exposed to perfluorooctanoic acid (PFOA).**  
H. Kim<sup>\*</sup>, M. W. Hong, H. Lee, and S. J. Lee, Kangwon National University, Chuncheon, Republic of Korea.
- P214 **Polymorphisms associated with bovine paratuberculosis: Investigation of their role in DNA-protein interactions and transcriptional regulation.**  
C. Beltramo, A. Dondo, K. Varello, M. Gorla, A. Di Blasio, S. Nodari, S. Colussi, P. Modesto, P. L. Acutis<sup>\*</sup>, and S. Peletto, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta.
- P215 **Immune-related microRNA absorption in newborn calves.**  
H. T. Do<sup>\*1,2</sup>, J. L. Williams<sup>1</sup>, T. Chen<sup>1</sup>, K. Petrovski<sup>1</sup>, and C. D. K. Bottema<sup>1</sup>, <sup>1</sup>School of Animal & Veterinary Sciences, Davies Research Centre, University of Adelaide, Roseworthy, Australia, <sup>2</sup>Vietnam National University of Agriculture, Hanoi, Vietnam.
- P216 **Combined transcriptomic analysis of ileocecal valve and peripheral blood in Holstein dairy cattle at different stages of *Mycobacterium avium* ssp. *paratuberculosis* (Map) infection revealed CXCL8/IL8 as a common effector molecule.**  
M. Alonso-Hearn<sup>\*1</sup>, M. Canive<sup>1</sup>, C. Blanco-Vázquez<sup>2</sup>, R. Torremocha<sup>3</sup>, B. Soriano<sup>4</sup>, A. Balseiro<sup>2</sup>, J. Amado<sup>5</sup>, R. Ramos<sup>3</sup>, C. Llorens<sup>4</sup>, and R. Casais<sup>2</sup>, <sup>1</sup>NEIKER-Instituto Vasco de Investigación y Desarrollo Agrario, Derio, Bizkaia, Spain, <sup>2</sup>SERIDA, Servicio Regional de Investigación y Desarrollo Agroalimentario, Deva, Asturias, Spain, <sup>3</sup>Science Park of Madrid, Genomic Unit, Madrid, Spain, <sup>4</sup>Biotechvana, Paterna, Valencia, Spain, <sup>5</sup>LSAPA, Animal Health Laboratory of the Principality of Asturias, Gijón, Asturias, Spain.
- P217 ***Salmonella* Typhimurium induces genome-wide expression and phosphorylation changes that modulate immune response, survival, and vesicle transport in porcine infected neutrophils.**  
S. Zaldívar-López<sup>\*1</sup>, J. Herrera-Urbe<sup>1</sup>, R. Bautista<sup>2</sup>, A. Jiménez<sup>1</sup>, A. Moreno<sup>1,3</sup>, M. G. Claros<sup>2,4</sup>, and J. J. Garrido<sup>1</sup>, <sup>1</sup>Animal Breeding and Genomics group, Department of Genetics, University of Córdoba, Córdoba, Spain, <sup>2</sup>Supercomputing and Bioinnovation Center, University of Málaga, Málaga, Spain, <sup>3</sup>Institute for Sustainable Agriculture, Córdoba, Spain, <sup>4</sup>Department of Molecular Biology and Biochemistry, University of Málaga, Málaga, Spain.
- P218 **Gene expression reveals the role of autophagy in *Salmonella* Typhimurium replication during intestinal epithelial cells infection.**  
N. Bellido-Carreras<sup>\*1</sup>, S. Zaldívar-López<sup>1</sup>, H. Argüello<sup>1</sup>, R. Bautista<sup>2</sup>, M. G. Claros<sup>2,3</sup>, and J. J. Garrido<sup>1</sup>, <sup>1</sup>Animal Breeding and Genomics Group, Department of Genetics, University of Córdoba, Spain, <sup>2</sup>Supercomputing and Bioinnovation Center, University of Málaga, Spain, <sup>3</sup>Department of Molecular Biology and Biochemistry, University of Málaga, Spain.
- P219 **CRISPR/Cas9-mediated precise genome editing of cellular host factor of avian influenza virus in chicken.**  
Y. H. Park<sup>\*</sup>, K. Chungu, S. B. Lee, Y. M. Kim, J. M. Kim, and J. Y. Han, Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.
- P220 **Allele specific and differential expression in the chicken splenic transcriptome in response to avian pathogenic *Escherichia coli*.**  
M. Monson<sup>\*1</sup>, M. Kaiser<sup>1</sup>, A. Wolc<sup>1,2</sup>, and S. Lamont<sup>1</sup>, <sup>1</sup>Iowa State University, Ames, IA, USA, <sup>2</sup>Hy-Line International, Dallas Center, IA, USA.
- P221 **Porcine epidemic diarrhea virus induces APN gene expression to facilitate viral propagation.**  
H. Wang<sup>\*</sup>, C. Zhao, S. Wu, and W. Bao, Yangzhou University, Yangzhou, Jiangsu Province, China.
- P222 **Using dual RNA sequencing to interrogate bovine macrophage-pathogen interactions.**  
M. Hassan<sup>\*</sup> and A. Gossner, Roslin Institute, University of Edinburgh, Edinburgh, UK.
- P223 **PRNP genotyping in sheep with scrapie disease.**  
A. Piestrzynska-Kajtoch<sup>\*1</sup>, M. P. Polak<sup>2</sup>, G. Smolucha<sup>1</sup>, and J. F. Zmudzinski<sup>2</sup>, <sup>1</sup>National Research Institute of Animal Production, Balice, Poland, <sup>2</sup>National Veterinary Research Institute, Pulawy, Poland.



- P224 **Identification of lncRNAs regulating variable stress-responding sheep naturally exposed to gastrointestinal nematode parasites.**  
A. Suárez-Vega<sup>\*1</sup>, E. A. Borkowski<sup>2</sup>, S. Dixon<sup>1</sup>, N. A. Karrow<sup>1</sup>, A. S. Peregrine<sup>2</sup>, P. Menzies<sup>3</sup>, B. A. Mallard<sup>2</sup>, M. N. Boareki<sup>1</sup>, F. S. Schenkel<sup>1</sup>, J. J. Arranz<sup>4</sup>, G. Tosser-Klopp<sup>5</sup>, C. Klopp<sup>6</sup>, and A. Cánovas<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada, <sup>2</sup>Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada, <sup>3</sup>Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada, <sup>4</sup>Departamento de Producción Animal, University of León, León, Castilla y León, Spain, <sup>5</sup>GenPhySE, Université de Toulouse, INRA, ENVT, Castanet Tolosan, Midi-Pyrénées, France, <sup>6</sup>Sigenae Platform, MIAT, INRA, Auzeville, Midi-Pyrénées, France.
- P225 **PRRSV subverts reticulophagy by downregulating *Fam134b* expression.**  
K. Guan<sup>\*</sup>, X. Zhou, and B. Liu, Huazhong Agricultural University, Wuhan, Hubei, China.
- P226 **Assessment of monthly tick count variation and mapping of genomic regions associated with cattle resistance to African ticks.**  
N. O. Mapholi<sup>\*1</sup>, A. Maiwashe<sup>2</sup>, O. Matika<sup>3</sup>, V. Riggio<sup>3</sup>, C. Banga<sup>2</sup>, and K. Dzama<sup>4</sup>, <sup>1</sup>University of South Africa, Florida, Gauteng, South Africa, <sup>2</sup>Agricultural Research Council, Pretoria, Gauteng, South Africa, <sup>3</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, UK, <sup>4</sup>University of Stellenbosch, Stellenbosch, Western Cape South Africa.
- P227 **Preliminary results: Heritability estimate for tick count and identification of genomic regions associated with tick tolerance in F<sub>2</sub> Nguni x Angus population.**  
N. Mkize<sup>\*1,2</sup>, G. B. Hutang<sup>1</sup>, B. Dube<sup>1</sup>, K. Dzama<sup>2</sup>, A. Maiwashe<sup>1</sup>, and N. O. Mapholi<sup>3</sup>, <sup>1</sup>Agricultural Research Council-Animal Production Institute, Pretoria, Gauteng, South Africa, <sup>2</sup>Stellenbosch University, Stellenbosch, Western Cape, South Africa, <sup>3</sup>University of South Africa, Florida, Gauteng, South Africa.
- P228 **Association of *TLR* gene variants with utility and health traits in Czech Simmental cattle population.**  
K. Novák<sup>\*1</sup>, M. Bjelka<sup>2</sup>, K. Samaké<sup>3</sup>, and T. Valčíková<sup>4</sup>, <sup>1</sup>Institute of Animal Science, Prague-Uhrineves, Czech Republic, <sup>2</sup>Department of Genetics and Microbiology, Charles University, Prague, Czech Republic, <sup>3</sup>Breeding Company CHD Impuls, Bohdalec, Czech Republic, <sup>4</sup>Department of Genetics and Breeding, Czech University of Life Sciences, Prague, Czech Republic.
- P229 **Time- and population-dependent genetic patterns underlie bovine milk somatic cell count.**  
A. Miles<sup>\*</sup> and H. Huson, Cornell University, Ithaca, NY, USA.
- P230 **Whole-genome re-sequence analysis reveals tick resistance and heat tolerance genes in Iraqi cattle breeds.**  
A. Alshawi<sup>\*1,2</sup>, A. Essa<sup>3</sup>, S. Al-Bayatti<sup>3</sup>, A. Tijjani<sup>1,4</sup>, S. Salman<sup>3</sup>, and O. Hanotte<sup>1,4</sup>, <sup>1</sup>School of Life Sciences, Faculty of Medicine and Health Sciences, University of Nottingham, United Kingdom, <sup>2</sup>Department of Internal and Preventive Medicine, College of Veterinary Medicine, University of Baghdad, Iraqi Ministry of Higher Education and Scientific Research, Iraq, <sup>3</sup>Animal Genetics Resources Department, the Ministry of Iraqi agriculture, Baghdad, Iraq, <sup>4</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.
- P231 **Integrative functional genomics of the bovine host response to infection with *Mycobacterium bovis*.**  
T. Hall<sup>\*1</sup>, M. Mullen<sup>2</sup>, C. Correia<sup>1</sup>, G. McHugo<sup>1</sup>, K. Killick<sup>1</sup>, J. Browne<sup>1</sup>, N. Nalpas<sup>4</sup>, S. Gordon<sup>2,5</sup>, and D. MacHugh<sup>1,2</sup>, <sup>1</sup>Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland, <sup>2</sup>Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland, <sup>3</sup>Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany, <sup>4</sup>UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, <sup>5</sup>UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.
- P450 **African Swine Fever Virus strains show different virulence associated with modulation of IFNs type I gene expression.**  
E. Razzuoli<sup>1</sup>, G. Franzoni<sup>2</sup>, I. Ferretti<sup>2</sup>, T. Carta<sup>4</sup>, S. Zinellu<sup>2</sup>, G. Galleri<sup>4</sup>, M. Amadori<sup>3</sup>, S. Dei Giudici<sup>2</sup>, P. Modesto<sup>\*1</sup>, and A. Oggiano<sup>2</sup>, <sup>1</sup>Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy, <sup>2</sup>Istituto Zooprofilattico Sperimentale della Sardegna, Sassari, Italy, <sup>3</sup>Istituto Zooprofilattico Sperimentale della Lombardia e Dell'Emilia Romagna, Brescia, Italy, <sup>4</sup>Università degli Studi di Sassari, Sassari, Italy.

## Genome Edited Animals

- P232 **Genome modification in chicken for therapeutic protein production.**  
Y. M. Kim<sup>\*</sup>, Y. H. Park, J. M. Kim, J. S. Park, H. J. Lee, K. Y. Lee, and J. Y. Han, Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.



### Horse Genetics and Genomics

- P233 **Detection of homozygous-by-descent segments revealed distinct age-related classes overlapping with known behavioural QTLs in Norwegian-Swedish Coldblooded Trotter.**  
M. Solé\*<sup>1</sup>, B. D. Velie<sup>2</sup>, C. F. Ihler<sup>3</sup>, E. Strand<sup>3</sup>, and G. Lindgren<sup>1,4</sup>, <sup>1</sup>Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>Faculty of Life and Environmental Science, University of Sydney, Sydney, Australia, <sup>3</sup>Department of Companion Animal Clinical Sciences, Norwegian School of Veterinary Science, Oslo, Norway, <sup>4</sup>Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium.
- P234 **Analysis of MSTN SNPs associated with speed in Polo Argentino breed.**  
M. M. Martinez\*<sup>1</sup>, M. Costa<sup>1</sup>, C. Ratti<sup>1</sup>, and M. N. Corvalán<sup>2</sup>, <sup>1</sup>Laboratorio de Genética Aplicada, Sociedad Rural Argentina, CABA, Buenos Aires, Argentina, <sup>2</sup>Crestview Genetics, Luján, Buenos Aires, Argentina.
- P235 **Genetic diversity and relationships among native Japanese horse breeds and horses outside of Japan using genome-wide SNP data.**  
T. Tozaki\*<sup>1,3,6</sup>, M. Kikuchi<sup>1</sup>, H. Kakoi<sup>1</sup>, K.-I. Hirota<sup>1</sup>, S.-I. Nagata<sup>1</sup>, D. Yamashita<sup>2</sup>, T. Ohnuma<sup>2</sup>, M. Takasu<sup>3</sup>, I. Kobayashi<sup>4</sup>, S. Hobo<sup>5</sup>, D. Manglai<sup>6</sup>, and J. Petersen<sup>7</sup>, <sup>1</sup>Genetic Analysis Department, Utsunomiya, Tochigi, Japan, <sup>2</sup>Japan Equine Affairs Association, Chuo-ku, Tokyo, Japan, <sup>3</sup>Department of Veterinary Medicine, Faculty of Applied Biological Sciences, Gifu University, Gifu, Gifu, Japan, <sup>4</sup>Sumiyoshi Livestock Science Station, Field Science Center, University of Miyazaki, Miyazaki, Miyazaki, Japan, <sup>5</sup>Joint Faculty of Veterinary Medicine, Kagoshima University, Kagoshima, Kagoshima, Japan, <sup>6</sup>College of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, <sup>7</sup>Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE, USA.
- P236 **Genomic scan of conformation traits in Icelandic horses.**  
M. K. Rosengren\*<sup>1</sup>, M. Solé<sup>1</sup>, Å. Wiklund<sup>1</sup>, S. Eriksson<sup>1</sup>, B. D. Velie<sup>2</sup>, J. J. Negro<sup>3</sup>, and G. Lindgren<sup>1,4</sup>, <sup>1</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>2</sup>School of Life & Environmental Sciences, University of Sydney, Sydney, Australia, <sup>3</sup>Department of Evolutionary Ecology, Doñana Biological Station, CSIC, Seville, Spain, <sup>4</sup>Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium.
- P237 **Jumping into selective sweeps for sport horse performance.**  
M. Ablondi\*<sup>1</sup>, S. Eriksson<sup>2</sup>, A. Sabbioni<sup>1</sup>, Å. Viklund<sup>2</sup>, and S. Mikko<sup>2</sup>, <sup>1</sup>Department of Veterinary Science, Università degli Studi di Parma, Parma, Italy, <sup>2</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- P238 **Intense artificial selection reflected by runs of homozygosity in Arabian horses.**  
M. Stefaniuk-Szmukier\*<sup>1</sup>, T. Szmatoła<sup>2</sup>, A. Gurgul<sup>2</sup>, K. Pawlina-Tyszko<sup>2</sup>, E. Semik-Gurgul<sup>2</sup>, I. Jasielczuk<sup>2</sup>, K. Ropka-Molik<sup>2</sup>, and M. Bugno-Poniewierska<sup>1,2</sup>, <sup>1</sup>University of Agriculture in Cracow, Kraków, Poland, <sup>2</sup>National Research Institute of Animal Production, Balice, Poland.
- P239 **Training-induced modification of apoptosis related genes in Arabian horses during flat-racing schedule.**  
K. Ropka-Molik<sup>1</sup>, K. Piórkowska<sup>1</sup>, A. D. Musiał<sup>2</sup>, and M. Stefaniuk-Szmukier\*<sup>3</sup>, <sup>1</sup>National Research Institute of Animal Production, Balice, Poland, <sup>2</sup>Jagiellonian University, Kraków, Poland, <sup>3</sup>University of Agriculture, Kraków, Poland.
- P242 **Genetic variability of Lusitano horse breed reared in Italy.**  
M. C. Cozzi\*<sup>1</sup>, P. Valiati<sup>1</sup>, M. G. Strillacci<sup>1</sup>, E. Gorla<sup>1</sup>, F. Genova<sup>1</sup>, and A. Bagnato<sup>1</sup>, Dipartimento di Medicina Veterinaria - Università degli Studi di Milano, Milano, Italy.
- P243 **FAM174A-11(G) allele is a poor indicator for equine metabolic syndrome.**  
CE Rodríguez-Sanz\*<sup>1</sup>, N. Sevane<sup>1</sup>, and S. Dunner<sup>1</sup>, Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid, Madrid, España.
- P244 **Whole-genome population structure analyses of the Jeju horse using the equine high-density SNP array.**  
H.-S. Seong\*<sup>1</sup>, S. A. Brooks<sup>2</sup>, I.-C. Cho<sup>3</sup>, B. C. Yang<sup>3</sup>, Y. H. Choy<sup>4</sup>, T.-J. Choi<sup>4</sup>, J. H. Woo<sup>3</sup>, S. M. Shin<sup>3</sup>, M. C. Shin<sup>3</sup>, J. H. Yoo<sup>3</sup>, J.-Y. Choi<sup>3</sup>, D.-H. Son<sup>1</sup>, J.-W. Choi<sup>1</sup>, and N.-Y. Kim<sup>3</sup>, <sup>1</sup>College of Animal Life Science, Kangwon National University, Chuncheon-si, Kangwon-do, Republic of Korea, <sup>2</sup>Department of Animal Science, University of Florida, Gainesville, FL, USA, <sup>3</sup>Subtropical Animal Research Institute, National Institute of Animal Science, RDA, Jeju, Jeju, Republic of Korea, <sup>4</sup>Animal Breeding and Genetics Division, National Institute of Animal Science, RDA, Cheonan-si, Chungcheongnam-do, Republic of Korea.
- P245 **Genome-wide association study of muscular activity to identify genomic regions associated with Polysaccharide storage myopathy type 1 in Austrian Noriker horses.**  
N. Khayatzaadeh\*<sup>1</sup>, R. R. Zsoldos<sup>1,2</sup>, T. F. Licka<sup>3,4</sup>, G. Mészáros<sup>1</sup>, B. Fuerst-Waltl<sup>1</sup>, T. Druml<sup>3</sup>, G. Brem<sup>3</sup>, and J. Sölkner<sup>1</sup>, <sup>1</sup>University of Natural Resources and Life Sciences (BOKU), Vienna, Austria, <sup>2</sup>University of Queensland, Gatton, Queensland, Australia, <sup>3</sup>University of Veterinary Medicine Vienna, Vienna, Austria, <sup>4</sup>University of Edinburgh, Midlothian, Scotland, United Kingdom.



