ISAG 2023

39th International Society for Animal Genetics

CONFERENCE

2 – 7 July 2023

CAPE TOWN, SOUTH AFRICA

www.isag.us/2023

Conference Program

@isag2023 #ISAG2023

https://www.isag.us/2023/

Illumina Workshop:
Applying Genomics to Agriculture

We will hold Illumina Workshop '**Applying Genomics to Agriculture**' at ISAG.

Date & Time	July 4, 2023, 17:30 – 18:30
Place	Hall 8; CTICC Convention Centre, 1 Lower Long St, Cape Town, 8001 South Africa
Speaker	André Eggen, AgriGenomics, Illumina
Talk	The genomic revolution through NGS and High Throughput Genotyping is only in its infancy in agriculture research and industry.
Capacity	500

Over the past 20 years, genomics has taken a growing role in agriculture, from sequencing reference genomes to genotyping for genome-wide association studies to genomic prediction, advances in technology and applications have led to breakthroughs in plant and animal science and food production: based on Next Generation Sequencing and high throughput genotyping using SNP arrays, genomic technologies can be considered as a molecular microscope, finding its way in many different area of agriculture research and in industry.

This workshop will cover how Illumina's genomics technologies have been used and applied in different areas, from whole genome sequencing to high throughput genotyping, from genomic breeding to biodiversity characterization, from food science to climate change challenges and how Illumina technologies will continue to deliver best in class solutions for agrigenomics.

Register now and be eligible for our exclusive lucky draw. Don't miss out on your chance to win a SONOS bluetooth speaker!

Click here or scan the QR code to register

Sonos One Voice Controlled Smart Speaker (White) [2nd Generation]

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Contents

Committees

ISAG 2023 Local Organising Committee

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Este van Marle-Koster, University of Pretoria
Cuthbert Banga, Botswana University of Agriculture and Natural Resources
Nkhanedzeni (Baldwin) Nengovhela, Department of Agriculture Land Reform and Rural Development
Khathutshelo Nephawe, Tshwane University of Technology

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Sofia Mikko, Swedish University of Agricultural Science, Sweden (Secretary)
Klaus Wimmers, FBN-Dummerstorf, Germany (Treasurer)
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Chris Tuggle, Iowa State University, USA
Hans Lenstra, Utrecht University, Netherlands (ex officio)
Ntanganedzeni Olivia Mapholi, University of South Africa (ex officio)

ISAG 2023 Workshop Chairs

Animal epigenetics
Kyle Schachtschneider, University of Illinois at Chicago, USA

Animal forensic genetics
Guillermo Giovambattista, Universidad Nacional De La Plata

Applied genetics and genomics in other species of economic importance
Amparo Martinez, Animal Breeding Consulting, S.L., Spain (Chair)
Marcela Martinez, Laboratorio De Genetica AplicadaSociedad Rural Argentina, Argentina (Co-Chair)

Small ruminant genetics and genomics
Meng-Hua Li, Institute of Zoology, Chinese Academy of Sciences, China (Chair)
Rebecca Simon, Justus Liebig University Giessen, Germany (Co-Chair)

Applied genetics of companion animals
Peter Dovc, University of Ljubljana, Biotechnical Faculty, Slovenia (Chair)
Jiansheng Qiu, Neogen GeneSeek, USA (Co-Chair)

Avian genetics and genomics
Susan Lamont, Iowa State University, Iowa, USA

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

Companion animal genetics and genomics
Heather Huson, Cornell University, Ithaca, New York, USA (Co-Chair)

Jeffrey Schoenebeck, Roslin Institute (University of Edinburgh), United Kingdom (Co-Chair)

Comparative and functional genomics
Christa Kühn, FBN Dummerstorf, Germany

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

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

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

Genetics and genomics of aquaculture species
Francesca Bertolini, University of Bologna, Italy (Chair)

Maria Saura, INIA, Spain (Co-Chair)

Genetics of immune response and disease resistance
Christopher Tuggle, Iowa State University, USA (Co-Chair)

Graham Plastow, Livestock Gentec, Dept of AFNS, Edmonton, Canada (Co-Chair)

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

Horse genetics and genomics
Leslie Bickel, Veterinary Genetics Lab UC Davis, USA (Chair)

Tomasz Zabek, National Research Institute of Animal Production, Poland (Co-Chair)

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

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

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

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

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

Pig genetics and genomics
Daniel Ciobanu, University of Nebraska, Lincoln, Nebraska, USA

Amanda Warr, The Roslin Institute, Edinburgh, United Kingdom

Ruminant genetics and genomics
Shannon Clarke, AgResearch, Mosgiel, New Zealand

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ThermoFisher SCIENTIFIC

Schedule of Events

Sunday, July 2, 2023		
16:00-18:00	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
16:00-18:00	Poster Board Setup	Hall 9 - Exhibition Hall

Monday, July 3, 2023		
07:00-18:30	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
08:00-09:00	Opening Ceremony	Hall 8
09:00-12:15	Plenary Session I: Genetics & Genomics, African Heritage & Changing Climates	Hall 8
12:15-14:00	Applied Genetics of Companion Animals—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Avian Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Cattle Molecular Markers and Parentage Testing—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Companion Animal Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Comparative and Functional Genomics—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Equine Genetics and Thoroughbred Parentage Testing—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Genetics and Genomics of Aquaculture Species—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Genetics of Immune Response and Disease Resistance—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Horse Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Microbiomes—Poster Sessions	Hall 9 - Exhibition Hall
12:15-14:00	Pig Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
13:00-13:45	ThermoFisher Scientific Lunch Symposium	Daisy
13:00-13:45	Neogen Lunch Symposium	Orchid
13:15-14:00	Lunch Break, Exhibition and Poster Viewing	Hall 9 - Exhibition Hall
14:00-17:30	Microbiomes	Freesia
14:00-17:30	Pig Genetics and Genomics	Hall 8
14:00-17:30	Cattle Molecular Markers and Parentage Testing	Nerina
14:00-17:30	Comparative and Functional Genomics	Orchid
14:00-17:30	Horse Genetics and Genomics	Daisy
17:30-20:00	Welcome Reception	Hall 9 - Exhibition Hall

Tuesday, July 4, 2023		
07:00-18:30	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
08:30-11:00	Plenary Session II: Exploring genomic "big" data	Hall 8
11:00-14:00	Comparative MHC Genetics—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Domestic Animal Sequencing and Annotation—Poster Sessions	Hall 9 - Exhibition Hall
11:00-13:00	International Goat Genome (IGGC)	Orchid
11:00-14:00	Small Ruminant Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	ISAG-FAO Genetic Diversity—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Livestock Genomics for Developing Countries—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Genome Edited Animals—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Ruminant Genetics and Genomics—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Animal Epigenetics—Poster Sessions	Hall 9 - Exhibition Hall
11:00-14:00	Animal Forensic Genetics—Poster Sessions	Hall 9 - Exhibition Hall
13:00–13:45	J.E.D.I Symposium	Orchid
13:00-13:45	Biosearch Technologies Lunch Symposium: High-throughput genotyping technologies to accelerate livestock breeding programmes	Hall 8
13:00-14:00	Lunch Break, Exhibition and Poster Viewing	Hall 9 - Exhibition Hall
14:00-18:00	ISAG-FAO Genetic Diversity	Nerina
14:00-17:30	Domestic Animal Sequencing and Annotation	Orchid
14:00-17:30	Animal Epigenetics	Hall 8
14:00-17:30	Applied Genetics and Genomics in Other Species of Economic Importance	Freesia
14:00-17:30	Genetics of Immune Response and Disease Resistance	Daisy
17:30-19:30	Animal Genetic Testing Standardization	Orchid
18:00-19:30	ISAG-FAO Advisory Group on Animal Genetic Diversity Business Meeting	Nerina
18:00-20:00	Illumina Workshop—Followed by cocktail reception in the exhibition hall (Hall 9)	Hall 8

Wednesday, July 5, 2023		
07:00-18:30	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
08:30-10:30	Words of Wisdom – Engaging with Future Generations Workshop	Freesia
08:30-10:15	Genome Edited Animals	Hall 8
08:30-10:30	Applied Genetics of Companion Animals	Orchid
08:30-10:45	Small Ruminant Genetics and Genomics	Nerina
08:30-10:30	Comparative MHC Genetics	Daisy
10:30-11:00	Tea/Coffee Break, Exhibition and Poster Viewing	Hall 9 - Exhibition Hall

Thursday, July 6, 2023		
07:00-18:30	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
08:30-10:30	Plenary Session III: Functional Genomics (FAANG)	Hall 8
10:30-10:30	Tea/Coffee Break, Exhibition and Poster Viewing	Hall 9 - Exhibition Hall
11:00-13:00	Animal Genetics Journal Editorial Meeting (By invite only)	Nerina
11:00-13:00	Companion Animal Genetics and Genomics	Hall 8
11:00-12:45	Animal Forensic Genetics	Orchid
11:00-13:00	FAANG Workshop	Daisy
13:00-13:00	Lunch Break, Exhibition and Poster Viewing	Hall 9 - Exhibition Hall
14:00-17:30	Genetics and Genomics of Aquaculture Species	Freesia
14:00-17:30	Equine Genetics and Thoroughbred Parentage Testing	Nerina
14:00-17:15	Livestock Genomics for Developing Countries	Daisy
14:00-17:30	Avian Genetics and Genomics	Orchid
14:00-17:30	Ruminant Genetics and Genomics	Hall 8
19:00-23:00	Gala Dinner & Awards Ceremony	Gold Restaurant

Friday, July 7, 2023		
07:00-18:30	Registration Desk Open	CTICC 2, Level 2, Foyer of Hall 9
09:00-10:50	Plenary Session IV: Genomics for SA livestock and wildlife	Hall 8
10:50-11:30	Tea/Coffee Break	Hall 8 Foyer
11:30-12:30	Business Meeting	Hall 8
12:30-13:00	Closing Ceremony	Hall 8

Join our lunch symposium!

High-throughput genotyping technologies to accelerate livestock breeding programmes

Feeding the world in the midst of climate change and an ever-growing population demands scientists have access to scalable, flexible and sustainable genomic tools that add value to animal breeding programmes. At LGC Biosearch Technologies, we partner with you to provide fit for purpose technologies to ensure your mission critical projects are a success.

In this workshop, industry experts will be showcasing how innovation and creativity are being leveraged to overcome technical hurdles in the application of genomic technologies to accelerate your breeding programme through high-throughput genotyping via PCR and Next Generation Sequencing (NGS).

LGC Biosearch Technologies' genotyping solutions can target from a few regions to entire genomes. These methods can be applied to any species and can leverage valuable previous marker information you already have for your population. A breeding programme must screen a large number of animals quickly, and we have built technologies that match this demand to genotype up to hundreds of thousands of animals per year with fast turn-around time. Flexibility and technical excellence are at the core of our technologies, and these genotyping methods can be updated and optimized over time as you advance your breeding populations to answer evolving goals.

Introduction: Marcus Wills, Strategy Development Director, LGC Biosearch Technologies

Individual talk titles

- Accelerating molecular breeding from sample to actionable data: Marcus Wills, Strategy Development Director, LGC Biosearch Technologies
- Innovating animal breeding with Flex-Seq, a flexible and targeted high-throughput genotyping technology: Leandro Neves, Senior Director of Research and Innovation, LGC Biosearch Technologies

When: Tuesday, 4 July – 13:00 – 14:00

Where: Hall 8

Add event to calendar!