- P246 **Population genetic structure evaluations of the Iranian horse breeds by SSR and SNP markers.**  
M. Abdoli\*<sup>1</sup>, M. B. Zandi<sup>1</sup>, and M. T. Harkinejad<sup>1</sup>, <sup>1</sup>University of Zanjan, Zanjan, Iran, <sup>2</sup>University of Zanjan, Zanjan, Iran, <sup>3</sup>University of Zanjan, Zanjan, Iran.
- P247 **Genetic diversity in Iranian Arab horse breed assessed from pedigree and STR analysis.**  
M. B. Zandi\*<sup>1</sup> and S. Rafiee<sup>2</sup>, <sup>1</sup>University of Zanjan, Zanjan, Iran, <sup>2</sup>University of Tehran, Karaj, Iran.
- P248 **Whole-genome sequencing reveals the genetic mechanisms underlying the high-altitude adaptation in Tibetan horses.**  
X. Liu\*, Y. Ma, and L. Jiang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China.*
- P249 **Identification of shared and species-specific k-mers in Equids and Caballines to characterize adaptive introgression events.**  
K. de Silva\*<sup>1</sup>, E. Bailey<sup>2</sup>, and T. S. Kalbfleisch<sup>2</sup>, <sup>1</sup>University of Louisville, Louisville, KY, USA, <sup>2</sup>University of Kentucky, Lexington, KY, USA.

### ISAG-FAO Genetic Diversity

- P250 **Population structure of Blanco Orejinegro (BON) cattle from germplasm bank using pedigree analysis.**  
R. J. Ocampo\*, E. J. Ramirez, and G. J. Restrepo, *Corporación Colombiana de Investigación Agropecuaria AGROSAVIA, San Roque, Antioquia, Colombia.*
- P251 **Evaluating genetic diversity in Zambian indigenous cattle.**  
E. Musimuko\*<sup>1</sup>, W. Muleya<sup>1</sup>, C. Bottema<sup>2</sup>, and P. Wayne<sup>2</sup>, <sup>1</sup>University of Zambia, Lusaka, Zambia, <sup>2</sup>University of Adelaide, Adelaide, SA, Australia.
- P252 **Whole-genome assessment of goat breeds in Russia.**  
T. Deniskova\*<sup>1</sup>, A. Dotsev<sup>1</sup>, M. Fornara<sup>1</sup>, M. Selionova<sup>2</sup>, H. Reyer<sup>3</sup>, K. Wimmers<sup>3</sup>, G. Brem<sup>1,4</sup>, and N. Zinovieva<sup>1</sup>, <sup>1</sup>L.K. Ernst Federal Science Center for Animal Husbandry, Podolsk, Moscow region, Russia, <sup>2</sup>All-Russian Research Institute of Sheep and Goat Breeding, Stavropol, Russia, <sup>3</sup>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Mecklenburg-Vorpommern, Germany, <sup>4</sup>Institute of Animal Breeding and Genetics, University of Veterinary Medicine, Vienna, Austria.
- P253 **Phylogenetic analysis of Nepalese goats using mtDNA D-loop region and SRY gene sequences.**  
Y. Nomura\*<sup>1</sup>, T. Kunieda<sup>2</sup>, M. Shah<sup>3</sup>, F. Kawaguchi<sup>1</sup>, S. Sasazaki<sup>1</sup>, and H. Mannen<sup>1</sup>, <sup>1</sup>Graduate School of Agricultural Science, Kobe University, Kobe, Japan, <sup>2</sup>Graduate School of Agricultural Science, Okayama University, Okayama, Japan, <sup>3</sup>Regional Agriculture Research Station in Kathmandu, Kathmandu, Nepal.
- P254 **Genetic diversity of mitochondrial DNA D-loop region in indigenous pig breeds of India.**  
S. Naskar\*<sup>1,2</sup>, L. Rongala<sup>1</sup>, Y. Vashi<sup>2</sup>, D. Kalita<sup>2</sup>, S. Banik<sup>2</sup>, and N. R. Sahoo<sup>2,3</sup>, <sup>1</sup>ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, Jharkhand, India, <sup>2</sup>ICAR-National Research Centre on Pig, Guwahati, Assam, India, <sup>3</sup>ICAR-Indian Veterinary Research Institute, Bareilly, Uttar Pradesh, India.
- P255 **Genetic diversity and structure in 11 native Asian goat populations analyzed by high density SNP array.**  
K. Iso\*<sup>1</sup>, S. Sasazaki<sup>1</sup>, F. Kawaguchi<sup>1</sup>, T. Yonezawa<sup>2</sup>, J. Wu<sup>3</sup>, K. Nomura<sup>2</sup>, Y. Takahashi<sup>2</sup>, E. Kobayashi<sup>4</sup>, M. Shah<sup>5</sup>, O. Faruque<sup>6</sup>, J. Masangkay<sup>7</sup>, M. Bakhtin<sup>8</sup>, P. Kazymbet<sup>8</sup>, T. Dorji<sup>9</sup>, H. Mannen<sup>1</sup>, <sup>1</sup>Laboratory of Animal Breeding and Genetics, Agricultural Science, Kobe University, Japan, <sup>2</sup>Faculty of Agriculture, Tokyo University of Agriculture, Japan, <sup>3</sup>School of Bioscience and Biotechnology, Tokyo Institute of Technology, Japan, <sup>4</sup>NARO Institute of Livestock and Grassland Science, Japan, <sup>5</sup>Regional Agriculture Research Station in Kathmandu, Nepal, <sup>6</sup>Faculty of Animal Husbandry, Bangladesh Agricultural University, Bangladesh, <sup>7</sup>University of the Philippines, Los Banos, Philippines, <sup>8</sup>Astana Medical University, Radiobiology Scientific Center, Kazakhstan, <sup>9</sup>Department of Livestock, Ministry of Agriculture, Bhutan.
- P256 **Genetic diversity of *Bos taurus* and *Bos indicus* using developed indel markers.**  
T. Yasui\*<sup>1</sup>, H. Yamanaka<sup>1</sup>, F. Kawaguchi<sup>1</sup>, S. Sasazaki<sup>1</sup>, T. Yonezawa<sup>2</sup>, J. Wu<sup>3</sup>, and H. Mannen<sup>1</sup>, <sup>1</sup>Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Japan, <sup>2</sup>Faculty of Agriculture, Tokyo University of Agriculture, Atsugi, Japan, <sup>3</sup>School of Bioscience and Biotechnology, Tokyo Institute of Technology, Yokohama, Japan.
- P257 **Changes in allelic frequencies when different genomic coancestry matrices are used for maintaining genetic diversity.**  
E. Morales-Gonzalez\*<sup>1</sup>, J. Fernandez<sup>1</sup>, R. Pong-Wong<sup>2</sup>, and B. Villanueva<sup>1</sup>, <sup>1</sup>Departamento de Mejora Genética Animal, INIA, Madrid, Spain, <sup>2</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, UK.

- P258 **The genetic diversity studies for natural treasure chicken of South Korea.**  
D. Seo\*<sup>1</sup>, D. H. Lee<sup>1</sup>, S. S. Lee<sup>1,2</sup>, S. H. Lee<sup>1</sup>, and J. H. Lee<sup>1</sup>, <sup>1</sup>Division of Animal and Dairy Science, Chungnam National University, Daejeon, South Korea, <sup>2</sup>Yeonsan Ogye Foundation, Nonsan, South Korea.
- P261 **Genomic analysis of sheep remains from the 4th to 5th century AD Roman villa at São Miguel de Odrinhas, Portugal.**  
D. Gaspar\*<sup>1,2</sup>, S. Guimarães<sup>2,3</sup>, I. Ureña<sup>2</sup>, S. Davis<sup>2,4</sup>, A. Gonçalves<sup>5</sup>, C. Detry<sup>6</sup>, A. E. Pires<sup>2,4</sup>, A. M. Ramos<sup>1,8</sup>, A. Gotherstrom<sup>7</sup>, and C. Ginja<sup>2</sup>, <sup>1</sup>CEBAL (Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo), Beja, Portugal, <sup>2</sup>CIBIO-InBIO (Centro de Investigação em Biodiversidade e Recursos Genéticos), Universidade do Porto, Vairão, Portugal, <sup>3</sup>Institución Milá i Fontanals, CSIC, Barcelona, Spain, <sup>4</sup>LARC, Laboratório de Arqueociências, Direcção Geral do Património Cultural, Lisbon, Portugal, <sup>5</sup>Museu Arqueológico de São Miguel de Odrinhas, Sintra, Portugal, <sup>6</sup>Uniarq, Faculdade de Letras, Universidade de Lisboa, Lisbon, Portugal, <sup>7</sup>Archaeological Research Laboratory, Department of Archaeology and Classical Studies, Stockholm University, Stockholm, Sweden, <sup>8</sup>Instituto de Ciências Agrárias e Ambientais Mediterrânicas (ICAAM), Universidade de Évora, Évora, Portugal.
- P263 **Ancestry diversity versus genetic diversity in Creole cattle.**  
A. Martínez\*<sup>1,2</sup>, J. Cañón<sup>3</sup>, and BioBovis Consortium1<sup>1</sup>, <sup>1</sup>Departamento de Genética, Universidad de Córdoba, Cordoba, Spain, <sup>2</sup>Animal Breeding Consulting S.L, Cordoba, Spain, <sup>3</sup>Departamento de Producción Animal, Universidad Complutense de Madrid, Madrid, Spain.
- P264 **Population structure and influence of inbreeding on reproduction traits in Sahiwal cattle through pedigree analysis.**  
S. Mumtaz\*<sup>1</sup>, K. Parveen<sup>2</sup>, P. Pathak<sup>3</sup>, and A. Mukherjee<sup>4</sup>, <sup>1</sup>ICAR-NDRI, Karnal, Haryana, India, <sup>2</sup>COVS&AH, Durg, Chhattisgarh, India, <sup>3</sup>ICAR-NDRI, Karnal, Haryana, India, <sup>4</sup>ICAR-NDRI, Karnal, Haryana, India.
- P265 **Genetic characterization of Spanish autochthonous chicken breeds using microsatellites.**  
J. L. Vega-Pla\*<sup>1</sup>, A. M. Martínez<sup>2,3</sup>, A. Pons<sup>7</sup>, A. Arando<sup>2</sup>, A. Canales<sup>2</sup>, N. García<sup>4</sup>, M. M. Gomez-Carpio<sup>2,3</sup>, C. Gonzalez-Felgueroso<sup>5</sup>, V. Landi<sup>2,3</sup>, J. M. Leon-Jurado<sup>6</sup>, M. Macri<sup>2,3</sup>, S. Nogales<sup>2</sup>, G. Pizarro<sup>2</sup>, S. Verges<sup>8</sup>, M. E. Camacho<sup>9</sup>, <sup>1</sup>Laboratorio de Investigación Aplicada, Servicio de Cría Caballar de las Fuerzas Armadas, Cordoba, Spain, <sup>2</sup>Departamento de Genética, Universidad de Cordoba, Cordoba, Spain, <sup>3</sup>Animal Breeding Consulting S.L., Universidad de Cordoba, Cordoba, Spain, <sup>4</sup>CICYTEX Finca La Orden-Valdesequera, Guadajira, Badajoz, Spain, <sup>5</sup>Asociacion de Criadores de Pita Pinta Asturiana, Oviedo, Asturias, Spain, <sup>6</sup>Centro Agropecuario, Diputacion de Cordoba, Cordoba, Spain, <sup>7</sup>SEMILLA, Palma, Spain, <sup>8</sup>FEPIRA, Ibiza, Spain, <sup>9</sup>IFAPA Alameda del Obispo, Cordoba, Spain.
- P266 **Integrating in situ and ex situ genomic data of domestic chicken breeds for conservation in China.**  
M. Zhang\* and K. Wu, China Agricultural University, Beijing, China.
- P267 **Towards a complete genomic characterization of African indigenous cattle.**  
A. Tijjani\*<sup>1,3</sup>, K. Marshal<sup>2,3</sup>, H. Kim<sup>4,5</sup>, H. Jianlin<sup>2,6</sup>, and O. Hanotte<sup>7,8</sup>, <sup>1</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>2</sup>International Livestock Research Institute (ILRI), Nairobi, Kenya, <sup>3</sup>Center for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom, <sup>4</sup>Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea, <sup>5</sup>C&K genomics, Seoul National University Research Park, Seoul, Republic of Korea, <sup>6</sup>ILRI-CAAS Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China, <sup>7</sup>LiveGene-CTLGH, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>8</sup>Cells, Organism and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, United Kingdom.

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- P268 **Climate resilient metamorphism in phenotype and genomic traits of genetic diversity.**  
S. R. Kapa\*, Sri Venkateswara Veterinary University, Tirupati, AP, India.
- P269 **Genome-wide association study of carcass quality using real-time ultrasound scans in South African Nguni cattle.**  
J. de Vos\*<sup>1</sup>, E. van Marle-Köster<sup>1</sup>, and DP Berry<sup>2</sup>, <sup>1</sup>Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, Gauteng, South Africa, <sup>2</sup>Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Co. Cork, Ireland.
- P270 **Genome-wide characterization of selection signatures in Ugandan goat breeds.**  
R. B. Onzima\*<sup>1,2</sup>, M. R. Upadhyay<sup>1,4</sup>, H. P. Doekes<sup>1</sup>, L. F. Brito<sup>3,5</sup>, M. Bosse<sup>1</sup>, E. Kanis<sup>1</sup>, M. A. M. Groenen<sup>1</sup>, and R. P. M. A. Crooijmans<sup>1</sup>, <sup>1</sup>Animal Breeding and Genomics, Wageningen University & Research, Wageningen, The Netherlands, <sup>2</sup>National Agricultural Research Organization (NARO), Entebbe, Uganda, <sup>3</sup>Department of Animal Biosciences, Centre for Genetic Improvement of Livestock (CGIL), University of Guelph, Guelph, ON, Canada, <sup>4</sup>Department of Veterinary Science, Ludwig Maximilian University of Munich, Munich, Germany, <sup>5</sup>Animal Sciences, College of Agriculture, University of Purdue, West Lafayette, IN, USA.



- P271 **Genome-wide insights of Ethiopian indigenous sheep populations reveal the population structure adheres to tail morphology than phylogeography.**  
A. Amane<sup>\*1,2</sup>, G. Belay<sup>1</sup>, Y. Nassir<sup>3</sup>, M. Kyalo<sup>3</sup>, T. Dessie<sup>4</sup>, A. Kebede<sup>1,2</sup>, T. Getachew<sup>5</sup>, J.-B. D. Entfellner<sup>3</sup>, Z. Edea<sup>6</sup>, O. Hanotte<sup>4</sup>, and G. Mekuriaw<sup>7,8</sup>, <sup>1</sup>Addis Ababa University, Addis Ababa, Ethiopia, <sup>2</sup>Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia, <sup>3</sup>Biosciences eastern and central Africa-International Livestock Research Institute, Nairobi, Kenya, <sup>4</sup>International Livestock Research Institute, Addis Ababa, Ethiopia, <sup>5</sup>International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia, <sup>6</sup>Chungbuk National University, Cheongju, South Korea, <sup>7</sup>Swedish University of Agricultural Science, Uppsala, Sweden, <sup>8</sup>Bahir Dar University, Bahir Dar, Ethiopia.
- P273 **Mitochondrial D-loop genetic diversity of the Djallonke sheep ecotype of the western highlands of Cameroon.**  
J. Ntsoli<sup>\*1,2</sup>, A.Z. Meka<sup>1</sup>, and F. Meutchieye<sup>1</sup>, <sup>1</sup>University of Dschang, Dschang, West, Cameroon, <sup>2</sup>University of Modena and Reggio Emilia, Reggio Emilia, Emilia Romagna, Italy.
- P274 **Investigating genetic variability in two Nigerian ecotypes of local chickens using inter simple sequence repeat (ISSR) markers.**  
H. Etta<sup>\*1</sup>, E. Okon<sup>1</sup>, E. Ikpeme<sup>2</sup>, and H. Sunday<sup>1</sup>, <sup>1</sup>Cross River University of Technology, Calabar, Cross River, Nigeria, <sup>2</sup>University of Calabar, Calabar, Cross River, Nigeria.
- P275 **Genetic diversity and structure of the Mexican Lidia breed bovine based on SNP data.**  
P. G. Eusebi<sup>\*1,2</sup>, O. Cortés<sup>1</sup>, S. Dunner<sup>1</sup>, and J. Cañon<sup>1</sup>, <sup>1</sup>Universidad Complutense de Madrid, Madrid, Spain, <sup>2</sup>VELOGEN.SL, Madrid, Spain.
- P276 **Linkage disequilibrium and haplotype block analysis of SNPs on the CAST gene in Boerka goat.**  
D. Maharani<sup>\*1</sup>, A. Antonius<sup>2</sup>, S. P. Ginting<sup>2</sup>, S. Elieser<sup>2</sup>, A. Tarigan<sup>2</sup>, I. G. S. Budisatria<sup>1</sup>, A. Batubara<sup>2</sup>, D. N. H. Hariyono<sup>1</sup>, and A. P. Z. N. L. Sari<sup>1</sup>, <sup>1</sup>Universitas Gadjah Mada, Yogyakarta, Indonesia, <sup>2</sup>Indonesian Goat Research Institute, Sei Putih, North Sumatera, Indonesia.
- P277 **Genetic diversity of interleukin genes in Egyptian goat breeds from different agro-climatic locations.**  
S. Ahmed<sup>\*1</sup>, A. Kropff<sup>2</sup>, and A. Kotzé<sup>2,3</sup>, <sup>1</sup>National Research Center, Dokki, Giza, Egypt, <sup>2</sup>South African National Biodiversity Institute, Pretoria, South Africa, <sup>3</sup>University of the Free State, Bloemfontein, South Africa.
- P278 **A comparative study on reproductive performance of zebu and taurus genotypes.**  
M. A. S. Khan<sup>\*</sup> and M. S. R. Siddiki, Bangladesh Agricultural University, Mymensingh, Mymensingh, Bangladesh.
- P279 **Genome adaptation of indigenous Ethiopian cattle to high altitude and heat stress.**  
E. Terefe<sup>\*1,2</sup>, G. Belay<sup>1</sup>, K. Marshal<sup>3,6</sup>, O. Hanotte<sup>4,5</sup>, and A. Tijani<sup>2,5</sup>, <sup>1</sup>Addis Ababa University, College of Natural Science, Microbial Cellular Molecular Biology, Addis Ababa, Ethiopia, <sup>2</sup>International Livestock Research Institutes, Addis Ababa, Ethiopia, <sup>3</sup>International Livestock Research Institute, Nairobi, Kenya, <sup>4</sup>LiveGene – CTLGH, International Livestock Research Institute, Addis Ababa, Ethiopia, <sup>5</sup>School of Life Sciences, University of Nottingham, University Park, Nottingham, UK, <sup>6</sup>Center for Tropical Livestock Genetics and Health, The Roslin Institute, University of Edinburgh, Edinburgh, UK.
- P280 **Integrating Ecological Niche Modelling with genomics to dissect tropical adaptation in Ethiopian indigenous chicken.**  
A. Vallejo<sup>\*1</sup>, A. Kabede<sup>2,3</sup>, M. Lozano<sup>4</sup>, D. Tadelles<sup>2</sup>, N. Sparks<sup>5</sup>, J. Smith<sup>5</sup>, O. Hanotte<sup>1,2</sup>, and A. Gheyas<sup>5,6</sup>, <sup>1</sup>Cells, Organism and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, United Kingdom, <sup>2</sup>LiveGene-CTLGH, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>3</sup>Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia, <sup>4</sup>Wageningen University & Research Animal Breeding and Genomics, Wageningen, The Netherlands, <sup>5</sup>The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom, <sup>6</sup>Centre for Tropical Livestock Genetics and health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom.
- P281 **Genetic diversity analysis of Creole cattle populations from Bolivia using a 50K SNP chip.**  
G. Bottani Claros<sup>\*2,1</sup>, E. Jonas<sup>1</sup>, and E. Strandberg<sup>1</sup>, <sup>1</sup>Sveriges lantbruksuniversitet, SLU, Uppsala, Sweden, <sup>2</sup>Universidad Mayor de San Simon, UMSS, Cochabamba, Bolivia.
- P283 **Common selection signatures identified in the genomes of Ethiopian cattle, sheep, and goats on local adaptation.**  
Z. E. Bedada<sup>\*1</sup> and K.-S. Kim<sup>4</sup>, <sup>1</sup>Chungbuk National University, Cheongju, South Korea, <sup>2</sup>International Livestock Research Institute, Addis Ababa, Ethiopia, <sup>3</sup>Ethiopian Biotechnology Institute, Addis Ababa, Ethiopia, <sup>4</sup>Chungbuk National University, Cheongju, South Korea.
- P284 **Genome-wide patterns of selection in Malawi, South Africa, Zimbabwe indigenous village chickens and conserved chicken flocks.**  
K. Hadebe<sup>\*1</sup>, E. F. Dzomba<sup>2</sup>, and F. C. Muchadeyi<sup>1</sup>, <sup>1</sup>Agricultural Research Council, Biotechnology Platform, Onderstepoort, South Africa, <sup>2</sup>University of KwaZulu-Natal, Scottsville, South Africa.

- P286 **Linkage disequilibrium and haplotype block partitioning in village, commercial and indigenous pigs of South Africa.**  
N. Hlongwane<sup>1,2</sup>, E. F. Dzomba<sup>2</sup>, K. Hadebe<sup>\*1</sup>, P. Soma<sup>3</sup>, and F. C. Muchadeyi<sup>1</sup>, <sup>1</sup>Agricultural Research Council, Biotechnology Platform, Onderstepoort, Gauteng, South Africa, <sup>2</sup>Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, KwaZulu-Natal, South Africa, <sup>3</sup>Agricultural Research Council, Animal Production Institute, Irene, Gauteng, South Africa.
- P287 **Differential mitochondrial proteomics reveals plateau adaptability of polled yak.**  
C. Liang<sup>\*1,2</sup>, D. Fu<sup>1,2</sup>, X. Ma<sup>1,2</sup>, C. Ji<sup>1,2</sup>, X. Wu<sup>1,2</sup>, Y. Gao<sup>1,2</sup>, and P. Yan<sup>1,2</sup>, <sup>1</sup>Lanzhou Institute of Animal Science and Veterinary Pharmaceutics, CAAS, Lanzhou, China, <sup>2</sup>Key Laboratory for Yak Breeding Engineering, Lanzhou, China.
- P288 **Autosomal genome evidence for introgression from other *Gallus* species into African and Middle East indigenous chicken.**  
A. S. Al-Jumaili<sup>\*1,2</sup>, A. Gheyas<sup>3,4</sup>, A. Kebede<sup>5,6</sup>, J. Smith<sup>3,4</sup>, and O. Hanotte<sup>1,5</sup>, <sup>1</sup>School of Life Sciences, University of Nottingham, University Park, Nottingham, United Kingdom, <sup>2</sup>University of Anbar, Anbar, Iraq, <sup>3</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush Campus, Midlothian, UK, <sup>4</sup>Centre for Tropical Livestock Genetics and Health, The Roslin Institute, Edinburgh, UK, <sup>5</sup>LiveGene, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>6</sup>Addis Ababa University (AAU), Addis Ababa, Ethiopia.

### Microbiomes

- P289 **Comparative analysis of rumen metagenome of Vechur and crossbred cattle of Kerala, India—A first report.**  
T. Sadan<sup>\*</sup>, T. V. Aravindakshan, G. Radhika, F. Anand Lali, and K. Ally, *College of Veterinary and Animal Sciences, Thrissur, Kerala, India.*
- P290 **Effect of *Bacillus* probiotics on microbial gut diversity in weaner pigs.**  
J. Rosenstrauch, E. van Marle-Köster<sup>\*</sup>, and C. Jansen van Rensburg, *University of Pretoria, Pretoria, South Africa.*
- P291 **Effect of selection for intramuscular fat content in the cecum microbiome content in rabbits.**  
A. Zubiri-Gaitán<sup>\*</sup>, M. Martínez-Alvaro, A. Blasco, and P. Hernández, *Universitat Politècnica de València, Valencia, Valencia, Spain.*
- P292 **Going full circle: Assembly of high-quality, single-contig microbial genomes from the rumen microbiome using long-read sequencing.**  
A. Warr<sup>\*1</sup>, R. Stewart<sup>1</sup>, M. Aufrett<sup>2</sup>, A. Walker<sup>3</sup>, R. Roehe<sup>2</sup>, and M. Watson<sup>1</sup>, <sup>1</sup>The Roslin Institute, Edinburgh, UK, <sup>2</sup>SRUC, Edinburgh, UK, <sup>3</sup>The Rowett Institute, Aberdeen, UK.
- P293 **High-throughput metagenome sequencing for prediction of quantitative traits.**  
M. Hess<sup>\*1</sup>, L. Zetouni<sup>1</sup>, J. Budel<sup>1</sup>, T. Van Stijn<sup>1</sup>, H. Henry<sup>1</sup>, R. Brauning<sup>1</sup>, A. McCulloch<sup>1</sup>, S. Hickey<sup>2</sup>, A. Hess<sup>1</sup>, M. Kirk<sup>3</sup>, S. Kumar<sup>3</sup>, N. Morton<sup>4</sup>, H. Flay<sup>5</sup>, S. Kittelmann<sup>3</sup>, G. Henderson<sup>3</sup>, <sup>1</sup>AgResearch Ltd, Mosgiel, New Zealand, <sup>2</sup>AgResearch Ltd, Ruakura, New Zealand, <sup>3</sup>AgResearch Ltd, Palmerston North, New Zealand, <sup>4</sup>University of Auckland, Auckland, New Zealand, <sup>5</sup>DairyNZ, Hamilton, New Zealand.

### Pig Genetics and Genomics

- P294 **Plant secondary metabolites affect pig's gastro-intestinal health.**  
H. H. Hofmann<sup>\*</sup>, M. J. Proell-Cornelissen, M. Schulte-Rosier, K. Schellander, and C. Neuhoﬀ, *Animal Breeding and Husbandry/Animal Genetics group; University of Bonn, Bonn, North Rhine-Westphalia, Germany.*
- P295 **Array genotyping and/or whole-genome sequencing facilitates detection of structural variants and chromosomal imbalance in pigs.**  
A. Letko<sup>\*1</sup>, A. Grahofner<sup>2</sup>, I. M. Häfliger<sup>1</sup>, V. Jagannathan<sup>1</sup>, A. Ducos<sup>3</sup>, O. Richard<sup>4</sup>, V. Peter<sup>5</sup>, H. Nathues<sup>2</sup>, and C. Drögemüller<sup>1</sup>, <sup>1</sup>Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>2</sup>Clinic for Swine, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>3</sup>GenPhyse, INRA, INPT, ENVT, Université de Toulouse, Castanet-Tolosan, France, <sup>4</sup>Institute of Animal Pathology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>5</sup>Division of Clinical Radiology, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern, Bern, Switzerland.