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GENOMIC ANALYSIS BY LGC

CONFERENCE INFORMATION

CONFERENCE VENUE

Cape Town International Convention Centre, **Block 2 (CTICC 2)**

Telephone: +27 (0) 21 410 5000

Address: Corner of Heerengracht and Rua Bartholomeu Dias, Foreshore, Cape Town, 8001 South Africa

GPS Coordinates: -33.915141°, 18.425657°

CTICC 2 is accessible through CTICC 1, which is across the road from Hotel Sky. The two buildings are joined by a sky bridge on the first floor of CTICC1. Alternatively, one can walk along Walter Sisulu Avenue, cross over Heerengracht Street, and the venue is on the corner of Heerengracht and Rua Bartholomeu Dias.

Parking is at your own expense.

REGISTRATION DESK

Location: CTICC 2, outside Hall 9 (first floor)

You will be able to collect your conference bag and name badge at this desk. The registration desk will be available and open during the following times to assist with registration and any queries you may have:

Sunday, July 2, 2023	16:00 – 18:00
Monday, July 3, 2023	07:00 – 18:30
Tuesday, July 5, 2023	07:30 – 18:00
Wednesday, July 6, 2023	07:30 – 14:00
Thursday, July 7, 2023	07:30 – 18:00
Friday, July 8, 2023	07:30 – 14:00

SPEAKER PREPARATION ROOM AND GUIDELINES

Location: CTICC 2, outside Hall 9 (first floor)

If you are a speaker, please note the following speaker preparation procedures.

Speakers are requested to check in at the Speaker Preparation Room.

The speaker preparation room will be operational on the following days and times:

Sunday, July 2, 2023	16:00 – 18:00
Monday, July 3, 2023	07:00 – 18:30
Tuesday, July 5, 2023	07:30 – 18:00
Wednesday, July 6, 2023	07:30 – 14:00
Thursday, July 7, 2023	07:30 – 18:00
Friday, July 8, 2023	07:30 – 12:30

Speakers are requested to load their presentations at the speaker preparation area no later than two hours prior to their sessions. Presentations cannot be loaded during the session in which presenters are speaking.

Speakers will be able to check their presentation(s) with a technician; once satisfied, the technician will assist with uploading the presentation onto the server.

At the time of your presentation, report directly to the meeting room you are presenting in, and your presentation will be available in the meeting room with the technician on duty in the room.

If your presentation includes embedded audio and video clips, please bring your audio and video clips as separate files. Should they not work in your presentation, this will allow the technician to assist you with re-embedding them.

Presentations should be prepared in Microsoft Office PowerPoint 2007 or later. Presentations should be in the widescreen (16:9) ratio format for optimal viewing. Presentations can also be provided in PDF format.

Please contact Kerry Firmani (kerryf@turnersconferences.co.za) for any speaker-related queries, including the submission of presentations.

EXHIBITION OPENING TIMES AND LOCATION

Location: CTICC 2, Hall 9

Monday, July 3, 2023	08:30 – 18:30
Tuesday, July 4, 2023	08:30 – 17:00
Wednesday, July 5, 2023	08:30 – 11:00
Thursday, July 6, 2023	08:30 – 15:45

SOCIAL EVENTS

The following social events will take place during the conference.

Welcome Reception Speeches
Date: Monday, July 3, 2023
Venue: CTICC2, Hall 8
Time: 17:30 – 18:30

Welcome Reception
Date: Monday, July 3, 2023
Venue: CTICC 2, Exhibition Hall 9
Time: 18:30 – 20:30

Gala Dinner
Date: Thursday, July 6, 2023
Venue: Gold Restaurant, 15 Bennett Street, Green Point, Cape Town
Time: 19:00 – 23:00
Dress: Smart or traditional attire

Transportation will be provided. The transport will depart from the CTICC Outside Entrance 3 (opposite the Sky Hotel Cape Town) to the restaurant from 18:00 to 18:45, and return to the appointed hotels from 22:00 to 23:00.

CONTACT DETAILS

Responsibility	Contact	Contact Details
General Queries	Gill Slaughter	Mobile: +27 83 269 0279 | Email: gills@turnersconferences.co.za
Programme	Kerry Firmani	Mobile: +27 60 557 3783 | Email: kerryf@turnersconferences.co.za
Accommodation	Bruce Rumble	Mobile: +27 83 263 3657 | Email: brucer@turnersconferences.co.za
Registration	Leanne Armoogam	Mobile: +27 78 191 8236 | Email: leannea@turnersconferences.co.za
Transportation and Excursions	Deveena Naiker	Mobile: +27 83 263 3657 | Email: deveenan@turnersconferences.co.za
Exhibition	Catherine Taylor	Mobile: +27 83 284 8592 | Email: catherinet@turnersconferences.co.za

ACCOMMODATION/HOTELS

Accommodation has been reserved for self-sponsored guests (who have indicated that a room be reserved) at the appointed hotels throughout the city.

An accommodation/hotel desk will be available at the conference center for the duration of the conference to assist with any queries and check-out procedures.

There will be no luggage-holding facility at the Cape Town International Conference Centre. We recommend that you plan to have your hotel hold your luggage until you are ready to depart for the airport.

EXCURSIONS

South Africa is often referred to as “a world in one country,” and we would like you to experience the beauty and splendor of Cape Town and the rest of the country for yourself. A fine selection of sightseeing excursions has been arranged using quality tour operators at preferential rates for conference participants. Turners Conferences excursion-booking desk will be available onsite for the duration of the conference.

CONFERENCE APP

The app allows you to plan your day, contact other attendees, find exhibitors through the interactive map, and keep up to date with the latest news. Please go to the ISAG 2023 website to download the app.

WiFi

There is complimentary WiFi at the CTICC for the duration of the conference.
WiFi network: CTICC
WiFi password: Explor3CTICC!

PASSPORTS AND VISAS

All visitors to South Africa must have a valid passport, and it is required that the document should have **at least two empty pages** when you arrive in South Africa. The passport must be valid for no fewer than 30 days after the final date of your intended stay in South Africa. Your passport needs to be machine-readable.

Nationals of some countries are exempt from visas; they are required for nationals of other countries. Visas must be obtained in your home country or from missions outside South Africa and cannot be applied for at South African ports of entry.

CAPE TOWN INTERNATIONAL AIRPORT AND TRANSPORT TO HOTELS

South African customs regulations require that all checked luggage be collected at your first airport of entry into South Africa, even though the airline may have checked that luggage through to your destination. Delegates arriving at O. R. Tambo International Airport in Johannesburg must collect their luggage at the international arrivals hall (Terminal A) and proceed through customs before making their way to domestic departures (Terminal B). Please recheck luggage to Cape Town.

SAFETY AND SECURITY

Cape Town has been host to numerous international and national events, and our beautiful city is well prepared for your arrival. As in any large city, we advise that you exercise good judgment when traveling alone or after dark. Ask your hotel concierge or the registration desk for advice on how to get around and where to go. Ostentatious displays of wealth in public places are not encouraged, and valuables such as wallets, laptop computers, cameras, and so forth should be kept in a secure place, such as your hotel safe-deposit facility. Please visit the many wonderful attractions, historical and cultural sites, restaurants, and shops that make Cape Town one of the world's most popular cities to visit.

CURRENCY AND MONEY EXCHANGE

You can exchange your money at the airport on arrival or at any of the many banks in Cape Town during banking hours. Hotels will also assist, but the exchange rates may be less favorable. Automated teller machines are available throughout the city for easy access to funds.

ELECTRICITY

South Africa's electricity supply runs at 220/230V, 50Hz AC. Sockets take round-pinned plugs, so you may need an adapter for your devices.

IMMUNISATIONS

Malaria: Cape Town is not considered a malaria-designated area. However, you are advised to take the necessary precautions if you are traveling to malaria-designated areas (located mainly in the northern areas of South Africa).

COVID restrictions: There are no COVID-19 restrictions in place in South Africa.

INSURANCE

The organizers are unable to accept any responsibility for damage or loss of personal property during the conference, and delegates are advised to ensure that such items are adequately insured.

MEDICAL EMERGENCIES

As with any travel, you are advised to take out travel insurance to cover the cost of private hospital treatment. In addition, Netcare Christiaan Barnard Memorial Hospital is located adjacent to the CTICC. If you require emergency medical assistance while at the CTICC, please alert the staff at the registration desk.

Join our symposium at ISAG 2023

Thermo Fisher Scientific provides agrigenomic solutions designed to deliver accurate and actionable data when you need it most. We are committed to providing instruments, reagents, and solutions for plant and animal genotyping applications: simple, scalable, and affordable next-generation solutions that will help drive remarkable agricultural innovations. These solutions enable producers to develop healthier, more efficient crops and livestock to help nourish the world's growing population.

Title:	Generations and Genetics: Advancements in Genetic Tools for Animal Genotyping
Date:	Monday 03 July, 2023
Time:	13:00 – 13:45
Location:	CTICC2, Level 2, Daisy

Speakers

Dr. Nina Schwensow
LABOKILN

Dr. Gabrielle Becker
University of Idaho

SOCIAL PROGRAMME

Welcome Reception
Date: Monday, July 3, 2023
Venue: Exhibition Hall (Hall 9)
Time: 18:30 – 20:30

Drinks and snacks will be served, along with some entertainment. You will have the opportunity of networking with fellow delegates and exhibitors.

Mid-Conference Tours
Date: Wednesday, July 5, 2023
Time: 11:00

City Sightseeing Hop On, Hop Off Bus Tour—Official Registration Tour

Departs Every 10 minutes.

Tickets are included in your registration pack.

The Red City route covers V&A Waterfront, Greenmarket Square, Free Walking tours, Table Mountain Cableway, The Camps Bay Strip, Sea Point, and Green Point Lighthouse.

Bus departure point is on Walter Sisulu Avenue, outside CTICC Entrance 3.

Spend the day at your leisure, the **Blue Mini Peninsula route** covers the V&A Waterfront, Two Oceans Aquarium, Greenmarket Square, Free Walking tours, Mount Nelson Hotel, South African Jewish Museum, Kirstenbosch Botanical Gardens, Constantia Winelands, World of Birds and Monkey Jungle, Imizamo Yethu Township Walking Tours, Mariners Wharf, The Camps Bay Strip Beach, Sea Point and Green Point Lighthouse.

Bus departure point is Lower Long Street, outside Hotel Sky.

Half-Day Cape Town City, Noon Gun, and Table Mountain Tour

This tour gives you the opportunity to discover the spirit of the Mother City, experience her vibrant cultures and history, and enjoy spectacular scenery.

Visit Table Mountain, weather permitting (otherwise Signal Hill), drive along the scenic coastal towns of Clifton and Sea Point. The tour includes a visit Green Market Square, District Six, and a walk through the Company Gardens. This scenic tour will also take you past the Houses of Parliament, City Hall, The Castle, and Slave Lodge.

Half-Day Cultural Township Tour

The tour offers you an insight into, and interaction with, diverse cultures, communities, and individuals living in our colourful society. Witness everyday life in a demanding environment and share in the hopes and the achievements of our people. Travel to District Six—visit the museum, Langa—visit a traditional healer "Sangoma" Tsoga Environmental Centre and a shebeen (informal pub), Gugulethu—visit Gugulethu Seven Memorial and Amy Biehl memorial, Crossroads, Bonteheuwel, and Khayelitsha—visit the Masikhule Kindergarten. You will have the opportunity to meet and talk to the local people and to buy arts and crafts manufactured by the local community.

Cape Point and Cape of Good Hope

Join us on Africa's premier tour route to the romantic meeting place of the Indian and Atlantic Oceans. Sir Francis Drake, the explorer, called it "the fairest Cape that we saw in the circumference of the Globe." This tour offers a full and exciting day out.