- P296 **Detecting deleterious variants in the pig.**  
M. Johnsson<sup>\*1,2</sup>, R. Ros-Freixedes<sup>1,3</sup>, A. Whalen<sup>1</sup>, G. Gorjanc<sup>1</sup>, D.-J. De Koning<sup>2</sup>, C.-Y. Chen<sup>4</sup>, M. A. Cleveland<sup>4</sup>, A. J. Mileham<sup>5</sup>, S. Rounsley<sup>5</sup>, W. Herring<sup>4</sup>, and J. M. Hickey<sup>1</sup>, <sup>1</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Midlothian, United Kingdom, <sup>2</sup>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, <sup>3</sup>Departament de Ciència Animal, Universitat de Lleida, Lleida, Spain, <sup>4</sup>Genus plc, Hendersonville, TN, USA, <sup>5</sup>Genus plc, DeForest, WI, USA.
- P297 **Sustainability of extensive Iberian pig production through improved feed efficiency and genomic selection.**  
W. M. Rauw<sup>\*1</sup>, L. A. García Cortés<sup>1</sup>, J. M. García Casco<sup>2</sup>, F. Gómez Carballar<sup>3</sup>, E. de la Serna Fito<sup>3</sup>, and L. Gomez-Raya<sup>1</sup>, <sup>1</sup>INIA, Dept de Mejora Genética Animal, Madrid, Spain, <sup>2</sup>INIA, Centro de I+D en Cerdo Ibérico, Zafra, Badajoz, Spain, <sup>3</sup>Sánchez Romero Carvajal Jabugo S.A, Jabugo, Huelva, Spain.
- P298 **Comparative transcriptomic analysis of dorsal subcutaneous fat from Portuguese local pig breeds.**  
A. Albuquerque<sup>\*1</sup>, C. Óvilo<sup>2</sup>, Y. Núñez<sup>2</sup>, R. Benítez<sup>2</sup>, A. López-García<sup>2</sup>, J. Ballesteros<sup>2</sup>, F. García<sup>2</sup>, M. Laranjo<sup>1</sup>, R. Charneca<sup>3</sup>, and J. M. Martins<sup>4</sup>, <sup>1</sup>ICAAM-Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Pólo da Mitra, Évora, Portugal, <sup>2</sup>Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, <sup>3</sup>ICAAM, Departamento de Medicina Veterinária, Universidade de Évora, Pólo da Mitra, Évora, Portugal, <sup>4</sup>ICAAM, Departamento de Zootecnia, Universidade de Évora, Pólo da Mitra, Évora, Portugal.
- P299 **Runs of homozygosity provide a genome landscape picture of inbreeding and genetic history of European autochthonous and cosmopolitan pig breeds.**  
G. Schiavo<sup>\*1</sup>, M. Muñoz<sup>2</sup>, S. Bovo<sup>1</sup>, J. García-Casco<sup>2</sup>, A. Ribani<sup>1</sup>, S. Tinarelli<sup>1,3</sup>, I. Djurkin-Kušec<sup>4</sup>, C. Radovic<sup>5</sup>, R. Savic<sup>6</sup>, M. Gallo<sup>3</sup>, M. Candek-Potokar<sup>7</sup>, A. Fernández<sup>2</sup>, C. Óvilo<sup>2</sup>, L. Fontanesi<sup>1</sup>, TREASURE consortium<sup>8</sup>, <sup>1</sup>Department of Agriculture and Food Sciences, Università di Bologna, Bologna, Italy, <sup>2</sup>Departamento Mejora Genética Animal, INIA, Madrid, Spain, <sup>3</sup>Associazione Nazionale Allevatori Suini (ANAS), Roma, Italy, <sup>4</sup>Faculty of Agrobiotechnical Sciences Osijek, University of Osijek, Osijek, Croatia, <sup>5</sup>Institute for Animal Husbandry-Pig Research Department, Belgrade-Zemun, Serbia, <sup>6</sup>University of Belgrade, Faculty of agriculture, Belgrade-Zemun, Serbia, <sup>7</sup>Kmetijski inštitut Slovenije, Ljubljana, Slovenia, <sup>8</sup>TREASURE Consortium, Ljubljana, Slovenia.
- P300 **The transcriptomic impact of maternal dietary resistant starch on piglet's liver and colon when challenged with a high fat diet.**  
M. Schroyen<sup>\*1</sup>, J. Leblois<sup>2</sup>, J. Uerlings<sup>1</sup>, B. Li<sup>1</sup>, E. A. Sureda<sup>1</sup>, J. Wavreille<sup>3</sup>, J. Bindelle<sup>1</sup>, and N. Everaert<sup>1</sup>, <sup>1</sup>Precision Livestock and Nutrition Laboratory, Teaching and Research Centre (TERRA), Gembloux AgroBioTech, University of Liège, Gembloux, Belgium, <sup>2</sup>Association Wallonne de l'Élevage (awé), Ciney, Belgium, <sup>3</sup>Production and Sectors Department, Walloon Agricultural Research Centre (CRA-W), Gembloux, Belgium.
- P301 **Differential expression analysis of genes correlated with reproduction in Gossypol-treated porcine granulosa cells.**  
M. W. Hong<sup>\*</sup>, S. Y. Choi, H. Kim, H. Lee, and S. J. Lee, Kangwon National University, Chuncheon-si, Gangwon-do, South Korea.
- P302 **Genomic mating as a sustainable breeding strategy in Chinese NingXiang pigs.**  
J. He<sup>\*1,2</sup>, X. Wu<sup>2,3</sup>, Q. Zeng<sup>4</sup>, H. Li<sup>2,3</sup>, H. Ma<sup>1</sup>, J. Jiang<sup>1,3</sup>, G. J. M. Rosa<sup>3</sup>, D. Gianola<sup>3</sup>, R. G. Tait Jr.<sup>2</sup>, and S. Bauck<sup>2</sup>, <sup>1</sup>College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China, <sup>2</sup>Biostatistics and Bioinformatics, Neogen GeneSeek, Lincoln, NE, USA, <sup>3</sup>Department of Animal Sciences, University of Wisconsin, Madison, WI, USA, <sup>4</sup>Ningxiang Pig Farm of Dalong Livestock Technology Co. Ltd, Ningxiang, Hunan, China.
- P304 **Structural variants detection by large-scale sequencing data of pig genomes.**  
H. Du<sup>\*</sup> and J.-F. Liu, China Agricultural University, Beijing, Beijing, China.
- P305 **Genome-wide association and high-resolution QTL analyses identify a major locus on SSC12 influencing fatty acid composition in the *longissimus dorsi* muscle in pigs.**  
J.-B. Lee<sup>1</sup>, H.-B. Park<sup>\*2</sup>, Y. J. Kang<sup>3</sup>, and I.-C. Cho<sup>3</sup>, <sup>1</sup>Korea Zoonosis Research Institute, Chonbuk National University, Iksan, Republic of Korea, <sup>2</sup>Department of Animal Resources Science, Kongju National University, Yesan, Republic of Korea, <sup>3</sup>National Institute of Animal Science, RDA, Jeju, Republic of Korea.
- P306 **Piglet genotype, hypothalamic transcriptome, and their relationship with growth and viability traits.**  
A. Heras-Molina<sup>\*1</sup>, C. García-Contreras<sup>1,2</sup>, M. Vázquez-Gómez<sup>3</sup>, R. Benítez<sup>2</sup>, Y. Núñez<sup>2</sup>, J. Ballesteros<sup>2</sup>, J.L. Pesántez-Pacheco<sup>1,4</sup>, V. Sanz-Fernández<sup>1</sup>, S. Astiz<sup>1</sup>, B. Isabel<sup>3</sup>, A. González-Bulnes<sup>1,3</sup>, and C. Óvilo<sup>2</sup>, <sup>1</sup>Department of Animal Reproduction, SGIT-INIA, Madrid, Spain, <sup>2</sup>Department of Animal Breeding, SGIT-INIA, Madrid, Spain, <sup>3</sup>Faculty of Veterinary Medicine, UCM, Madrid, Spain, <sup>4</sup>School of Veterinary Medicine and Zootechnics, UCuenca, Cuenca, Ecuador.
- P307 **MC1R gene polymorphism of Polish wild boar (*Sus scrofa scrofa*) and swine (*Sus scrofa f. domestica*).**  
A. Koseniuk<sup>\*</sup>, G. Smolucha, D. Rubis, A. Szumiec, A. Radko, and K. Ropka-Molik, The National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland.

- P308 **Integrative analysis of genomic data related with pig intramuscular fat.**  
R. Gonzalez-Prendes\*<sup>1</sup>, Y. Ramayo-Caldas<sup>2</sup>, R. Ros-Freixedes<sup>1</sup>, E. Solé<sup>1</sup>, J. Estany<sup>1</sup>, and R. N. Pena<sup>1</sup>, <sup>1</sup>Department of Animal Science, University of Lleida–Agrotecnio Center, Lleida, Spain, <sup>2</sup>Animal Breeding and Genetics Program, IRTA, Caldes de Montbui, Barcelona, Spain.
- P309 **Variant discovery rate and genotype concordance of sequencing at a moderate coverage.**  
R. Ros-Freixedes\*, R. González-Prendes, S. Gol, E. Solé, R. N. Pena, and J. Estany, *Departament de Ciència Animal, Universitat de Lleida–Agrotecnio Center, Lleida, Spain.*
- P310 **The variance of gene expression in the porcine skeletal muscle changes in response to food intake.**  
E. Mármol-Sánchez\*<sup>1</sup>, R. Quintanilla<sup>2</sup>, TF Cardoso<sup>3</sup>, J. Tibau<sup>4</sup>, and M. Amills<sup>1,5</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>2</sup>Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Spain, <sup>3</sup>CAPEF Foundation, Ministry of Education of Brazil, Brasília D. F., Brazil, <sup>4</sup>IRTA-Monells, Monells, Spain, <sup>5</sup>Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.
- P311 **Integration of phenomics, transcriptomics, epigenetics and glycomics to reveal the mechanism underlying the embryo-maternal interaction during implantation in pigs.**  
F. Wang\*, K. Han, J. Huang, D. Deng, W. Wang, and M. Yu, *Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China.*
- P312 **Combining metabolomics and genomics to elucidate physiological processes related to tail damage score in pigs.**  
E. Dervishi\*<sup>1</sup>, L. van der Zande<sup>2</sup>, T. da Silva Valente<sup>1</sup>, I. Reimert<sup>3</sup>, P. Mathur<sup>2</sup>, M. S. Lopes<sup>2,4</sup>, E. F. Knol<sup>2</sup>, and G. S. Plastow<sup>1</sup>, <sup>1</sup>University of Alberta, Edmonton, Alberta, Canada, <sup>2</sup>Topigs Norsvin Research Center, Beuningen, The Netherlands, <sup>3</sup>Wageningen University & Research, Wageningen, The Netherlands, <sup>4</sup>Topigs Norsvin, Curitiba, Paraná, Brazil.
- P313 **Investigation of gene expression profiles for correlation between female reproductive hormones and estrous cycle in the ovary, oviduct, and endometrium in swine.**  
W. Park\*<sup>1</sup>, B.-H. Choi<sup>1</sup>, J.-M. Kim<sup>3</sup>, J.-E. Park<sup>1</sup>, H. Ka<sup>4</sup>, K.-T. Lee<sup>2</sup>, and D. Lim<sup>1</sup>, <sup>1</sup>Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju, Republic of Korea, <sup>2</sup>Animal Genetics and Breeding Division, National Institute of Animal Science, RDA, Wanju, Republic of Korea, <sup>3</sup>Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea, <sup>4</sup>Division of Biological Science and Technology, Yonsei University, Wonju, Republic of Korea.
- P314 **Whole-genome sequencing reveals selective signals for high-altitude adaptation in Tibetan pigs.**  
Y. W. Zhang\*, H. Zhang, and C. X. Wu, *College of Animal Science and Technology, China Agricultural University, Beijing, China.*
- P315 **Genetic relationship between Okinawa indigenous Agu pigs, wild boars in Japan and Asian pig breeds.**  
A. Arakawa\*<sup>1</sup>, S. Touma<sup>2</sup>, M. Taniguchi<sup>1</sup>, T. Eguchi-Ogawa<sup>3</sup>, S. Mikawa<sup>1</sup>, and H. Uenishi<sup>3</sup>, <sup>1</sup>Institute of Livestock and Grassland Science, NARO, Tsukuba, Ibaraki, Japan, <sup>2</sup>Okinawa Prefectural Livestock and Grassland Research Center, Nakijin, Okinawa, Japan, <sup>3</sup>Institute of Agrobiological Sciences, NARO, Tsukuba, Ibaraki, Japan.
- P316 **Fetal genotype effects on morphomics, fatty acids composition and transcriptomics in swine.**  
C. García-Contreras\*<sup>1,4</sup>, M. Vazquez-Gomez<sup>2</sup>, O. Madsen<sup>3</sup>, M. A. M. Groenen<sup>3</sup>, S. Astiz<sup>4</sup>, Y. Nuñez<sup>1</sup>, R. Benitez<sup>1</sup>, A. Heras-Molina<sup>4</sup>, A. Fernandez<sup>1</sup>, B. Isabel<sup>2</sup>, A. I. Rey<sup>2</sup>, A. Gonzalez-Bulnes<sup>4</sup>, and C. Ovilo<sup>1</sup>, <sup>1</sup>Department of Animal Breeding. Instituto Nacional de Investigación y tecnología Agraria y Alimentaria (INIA), Madrid, Madrid, Spain, <sup>2</sup>Faculty of Veterinary Medicine, Universidad Complutense de Madrid (UCM), Madrid, Madrid, Spain, <sup>3</sup>Animal Breeding and Genomics, Wageningen University & Research, Wageningen, The Netherlands, <sup>4</sup>Department of Animal Reproduction. Instituto Nacional de Investigación y tecnología Agraria y Alimentaria (INIA), Madrid, Madrid, Spain.
- P317 **Selection and validation in the pig production chain of genetic markers associated with quality of thighs for dry cured ham.**  
R. Davoli<sup>1</sup>, M. Zappaterra<sup>1</sup>, C. Schivazappa<sup>2</sup>, N. Simoncini<sup>2</sup>, R. Virgili<sup>2</sup>, and P. Zambonelli\*<sup>1</sup>, <sup>1</sup>Department of Agricultural and Food Sciences (DISTAL), University of Bologna, Bologna, Italy, <sup>2</sup>Stazione Sperimentale per l'Industria delle Conserve Alimentari (SSICA), Parma, Italy.
- P318 **A survey of genomic variants in commercial swine germplasm identified from whole-genome sequence.**  
B. N. Keel\*, D. J. Nonneman, A. K. Lindholm-Perry, W. T. Oliver, and G. A. Rohrer, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA.*
- P319 **Differences in longissimus transcriptome between Iberian pigs divergent for meat tenderness.**  
M. A. Fernandez-Barroso\*<sup>1</sup>, J. M. García-Casco<sup>1</sup>, L. Sillio<sup>2</sup>, C. Rodriguez<sup>2</sup>, Y. Nuñez<sup>2</sup>, F. Sanchez-Esquiliche<sup>3</sup>, C. Caraballo<sup>1</sup>, and M. Muñoz<sup>1</sup>, <sup>1</sup>Centro de I+D en Cerdo Ibérico, INIA, Zafra, Extremadura, Spain, <sup>2</sup>Departamento de Mejora Genética Animal, INIA, Madrid, Spain, <sup>3</sup>Sánchez-Romero Carvajal, Jabugo, Huelva, Spain.