The tour's most memorable features include a visit to Hout Bay where you can take an optional 30-minute cruise to the Seal colony. Chapman's Peak Drive, Cape Point Nature Reserve, Cape Point and Cape of Good Hope. You can also visit the penguin colony (optional).

We will stop for lunch at the Fish Hoek Galley or similar (lunch is optional). Visit Simonstown, Constantia, and Kirstenbosch Botanical Gardens.

The Winelands—Paarl, Franschhoek, and Stellenbosch

Enjoy a full day in the Capes finest winelands. Your day will include the following highlights:

- Visit a Wine Estate for a cellar tour and tasting.
- Visit the town of Paarl, Former Victor Verster Prison, where Nelson Mandela was released in February 1990.
- Cheese and wine tasting.
- A lunch (optional) stop will be made in the town of Stellenbosch where you will also enjoy a tour of the town including the Village Museum.

Gala Dinner
Date: Thursday, July 6, 2023
Venue: Gold Restaurant
Time: 19:00 – 23:00

Enjoy dinner and entertainment from the African Continent.

Coach Shuttle transport will depart from 17:30 until 19:00 from outside the CTICC. The return shuttle will be available from 22:00 and will drop delegates off at the appointed hotels.

POSTER SCHEDULE

POSTER SESSIONS

Poster Room: Hall 9 – Exhibition Hall

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

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

Poster presenters should make themselves available to discuss their poster during the designated poster session that take place 12:15-14:00 on Monday and Tuesday from 11:00-14:00.

Monday **Presenters of the poster below should make themselves available to discuss their poster from 12:15-14:00 on Monday**	
Poster Number	**Section**
P20-P22	**Applied Genetics of Companion Animals**
P24-P64	**Avian Genetics and Genomics**
P66-P71	**Cattle Molecular Markers and Parentage Testing**
P72-P82	**Companion Animal Genetics and Genomics**
P83-P106	**Comparative and Functional Genomics**
P119-P124	**Equine Genetics and Thoroughbred Parentage Testing**
P125-P140	**Genetics and Genomics of Aquaculture Species**
P141-P164	**Genetics of Immune Response and Disease Resistance**
P173-P196	**Horse Genetics and Genomics**
P250-P267	**Microbiomes**
P268-P313	**Pig Genetics and Genomics**

Tuesday **Presenters of the poster below should make themselves available to discuss their poster from 11:00-14:00 on Tuesday**	
Poster Number	**Section**
P1-P11	**Animal Epigenetics**
P12-P19	**Animal Forensic Genetics**
P107-P108	**Comparative MHC Genetics**
P109-P118	**Domestic Animal Sequencing and Annotation**
P165-P172	**Genome Edited Animals**
P198-P211	**ISAG-FAO Genetic Diversity**
P212-P249	**Livestock Genomics for Developing Countries**
P314-P395	**Ruminant Genetics and Genomics**
P396-P434	**Small Ruminant Genetics and Genomics**

ISAG 2023
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Monday, 3rd July 2023
1pm - 1.45pm

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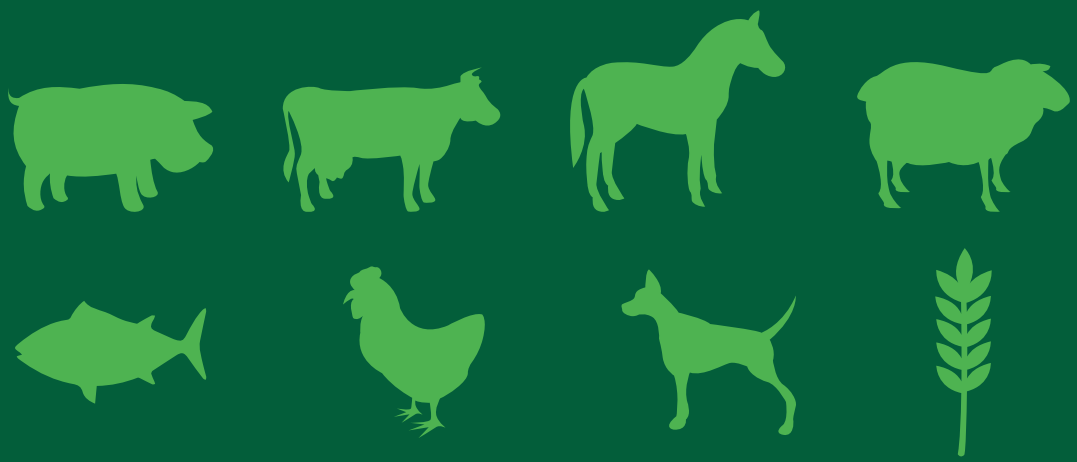

Monday, July 3

Opening Ceremony

Hall 8
8:00 AM - 9:00 AM

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions

Plenary Session I: Genetics & Genomics, African Heritage & Changing Climates

Chair: **Talks 1 & 2: Prof N Mapholi & Prof C Gill;**
Talk 3: Prof K Watson & Prof N Maiwashe
Hall 8
9:00 AM - 12:15 PM

9:00 AM OP1 **Understanding African health through genetic diversity.**
M. Ramsay*, *Sydney Brenner Institute for Molecular Bioscience, Faculty of Health Sciences, University of the Witwatersrand, South Africa*.

9:55 AM OP2 **Experiences in genomic selection for improved animal health and adaptability in Africa.**
A. Djikeng*[1,2], E. Rege[3], N. Mapholi[4], E. Ibeagha Awemu[5], S. E. Aggrey[6], R. Mrode[1,2,7], and O. Mwai[1], [1]*The International Livestock Research Institute (ILRI), Nairobi, Kenya*, [2]*The University Edinburgh, Scotland*, [3]*Emerge Centre for Innovations-Africa (ECI-Africa), Kenya*, [4]*University of South Africa (UNISA), South Africa*, [5]*Agriculture and Agri-Food Canada, Canada*, [6]*University of Georgia, Athens, GA*, [7]*Scotland's Rural College (SRUC), Scotland*.

10:50 AM **Tea/Coffee Break, Exhibition and Poster Viewing.**

11:20 AM OP3 **Genetics and genomics for genetic improvement and sustainability of animals—A world perspective.**
C. Baes*, *Department of Animal Biosciences at the University Guelph, Guelph, Ontario, Canada*.

OTHER EVENTS

Neogen Lunch Symposium
Orchid
1:00 PM - 1:45 PM

ThermoFisher Scientific Lunch Symposium
Daisy
1:00 PM - 1:45 PM

Lunch Break, Exhibition and Poster Viewing
Hall 9 - Exhibition Hall
1:15 PM - 2:00 PM

SYMPOSIA AND ORAL SESSIONS

Cattle Molecular Markers and Parentage Testing

Chair: **Jiansheng Qiu, Neogen Genomics, Lincoln, Nebraska, United States**
Nerina
2:00 PM - 5:30 PM

2:00 PM		**Welcoming remarks.**
2:05 PM		**Cattle STR/SNP Comparison Test 2022-2023.**
2:15 PM		**Presentation by Duty Lab.**
2:30 PM		**Presentation of STR results.**
2:45 PM		**Presentation of SNP results.**
3:00 PM		**Next Comparison Test (2024-2025).**
3:30 PM		**Tea/Coffee Break, Exhibition and Poster Viewing.**
4:00 PM	OP4	**ISAG Bursary Award: Population genomics of indigenous African cattle inferred from 537 whole-genome sequencing.** A. Tijjani[1,2], S. Kambal*[3,4], K. Marshall[5], O. Hanotte[1,3,6], and on behalf of the African Cattle Genomics Consortium[1], [1]*Centre for Livestock Genetics and Health (CTLGH), International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [2]*The Jackson Laboratory, Bar Harbor, ME*, [3]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [4]*University of Khartoum, Khartoum, Sudan*, [5]*International Livestock Research Institute (ILRI), Nairobi, Kenya*, [6]*School of Life Sciences, University of Nottingham, University Park Campus, Nottingham, UK.*
4:20 PM	OP5	**Low-density genotype panels performance for parentage verification in South African beef cattle breeds.** Y. Sanarana*[1,2], D. Berry[1,3], A. Maiwashe[2], C. Banga[2,4], and E. Van Marle-Köster[1], [1]*University of Pretoria, University of Pretoria, Hatfield, Pretoria, Gauteng, South Africa*, [2]*Agricultural Research Council, Irene, Pretoria, Gauteng, South Africa*, [3]*Teagasc, Fermoy, County Cork, Ireland*, [4]*Botswana University of Agriculture and Natural Resources, Gaborone, Botswana*.
4:40 PM	OP6	**Genetic diagnosis of sex chromosome aberrations in cattle based on parentage test by microsatellite DNA, X- and Y-linked markers.** L. Borreguero*[1], M. R. Maya[2], A. Trigo[2], I. Bonet[2], and J. A. Bouzada[1], [1]*Laboratorio Central de Veterinária, Algete, Madrid, Spain*, [2]*Tecnologias y Servicios Agrarios S.A, Madrid, Spain*.
5:00 PM		**Business Meeting and Closing Remarks.**

Comparative and Functional Genomics

Chair: **Christa Kühn, FBN Dummerstorf, Dummerstorf, Germany**
Orchid
2:00 PM - 5:30 PM

2:00 PM	OP7	**Exploring tissue-specificity in the regulatory landscape of bovine genome.** G. Costa Monteiro Moreira*[1], C. Yuan[1], S. Dupont[1], L. Tang[1], Y. Lee[1], D. Becker[2], M. Salavati[3], R. Clark[4], E. Clark[3], G. Plastow[5], C. Kühn[2,6], C. Charlier[1], and BovReg consortium[7], [1]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [3]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [4]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [7]*https://www.bovreg.eu/project/consortium/*.

2:15 PM OP8 **A multi-tissue porcine single-cell immune atlas: Resources for comparative and systems immunology.**
C. Tuggle*[1,2], L. Daharsh[1], M. Kapoor[1,2], P. Bk[2], S. Sivasankaran[3], K. Byrne[3], J. Herrera-Uribe[1], and C. Loving[3], [1]*Department of Animal Science, Iowa State University, Ames, IA*, [2]*Bioinformatics and Computation Biology, Iowa State University, Ames, IA*, [3]*USDA-Agriculture Research Service, National Animal Disease Center, Food Safety and Enteric Pathogens Research Unit, Ames, IA*.

2:30 PM OP9 **ISAG Bursary Award: Single cell atlas of developing ovine tail tissue reveals multi-cellular origins contributing to fat deposition.**
J. Han*[1,2], [1]*Institute of Animal Science, Chinese Academy of Agriculture Science, Beijing, China*, [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*.

2:45 PM OP10 **A multi-omic approach to understanding genetic and phenotypic variation in mass-reared Black Soldier Flies (*Hermetia illucens*).**
C. Rhode*, K. Hull, and M. Greenwood, *Stellenbosch University, Stellenbosch, Western Cape, South Africa*.

3:00 PM OP11 **ISAG Bursary Award: Ribosome profiling reveals stage-specific translational regulation during muscle differentiation.**
A. Goldkamp*[1], L. Okamoto[2], K. Thornton[2], and D. Hagen[1], [1]*Oklahoma State University, Stillwater, OK*, [2]*Utah State University, Logan, UT*.

3:15 PM OP12 **Chromosome conformation comparison in Piedmontese × Gaur F_1 fetal muscle tissue.**
M. R. Stegemiller*[1], K. L. Kuhn[2], T. P. Smith[2], B. D. Rosen[3], and B. M. Murdoch[1], [1]*Department of Animal, Veterinary, and Food Sciences, University of Idaho, Moscow, ID*, [2]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*, [3]*USDA, ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP13 **ISAG Bursary Award: DNA methylation dynamics regulating embryonic development in pig.**
J. de Vos*[1], M. Derks[1], H. Acloque[2], S. Djebali[3], S. Foissac[4], C. Guyomar[4], C. Kurylo[4], E. Giuffra[2], M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University, Wageningen, the Netherlands*, [2]*Paris-Saclay University, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*IRSD, Université de Toulouse, INSERM, INRA, ENVT, UPS, Toulouse, France*, [4]*GenPhySE, Université de Toulouse, INRAE, ENVT, Toulouse, France*.

4:15 PM OP14 **Genomic and functional characterization of frequently used bovine cell lines.**
D. Becker*[1], G. C. M. Moreira[2], C. Mörke[1], M. Charles[3], F. Hadlich[1], C. Lopez-Roques[9], M. Schmicke[4], V. Blanchet[5], H. Taniguchi[6], E. Clark[7], C. Pfarrer[8], J. Vanselow[1], C. Charlier[2], D. Rocha[3], C. Kuehn[1,10], [1]*Research Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Unit of Animal Genomics, GIGA, Liege, Belgium*, [3]*INRAE, Jouy-en-Josas, France*, [4]*Veterinary Endocrinology and Laboratory Diagnostics, University of Veterinary Medicine Hannover, Foundation, Hannover, Germany*, [5]*Unité de Génétique Moléculaire Animale (UGMA), University of Limoges, Limoges, France*, [6]*Institute of Genetics & Animal Biotechnology, Polish Academy of Sciences, Magdalenka, Poland*, [7]*The Roslin Institute, Edinburgh, UK*, [8]*Institute of Anatomy, University of Veterinary Medicine Hannover, Foundation, Hannover, Germany*, [9]*INRAE, US 1426, GeT-PlaGe, Genotoul, Castanet-Tolosan, France*, [10]*Agricultural and Environmental Faculty, University Rostock, Rostock, Germany*.

4:30 PM OP15 **Competing endogenous RNA (ceRNA) in a non-model animal: Non-coding RNAs respond to heat stress in rainbow trout (*Oncorhynchus mykiss*) through ceRNA-regulated mechanisms.**
J. Quan*, *Gansu Agricultural University, Lanzhou, China*.

4:45 PM OP16 **ISAG Bursary Award: Functional variants associated with male fertility in reproductive tissues of Brown Swiss bulls.**
X. Mapel*, N. Kadri, Q. He, A. Leonard, A. Lloret-Villas, and H. Pausch, *ETH Zürich, Zürich, Switzerland*.

5:00 PM OP17 **Transcriptome and histological analysis of skin of Brangus cattle under heat stress conditions.**
P. Alvarez Cecco*[1], M. Balbi[1], M. Bonamy[1], A. Rogberg-Muñoz[2], L. H. Olivera[1], G. Giovambattista[1], and M. E. Fernández[1], [1]*Intituto de Genética Veterinaria (IGEVET), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*Instituto de investigaciones en Producción Animal (INPA), Universidad de Buenos Aires, CONICET, Buenos Aires, Buenos Aires, Argentina*.

5:15 PM **Business meeting.**

Horse Genetics and Genomics

Chair: **Leslie Bickel (1), Tomasz Zabek (2), Veternary Genetics Lab UC Davis, Davis, CA, United States (1), National Research Institute of Animal Production, Balice, Poland (2)**

Daisy

2:00 PM - 5:30 PM

2:00 PM **Invited Workshop Presentation: FAANG Update.**
J.L. Petersen, University of Nebraska-Lincoln, Lincoln, NE, U.S.A.

2:30 PM OP18 **ISAG Bursary Award: The epigenetic landscape of the satellite-free centromere of horse chromosome 11.**
E. Cappelletti*[1], F. Piras[1], L. Sola[1], S. Peng[2], A. Barber[3], M. Santagostino[1], J. Petersen[3], R. Bellone[2,4], C. Finno[2], T. Kalbfleisch[5], E. Bailey[5], S. Nergadze[1], and E. Giulotto[1], [1]*Department of Biology and Biotechnology, University of Pavia, Pavia, Italy*, [2]*School of Veterinary Medicine, Department of Population Health and Reproduction, University of California–Davis, Davis, CA*, [3]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE*, [4]*School of Veterinary Medicine, Veterinary Genetics Laboratory, University of California–Davis, Davis, CA*, [5]*Gluck Equine Research Center, University of Kentucky, Lexington, KY*.

2:45 PM OP19 **Genomics of Thoroughbred stallion subfertility.**
C. Castaneda, R. Juras, B. W. Davis, and T. Raudsepp*, *School of Veterinary Medicine, Texas A&M University, College Station, TX*.

3:00 PM OP20 **Whole-genome trio sequencing to reveal the genetics of equine microphthalmia.**
I. Shutava[1], B. Ekesten[1], C.-J. Rubin[2], S. Mäkeläinen[2], T. Bergström[1], J. Tetens[3], and S. Mikko*[1], [1]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [2]*Uppsala University, Uppsala, Sweden*, [3]*University of Göttingen, Göttingen, Germany*.

3:15 PM OP21 **Changes in the gene expression profile of equine mesenchymal stem cells (MSC) after their allogeneic administration in horses matched or mismatched for the major histocompatibility complex (MHC).**
A. Cequier[1,2], E. Bernad[1], M. García-Martínez[1], B. Serrano[1], F. Vázquez[1,2], A. Romero[1,2], A. Vitoria[1,2], L. Barrachina[1,2], and C. Rodellar*[1], [1]*Laboratorio de Genética Bioquímica LAGENBIO–Instituto Agroalimentario de Aragón–IA2 (Universidad de Zaragoza-CITA)–Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP22 **A missense mutation of BCHE promotes the butyrylcholinesterase activity in Chinese horses.**
Y. Zhang*[1], X. Liu[2,1], and l. Jiang[1], [1]*Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [2]*Centre d'Anthropobiologie et de Génomique de Toulouse, Toulouse, France*.

4:15 PM OP23 **Genomics of gaits in Icelandic horses is more complex than DMRT3.**
H. Sigurdardottir*[1,3], E. Albertsdottir[2], T. Kristjansson[3], M. Rhodin[4], G. Lindgren[1,5], and S. Eriksson[1], [1]*Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, Sweden*, [2]*The Icelandic Agricultural Advisory Centre, Reykjavik, Iceland*, [3]*Agricultural University of Iceland, Faculty of Agricultural Sciences, Hvanneyri, Borgarbyggð, Iceland*, [4]*Swedish University of Agricultural Sciences, Department of Anatomy, Physiology and Biochemistry, Uppsala, Sweden*, [5]*KU Leuven, Livestock Genetics, Department of Biosystems, Leuven, Belgium*.

4:30 PM OP24 **ISAG Bursary Award: Identification of personality-related genes associated with tractability of handling in Thoroughbred horses.**
T. Yokomori*[1], A. Ohnuma[2], T. Tozaki[2], M. Ishimaru[3], F. Sato[3], Y. Hori[4], T. Segawa[1], and I. Takuya[1], [1]*Nihon University, Fujisawa, Kanagawa, Japan*, [2]*Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [3]*Japan Racing Association, Urakawa, Hokkaido, Japan*, [4]*The University of Tokyo, Meguro, Tokyo, Japan*.

4:45 PM OP25 **A resource for documenting and tracking genetic diversity in US Thoroughbred horses.**
J. L. Petersen*[2], T. S. Kalbfleisch[1], J. N. Cullen[3], and E. F. Bailey[1], [1]*University of Kentucky, Lexington, KY*, [2]*University of Nebraska–Lincoln, Lincoln, NE*, [3]*University of Minnesota, Minneapolis, MN*.

5:15 PM OP26 **Construction of genome-wide INDEL database, application to a parentage test using INDELs for horse registration, and a gene-editing test for doping control.**
T. Tozaki*, A. Ohnuma, M. Kikuchi, T. Ishige, H. Kakoi, K.-I. Hirota, and S.-I. Nagata, *Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*.

Microbiomes

Chair: **Jordi Estelle (1), Oscar Gonzalez-Recio (2), INRAE Jouy-en-Josas, France (1); INIA Madrid, Spain (2)**
Freesia
2:00 PM - 5:30 PM

2:00 PM OP27 **Analysis of the gut microbiome sheds insights into breed resilience to challenges of antimicrobial resistance in Dohne Merino sheep.**
A. Khwela*[1,2], E. F. Dzomba[2], R. Pierneef[1], and F. C. Muchadeyi[1], [1]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Gauteng, South Africa*, [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, KwaZulu-Natal, South Africa*.

2:15 PM OP28 **Using a Snakemake workflow for metagenomic analysis of sheep rumen microbiome divergently selected for methane emissions.**
B. Perry, A. Kim, H. Henry, T. Bilton, A. McCulloch, K. McRae, S. Clarke*, P. Janssen, J. McEwan, and S. Rowe, *AgResearch Limited, Lincoln, Canterbury, New Zealand*.

2:30 PM OP29 **ISAG Bursary Award: Study of gut microbes and body metabolism function between Dorper and Tan sheep.**
Y. Ma*[1], X. Yang[1], G. Hua[1], G. Cai[1], X. Li[2], D. Feng[2], and X. Deng[1], [1]*Key Laboratory of Animal Genetics, Breeding, and Reproduction of the Ministry of Agriculture and Beijing Key Laboratory of Animal Genetic Improvement, China Agricultural University, Beijing, China*, [2]*Department of Animal Science and College of Agriculture, Ningxia University, Ningxia Hui Autonomous Region, China*.

2:45 PM OP30 **Comparative metagenomic along the gut biogeography of indigenous chicken.**
A. Tangomo Ngnintedem*[1,2], E. Machuka[3], B. Waweru[3], J.-B. Domelevo Entfellner[3], M. Gitau Gicheha[4], J. Maina Kagira[4], R. Pelle[3], A. Djikeng[5], and C. Keambou Tiambo[6], [1]*Biotechnology and Bioinformatics Research and Training Unit, Department of Anim. Sci, FASA, University of Dschang, Dschang, Cameroon*, [2]*Department of Molecular Biology and Biotechnology, Pan-African University Institute of Basic Sciences, Technology and Innovation, Nairobi, Kenya*, [3]*Biosciences Eastern and Central Africa–International Livestock Research Institute (BecA–ILRI) Hub, Nairobi, Kenya*, [4]*Department of Animal Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya*, [5]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush Campus, Edinburgh, UK*, [6]*Centre for Tropical Livestock Genetics and Health (CTLGH), ILRI Kenya, Nairobi, Kenya*.

3:00 PM OP31 **Bacterial diversity associated with feeding Boschveld chicken with the South African red sorghum variety.**
N. Nemukondeni*[1], C. A. Mbajiorgu[1], A. N. Sebola[1], O. M. Letsoalo[1], T. Mafuna[2], and M. Mabelebele[1], [1]*University of South Africa, Florida, South Africa*, [2]*University of Johannesburg, Auckland Park, South Africa*.

3:05 PM OP32 **Bacterial metagenomics sequencing of chickens fed tannins.**
T. Manyelo*, E. Malematja, N. Sebola, S. Kolobe, and M. Mabelebele, *University of South Africa, Gauteng, South Africa*.