- P320 **Transcriptomic profiles can explain differences in meat quality between two Iberian pig varieties.**  
A. Vilaplana<sup>1,2</sup>, N. Ibanez-Escriche<sup>\*3</sup>, R. Pena<sup>4</sup>, L. Muñoz<sup>5</sup>, E. González<sup>7</sup>, J. F. Tejada<sup>7</sup>, and J. L. Noguera<sup>5</sup>, <sup>1</sup>The Roslin Institute, Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, UK, <sup>2</sup>Centre for Medical Informatics, User Institute, Edinburgh, UK, <sup>3</sup>Department for Animal Science and Technology, Universitat Politècnica de València, Valencia, Spain, <sup>4</sup>Departament de Ciència Animal, Universitat de Lleida-Agrotecnio Center, Lleida, Spain, <sup>5</sup>IRTA, Genètica i Millora Animal, Lleida, Spain, <sup>6</sup>NGA FOOD S.A, Almendralejo, Spain, <sup>7</sup>Tecnología de los alimentos, Universidad de Extremadura, Badajoz, Spain.
- P321 **Genetic relationship of linoleic to arachidonic acid pathway with intramuscular fat in pigs.**  
S. Gol<sup>\*1</sup>, R. González-Prendes<sup>1</sup>, L. Bosch<sup>2</sup>, M. Tor<sup>1</sup>, J. Reixach<sup>3</sup>, R. N. Pena<sup>1</sup>, and J. Estany<sup>1</sup>, <sup>1</sup>Department of Animal Science, University of Lleida-Agrotecnio Center, Lleida, Spain, <sup>2</sup>Department of Agriculture Engineering and Food Technology, University of Girona, Girona, Spain, <sup>3</sup>Selección Batallé, Riudarenes, Spain.
- P322 **Predicting variant deleteriousness in non-human species: Applying the CADD approach in pig.**  
C. Gross<sup>\*1,2</sup>, M. Derks<sup>3</sup>, H. J. Megens<sup>3</sup>, M. Bosse<sup>3</sup>, M. A. M. Groenen<sup>3</sup>, M. Reinders<sup>1</sup>, and D. de Ridder<sup>2</sup>, <sup>1</sup>Delft Bioinformatics Lab, Delft University of Technology, Delft, The Netherlands, <sup>2</sup>Bioinformatics Group, Wageningen University & Research, Wageningen The Netherlands, <sup>3</sup>Animal Breeding and Genomics Centre, Wageningen University & Research, Wageningen The Netherlands.
- P323 **Genome-wide association studies for feed efficiency with imputed genotypes in pigs.**  
E. Delpuech<sup>\*</sup>, Y. Labrune, A. Aliakbari, H. Gilbert, and J. Riquet, *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet-Tolosan, Toulouse, France.*
- P324 **Population structure and genome characterization of synthetic pig breed based on Korean native pig.**  
D.-H. Son<sup>\*1</sup>, H.-S. Seong<sup>1</sup>, J.-W. Choi<sup>1</sup>, Y.-M. Kim<sup>1,2</sup>, and E.-S. Cho<sup>2</sup>, <sup>1</sup>College of Animal Life Science, Kangwon National University, Chuncheon, Republic of Korea, <sup>2</sup>Division of Swine Science, National Institute of Animal Science, RDA, Cheonan, Republic of Korea.
- P325 **QTL analysis of serum traits in an F<sub>2</sub> intercross between Landrace and Korean native pigs.**  
I.-C. Cho<sup>\*1</sup>, M. U. Kang<sup>2</sup>, M. S. Choi<sup>2</sup>, N.-Y. Kim<sup>1</sup>, M.-C. Shin<sup>1</sup>, S.-M. Shin<sup>1</sup>, J.-K. Son<sup>1</sup>, J.-H. Woo<sup>1</sup>, J.-H. Yoo<sup>1</sup>, N.-G. Park<sup>1</sup>, H.-B. Park<sup>1</sup>, and B.-C. Yang<sup>1</sup>, <sup>1</sup>National Institute of Animal Science, Jeju, Jeju, South Korea, <sup>2</sup>Foundation of Agri. Tech. Commercialization and Transfer, Iksan, Jeollabuk-do, South Korea.
- P327 **Whole-genome resequencing reveals signatures of selection in European pig breeds and wild boars.**  
S. Bovo<sup>\*1</sup>, G. Schiavo<sup>1</sup>, A. Ribani<sup>1</sup>, F. Di Palma<sup>2</sup>, V. J. Utzeri<sup>1</sup>, G. Moscatelli<sup>1</sup>, C. Geraci<sup>1</sup>, M. Gallo<sup>3</sup>, M. Muñoz<sup>4</sup>, A. I. Fernandez<sup>4</sup>, G. Usai<sup>5</sup>, J. Riquet<sup>6</sup>, R. Charneca<sup>7</sup>, I. Djurkin-Kušec<sup>8</sup>, Č. Radović<sup>9</sup>, R. Savić<sup>10</sup>, J. P. Araujo<sup>11</sup>, R. Quintanilla<sup>12</sup>, V. Razmaite<sup>13</sup>, M. J. Mercat<sup>14</sup>, C. Zimmer<sup>15</sup>, D. Karolyi<sup>16</sup>, M. Candek-Potokar<sup>17</sup>, F. García<sup>4</sup>, Y. Nuñez<sup>4</sup>, C. Ovilo<sup>4</sup>, L. Fontanesi<sup>1</sup>, and TREASURE Consortium<sup>18</sup>, <sup>1</sup>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, <sup>2</sup>Earlham Institute, Norwich, United Kingdom, <sup>3</sup>Associazione Nazionale Allevatori Suini (ANAS), Rome, Italy, <sup>4</sup>Departamento Mejora Genética Animal, INIA, Madrid, Spain, <sup>5</sup>AGRIS SARDEGNA, Loc. Bonassai, Sassari, Italy, <sup>6</sup>Génétique Physiologie et Système d'Élevage, INRA, Castanet-Tolosan, France, <sup>7</sup>Instituto de Ciências Agrárias e Ambientais Mediterrânicas (ICAAM), Universidade de Évora, Évora, Portugal, <sup>8</sup>University of Osijek, Faculty of Agrobiotechnical Sciences, Osijek, Croatia, <sup>9</sup>Institute for Animal Husbandry-Pig Research Department, Belgrade-Zemun, Serbia, <sup>10</sup>University of Belgrade, Faculty of Agriculture, Belgrade-Zemun, Serbia, <sup>11</sup>Instituto Politecnico de Viana do Castelo, Viana do Castelo, Portugal, <sup>12</sup>Programa de Genética y Mejora Animal, IRTA, Barcelona, Spain, <sup>13</sup>Animal Science Institute, Lithuanian University of Health Sciences, Baisogala, Lithuania, <sup>14</sup>Institut du Porc, IFIP, Le Rheu, France, <sup>15</sup>Bäuerliche Erzeugergemeinschaft Schwäbisch Hall, Schwäbisch Hall, Germany, <sup>16</sup>Department of Animal Science, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia, <sup>17</sup>Kmetijski inštitut Slovenije, Ljubljana, Slovenia, and <sup>18</sup>TREASURE Consortium, Ljubljana, Slovenia.
- P328 **Identification and experimental validation of enhancers in 11 tissues in the genome of lean and fatty type pigs.**  
Q. Xiaolong<sup>\*1</sup>, H. Mingyang<sup>1</sup>, H. Ye<sup>1</sup>, Z. Yuxia<sup>1</sup>, L. Yu<sup>1</sup>, L. Tingting<sup>2</sup>, Y. Hongbo<sup>2</sup>, Y. Feng<sup>2</sup>, Z. Shuhong<sup>1</sup>, and L. Xinyun<sup>1</sup>, <sup>1</sup>College of Animal Science & Technology College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China, <sup>2</sup>Department of Biochemistry and Molecular Biology, College of Medicine, The Pennsylvania State University, Hershey, PA, USA.
- P329 **Analysis of porcine muscle transcriptome reveals regulators and pathways associated with feed efficiency.**  
Y. Ramayo-Caldas<sup>\*1,3</sup>, E. Mármol-Sánchez<sup>2</sup>, M. Ballester<sup>1</sup>, R. González-Prendes<sup>2</sup>, M. Amills<sup>2,3</sup>, and R. Quintanilla<sup>1</sup>, <sup>1</sup>Institute for Research and Technology in Food and Agriculture, Caldes de Montbuit, Barcelona, Spain, <sup>2</sup>Department of Animal Genetics, Centre for Research in Agricultural Genomics, Universitat Autònoma de Barcelona, Barcelona, Spain, <sup>3</sup>Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Universitat Autònoma de Barcelona, Barcelona, Spain.
- P330 **Analysis of porcine miRNA-33b expression in liver and longissimus dorsi muscle and its role in fatty acid metabolism.**  
L. Criado-Mesas<sup>\*1</sup>, M. Ballester<sup>2</sup>, D. Crespo-Piazuelo<sup>1,3</sup>, A. Castelló<sup>1,3</sup>, and J. M. Folch<sup>1,3</sup>, <sup>1</sup>Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Barcelona, Spain, <sup>2</sup>Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain, <sup>3</sup>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain.



- P331 **From population genetics to single gene variants: Molecular background of breed specific effects at a QTL for thoracic vertebrae in pigs.**  
M. van Son<sup>1</sup>, M. Lopes<sup>2</sup>, H. Martell<sup>3</sup>, M. Derks<sup>4</sup>, J. Kongsro<sup>1</sup>, E. Grindfle<sup>1</sup>, and B. Harlizius<sup>\*2</sup>, <sup>1</sup>Norsvin SA, Hamar, Norway, <sup>2</sup>Topigs Norsvin Research Center, Beuningen, The Netherlands, <sup>3</sup>University of Kent, Canterbury, UK, <sup>4</sup>Wageningen University, Wageningen, The Netherlands.
- P332 **Transcription profile of *Semimembranosus* muscle in Italian Large White pigs with high and low intramuscular fat content and comparative analysis.**  
M. Zappaterra<sup>\*1</sup>, S. Gioiosa<sup>2</sup>, G. Chillemi<sup>3</sup>, T. Castrignanò<sup>2</sup>, P. Zambonelli<sup>1</sup>, and R. Davoli<sup>1</sup>, <sup>1</sup>Department of Agricultural and Food Sciences (DISTAL), Alma Mater Studiorum-University of Bologna, Bologna, Italy, <sup>2</sup>CINECA SuperComputing Applications and Innovation Department (SCAI), Roma, Italy, <sup>3</sup>Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), La Tuscia University of Viterbo, Viterbo, Italy.
- P333 **Genome-wide analysis of expression QTL (eQTL) and allelic specific expression QTL (aseQTL) in porcine muscle highlight candidate genes for meat quality traits.**  
Y. Liu<sup>1,2</sup>, T. Ma<sup>1,2</sup>, Y. Liu<sup>1,2</sup>, S. Zhao<sup>1,2</sup>, and X. Xu<sup>\*1,2</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China, <sup>2</sup>The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China.
- P334 **Association of *SCD* and *LEPR* genes with litter size and weight in pigs.**  
E. Solé<sup>\*1</sup>, R. N. Pena<sup>1</sup>, M. Tor<sup>1</sup>, J. Reixach<sup>2</sup>, and J. Estany<sup>1</sup>, <sup>1</sup>University of Lleida, Lleida, Spain, <sup>2</sup>Selección Batallé, Riudarenes, Spain.
- P335 **Low birth weight affects porcine intestinal gene expression and impairs intestinal development.**  
M. Ayuso<sup>\*1</sup>, S. Van Cruchten<sup>1</sup>, C. P. Walsh<sup>2</sup>, R. Irwin<sup>2</sup>, and C. Van Ginneken<sup>1</sup>, <sup>1</sup>Department of Veterinary Medicine, Faculty of Pharmaceutical, Biomedical and Veterinary Sciences, University of Antwerp, Wilrijk, Belgium, <sup>2</sup>School of Biomedical Sciences, Faculty of Life & Health Sciences; Ulster University, Coleraine, United Kingdom.
- P336 **Transcriptome-wide analysis of glucocorticoid regulated genes in pigs in the context of a gain-of-function mutation in the glucocorticoid receptor.**  
E. Murani<sup>\*</sup>, N. Trakooljul, F. Hadlich, S. Ponsuksili, and K. Wimmers, Leibniz Institute for Farm Animal Biology (FBN Dummerstorf), Institute for Genome Biology, Dummerstorf, Germany.
- P337 **Genetic regulation of liver metabolites and transcripts linking to biochemical-clinical parameters.**  
S. Ponsuksili, N. Trakooljul, F. Hadlich, E. Murani, and K. Wimmers<sup>\*</sup>, Leibniz-Institute for Farm Animal Biology (FBN), Genome Biology, Dummerstorf, Germany.
- P338 **Profiling of miR-874 and its predicted target gene *citron kinase* during myogenesis *in vitro*.**  
K. R. Daza<sup>\*</sup>, L. M. Ford, D. Velez-Irizarry, N. E. Raney, and C. W. Ernst, Michigan State University, East Lansing, MI, USA.
- P339 **Genotype-environment interactions for quantitative traits of purebred pig population in Korea.**  
D. Shin<sup>\*</sup>, J.-D. Oh, K.-D. Song, and H.-K. Lee, Chon-buk National University, Jeonju-si, Jeollabuk-do, Korea.
- P340 **Comprehensive analysis of the CircRNA expression profiles uncover ceRNA network involving fat deposition from castrated and intact full-sib pair Yorkshire male pigs.**  
X. Liu<sup>\*</sup> and M. Fang, China Agricultural University, Beijing, Beijing, China.
- P341 **A genome-wide association study for the robustness of piglets at weaning.**  
M. Revilla<sup>\*1,2</sup>, F. Blanc<sup>1</sup>, R. Muñoz-Tamayo<sup>2</sup>, G. Lemonnier<sup>1</sup>, J.-J. Leplat<sup>1</sup>, M.-J. Mercat<sup>3</sup>, L. Ravon<sup>4</sup>, Y. Billon<sup>4</sup>, N. C. Friggens<sup>2</sup>, J.-P. Bidanel<sup>1</sup>, C. Rogel-Gaillard<sup>1</sup>, N. Le-Floc'h<sup>5</sup>, and J. Estellé<sup>1</sup>, <sup>1</sup>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, <sup>2</sup>MoSAR, INRA, AgroParisTech, Université Paris-Saclay, Paris, France, <sup>3</sup>IFIP-Institut du porc and Alliance R&D, Le Rheu, France, <sup>4</sup>GenESI, INRA, Surgères, France, <sup>5</sup>PEGASE, INRA, AgroCampus Ouest, Saint-Gilles, France.
- P342 **Genetic parameters of protein of nitrogen efficiency in a Swiss Large White pig population: Preliminary results.**  
C. Kasper<sup>\*</sup>, I. Ruiz-Ascacibar, P. Stoll, and G. Bee, Agroscope, Posieux, Switzerland.
- P343 **Application of STR markers and their evaluation for parentage verification of pigs in Poland.**  
A. Radko, A. Koseniuk<sup>\*</sup>, G. Smolucha, and A. Podbielska, The National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland.