3:10 PM OP33 **High-throughput metagenomic characterization of the fecal microbiota of peste des petits ruminants–infected West African Dwarf goats.**
I. Muritala*[1], B. O. Sodimu[1], M. N. Bemji[1], M. A. Busari[1], G. F. Farayola[1], S. Saleem[2], N. Kumari[3], S. Jaiswal[3], M. A. Iquebal[3], S. M. Ahmad[2], A. O. Sonibare[4], M. Wheto[1], and E. M. Ibeagha-Awemu[5], [1]*Department of Animal Breeding and Genetics, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [2]*Division of Animal Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shuhama, Jammu and Kashmir, India*, [3]*Division of Agricultural Bioinformatics, ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India*, [4]*Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [5]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Québec, Canada*.

3:15 PM OP34 **ISAG Bursary Award: Nasal microbiome diversity in West African Dwarf goats with peste des petits ruminants viral infection.**
I. Muritala*[1], M. N. Bemji[1], M. A. Busari[1], B. O. Sodimu[1], S. M. Ahmad[2], A. Negi[3], S. Jaiswal[3], M. A. Iquebal[3], B. Bhat[2], M. O. Ozoje[1], O. L. Ajayi[4], and E. M. Ibeagha-Awemu[5], [1]*Department of Animal Breeding and Genetics, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [2]*Division of Animal Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shuhama, Jammu and Kashmir, India*, [3]*Division of Agricultural Bioinformatics, ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India*, [4]*Department of Pathology, College of Veterinary Medicine, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [5]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Québec, Canada*.

3:20 PM OP35 **Optimising metagenomic sequencing: A comparative study of ONT Adaptive Sampling strategies to improve microbial DNA recovery.**
E. L. Reinoso-Peláez*[1,2], M. Saura[1], C. González[1], F. Puente-Sánchez[3], and M. Serrano[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*ETSIAAB, Universidad Politécnica de Madrid, Madrid, Spain*, [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden*.

3:25 PM **Questions on Flash Talks.**

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP36 **Possible coevolution of balanced polymorphisms in the pig host and its intestinal microbiome.**
C. Hupperts*[1], M. Mni[1], W. Coppieters[1,2], C. Charlier[1], and M. Georges[1], [1]*Unit of Animal Genomics, GIGA-R and Faculty of Veterinary Medicine, Liège, Liège, Belgium*, [2]*GIGA–Genomics Platform, University of Liège, Liège, Liège, Belgium*.

4:15 PM OP37 **Genetic selection of the host drives gut microbiota enterotypes across generations.**
J. Estellé*[1], C. Larzul[2], M. Borey[1], F. Blanc[1], G. Lemonnier[1], Y. Billon[3], M. Thiam[4], B. Quinquis[4], N. Galleron[4], D. Jardet[3], J. Lecardonnel[3], F. Plaza-Oñate[4], and C. Rogel-Gaillard[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [3]*INRAE, GenESI, Surgères, France*, [4]*Université Paris-Saclay, INRAE, MGP, Jouy-en-Josas, France*.

4:30 PM OP38 **Differential miRNA profile in response to dietary treatment and their possible impact in the host-microbiota genetic regulation.**
T. Porto[1], T. Cardoso[2], J. Bruscadin[1], L. Conteville[2], P. Oliveira[1], G. Mourao[3], L. Coutinho[3], A. Zerlotini[4], J. Reecy[5], and L. Regitano*[2], [1]*Post-graduation Program of Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, Sao Carlos, SP, Brazil*, [2]*Embrapa Southeast Livestock Research Center, Sao Carlos, SP, Brazil*, [3]*Department of Animal Science, University of São Paulo, Piracicaba, SP, Brazil*, [4]*Embrapa Digital Agriculture, Campinas, SP, Brazil*, [5]*Department of Animal Science, Iowa State University, Ames, IA*.

4:45 PM OP39 **Host genomic regions associated with ewes' vaginal microbiota.**
M. Ramon*[1], E. Reinoso-Pelaez[2], M. Saura[2], O. González-Recio[2], C. Gonzalez[2], R. Arias[1], M. Pérez-Guzman[1], I. Beltrán de Heredia[3], J. Calvo[4], and M. Serrano[2], [1]*CERSYRA-IRIAF, Valdepeñas, Ciudad Real, Spain*, [2]*INIA-CSIC, Madrid, Spain*, [3]*NEIKER, Arkaute, Spain*, [4]*CITA-ARAID-IA2, Zaragoza, Aragón, Spain*.

4:50 PM OP40 **Links between gut microbiome functions and feed efficiency in growing pigs fed a conventional or a high-fiber diet.**
A. Cazals[1], O. Zemb[2], V. Déru[2,3], J. Bidanel[4], H. Gilbert[2], and J. Estellé*[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [3]*France Génétique Porc, Le Rheu, France*, [4]*IFIP-Institut du Porc, Le Rheu, France*.

4:55 PM OP41 **Comparison of rumen microbial analysis pipelines based on 16S rRNA gene sequencing.**
X. Ye*, Z. Cai, and M. Lund, *Center for Quantitative Genetics and Genomics, Aarhus University, Aarhus, Denmark*.

5:00 PM OP42 **Exploring links between porcine genome copy number variants, the diversity and composition of pig gut eukaryote and prokaryote microbial communities.**
M. Ballester*[1], D. Crespo-Piazuelo[1], J. Morata[2], L. Ramírez[1], O. González-Rodríguez[1], C. Sebastià[3,4], A. Castelló[3,4], A. Dalmau[5], S. E. Ramos-Onsins[3], K. Alexiou[3], J. M. Folch[3,4], R. Quintanilla[1], and Y. Ramayo-Caldas[1], [1]*IRTA, Torre Marimon, Caldes de Montbui, Spain*, [2]*CNAG-CRG, Baldiri i Reixac 4, Barcelona, Spain*, [3]*CRAG, Campus UAB, Bellaterra, Spain*, [4]*UAB, Bellaterra, Spain*, [5]*IRTA, Monells, Girona, Spain*.

5:05 PM OP43 **Impact of the vaginal microbiota on the pregnancy rate by artificial insemination in three Spanish sheep breeds.**
E. L. Reinoso[1,2], F. Puente-Sánchez[3], C. González[1], J. H. Calvo[4], M. Serrano[1], and M. Saura*[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*ETSIAAB Universidad Politécnica de Madrid, Madrid, Spain*, [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [4]*CITA-IA2, Zaragoza, Spain*.

5:10 PM OP44 **Preliminary results: Bacterial abundance in the microbiome from South African beef faecal samples through 16S rRNA targeted sequencing.**
O. P. Monchusi[1,2], K. P. Montso[2], C. N. Ateba[2], A. A. Zwane[1], and M. M. Makgahlela*[1], [1]*Agricultural Research Council, Old Olifantsfonteing, Irene, Centurion, Gauteng, South Africa*, [2]*North-West University, Mahikeng, South Africa*.

5:15 PM **Questions on Flash Talks.**

5:20 PM **Meeting of Microbiomes Committee.**

Pig Genetics and Genomics

Chair: **Daniel Ciobanu (1), Amanda Warr (2), University of Nebraska Lincoln, Nebraska, United States (1); The Roslin Institute, Edinburgh, United Kingdom (2)**

Hall 8

2:00 PM - 5:30 PM

2:00 PM OP45 **Initiative for African Indigenous Pig Genome Project.**
A. C. Adeola*[1,2], X. Shi[1], X. Liu[3], O. F. Olaniyan[4], C. A. M. S. Djagoun[5], G. Msalya[6], D. H. Mauki[7], N. K. Wanzie[8], G. Niba[9], P. D. Luka[10], S. C. Olaogun[11], V. M. O. Okoro[12], J.-L. Han[13], M.-S. Peng[1,2], Y.-P. Zhang[1,2], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*Sino-Africa Joint Research Centre, Chinese Academy of Sciences, Kunming, Yunnan, China*, [3]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [4]*West Africa Livestock Innovation Centre, Banjul, The Gambia*, [5]*Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin*, [6]*Sokoine University of Agriculture, Morogoro, Tanzania*, [7]*Center for Cancer Immunology, Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences (CAS), Shenzhen, China*, [8]*Department of Zoology, University of Douala, Douala, Cameroon*, [9]*National Centre for Animal Husbandry, Veterinary and Halieutic Training, Jakiri, Cameroon*, [10]*National Veterinary Research Institute, Vom, Nigeria*, [11]*Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria*, [12]*Department of Animal Science and Technology, School of Agriculture and Agricultural Technology, Federal University of Technology, Owerri, Nigeria*, [13]*International Livestock Research Institute, Nairobi, Kenya*.

2:13 PM OP46 **Identification of new transcription factors using eGWAS in four porcine tissues.**
S. Hosseini[1], M. Gòdia[1], M. Derks[1], B. Harlizius[2], O. Madsen[1], and M. Groenen*[1], [1]*Wageningen University & Research, Wageningen, the Netherlands*, [2]*Topigs Norsvin Research Center, Beuningen, the Netherlands*.

2:26 PM OP47 **ISAG Bursary Award: Comprehensive identification of functional DNA elements and 3D chromatin interaction map in the pig genome.**
D. Wang*[1], M. Hu[1], Y. Guo[1], R. Kuang[1], H. Zhou[1], R. Ma[1], Z. Han[1], L. Li[1], H. Peng[1], Z. Xu[1], Y. Zhang[1], M. Zhu[1,3], C. K. Tuggle[4], Y. Zhao[1], S. Zhao[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, Hubei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China*, [4]*Department of Animal Science, Iowa State University, Ames, IA*.

2:39 PM OP48 **Multi-breed, multi-tissue, and multi-omics aiding the quest for key porcine regulators.**
D. Crespo-Piazuelo[1], A. Reverter[2], Y. Ramayo-Caldas[1], R. Quintanilla[1], H. Acloque[3], M.-J. Mercat[4], M. C. A. M. Bink[5], A. E. Huisman[5], and M. Ballester*[1], [1]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Torre Marimon, Caldes de Montbui, Spain*, [2]*CSIRO Agriculture and Food, St. Lucia, Brisbane, Queensland, Australia*, [3]*INRAE GABI, Domaine de Vilvert, Jouy-en-Josas, France*, [4]*IFIP-Institut du Porc and Alliance R&D, La Motte au Vicomte, Le Rheu, France*, [5]*Hendrix Genetics, Boxmeer, the Netherlands*.

2:52 PM OP49 **ISAG Bursary Award: Allele-specific expression in pig genomic makeup and phenotypic implications.**
W.-Y. Yao*[1,2], L. Bai[2], K. Li[2], L. Fang[3], M. A. M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands*, [2]*Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China*, [3]*Center for Quantitative Genetics and Genomics (QGG), Aarhus University, Aarhus, Denmark*.

3:05 PM OP50 **Combined targeted and untargeted metabolomics in pigs coupled with genomic information: Towards a comprehensive genetic characterization of the pig metabolome.**
S. Bovo[1], G. Schiavo[1], F. Fanelli[2], A. Ribani[1], F. Bertolini*[1], M. Gallo[3], G. Galimberti[4], S. Dall'Olio[1], P. Martelli[5], R. Casadio[5], U. Pagotto[2], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Department of Surgical and Medical Sciences, Endocrinology Unit, University of Bologna, Bologna, Italy*, [3]*Associazione Nazionale Allevatori Suini, Roma, Italy*, [4]*Department of Statistical Sciences "Paolo Fortunati," University of Bologna, Bologna, Italy*, [5]*Biocomputing Group, Department of Pharmacy and Biotechnology, University of Bologna, Bologna, Italy*.

3:18 PM OP51 **ISAG Bursary Award: Enhancer-promoter interaction map in the maternal-fetal interface during implantation reveals important regulatory regions and variations in pigs.**
Y. Sun*[1,2], R. Liu[1,2], H. Liang[1,2], K. Han[1,2], F. Wang[1,2], J. Cao[1,2], and M. Yu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China*.

3:31 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:01 PM OP52 **ISAG Bursary Award: On the genetic basis of porcine semen traits: A large-scale genome-wide study on a synthetic line.**
P. Sá*[1], R. Godinho[2], M. Gòdia[1], C. Sevillano[2], B. Harlizius[2], O. Madsen[1], and H. Bovenhuis[1], [1]*Wageningen University and Research, Wageningen, the Netherlands*, [2]*Topigs Norsvin Research Center, Beuningen, the Netherlands*.

4:14 PM OP53 **Towards identification of new genetic determinants for post-weaning diarrhea in piglets.**
E. Ibragimov, E. Ø. Eriksen, J. P. Nielsen, C. B. Jørgensen, M. Fredholm, and P. Karlskov-Mortensen*, *University of Copenhagen, Frederiksberg, Denmark*.

4:27 PM OP54 **Identification of genomic regions associated with fatty acid metabolism across four tissues in pigs.**
J. Liu*[1,2], C. Sebastià[1,2], T. Jové-Juncà[3], R. Quintanilla[3], O. González-Rodríguez[3], M. Passols[1,2], A. Castelló[1,2], A. Sánchez[1,2], M. Ballester[3], and J. M. Folch[1,2], [1]*Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Spain*, [3]*Animal Breeding and Genetics Program, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain*.

4:40 PM OP55 **ISAG Bursary Award: Integrated analysis of genome-wide association studies and 3D epigenomic characteristics reveal the *BMP2* gene regulating loin muscle depth in Yorkshire pigs.**
S. Wan*[1], Y. Miao[2], Y. Zhao[1], S. Zhao[1], X. Xu[1], and T. Xiang[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei Province, China*, [2]*Research Institute of Agricultural Biotechnology, Jingchu University of Technology, Jingmen, Hubei Province, China*.

4:53 PM OP56 **ISAG Bursary Award: Sequence-based GWAS identifies novel loci influencing growth and reproduction traits in pigs.**
A. Boshove*[1], M. F. L. Derks[1,2], B. Harlizius[1], E. F. Knol[1], M. S. Lopes[3], M. van Son[4], and C. A. Sevillano[1], [1]*Topigs Norsvin Research Center, Beuningen, the Netherlands*, [2]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands*, [3]*Topigs Norsvin, Curitiba, Brazil*, [4]*Norsvin SA, Hamar, Norway*.

5:06 PM OP57 **Methods to predict lameness in sows.**
G. A. Rohrer*[1], L. Ostrand[2], L. A. Rempel[1], T. Schmidt[2], and B. Mote[2], [1]*USDA-ARS US Meat Animal Research Center, Clay Center, NE*, [2]*University of Nebraska, Lincoln, NE*.

5:19 PM **Business Meeting.**

OTHER EVENTS

Welcome Reception
Hall 9 - Exhibition Hall
5:30 PM - 8:00 PM

Tuesday, July 4

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions

Plenary Session II: Exploring genomic "big" data
Chair: **Talk 1: Prof N Mapholi & Prof C Gill; Talk 2: Dr J Heon & Dr B Nkhane**
Hall 8
8:30 AM - 11:00 AM

8:30 AM OP58 **Big data integration in the era of animal omics: Current and future challenges.**
L. Fang*, *QGG, Aarhus University, Aarhus, Denmark*.

9:30 AM OP59 **Microbiome solutions for improving the sustainability of cattle production.**
L. Guan*, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Alberta, Canada*.

10:30 AM **Tea/Coffee Break, Exhibition and Poster Viewing.**

International Goat Genome (IGGC)

Chair: **Marcel Amills, Universitat Autonoma de Barcelona, Spain**
Orchid
11:00 AM - 1:00 PM

11:00 AM OP60 **Combining ATAC-Seq and RNA-Seq data to investigate the molecular basis of lactation in goats.**
A. Noce*[1], M. Luigi-Sierra[1], A. Martínez[2], M. Wang[1], M. Macri[2], J. Delgado[2], A. Salama[3], X. Such[3], J. Jordana[3], and M. Amills[1,3], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra, Spain*, [2]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*, [3]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

11:20 AM OP61 **ISAG Bursary Award: Identification of long non-coding RNAs differentially expressed in the mammary gland of lactating and dry goats.**
M. Wang*[1], E. Varela-Martínez[1], M. Luigi-Sierra[1], A. Noce[1], A. Martínez[2], J. Delgado[2], A. Salama[3], X. Such[3], J. Jordana[3], and M. Amills[1,3], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [2]*Departamento de Genética, Universidad de Córdoba, Córdoba, Córdoba, Spain*, [3]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*.

11:40 AM OP62 **Genomic improvement in dairy goats using DNA sequencing.**
A. Caulton*[1], M. Wheeler[2], S. Clarke[1], R. Brauning[1], T. Van Stijn[1], H. Baird[1], R. Anderson[1], B. Foote[3], J. Foote[3], S. Cameron[4], T. Blichfeldt[5], J. Jakobsen[5], K. Dodds[1], and J. McEwan[1], [1]*AgResearch, Mosgiel, Otago, New Zealand*, [2]*AgResearch, Hamilton, Waikato, New Zealand*, [3]*Footes, Hikurangi, Northland, New Zealand*, [4]*Meredith Dairy, Meredith, Victoria, Australia*, [5]*NSG, As, Norway*.

12:00 PM OP63 **Heritability estimates of hematological, serological, morphological and productive traits in Murciano-Granadina goats, using a univariate animal model.**
M. Macrì[1,2], M. Amills[3,4], J. León Jurado[5], L. Gama[6], M. Luigi-Sierra[3], J. Delgado[2], J. Fernández[7], and A. Martínez Martínez*[2], [1]*Animal Breeding Consulting, Córdoba, Spain*, [2]*Universidad de Córdoba, Córdoba, Spain*, [3]*CRAG, CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Spain*, [4]*Universitat Autònoma de Barcelona, Bellaterra, Spain*, [5]*Diputación Provincial de Córdoba, Córdoba, Spain*, [6]*Universidad de Lisboa, Lisboa, Portugal*, [7]*Asociación Nacional de Criadores de Caprino de Raza Murciano-Granadina (CAPRIGRAN), Granada, Spain*.

12:20 PM OP64 **Ascertaining the variability and demographic history of the Canarian goat breeds through the use of genome-wide SNPs data.**
G. Senczuk*[1], M. Macrì[2,3], S. Mastrangelo[4], M. Di Civita[1], M. del Rosario Fresno[5], J. Capote[5], F. Pilla[1], J. V. Delgado[3], M. Amills[6], and A. Martínez[3], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Animal Breeding Consulting S.L, Córdoba, Spain*, [3]*Universidad de Córdoba, Córdoba, Spain*, [4]*Department of Agricultural, Food and Forest Sciences, University of Palermo, Palermo, Italy*, [5]*Instituto Canario de Investigaciones Científicas, Tenerife, Spain*, [6]*CRAG, CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

12:40 PM OP65 **The extreme genotypes of *CSN1S1* gene have a significant effect on milk composition and cheese yield in Carpathian goat.**
V. A. Balteanu*[1], R. K. Sigartau[2], D. Nadolu[3], and A. H. Anghel[4], [1]*University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Institute of Life Sciences, Cluj-Napoca, Cluj, Romania*, [2]*Babes-Bolyai University, Faculty of Mathematics and Computer Science, Cluj-Napoca, Cluj, Romania*, [3]*ICDCOC Palas, Constanta, Constanta, Romania*, [4]*Ovidius University, Constanta, Constanta, Romania*.

OTHER EVENTS

Biosearch Technologies Lunch Symposium:
High-throughput genotyping technologies to accelerate livestock breeding programmes
Hall 8
1:00 PM - 1:45 PM

Lunch Break, Exhibition and Poster Viewing
Hall 9 - Exhibition Hall
1:00 PM - 2:00 PM

SYMPOSIA AND ORAL SESSIONS

J.E.D.I Symposium

Chair: **Ntanganedzeni Mapholi, University of South Africa**
Orchid
1:00 PM - 1:45 PM

1:00 PM OP200 **Decolonizing science: A primer on centering justice, equity, diversity, and inclusion within animal genetics and genomics.**
S. Paez*[1,2], [1]*Rockefeller University, New York, New York*, [2]*New York University, New York, New York.*

Animal Epigenetics

Chair: **George Liu (1) and Luciana Correia de Almeida Regitano (2), (1) USDA/ARS, (2) Embrapa**
Hall 8
2:00 PM - 5:30 PM

2:00 PM OP66 **Annotation of functional variations in four livestock genomes utilizing *cis*-regulatory elements datasets.**
R. Ma*[1], R. Kuang[1], M. Hu[1], Y. Guo[1], D. Wang[1], H. Zhou[1], Z. Han[1], L. Li[1], Z. Xu[1], Y. Zhang[1], Y. Zhao[1], X. Li[1,2], and S. Zhao[1,2], [1]*Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, China*.

2:15 PM OP67 **DNA methylation alteration patterns in repeat elements are similar during subclinical mastitis caused by *Staphylococcus chromogenes* and *Staphylococcus aureus*.**
M. Wang[1,2], N. Bissonnette[1], M. Laterrière[3], D. Gagné[3], and E. M. Ibeagha-Awemu*[1], [1]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Québec, Canada*, [2]*Département des Sciences Animales, Université Laval, Québec, Québec, Canada*, [3]*3Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Québec, Québec, Canada*.

2:30 PM OP68 **Extending Ensembl regulatory annotation to farmed animals.**
G. R. Ilsley*, G. A. Merino, P. R. Branco Lins, M. Perry, D. Urbina-Gomez, and P. Harrison, *European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridge, UK*.

2:45 PM OP69 **Genome-wide acetylation modification of H3K27ac in bovine rumen cell following butyrate exposure.**
X. Kang[1,2], C. Li[2], R. L. Baldwin[1], G. Liu[1], and C. Li*[1], [1]*ARS, USDA, Beltsville, MD*, [2]*Ningxia University, Yinchuan, Ningxia, China*.

3:00 PM OP70 **Long-term selection impacts the rewiring of chromatin structure in chickens.**
D. Guan[1], Y. Wang[1], S. Aggrey[2], R. Okimoto[3], R. Hawken[3], and H. Zhou*[1], [1]*University of California, Davis, Davis, CA*, [2]*University of Georgia, Athens, GA*, [3]*Cobb-Vantress Inc, Siloam Springs, AR*.

3:15 PM OP71 **M6A demethylase ALKBH5 regulates PRRSV replication by manipulating host immune response.**
Q. Su*[1], X. Meng[1], B. Liu[1,2], and X. Zhou[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Wuhan, China*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP72 **ISAG Bursary Award: Relationship between spleen and uterus gene expression and DNA methylation according to developmental stages of pigs.**
B. Ahn*[1], M. Kang[1], M. Choi[1,2], L. Rund[3], L. Shook[3], and C. Park[1], [1]*Department of Stem Cell and Regenerative Biotechnology, Konkuk University, Seoul, Korea*, [2]*Living Systems Institute, University of Exeter, Exeter, United Kingdom*, [3]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL*.

4:15 PM OP73 **RNA methylation as a mechanistic link between epigenotype and phenotype.**
S. Xie[1], B. Murdoch[1], and S. McKay*[2,3], [1]*University of Idaho, Moscow, ID*, [2]*University of Vermont, Burlington, VT*, [3]*University of Missouri, Columbia, MO*.