- P344 **Effects of fiber addition and dietary protein on phenotype and muscle transcriptome in Iberian pigs.**  
A. López-García\*<sup>1</sup>, Y. Núñez<sup>1</sup>, R. Benítez<sup>1</sup>, L. Fontanesi<sup>4</sup>, F. I. Hernández<sup>2</sup>, I. Seiquer<sup>3</sup>, P. Palma-Granados<sup>5,3</sup>, M. Izquierdo<sup>2</sup>, R. Nieto<sup>3</sup>, and C. Óvilo<sup>1</sup>, <sup>1</sup>Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain, <sup>2</sup>Centro de Investigaciones Científicas y Tecnológicas de Extremadura (CICYTEX), Guadajira, Badajoz, Spain, <sup>3</sup>Estación Experimental del Zaidín (EEZ), CSIC, Granada, Spain, <sup>4</sup>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, <sup>5</sup>Centro de I+D del Cerdo Ibérico, INIA, Zafra, Badajoz, Spain.
- P345 **Genomic differentiation among varieties of Iberian pig.**  
I. Alonso<sup>1</sup>, N. Ibañez-Escriche<sup>2</sup>, J. L. Noguera\*<sup>3</sup>, J. Casellas<sup>4</sup>, and L. Varona<sup>1,5</sup>, <sup>1</sup>Universidad de Zaragoza, Zaragoza, Spain, <sup>2</sup>Universitat Politècnica de Valencia, Valencia, Spain, <sup>3</sup>IRTA, Lleida, Spain, <sup>4</sup>Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>5</sup>Instituto Agroalimentario de Aragón(IA2), Zaragoza, Spain.
- P346 **Estimation of genomic regions associated with assortative mating.**  
L. Gomez-Raya\*, L. A. Garcia-Cortes, and W. M. Rauw, *Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria INIA, Madrid, Spain.*
- P347 **Genetic determinism of immunity traits in pigs: An opportunity for selecting robustness.**  
R. Quintanilla\*<sup>1</sup>, J. Reixach<sup>2</sup>, O. González-Rodríguez<sup>1</sup>, M. Pascual<sup>1</sup>, Y. Ramayo-Caldas<sup>1</sup>, M. Díaz<sup>2</sup>, J. Tibau<sup>1</sup>, and M. Ballester<sup>1</sup>, <sup>1</sup>Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Spain, <sup>2</sup>Selección Batallé S.A, Riudarenes, Spain.
- P348 **Allele-specific expression in *longissimus dorsi* muscle transcriptomes associated with phenotypic traits in pigs.**  
D. Vélez-Irizarry\*<sup>1</sup>, K. R. Daza<sup>1</sup>, R. O. Bates<sup>1</sup>, N. E. Raney<sup>1</sup>, J. P. Steibel<sup>1,2</sup>, and C. W. Ernst<sup>1</sup>, <sup>1</sup>Department of Animal Science, Michigan State University, East Lansing, MI, USA, <sup>2</sup>Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI, USA.
- P349 **Altered hippocampal epigenetic regulation underlying reduced cognitive development in response to early life environmental insults.**  
K. M. Schachtschneider\*<sup>1,2</sup>, M. E. Welge<sup>2,3</sup>, L. S. Auvil<sup>2</sup>, S. Chaki<sup>2</sup>, L. A. Rund<sup>2</sup>, O. Madsen<sup>4</sup>, M. R. P. Elmore<sup>2</sup>, R. W. Johnson<sup>2</sup>, M. A. M. Groenen<sup>4</sup>, and L. B. Schook<sup>1,2</sup>, <sup>1</sup>University of Illinois at Chicago, Chicago, IL, USA, <sup>2</sup>University of Illinois at Urbana-Champaign, Urbana, IL, USA, <sup>3</sup>Mayo-Illinois Alliance for Technology-Based Healthcare, Urbana, IL, USA, <sup>4</sup>Wageningen University, Wageningen, The Netherlands.
- P350 **Estimating the shared genetic architecture between site-specific RNA editing and economically important traits in pigs.**  
S. A. Funkhouser\*, J. P. Steibel, D. Velez-Irizarry, and C. W. Ernst, *Michigan State University, East Lansing, MI, USA.*
- P351 **miRNA and mRNA differential expression in peripheral blood mononuclear cells of pigs exposed to topsoil in early life.**  
M. de Souza<sup>1</sup>, D. Koltes<sup>1</sup>, H. Beiki<sup>1</sup>, T. Tsai<sup>2</sup>, M. Sales<sup>2</sup>, C. Maxwell<sup>2</sup>, J. Zhao<sup>2</sup>, and J. Koltes\*<sup>1</sup>, <sup>1</sup>Iowa State University, Ames, IA, USA, <sup>2</sup>University of Arkansas-Division of Agriculture, Fayetteville, AR, USA.
- P353 **Multiple domestication centers reveal the domestication and geographical distribution of Chinese native pig.**  
J. Quan\*<sup>1</sup>, C. Gao<sup>2</sup>, Y. Cai<sup>1</sup>, T. Jiao<sup>3</sup>, and S. Zhao<sup>1</sup>, <sup>1</sup>College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China, <sup>2</sup>Harbin Veterinary Research Institute, Harbin, China, <sup>3</sup>College of Grassland, Gansu Agricultural University, Lanzhou, China.
- P354 **Circular RNAs as biomarkers for porcine sperm motility.**  
M. Gòdia\*<sup>1</sup>, A. Castelló<sup>1,2</sup>, M. Rocco<sup>1,3</sup>, J.-E. Rodríguez-Gil<sup>3</sup>, A. Sánchez<sup>1,2</sup>, and À. Clop<sup>1,4</sup>, <sup>1</sup>Center for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Bellaterra, Catalonia, Spain, <sup>2</sup>Unit of Animal Science, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Catalonia, Spain, <sup>3</sup>Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Universitat Autònoma de Barcelona, Bellaterra, Catalonia, Spain, <sup>4</sup>Consejo Superior de Investigaciones Científicas (CSIC), Barcelona, Catalonia, Spain.
- P355 **An integrative GWAS and RNA-seq study to identify SNPs and transcripts related to sperm quality traits in pigs.**  
M. Gòdia\*<sup>1</sup>, A. Reverter<sup>2</sup>, R. González-Prendes<sup>3</sup>, Y. Ramayo-Caldas<sup>4</sup>, A. Castelló<sup>1,5</sup>, J.-E. Rodríguez-Gil<sup>6</sup>, A. Sánchez<sup>1,5</sup>, and À. Clop<sup>1,7</sup>, <sup>1</sup>Center for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Bellaterra, Catalonia, Spain, <sup>2</sup>CSIRO Agriculture and Food, St Lucia, Queensland, Australia, <sup>3</sup>Department of Animal Production, University of Lleida, Lleida, Catalonia, Spain, <sup>4</sup>Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Catalonia, Spain, <sup>5</sup>Unit of Animal Science, Department of Animal and Food Science, Universitat Autònoma de Barcelona, Bellaterra, Catalonia, Spain, <sup>6</sup>Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Universitat Autònoma de Barcelona, Bellaterra, Catalonia, Spain, <sup>7</sup>Consejo Superior de Investigaciones Científicas (CSIC), Barcelona, Catalonia, Spain.
- P356 **Promotion of muscle growth and development by IGFBP7 is regulated by CKM and miR-142-5p in pigs.**  
Q. Xu\* and M. Fang, *China Agricultural University, Beijing, China.*

- P358 **Effect of *MUC4* and *FUT1* genotypes on piglets infected with enterotoxigenic *Escherichia coli* F4 and F18.**  
F. R. Massacci\*<sup>1,3</sup>, S. Tofani<sup>2</sup>, M. Tentellini<sup>2</sup>, S. Orsini<sup>2</sup>, C. Forte<sup>2</sup>, C. Lovito<sup>2</sup>, D. Luise<sup>3</sup>, C. Bevilacqua<sup>1</sup>, M. Bertocchi<sup>3</sup>, L. Marchi<sup>2</sup>, C. Rogel-Gaillard<sup>1</sup>, G. Pezzotti<sup>3</sup>, J. Estellé<sup>1</sup>, P. Trevisi<sup>3</sup>, C. F. Magistrali<sup>2</sup>, <sup>1</sup>INRA, GABI, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France, <sup>2</sup>Istituto Zooprofilattico Sperimentale Umbria e Marche "Togo Rosati," SC3RS, Perugia, Italy, <sup>3</sup>University of Bologna, DISTAL, Bologna, Italy.
- P359 **Genome-wide association study reveals candidate genes for growth relevant traits in pigs.**  
Z. Tang\*<sup>1,2</sup>, J. Xu<sup>1,2</sup>, L. Yin<sup>1,2</sup>, D. Yin<sup>1,2</sup>, M. Zhu<sup>1,2</sup>, M. Yu<sup>1,2</sup>, X. Li<sup>1,2</sup>, S. Zhao<sup>1,2</sup>, and X. Liu<sup>1,2</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China, <sup>2</sup>Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei, China.
- P360 **Circular analysis of breeding seasonality in Iberian sows under an intensive production system.**  
M. M. de Hijas-Villalba\*<sup>1</sup>, L. Varona<sup>2</sup>, N. Ibáñez-Escriche<sup>3</sup>, J. P. Rosas<sup>4</sup>, J. L. Noguera<sup>5</sup>, and J. Casellas<sup>1</sup>, <sup>1</sup>Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>2</sup>Departamento de Anatomía Embriología y Genética Animal, Universidad de Zaragoza, Zaragoza, Spain, <sup>3</sup>Departament de Ciència Animal, Universitat Politècnica de València, Valencia, Spain, <sup>4</sup>Programa de Mejora Genética "Castúa," INGA FOOD SA, Almendralejo, Spain, <sup>5</sup>Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries, Lleida, Spain.
- P361 **Assessment of punctual  $\Delta 9$ -desaturase activity in porcine adipose tissue.**  
L. Sarri\*, G. De la Fuente, A. R. Seradj, J. Estany, R. N. Pena, J. Balcells, and M. Tor, Animal Science Department, University of Lleida- Agrotecnio Center, Lleida, Spain.
- P362 **Genome-wide identification of splicing QTL (sQTL) in the pig *Longissimus dorsi* muscle.**  
Z. Zheng\*<sup>1,2</sup>, R. Zhang<sup>1,2</sup>, Y. Liu<sup>1,2</sup>, Y. Liu<sup>1,2</sup>, and X. Xu<sup>1,2</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China, <sup>2</sup>The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China.
- P363 **Progress on study of the genetic diversity of different pig breeds from China and Africa.**  
W. Feng<sup>1,2</sup>, R. Mrode<sup>2</sup>, E. Okoth<sup>2</sup>, and J.-F. Liu\*<sup>1</sup>, <sup>1</sup>College of Animal Science and Technology, China Agricultural University, Beijing, China, <sup>2</sup>International Livestock Research Institute, Nairobi, Kenya.
- P364 **Breed feature characteristics and genome variation based genome-wide association study on pigs.**  
J. Xu\*<sup>1,2</sup>, Y. Fu<sup>1,2</sup>, Y. Zhou<sup>1,2</sup>, L. Yin<sup>1,2</sup>, Z. Tang<sup>1,2</sup>, D. Yin<sup>1,2</sup>, M. Zhu<sup>1,2</sup>, M. Yu<sup>1,2</sup>, X. Li<sup>1,2</sup>, X. Liu<sup>1,2</sup>, and S. Zhao<sup>1,2</sup>, <sup>1</sup>Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education & College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China, <sup>2</sup>Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei, China.
- P365 **Mitochondrial and SNP data analysis confirm the complex origin of Bazna pigs from Romania.**  
VA Bâlțeanu\*<sup>1</sup>, T. Figueiredo-Cardoso<sup>2</sup>, M. Amills<sup>2</sup>, and A. Zsolnai<sup>3</sup>, <sup>1</sup>University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania, <sup>2</sup>Center for Research in Agricultural Genomics (CSIC-IRTA-UAB-UB), Campus Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>3</sup>NARIC-Research Institute for Animal Breeding, Nutrition and Meat Science (ÁTHK), Herceghalom, Hungary.

### Ruminant Genetics and Genomics

- P366 **Development and validation of a qPCR assay for the non-invasive determination of fetal sex in cattle and African Buffalo.**  
D. M. De Villiers\*<sup>2,1</sup>, R. Van der Sluis<sup>1</sup>, and B. C. Vorster<sup>1</sup>, <sup>1</sup>North-West University, Potchefstroom, North-West, South Africa, <sup>2</sup>Lumen Laboratories, Potchefstroom, North-West, South Africa.
- P367 **Mapping the *SCURS* locus in the South African Bonsmara beef cattle breed.**  
R. Grobler\*, C. Visser, and E. van Marle-Köster, Department Animal and Wildlife Sciences, University of Pretoria, Pretoria, Gauteng, South Africa.
- P368 **Bioinformatic investigation of the cattle *POLLED* variants.**  
J. E. Aldersey\*<sup>1</sup>, W. Y. Low<sup>1</sup>, N. Liu<sup>2</sup>, R. Tearle<sup>1</sup>, J. L. Williams<sup>1</sup>, and C. D. K. Bottema<sup>1</sup>, <sup>1</sup>Davies Research Centre, School of Animal & Veterinary Sciences, University of Adelaide, Roseworthy Campus, Roseworthy, SA, Australia, <sup>2</sup>Bioinformatics Hub, School of Biological Sciences, University of Adelaide, North Terrace Campus, Adelaide, SA, Australia.



- P369 **Genetic parameter estimation and dynamics of fatty acid composition in Korean Holstein cattle.**  
R. Umanthi<sup>1</sup>, C. H. Park<sup>2</sup>, C. G. Dang<sup>3</sup>, and C. H. Do\*<sup>1</sup>, <sup>1</sup>Chungnam National University, Daejeon, Korea, <sup>2</sup>Korea Animal Improvement Association, Seoul, Korea, <sup>3</sup>National Institute of Animal Science, RDA, Cheonan, Korea.
- P371 **Effects of including sequence variants on imputation accuracy.**  
M. Spengeler\*<sup>1</sup>, I. M. Häfliger<sup>2</sup>, C. Drögemüller<sup>2</sup>, H. Pausch<sup>3</sup>, and F. R. Seefried<sup>1</sup>, <sup>1</sup>Qualitas AG, Zug, Switzerland, <sup>2</sup>Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>3</sup>Animal Genomics, Institute of Agricultural Sciences, Lindau, Zurich, Switzerland.
- P372 **Expressions of  $\beta$ -defensin family genes in cisternal lining epithelial cells of dairy cattle mammary gland infected with staphylococci.**  
E. Bagnicka<sup>1</sup>, E. Kosciuczuk<sup>1</sup>, J. Jarczak<sup>2</sup>, P. Lisowski<sup>1</sup>, M. Rzewuska<sup>3</sup>, M. Zalewska<sup>1</sup>, E. Kawecka<sup>1</sup>, T. Zabek\*<sup>4</sup>, S. Marczak<sup>1</sup>, S. Petrykowski<sup>1</sup>, D. Sloniewska<sup>1</sup>, and L. Zwierzchowski<sup>1</sup>, <sup>1</sup>Institute of Genetics and Animal Breeding PAS, Jastrzebiec, Poland, <sup>2</sup>Biobank Lab, Department of Molecular Biophysics, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland, <sup>3</sup>Department of Pre-Clinical Sciences, Faculty of Veterinary Medicine, Warsaw University of Life Sciences - SGGW, Warsaw, Poland, <sup>4</sup>National Research Institute of Animal Production, Balice, Poland.
- P373 **Differences in miRNAs expression between blood leukocytes and milk somatic cells of SRLV-seropositive and seronegative goats.**  
E. Bagnicka<sup>1</sup>, D. Reczynska\*<sup>1</sup>, M. Czopowicz<sup>2</sup>, J. Kaba<sup>2</sup>, J. Jarczak<sup>3</sup>, D. Sloniewska<sup>1</sup>, K. Horbanczuk<sup>1</sup>, and L. Zwierzchowski<sup>1</sup>, <sup>1</sup>Institute of Genetics and Animal Breeding PAS, Jastrzebiec, Poland, <sup>2</sup>Warsaw University of Life Sciences, Laboratory of Veterinary Epidemiology and Economics, Faculty of Veterinary Medicine, Warsaw, Poland, <sup>3</sup>Biobank Lab, Department of Molecular Biophysics, Faculty of Biology and Environmental Protection, University of Łódź, Lodz, Poland.
- P374 **Genetic and genomic analyses for predicted methane-related traits in Japanese Black cattle.**  
Y. Uemoto\*<sup>1</sup>, M. Takeda<sup>1,2</sup>, A. Ogino<sup>3</sup>, T. Nozaki<sup>3</sup>, K. Kurogi<sup>3</sup>, T. Yasumori<sup>4</sup>, S. Ogawa<sup>1</sup>, M. Satoh<sup>1</sup>, and F. Terada<sup>1</sup>, <sup>1</sup>Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan, <sup>2</sup>National Livestock Breeding Center, Nishigo, Fukushima, Japan, <sup>3</sup>Maebashi Institute of Animal Science, Livestock Improvement Association of Japan Inc, Maebashi, Gunma, Japan, <sup>4</sup>Cattle Breeding Department, Livestock Improvement Association of Japan Inc, Tokyo, Japan.
- P376 **Simulation study on the power of QTL detection and genomic prediction accuracy using small effective population sizes.**  
M. Takeda\*<sup>1,2</sup>, Y. Uemoto<sup>2</sup>, and M. Satoh<sup>2</sup>, <sup>1</sup>National Livestock Breeding Center, Nishigo, Fukushima, Japan, <sup>2</sup>Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan.
- P377 **A genome-wide association analysis for dairy traits in Murciano-Granadina goats.**  
D. Guan\*<sup>1</sup>, V. Landi<sup>2</sup>, M. G. Luigi<sup>1</sup>, J. V. Delgado<sup>2</sup>, A. Castelló<sup>1,3</sup>, B. Cabrera<sup>1,3</sup>, E. Mármol-Sánchez<sup>1</sup>, J. F. Alvarez<sup>4</sup>, A. Martínez<sup>2</sup>, X. Such<sup>3</sup>, J. Jordana<sup>3</sup>, and M. Amills<sup>1,3</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>2</sup>Departamento de Genética, Universidad de Córdoba, Córdoba, Spain, <sup>3</sup>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>4</sup>Asociación Nacional de Criadores de Caprino de Raza Murciano-Granadina (CAPRIGRAN), Granada, Spain.
- P378 **ASIP: Transcripts and expression in llamas with different coat color.**  
M. Anello\*<sup>1</sup>, M. S. Daverio<sup>1,2</sup>, S. R. Romero<sup>3</sup>, L. B. Vidal Rioja<sup>1</sup>, C. Renieri<sup>4</sup>, and F. Di Rocco<sup>1</sup>, <sup>1</sup>Instituto Multidisciplinario de Biología Celular (IMBICE), CONICET-UNLP-CIC, La Plata, Buenos Aires, Argentina, <sup>2</sup>Cátedra de Biología, Departamento de Ciencias Biológicas, Facultad de Ciencias Exactas, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina, <sup>3</sup>Instituto de Investigaciones y Desarrollo Tecnológico para la Agricultura Familiar (IPAF), INTA, Maimara, Jujuy, Argentina, <sup>4</sup>School of Pharmacy, University of Camerino, Camerino, Marche, Italia.
- P379 **Mapping copy number variation in Murciano-Granadina goats.**  
D. Guan\*<sup>1</sup>, A. Castelló<sup>1,3</sup>, V. Landi<sup>2</sup>, M. G. Luigi<sup>1</sup>, J. V. Delgado<sup>2</sup>, J. F. Alvarez<sup>4</sup>, A. Martínez<sup>2</sup>, X. Such<sup>3</sup>, J. Jordana<sup>3</sup>, and M. Amills<sup>1,3</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>2</sup>Departamento de Genética, Universidad de Córdoba, Córdoba, Spain, <sup>3</sup>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, Spain, <sup>4</sup>Asociación Nacional de Criadores de Caprino de Raza Murciano-Granadina (CAPRIGRAN), Granada, Spain.
- P380 **Interplay among miRNA, gene expression, and mineral metabolism in Nelore cattle.**  
W. J. S. Diniz\*<sup>1,2</sup>, P. Banerjee<sup>2</sup>, G. Mazzoni<sup>2</sup>, L. L. Coutinho<sup>4</sup>, A. S. M. Cesar<sup>4</sup>, J. Afonso<sup>3</sup>, C. F. Gromboni<sup>5</sup>, A. R. A. Nogueira<sup>3</sup>, H. N. Kadarmideen<sup>2</sup>, and L. C. A. Regitano<sup>3</sup>, <sup>1</sup>Federal University of São Carlos, São Carlos, São Paulo, Brazil, <sup>2</sup>Technical University of Denmark, Kgs. Lyngby, Denmark, <sup>3</sup>Embrapa Pecuária Sudeste, Empresa Brasileira de Pesquisa Agropecuária, São Carlos, São Paulo, Brazil, <sup>4</sup>University of São Paulo, Piracicaba, São Paulo, Brazil, <sup>5</sup>Bahia Federal Institute of Education, Science and Technology, Ilhéus, Bahia, Brazil.