4:30 PM OP74 **Super-accessible chromatin regions are associated with increased gene transcription and regulation of cell differentiation in mammals.**
M. Hu*[1], Y. Zhao[1], X. Qi[1], H. Zhou[1], Y. Guo[1], L. Li[1], R. Kuang[1], R. Ma[1], G. Sun[4], L. Li[4], M. Zhu[1,3], X. Li[1,3], and S. Zhao[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, Hubei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China*, [4]*College of Biomedicine and Health, Huazhong Agricultural University, Wuhan, Hubei, China*.

4:45 PM OP75 **Beyond the genome: Establishing molecular phenotypes to accelerate adaptation to a changing environment.**
A. Caulton*[1], R. Brauning[1], K. M. McRae[1], K. G. Dodds[1], C. Couldrey[2], P. L. Johnson[1], and S. M. Clarke[1], [1]*AgResearch, Invermay Agricultural Centre, Mosgiel, Otago, New Zealand*, [2]*Livestock Improvement Corporation, Hamilton, New Zealand*.

5:00 PM OP76 **African swine fever infection enhances the host transcriptional regulation of membrane protein-encoding genes mediated by changes in chromatin state.**
X. Qi*[1], Y. Xiang[1], L. Sun[3,4], L. Xing[3], S. Zhang[1], Q. Zhao[1], L. Zhang[1], J. Li[1], P. Zhou[1], Z. Zheng[1], X. Li[1], L. Fu[1,2], G. Peng[3,4], and S. Zhao[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China*, [3]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China*, [4]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China*.

5:15 PM **Business meeting.**

Applied Genetics and Genomics in other Species of Economic Interest

Chair: **Amparo Martinez (1), Marcela Martinez (2), Animal Breeding Consulting, S.L., Cordoba, Spain (1); Laboratorio De Genetica AplicadaSociedad Rural Argentina, Buenos Aires, Argentina (2)**
Freesia
2:00 PM - 5:30 PM

2:00 PM **Welcoming remarks.**

2:10 PM **Pig CT Discussion.**

2:20 PM **Dromedary CT Discussion.**

2:30 PM **Alpaca/Llama CT Discussion.**

2:40 PM **Pigeon CT Discussion.**

2:50 PM **Sheep CT Discussion.**

3:00 PM **Goat CT Discussion.**

3:10 PM **A future buffalos CT proposal.**

3:20 PM **Election of committee and any other business.**

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP77 **ISAG Bursary Award: The development of a 61K Illumina SNP chip for dromedaries under the frame of the 2019 Agricultural Greater Good (AGG) initiative.**
M. Di Civita*[1], G. Senczuk[1], S. Bruno[2], V. Landi[3], S. Brooks[4], F. Almathen[5,6], B. Faye[7], S. B. S. Gaouar[8], M. Piro[9], K. S. Kim[10], H. Dadi[11], P. C. Iglesias[12], H. Al-Haddad[13], M. Al-Abri[14], F. Pilla[1], X. David[15], A. Eggen[15], P. Burger[16], and E. Ciani[2], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Department of Biosciences, Biotechnologies and Environment, University of Bari "Aldo Moro," QQBari, Italy*, [3]*Department of Veterinary Medicine, University of Bari "Aldo Moro," QQValenzano, Bari, Italy*, [4]*Department of Animal Sciences, University of Florida, Gainesville, FL*, [5]*Department of Public Health, College of Veterinary Medicine, King Faisal University, Al-Ahsa, Saudi Arabia*, [6]*Camel Research Center, King Faisal University, Al-Ahsa, Saudi Arabia*, [7]*CIRAD-ES, UMR SELMET, Montpellier, France*, [8]*Department of Biology, Abou Bakr Belkaid University of Tlemcen, Tlemcen, Algeria*, [9]*Department of Medicine, Surgery and Reproduction, Institut Agronomique et Vétérinaire Hassan II, Rabat BP, Morocco*, [10]*Department of Animal Sciences, Chungbuk National University, Chungbuk, Korea*, [11]*Ethiopian Biotechnology Institute (EBTi), Addis Ababa, Etiopia*, [12]*Department of Genetics, Faculty of Veterinary Sciences, University of Córdoba, Córdoba, Spain*, [13]*Department of Biological Sciences, Kuwait University, Kuwait City, Kuwait*, [14]*Department of Animal and Veterinary Sciences, Sultan Qaboos University, Muscat, Oman*, [15]*Illumina, Agrigenomics, Evry, France*, [16]*Research Institute of Wildlife Ecology, Vetmeduni, Vienna, Austria.*

4:15 PM OP78 **Selection of an ovine SNP parentage panel for consideration as the ISAG comparison test panel.**
R. Ferretti*[1], K. Schutt[2], M. Dowling[2], J. Qiu[1], and R. Tait[1], [1]*Neogen GeneSeek Operations, Lincoln, NE*, [2]*Neogen Australasia, Ipswitch, QLD, Australia*.

4:30 PM OP79 **High-throughput detection of single nucleotide polymorphisms with flexible content panels.**
S. Camiolo[1], J. Yeakley[1], E. Clark[2], B. Seligmann[1], and J. McComb*[1], [1]*BioSpyder Technologies Inc, Carlsbad, CA*, [2]*Zoetis Inc, Kalamazoo, MI*.

4:45 PM OP80 **Genetic differentiation of *Camelus bactrianus* from Kazakhstan.**
K. Dossybayev*[1,2], D. Ualiyeva[1], M. Amandykova[1,2], T. Kapasuly[1,2], A. Mussayeva[1], Z. Orazymbetova[1], G. Shaltenbay[1,2], and B. Bekmanov[1,2], [1]*Laboratory of Genetics and Cytogenetics, Institute of Genetics and Physiology, Almaty, Kazakhstan*, [2]*Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan*.

5:00 PM OP81 **Genetic diversity and population structure among Central European native sheep breeds using microsatellite markers.**
Z. Sztankoova, M. Milerski, M. Brzáková, J. Rychtárová, and J. Kyselova*, *Institute of Animal Science, Praha-Uhrineves, Czech Republic*.

5:15 PM OP82 **Genome-wide association study between copy number variations and economically important traits in American mink.**
P. Davoudi*[1], D. Ngoc Do[1], B. Rathgeber[1], S. Colombo[1], M. Sargolzaei[2,3], G. Plastow[4], Z. Wang[4], G. Hu[1], S. Valipour[1], and Y. Miar[1], [1]*Department of Animal Science and Aquaculture, Dalhousie University, Truro, NS, Canada*, [2]*Department of Pathobiology, University of Guelph, Guelph, ON, Canada*, [3]*Select Sires Inc, Plain City, OH*, [4]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

Domestic Animal Sequencing and Annotation

Chair: **Brenda Murdoch, University of Idaho, Moscow, Idaho, United States**
Orchid
2:00 PM - 5:30 PM

2:00 PM OP83 **Invited Workshop Presentation: The human genome is finally complete, now what?**
S. Koren*, *National Human Genome Research Institute, National Institutes of Health, Bethesda, MD*.

2:40 PM OP84 **ISAG Bursary Award: An organism-wide ATAC-Seq peak catalogue for the bovine and its use to identify regulatory variants.**
C. Yuan*[1], L. Tang[1], T. Lopdell[2], C. Oget-Ebrad[1], G. Costa Monteiro Moreira[1], J. L. Gualdron[1], Z. Cheng[3], M. Salavati[3], D. C. Wathes[3], M. A. Crowe[4], W. Coppieters[1], C. Charlier[1], T. Druet[1], M. Georges[1], H. Takeda[1], [1]*GIGA Institute, University of Liège, Liège, Belgium*, [2]*Livestock Improvement Corporation, Hamilton, New Zealand*, [3]*Royal Veterinary College, Herts, UK*, [4]*School of Veterinary Medicine, University College Dublin, Dublin, Ireland*.

3:00 PM OP85 **Development of genomic tools for American mink (*Neogale vison*).**
Y. Miar*, *Dalhousie University, Truro, Nova Scotia, Canada*.

3:15 PM OP86 **ISAG Bursary Award: Identification and comparison of plant-derived miRNAs based on massive public data.**
H. Liu*[1], P. Xu[1], Y. Liao[1], C. Li[1], J. Dou[1], Y. Wang[1], Z. Tang[1], J. Xu[1], D. Yin[1], S. Zhu[1], L. Yin[1,2], M. Yu[1], S. Zhao[1,2], X. Liu[1,2], Y. Fu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, China*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP87 **Overview of Ruminant T2T Consortium.**
B. M. Murdoch*[1], S. D. McKay[2], B. D. Rosen[3], and T. P. L. Smith[4], [1]*University of Idaho, Moscow, ID*, [2]*University of Missouri, Columbia, MO*, [3]*USDA, Agricultural Research Service, Animal Genomics and Improvement Laboratory, Beltsville Agricultural Research Center, Beltsville, MD*, [4]*USDA, Agricultural Research Service, Genetics and Animal Breeding, Clay Center, NE*.

4:20 PM OP88 **Discovering the missing structural variation in the bovine genome.**
A. Chamberlain*[1,2], T. Nguyen[1], J. Wang[1], and I. Macleod[1,2], [1]*Agriculture Victoria, Bundoora, Victoria, Australia*, [2]*La Trobe University, Bundoora, Victoria, Australia*.

4:40 PM OP89 **Discovery of deleterious genetic variants in farmed animals.**
X. R. Arias[1], J. L. Petersen[2], B. M. Murdoch[3], F. M. McCarthy[4], and T. S. Kalbfleisch*[1], [1]*University of Kentucky, Lexington, KY*, [2]*University of Nebraska–Lincoln, Lincoln, NE*, [3]*University of Idaho, Moscow, ID*, [4]*University of Arizona, Tucson, AZ*.

5:00 PM OP90 **Assessment of different enrichment methods to characterize bovine circRNAs.**
Y. Wang[1,2], J. Wang[3], R. J. Gruninger[4], T. A. McAllister[4], and L. L. Guan*[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [2]*Institute of Animal Genetics and Breeding, College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, Sichuan, China*, [3]*State Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, College of Animal Science and Technology, Guangxi University, Nanning, Guangxi, China*, [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*.

5:15 PM **Business meeting.**

Genetics of Immune Response and Disease Resistance

Chair: **Christopher Tuggle, Iowa State University Ames, Iowa, United States**

Daisy

2:00 PM - 5:30 PM

2:00 PM OP91 **Invited Workshop Presentation: Uncovering the basis of natural tolerance to African cattle diseases using integrative omics.**
J. Prendergast*, *Roslin Institute, University of Edinburgh, Scotland, UK*.

2:40 PM OP92 **ISAG Bursary Award: IUIS-VIC Travel Award 1: Transcriptomic signatures of peripheral immune cells associated with immune competence traits in Australian Angus cattle.**
A. Wilson*[1], P. Alexandre[2], T. Legrand[2], S. Denman[2], T. Reverter[2], C. Stewart[1], and R. Farr[1], [1]*Commonwealth Scientific and Industrial Research Organization, East Geelong, VIC, Australia*, [2]*Commonwealth Scientific and Industrial Research Organization, St Lucia, QLD, Australia*.

2:50 PM OP93 **Association of variants in antibacterial *TLR* genes with reproductive traits in Czech Simmental cattle.**
K. Novak*[1], K. Samake[2], and M. Bjelka[3], [1]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*, [2]*Charles University, Prague, Czech Republic*, [3]*Breeding Company CHD Impuls, Bohdalec, Czech Republic*.