- P381 **Inclusion of herdmate data improves genomic prediction for milk production and feed efficiency traits within North American dairy herds.**  
N. Schultz\* and K. Weigel, *University of Wisconsin, Madison, WI, USA.*
- P382 **Genome-wide tests and sequencing point to candidate gene variants for body temperature maintenance under the cold stress in Siberian cattle population.**  
A. V. Igoshin\*<sup>1</sup>, A. A. Yurchenko<sup>1</sup>, N. M. Belonogova<sup>1</sup>, D. V. Petrovsky<sup>1</sup>, R. B. Aitnazarov<sup>1</sup>, V. A. Soloshenko<sup>2</sup>, N. S. Yudin<sup>1,3</sup>, and D. M. Larkin<sup>1,4</sup>, <sup>1</sup>*The Federal Research Center Institute of Cytology and Genetics, The Siberian Branch of the Russian Academy of Sciences (ICG SB RAS), Novosibirsk, Russia*, <sup>2</sup>*Siberian Research Institute of Animal Husbandry, Krasnoobsk, Russia*, <sup>3</sup>*Novosibirsk State University, Novosibirsk, Russia*, <sup>4</sup>*Royal Veterinary College, University of London, London, UK.*
- P383 **RNA-seq analysis of the effect of melatonin on the expression of genes related to hair follicle development in Inner Mongolia cashmere goats.**  
Y. Zhao\*, Y. Wang, Q. Mu, Z. Wu, and Z. Liu, *College of Animal Science, Inner Mongolia Agricultural University Hohhot, Inner Mongolia.*
- P384 **Validation of candidate SNPs for fat percentage in bovine rib-eye area using genotyping integrated fluidic circuit.**  
R. Yamamoto\*, S. Toyomoto<sup>1</sup>, N. Kohama<sup>2</sup>, T. Akiyama<sup>2</sup>, E. Yoshida<sup>3</sup>, E. Kobayashi<sup>4</sup>, K. Oyama<sup>5</sup>, H. Mannen<sup>1</sup>, and S. Sasazaki<sup>1</sup>, <sup>1</sup>*Graduate School of Agricultural Science, Kobe University, Kobe, Hyogo, Japan*, <sup>2</sup>*Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, Asago, Hyogo, Japan*, <sup>3</sup>*Hyogo Prefectural Technology Center for Agriculture, Forestry and Fisheries, Kasai, Hyogo, Japan*, <sup>4</sup>*Division of Animal Breeding and Reproduction Research, Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan*, <sup>5</sup>*Food Resources Education & Research Center, Kobe University, Kasai, Hyogo, Japan.*
- P385 **Effect of stage of lactation and polymorphisms in *CSN1S1* 5' flanking region on milk production traits in White Fulani cattle breed in Benin.**  
I. Houaga\*<sup>1,2</sup>, A. W.T. Muigai<sup>3</sup>, F. M. Ng'ang'a<sup>4</sup>, F. Stomeo<sup>4</sup>, I. A.K. Youssao<sup>2</sup>, V. C. Yapi-Gnaoré<sup>1</sup>, and E. M. Ibeagha-Awemu<sup>5</sup>, <sup>1</sup>*Centre International de Recherche-Développement sur l'Élevage en zone subhumide, Bobo-Dioulasso, Burkina Faso*, <sup>2</sup>*Department of Botany, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya*, <sup>3</sup>*Biosciences Eastern and Central Africa-International Livestock Research Institute (BeCA-ILRI) Hub, Nairobi, Kenya*, <sup>4</sup>*Laboratory of Animal Biotechnology and Meat Technology, Department of Animal Health and Production, Polytechnic School of Abomey-Calavi University, Cotonou, Benin Republic*, <sup>5</sup>*Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada.*
- P386 **Accuracy of genomic estimated breeding value in Hanwoo (Korean Native Cattle) cows.**  
D. J. Lee\*<sup>1</sup>, S. H. Lee<sup>2</sup>, S. E. Park<sup>1</sup>, and D. H. Yoon<sup>1</sup>, <sup>1</sup>*Department of Animal Science and Biotechnology, Kyungpook National University, Sangju, Korea*, <sup>2</sup>*Division of Animal and Dairy Science, Chungnam National University, Daejeon, Korea.*
- P387 **Gene expression profile of heat shock proteins from Caracu and Nelore cattle breeds in response to thermal stress.**  
B. V. Pires\*<sup>1</sup>, S. P. Lima<sup>2</sup>, N. B. Stafuzza<sup>2</sup>, and C. C. P. Paz<sup>1,2</sup>, <sup>1</sup>*Departamento de Genética, Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo, Ribeirão Preto, SP, Brazil*, <sup>2</sup>*Instituto de Zootecnia, Centro APTA Bovinos de Corte, Sertãozinho, SP, Brazil.*
- P388 **Metabolome fingerprinting and potential biomarkers of hypocalcemia in dairy cows.**  
E. Dervishi\*<sup>1</sup>, M. Zhu<sup>1</sup>, M. Colazo<sup>2</sup>, L. Li<sup>1</sup>, and G. S. Plastow<sup>1</sup>, <sup>1</sup>*University of Alberta, Edmonton, Alberta, Canada*, <sup>2</sup>*Alberta Agriculture and Forestry, Edmonton, Alberta, Canada.*
- P389 **Genetic relationship of maternal haplotypes of the endangered long-tailed goral (*Naemorhedus caudatus*) populations in South Korea.**  
S.-H. Han\*, J.-Y. Moon, Y.-H. Lee, S.-J. Jeong, G.-C. Kim, D.-W. Lee, J.-I. Son, and C.-U. Cho, *Species Restoration Technology Institute, Korea National Park Service, Gurye, South Korea.*
- P390 **Whole-genome sequence analysis reveals insights into the genetic diversity and structure of the Cuban Charolais, a taurine breed adapted to tropical climate.**  
L. C. Ramírez-Ayala\*<sup>1</sup>, S. E. Ramos-Onsins<sup>1</sup>, J. Leno-Colorado<sup>1</sup>, Y. Rodríguez-Valera<sup>2</sup>, D. Rocha<sup>3</sup>, Y. Ramayo-Caldas<sup>4,5</sup>, and M. Pérez-Enciso<sup>1,6</sup>, <sup>1</sup>*Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Barcelona, Spain*, <sup>2</sup>*Facultad de Ciencias Agropecuarias, Universidad de Granma, Granma, Cuba*, <sup>3</sup>*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France*, <sup>4</sup>*Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain*, <sup>5</sup>*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain*, <sup>6</sup>*Institut Català de Recerca i Estudis Avançats (ICREA), Barcelona, Spain.*



- P391 **Whole-genome sequencing and hybrid assembly of Malnad Gidda cattle—A unique dwarf breed from Western Ghats of Karnataka, India.**  
K. P. Ramesha\*<sup>1</sup>, R. C. Vinod Kumar<sup>1,2</sup>, A. H. Patil<sup>3</sup>, N. Azharuddin<sup>1,2</sup>, U. Kannegundla<sup>1</sup>, P. Mol<sup>4,5</sup>, K. Sandeep<sup>3</sup>, S. K. Behera<sup>3</sup>, S. Jeyakumar<sup>1</sup>, A. Kumaresan<sup>1</sup>, M. Katakataware<sup>1</sup>, A. Manimaran<sup>1</sup>, D. N. Das<sup>1</sup>, and T. S. Keshava Prasad<sup>3,4</sup>, <sup>1</sup>ICAR-National Dairy Research Institute (Deemed University), Bengaluru, Karnataka, India, <sup>2</sup>Department of Animal Husbandry and Veterinary Services, Government of Karnataka, Bengaluru, Karnataka, India, <sup>3</sup>Center for Systems Biology and Molecular Medicine, Yenepoya Research Centre, Yenepoya (Deemed to be University), Mangalore, Karnataka, India, <sup>4</sup>Institute of Bioinformatics, International Tech Park, Bangalore, Karnataka, India, <sup>5</sup>Amrita School of Biotechnology, Amrita Vishwa Vidyapeetham, Kollam, Kerala, India, <sup>6</sup>Manipal Academy of Higher Education, Manipal, Karnataka, India.
- P392 **Genomic analyses reveal distinct genetic architectures and selective pressures in buffaloes.**  
T. Sun\*<sup>1</sup>, J. Shen<sup>1</sup>, N. Chen<sup>1</sup>, A. Achilli<sup>2</sup>, Y. Jiang<sup>1</sup>, and C. Lei<sup>1</sup>, <sup>1</sup>Northwest A&F University, Yangling, Shaanxi, China, <sup>2</sup>Università di Pavia, Pavia, Italy.
- P393 **Genome insights into past and recent dynamics of goat pastoralism in northeast and eastern Africa.**  
N. Khayatzaadeh<sup>1</sup>, G. M. Tarekegn<sup>2</sup>, T. Dessie<sup>3</sup>, A. Djikeng<sup>4</sup>, A. Haile<sup>5</sup>, B. Rischkowsky<sup>5</sup>, and J. M. Mwacharo\*<sup>5</sup>, <sup>1</sup>University of Natural Resources and Life Sciences, Vienna, Austria, <sup>2</sup>Department of Animal Production and Technology, Bahir Dar University, Bahir Dar, Ethiopia, <sup>3</sup>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, <sup>4</sup>Beca-ILRI Hub, Nairobi, Kenya, <sup>5</sup>Small Ruminant Genomics Group, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia.
- P394 **Identification of genomic regions associated with morphological traits in Murciano-Granadina goats.**  
M. G. Luigi-Sierra\*<sup>1</sup>, V. Landi<sup>2</sup>, D. Guan<sup>1</sup>, J. V. Delgado<sup>2</sup>, A. Castelló<sup>1,3</sup>, B. Cabrera<sup>1,3</sup>, E. Mármol-Sánchez<sup>1</sup>, J. Fernández-Alvarez<sup>4</sup>, A. Martínez<sup>2</sup>, X. Such<sup>3</sup>, J. Jordana<sup>3</sup>, and M. Amills<sup>1,3</sup>, <sup>1</sup>Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>2</sup>Departamento de Genética, Universidad de Córdoba, Córdoba, Córdoba, Spain, <sup>3</sup>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, <sup>4</sup>Asociación Nacional de Criadores de Caprino de Raza Murciano-Granadina, Granada, Granada, Spain.
- P395 **Using RNA-seq data in the genomic prediction model to increase the accuracy of Hanwoo (Korean cattle) intramuscular fat-related traits.**  
S. B. Jang\*<sup>1</sup>, Y. J. Chung<sup>1</sup>, J. M. Kang<sup>1</sup>, D. Seo<sup>1</sup>, D. J. Kim<sup>2</sup>, J. H. Lee<sup>1</sup>, and S. H. Lee<sup>1</sup>, <sup>1</sup>Chungnam National University, Daejeon, South Korea, <sup>2</sup>TNT research, Anyang-si, South Korea.
- P396 **Effect of the *PLAG1* gene polymorphism on carcass weight and oleic acid percentage in Japanese Black cattle populations.**  
F. Kawaguchi\*<sup>1</sup>, H. Kigoshi<sup>1</sup>, R. Yasuzumi<sup>1</sup>, K. Oyama<sup>2</sup>, H. Mannen<sup>1</sup>, and S. Sasazaki<sup>1</sup>, <sup>1</sup>Laboratory of Animal Breeding and Genetics, Kobe, Hyogo, Japan, <sup>2</sup>Food Resources Education & Research Center, Kasai, Hyogo, Japan.
- P397 **Expression profiling identifies candidate drivers of sexual dimorphism in bovine placenta and somatic tissues.**  
R. Liu\*<sup>1</sup>, R. Tearle<sup>1</sup>, T. Chen<sup>1</sup>, D. Thomsen<sup>1,2</sup>, T. P. L. Smith<sup>3</sup>, J. L. Williams<sup>1</sup>, and S. Hiendleder<sup>1,2</sup>, <sup>1</sup>Davies Research Centre, School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, South Australia, Australia, <sup>2</sup>Robinson Research Institute, The University of Adelaide, Adelaide, South Australia, Australia, <sup>3</sup>USMARC, USDA-ARS-US Meat Animal Research Center, Clay Center, NE, USA.
- P398 **Genomic diversity in a local Swiss cattle breed.**  
M. Bhati\*<sup>1</sup>, D. Crysanto, and H. Pausch, *Animal Genomics, Institute of Agricultural Sciences, ETH, Zurich, Switzerland.*
- P399 **Multi-variate mixed-models for the normalization of RNA-Seq data: Application to onset of puberty in beef cattle.**  
L. Tusell\*<sup>1</sup>, I. David<sup>1</sup>, A. Canovas<sup>2</sup>, M. G. Thomas<sup>3</sup>, and A. Reverter<sup>4</sup>, <sup>1</sup>GenPhySE, Université de Toulouse, INRA, INPT, ENSAT, Castanet-Tolosan, France, <sup>2</sup>Department of Animal Biosciences, Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, <sup>3</sup>Department of Animal Sciences, Colorado State University, Fort Collins, CO, USA, <sup>4</sup>CSIRO Agriculture & Food, St. Lucia, Brisbane, Australia.
- P400 **Genomic characterization of a set of endangered Spanish bovine breeds: Morenas Galegas.**  
M. A. García-Atance<sup>1</sup>, J. Cañon<sup>1</sup>, P. G. Eusebi<sup>1</sup>, S. Dunner<sup>1</sup>, C. J. Rivero<sup>2</sup>, R. Justo<sup>3</sup>, and O. Cortes\*<sup>1</sup>, <sup>1</sup>Veterinary Faculty, University Complutense of Madrid, Madrid, Spain, <sup>2</sup>Centro de Recursos Zootécnicos de Galicia, Ourense, Spain, <sup>3</sup>Federación de Razas Autóctonas de Galicia-BOAGA, Ourense, Spain.
- P401 **Epigenetic changes of photoperiod responsiveness were identified in DNA methylation maps and transcriptome profiles using ovariectomized and estradiol treatment (OVX+E<sub>2</sub>) sheep.**  
X. He\*<sup>1</sup>, R. Di<sup>1</sup>, X. Wang<sup>1</sup>, W. Hu<sup>1</sup>, X. Zhang<sup>2</sup>, J. Zhang<sup>2</sup>, Q. Liu<sup>1</sup>, and M. Chu<sup>1</sup>, <sup>1</sup>Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, <sup>2</sup>Tianjin Institute of Animal Sciences, Tianjin, China.

- P402 **Identification of new *DGAT1* and *Casein* sequence variants in goats using capture sequencing.**  
S. A. Rahmatalla\*<sup>1,2</sup>, D. Arends<sup>1</sup>, M. Reissmann<sup>1</sup>, L. M. A. Hassan<sup>1,3</sup>, S. Krebs<sup>4</sup>, and G. A. Brockmann<sup>1</sup>, <sup>1</sup>Albrecht Daniel Thaer-Institut für Agrar- und Gartenbauwissenschaften, Humboldt-Universität zu Berlin, Berlin, Germany, <sup>2</sup>Department of Dairy Production, Faculty of Animal Production, University of Khartoum, Khartoum North, Sudan, <sup>3</sup>Wildlife Research Center, Animal Resource Research Corporation, Federal Ministry of Livestock, Fisheries and Rangelands, Khartoum, Sudan, <sup>4</sup>Laboratory of Functional Genome Analysis, Gene Center, University of Munich (LMU), München, Germany.
- P403 **Annotation of selection signatures in the bovine breed Asturiana de Valles.**  
C. Paris<sup>1</sup>, S. Boitard<sup>1</sup>, B. Servin<sup>1</sup>, N. Sevane<sup>2</sup>, and S. Dunner\*<sup>2</sup>, <sup>1</sup>GenPhySE, Université de Toulouse, INRA, INPT, INP-ENVT, Castanet Tolosan, France, <sup>2</sup>Facultad de Veterinaria. Universidad Complutense de Madrid, Madrid, Spain.
- P404 **Rumen epithelial transcriptome profile of beef cattle with liver abscesses.**  
A. K. Lindholm-Perry\*<sup>1</sup>, B. N. Keel<sup>1</sup>, S. Fernando<sup>2</sup>, J. Wells<sup>1</sup>, and K. E. Hales<sup>1</sup>, <sup>1</sup>USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA, <sup>2</sup>Department of Animal Science, University of Nebraska-Lincoln, Lincoln, NE, USA.
- P405 **Genome-wide association analyses of blood metabolites in crossbred beef cattle.**  
J. Li\*<sup>1</sup>, E. Akanno<sup>1</sup>, T. Valente<sup>1,2</sup>, M. Abo-Ismail<sup>1,3</sup>, B. Karisa<sup>4</sup>, Z. Wang<sup>1</sup>, and G. Plastow<sup>1</sup>, <sup>1</sup>Livestock Gentec, Dept. of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, Canada, <sup>2</sup>Ethology and Animal Ecology Research Group, Dept. of Animal Science, Sao Paulo State University, Jaboticabal, Brazil, <sup>3</sup>Department of Animal and Poultry Production, Damanshour University, Damanshour, Egypt, <sup>4</sup>Alberta Agriculture and Forestry, Edmonton, Canada.
- P406 **Relationship among the gene expression of *SCD1*, *SCD5*, *SREBP1* and the fatty acid profile of Holstein-Friesian steers finished under different pasture systems.**  
D. Gamarra<sup>1</sup>, N. Aldai<sup>2</sup>, A. Carvajal<sup>3</sup>, M. M. de Pancorbo<sup>1</sup>, M. Taniguchi\*<sup>4</sup>, and R. Morales<sup>3</sup>, <sup>1</sup>Biomics Research Group, Lascaray Research Center, UPV/EHU, Vitoria-Gasteiz, Álava, Spain, <sup>2</sup>Lactiker Research Group, Lascaray Research Center, UPV/EHU, Vitoria-Gasteiz, Álava, Spain, <sup>3</sup>Instituto de Investigaciones Agropecuarias, INIA Remehue, Osorno, Chile, <sup>4</sup>Animal Genome Unit, Institute of Livestock and Grassland Science (NARO), Tsukuba, Ibaraki, Japan.
- P407 **Influence of the genotype array density on copy number variants identification with PennCNV.**  
A. M. Butty\*<sup>1</sup>, T. C. S. Chud<sup>1</sup>, F. Miglior<sup>1</sup>, F. S. Schenkel<sup>1</sup>, P. Stothard<sup>2</sup>, I. M. Häfliger<sup>3</sup>, C. Drögemüller<sup>3</sup>, and C. F. Baes<sup>1,3</sup>, <sup>1</sup>University of Guelph, Guelph, ON, Canada, <sup>2</sup>University of Alberta, Edmonton, AB, Canada, <sup>3</sup>University of Bern, Bern, BE, Switzerland.
- P408 **Association of SNPs related to Johne's disease with Holstein bulls EBVs for milk ELISA test scores.**  
S. Mallikarjunappa<sup>1,2</sup>, F. S. Schenkel<sup>1</sup>, L. F. Brito<sup>1,3</sup>, N. Bissonnette<sup>4</sup>, K. G. Meade<sup>2</sup>, F. Miglior<sup>1</sup>, J. Chesnais<sup>5</sup>, M. Lohuis<sup>5</sup>, and N. A. Karrow\*<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Teagasc Animal and Bioscience Research Department, Grange, Co. Meath, Ireland, <sup>3</sup>Department of Animal Sciences, Purdue University, West Lafayette, IN, USA, <sup>4</sup>Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, <sup>5</sup>The Semex Alliance, Guelph, ON, Canada.
- P409 **A transcriptional landscape of long noncoding RNAs in tissues from cattle differing in metabolic efficiency.**  
R. Weikard\*<sup>1</sup>, W. Nolte<sup>1</sup>, H. M. Hammon<sup>1</sup>, R. M. Brunner<sup>1</sup>, E. Albrecht<sup>1</sup>, A. Reverter<sup>2</sup>, and C. Kuehn<sup>1,3</sup>, <sup>1</sup>Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, <sup>2</sup>Commonwealth Scientific and Industrial Research Organisation (CSIRO) Agriculture and Food, Brisbane, Queensland, Australia, <sup>3</sup>University of Rostock, Faculty of Agricultural and Environmental Sciences, Rostock, Germany.
- P410 **Genomic selection through single-step genomic BLUP improves the accuracy of evaluation in Korean Hanwoo cattle.**  
M. N. Park\*<sup>1</sup>, M. Alam<sup>1</sup>, S. Kim<sup>1</sup>, B. Park<sup>1</sup>, S. H. Lee<sup>2</sup>, and S. S. Lee<sup>3</sup>, <sup>1</sup>National Institute of Animal Science, Rural Development Administration, Cheonan, Republic of Korea, <sup>2</sup>Chungnam National University, Daejeon, Republic of Korea, <sup>3</sup>Hanwoo Genetic Improvement Center, NongHyup Agribusiness Group Inc, Seosan, Republic of Korea.
- P411 **Long non-coding RNAs modulate metabolic efficiency in cattle and are linked to arginine biosynthesis.**  
W. Nolte\*<sup>1</sup>, R. Weikard<sup>1</sup>, R. M. Brunner<sup>1</sup>, E. Albrecht<sup>1</sup>, H. Hammon<sup>1</sup>, A. Reverter<sup>2</sup>, and C. Kühn<sup>1,3</sup>, <sup>1</sup>Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Mecklenburg-Vorpommern, Germany, <sup>2</sup>Commonwealth Scientific and Industrial Research Organisation (CSIRO), Brisbane, Queensland, Australia, <sup>3</sup>University of Rostock, Rostock, Mecklenburg-Vorpommern, Germany.
- P412 **A case of pulmonary hypoplasia and anasarca syndrome in Holstein cattle due to trisomy of chromosome 19.**  
I. M. Häfliger\*<sup>1</sup>, J. S. Agerholm<sup>2</sup>, and C. Drögemüller<sup>1</sup>, <sup>1</sup>Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, <sup>2</sup>Department of Veterinary Clinical Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C, Denmark.



- P413 **Hong Kong feral cattle: A distinct genetic pool?**  
M. Barbato<sup>1</sup>, M. Reichel<sup>2</sup>, M. Passamonti<sup>1</sup>, W. L. Low<sup>3</sup>, L. Colli<sup>1</sup>, R. Tearle<sup>\*3</sup>, J. Williams<sup>3</sup>, and P. Ajmone-Marsan<sup>1</sup>, <sup>1</sup>Department of Animal Science, Food and Nutrition - DIANA, Università Cattolica del Sacro Cuore, Piacenza, Italy, <sup>2</sup>Jockey Club College of Veterinary Medicine and Life Sciences, City University of Hong Kong, Kowloon, Hong Kong, <sup>3</sup>Davies Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, Australia.
- P414 **Imputation of copy number variants from flanking single nucleotide polymorphism haplotypes in cattle.**  
P. Rafter<sup>\*1,2</sup>, I. C. Gormley<sup>2</sup>, A. C. Parnell<sup>3</sup>, J. F. Kearney<sup>4</sup>, and D. P. Berry<sup>1</sup>, <sup>1</sup>Teagasc, Fermoy, Cork, Ireland, <sup>2</sup>University College Dublin, Belfield, Dublin, Ireland, <sup>3</sup>Maynooth University, Maynooth, Kildare, Ireland, <sup>4</sup>Irish cattle breeding federation, Bandon, Cork, Ireland.
- P415 **Choosing animals for a reference population that maximize both the captured variability and the probability of correct imputation.**  
C. Diaz<sup>\*1</sup>, C. Meneses<sup>1</sup>, M. J. Carabaño<sup>1</sup>, M. A. Toro<sup>2</sup>, and K. J. Abraham<sup>3</sup>, <sup>1</sup>Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Depto. Mejora Genética Animal, Madrid, Spain, <sup>2</sup>Universidad Politécnica, UPM, Depto. de Producción Agraria, Madrid, Spain, <sup>3</sup>University of São Paulo, Ribeirão Preto SP, Brazil.
- P416 **Identification of expressional quantitative trait loci (eQTL) influencing gene expression after *Mycobacterium avium* ssp. *paratuberculosis* infection in Holstein Friesian cattle using a genome- and transcriptome-wide approach.**  
M. Canive<sup>\*1</sup>, N. Fernandez-Jimenez<sup>2</sup>, J. R. Bilbao<sup>2</sup>, R. Casais<sup>3</sup>, and M. Alonso-Hearn<sup>1</sup>, <sup>1</sup>NEIKER-Instituto Vasco de Investigación y Desarrollo Agrario, Derio, Bizkaia, Spain, <sup>2</sup>University of the Basque Country, UPV/EHU, Leioa, Bizkaia, Spain, <sup>3</sup>SERIDA, Servicio Regional de Investigación y Desarrollo Agroalimentario, Centro de Biotecnología, Deva, Asturias, Spain.
- P417 **Estimation of phenotypic and genetic parameters of milk yield and conformation traits in dairy cattle: A multi-genotype and multi-location study.**  
O. M. Akinsola<sup>\*1</sup> and R. O. Okeke<sup>1</sup>, <sup>1</sup>University of Jos, Jos, Plateau, Nigeria, <sup>2</sup>Ahmadu Bello University, Zaria, Kaduna, Nigeria.
- P419 **Genome-wide association study for hair coat length in Brahman-Angus crossbred heifers.**  
K. M. Sarlo Davila<sup>\*1</sup>, F. Rezende<sup>1</sup>, S. Dikmen<sup>2,1</sup>, and R. G. Mateescu<sup>1</sup>, <sup>1</sup>University of Florida, Gainesville, FL, USA, <sup>2</sup>Bursa Uludag University, Bursa, Turkey.
- P420 **A genomic landscape of mitochondrial DNA insertions (NUMTs) into the cattle genome.**  
G. Schiavo, S. Bovo, A. Ribani, H. Kazemi, and L. Fontanesi<sup>\*</sup>, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy.
- P421 **Inbreeding across generations after the crossbreeding in a composite breed in cattle.**  
T. P. Paim<sup>\*1,2</sup>, E. H. A. Hay<sup>3</sup>, C. Wilson<sup>4</sup>, M. Thomas<sup>5</sup>, L. A. Kuehn<sup>6</sup>, S. R. Paiva<sup>7</sup>, C. McManus<sup>2</sup>, and H. Blackburn<sup>4</sup>, <sup>1</sup>Instituto Federal de Educação, Ciência e Tecnologia Goiano, Iporá, GO, Brazil, <sup>2</sup>Universidade de Brasília, Brasília, DF, Brazil, <sup>3</sup>Fort Keogh Livestock and Range Research Laboratory, Agricultural Research Service, USDA, Miles City, MT, USA, <sup>4</sup>National Center for Genetic Resources Preservation, Agricultural Research Service, USDA, Fort Collins, CO, USA, <sup>5</sup>Department of Animal Sciences, Colorado State University, Fort Collins, CO, USA, <sup>6</sup>US Meat Animal Research Center, Agricultural Research Service, USDA, Clay Center, Nebraska, USA, <sup>7</sup>Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil.
- P422 **Identifying genomics regions affecting meat tenderness in *Longissimus Dorsi* muscle in crossbred beef cattle.**  
S. Nayeri<sup>\*1</sup>, G. Plastow<sup>2</sup>, G. Vander Voort<sup>3</sup>, F. Schenkel<sup>1</sup>, M. M. Magalhães<sup>1,4</sup>, L. Gálvao de Albuquerque<sup>4</sup>, M. McMorris<sup>3</sup>, R. Ventura<sup>5</sup>, M. Miller<sup>2,6</sup>, and A. Cánovas<sup>1</sup>, <sup>1</sup>Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, ON, Canada, <sup>2</sup>Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, <sup>3</sup>AgSights, Elora, ON, Canada, <sup>4</sup>Department of Animal Science, School of Agricultural and Veterinarian Sciences, São Paulo State University (Unesp), Jaboticabal, São Paulo, Brazil, <sup>5</sup>Department of Animal Nutrition and Production, FMVZ-USP, Pirassununga, São Paulo, Brazil, <sup>6</sup>Neogen Corporation, Enterprise Square, Edmonton, AB, Canada.
- P423 **Genotype by environment interaction assessing phenotypic and genomic method for the dairy Gyr cattle from Brazil and Colombia.**  
A. M. T. Ospina<sup>\*1</sup>, I. Aguilar<sup>2</sup>, R. A. S. Faria<sup>1</sup>, L. G. González Herrera<sup>3</sup>, A. C. Espasandin<sup>4</sup>, A. E. Vercesi Filho<sup>5</sup>, and J. A. de Vasconcelos Silva<sup>1</sup>, <sup>1</sup>Sao Paulo State University, Unesp, FMVZ, Botucatu, Sao Paulo, Brazil, <sup>2</sup>Instituto Nacional de Investigación Agropecuaria, las Brujas, Uruguay, <sup>3</sup>Universidad Nacional de Colombia, Medellin, Antioquia, Colombia, <sup>4</sup>Universidad de la Republica, Montevideo, Uruguay, <sup>5</sup>Instituto de Zootecnia, Nova Odessa, Sao Paulo, Brazil.
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