2:58 PM OP94 **ISAG Bursary Award: CRISPR-SpRY-mediated base-editing screening identifies TMEM41B amino acids that are critical for transmissible gastroenteritis virus replication in pig.**
Y. Zhou*[1], J. Zhang[1], Y. Zhang[1], X. Li[1,3], S. Xie[1,2], C. Zhao[1,2], and S. Zhao[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hu Bei, China*, [2]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hu Bei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hu Bei, China*.

3:10 PM OP95 **Genome-scale CRISPR screen identifies TRIM2 and SLC35A1 associated with porcine epidemic diarrhea virus infection.**
H. Liu[1], J. Wang[2], Z. Guo[1], X. Zeng[2], Y. Yang[1], S. Li[1], X. Li[1,4], S. Zhao[1,3], C. Wang[2], and S. Xie*[1,3], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei, P. R. China*, [2]*Key Laboratory of Pig Molecular Quantitative Genetics of Anhui Academy of Agricultural Sciences, Livestock and Poultry Epidemic Diseases Research Center of Anhui Province, Anhui Provincial Key Laboratory of Livestock and Poultry Product Safety Engineering, Hefei, Anhui, P. R. China*, [3]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, P. R. China*, [4]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hubei, P. R. China*.

3:22 PM OP96 **ISAG Bursary Award: LncRNA446 regulates tight junctions by inhibiting the ubiquitinated degradation of Alix after porcine epidemic diarrhea virus infection.**
Y. Xiao*, W. Qin, H. Wang, and W. Bao, *Yangzhou University, Yangzhou, Jiangsu, China*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP97 **ISAG Bursary Award: Multi-omics integration analysis deciphering genetic basis of host resistance to PRRSV.**
Q. Wu*[1], T. Zhang[1], X. Wu[1], X. Zhou[1,2], and B. Liu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Wuhan, China*.

4:12 PM OP98 **Superior survivability of *GBP1* and *GBP5* heterozygous pigs undergoing porcine respiratory syndrome outbreaks.**
R. Pena*[1], K. Keutgens[2], and L. Fraile[1], [1]*Universitat de Lleida-AGROTECNIO Centre, Lleida, Spain*, [2]*PXL University of Applied Sciences and Arts, Hasselt, Belgium*.

4:20 PM OP99 **IUIS-VIC Travel Award 2: Due to their improved immunity, disease-resistant common carp fish are also less infective.**
B. Dorfman*, E. Marcos-Hadad, R. Tadmor-Levi, and L. David, *Department of Animal Sciences, R.H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Israel*.

4:30 PM OP100 **ISAG Bursary Award: Functional diversity of Toll signaling pathway in Czech Simmental cattle with respect to health and resilience traits.**
K. Samake*[1], T. Valcikova[2], M. Bjelka[3], and K. Novak[4], [1]*Charles University, Prague, Czech Republic*, [2]*Czech University of Life Sciences, Prague, Czech Republic*, [3]*Breeding Company CHD Impuls, Bohdalec, Czech Republic*, [4]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*.

4:45 PM OP101 **ISAG Bursary Award: Genomic markers associated with immune traits in Sasso chickens raised in Ethiopia.**
M. Girma*[1,2], M. Katrina[3], S. Kate[3], W. Esatu[2], B. Solomon[2], T. Dessie[2], P. Androniki[3,4], V. Lonneke[3], H. Olivier[2,5], B. Georgios[3,6], and M. Dikeledi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Florida, South Africa*, [2]*CTLGH-LiveGene, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [3]*Centre for Tropical Livestock Genetics and Health, The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK*, [4]*The Royal Veterinary College, Hawkshead Lane, Hatfield, Hertfordshire, UK*, [5]*Cells, Organisms and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, UK*, [6]*Scotland's Rural College (SRUC), Animal and Veterinary Sciences, Easter Bush, Midlothian, UK*.

4:57 PM OP102 **ISAG Bursary Award: Assessment of haemagglutination titre and serum lysozyme concentration in Nigerian indigenous chicken genotypes.**
U. Akpan*, A. S. Adenaike, M. I. Takeet, A. A. Bello-Ibiyemi, and C. O. N. Ikeobi, *Federal University of Agriculture, Abeokuta, Ogun State, Nigeria*.

5:05 PM OP103 **Exploring, evaluating, and quantifying the mammalian alveolar macrophage response to intracellular mycobacterial pathogens using an integrative multi-omics approach.**
T. J. Hall[1], M. Mittermite[2], J. A. Browne[1], G. P. McHugo[1], J. F. O'Grady[1], E. L. Clark[3], M. Salavati[3,4], S. V. Gordon[2,5], and D. E. MacHugh*[1,5], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*, [3]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, United Kingdom*, [4]*Dairy Research and Innovation Centre, SRUC South and West Faculty, Barony Campus, Parkgate, Dumfries, Scotland, United Kingdom*, [5]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*.

5:17 PM **Genetics of Immune Response and Disease Resistance Business Meeting.**

ISAG-FAO Genetic Diversity

Chair: **Juha Kantanen (1), Catarina Ginja (2), Natural Resources Institute Finland, Jokioinen, Finland, (1); CIBIO-InBIO, Universidade do Porto, Porto, Portugal (2)**

Nerina

2:00 PM - 6:00 PM

2:00 PM OP104 **Genomic tools for the monitoring of genetic diversity.**
P. Boettcher*[1], R. Baumung[1], P. Burger[2], L. Colli[3], I. Curik[4], G. Leroy[1], C. Looft[5], A. Manunza[6], G. Mészáros[7], D. Ouedraogo[8], B. Rosen[9], A. Stella[6], Y. Utsunomiya[10], J. Windig[11], J. Soelkner[7], [1]*Food and Agriculture Organization of the UN, Rome, RM, Italy*, [2]*University of Veterinary Medicine Vienna, Vienna, WI, Austria*, [3]*Università Cattolica del Sacro Cuore, Piacenza, PC, Italy*, [4]*University of Zagreb, Zagreb, Croatia*, [5]*University of Applied Science Neubrandenburg, Neubrandenburg, MV, Germany*, [6]*IBBA-CNR, Milan, MI, Italy*, [7]*BOKU, Vienna, WI, Austria*, [8]*Joseph KI-ZERBO University, Ouagadougou, KAD, Burkina Faso*, [9]*United States Department of Agriculture, Beltsville, MD*, [10]*São Paulo State University, São Paulo, SP, Brazil*, [11]*Wageningen University and Research, Wageningen, GE, the Netherlands*.

2:15 PM OP105 **Genetic characterization of deleterious alleles in traditional cattle populations in Europe and Africa.**
R. Crooijmans*[1], R. Gonzalez-Prendes[1], M. Derks[1], N. Ghanem[2], C. Ginja[3], D. Kugonza[4], L. Makgahlela[5], and K. Juha[6], [1]*Wageningen University and Research, Animal Breeding and Genomics, Wageningen, the Netherlands*, [2]*University of Cairo, Animal Reproduction Department, Cairo, Egypt*, [3]*University of Porto, Centro de Investigacão em Biodiversidade e Resursos Genéticos, Vairão, Portugal*, [4]*Makerere University, Animal Breeding and Genetics, Kampala, Uganda*, [5]*Agricultural Research Council, Animal Breeding and Genetics, Pretoria, South Africa*, [6]*Natural Resources Institute Finland, Jokioinen, Finland*.

2:30 PM OP106 **Genetic structure of Criollo sheep populations with Iberian and African breeds.**
J. Cappello[1,2], M. Revidatti*[1,2], S. De la Rosa[1,2], V. Morales[1,2], E. Tejerina[1,2], BiOvis Consortium[2], and A. Martínez[2,3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional del Nordeste, Corrientes, Argentina*, [2]*Red CONBIAND, Córdoba, España*, [3]*Facultad de Veterinaria, Universidad de Córdoba, Córdoba, España*.

2:45 PM OP107 **ISAG Bursary Award: An insight into whole-genome resequencing data of Indian native goats with global breeds reveals high within-breed genetic diversity and distinct population structure.**
N. Balasubramaniam*[1,2], S. Dixit[2], S. Singh[2], S. Koloi[1,2], and I. Ganguly[2], [1]*ICAR-National Dairy Research Institute, Karnal, Haryana, India*, [2]*ICAR-National Bureau of Animal Genetic Resources, Karnal, Haryana, India*.

3:00 PM OP108 **Differences in effective population sizes and breed contributions to genetic variation in Estonian farm animal breeds.**
E. Sild*, S. Värv, T. Põlluäär, H. Viinalass, and T. Kaart, *Estonian University of Life Sciences, Institute of Veterinary Medicine and Animal Sciences, Tartu, Estonia*.

3:15 PM OP109 **Genetic diversity of Clydesdale and Shire draft horses with implications for management.**
J. L. Petersen*, A. M. Barber, A. M. Fuller, and I. Grazian, *University of Nebraska–Lincoln, Lincoln, NE*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP110 **History and genetic diversity of African sheep: Perpendicular contrasts of phenotypes and genomic diversity.**
A. Da Silva[1], A. Ahbara[2], S. Ben Jemaa[3], Y. Cao[4], E. Ciani[5], E. Dzomba[6], O. Hanotte[7], S. Mastrangelo[8], A. Missohou[9], A. Molotsi[10], A. Muchadeyi[11], J. Mwacharo[12], M.-L. Li[4], S. Hall[13], J. Lenstra*[14], [1]*PEREINE/E2LIM, Faculty of Science and Technics, Limoges, France*, [2]*Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya*, [3]*Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Université de Carthage, Ariana, Tunisia*, [4]*CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing, China*, [5]*Department of Biosciences, Biotechnologies and Biopharmaceutics, University of Bari "Aldo Moro," QQBari, Italy*, [6]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa*, [7]*School of Life Sciences, University of Nottingham, Nottingham, UK*, [8]*Dipartimento Scienze Agrarie, Alimentari e Forestali, University of Palermo, Palermo, Italy*, [9]*Animal Production and Nutrition Unit, Inter-State School of Veterinary Science and Medicine (EISMV), Dakar, Senegal*, [10]*Department of Animal Sciences, University of Stellenbosch, Matieland, Stellenbosch, South Africa*, [11]*Agricultural Research Council, Biotechnology, Platform, Onderstepoort, South Africa*, [12]*International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [13]*Department of Environmental Protection and Landscape, Estonian University of Life Sciences, Tartu, Estonia*, [14]*Faculty of Veterinary Medicine, Utrecht University, Utrecht, Utrecht, the Netherlands*.

4:15 PM OP111 **An archaeogenomics study of Iron Age cattle from Althiburos, Tunisia.**
C. Ginja*[1], S. Guimarães[1], R. da Fonseca[2], R. Rasteiro[3], R. Rodríguez-Varela[4], L. G. Simões[5], C. Sarmento[1], M. Carme Belarte[6], N. Kallala[7], J. Ramon Torres[8], J. Sanmartí[9], A. M. Arruda[10], C. Detry[10], S. Davis[11], J. Matos[12,13], A. Götherström[4], A. E. Pires[1,14], S. Valenzuela-Lamas[10,15], [1]*BIOPOLIS/CIBIO/InBIO, Universidade do Porto, Vairão, Portugal*, [2]*GLOBE Institute, University of Copenhagen, Copenhagen, Denmark*, [3]*Bristol Medical School, University of Bristol, Bristol, UK*, [4]*CPG-Centre for Palaeogenetics, Stockholm University, Stockholm, Sweden*, [5]*Human Evolution, Department of Organismal Biology, Uppsala University, Uppsala, Sweden*, [6]*ICREA-ICAC, Institut Català de Recerca i Estudis Avançats i d'Arqueologia Clàssica, Barcelona, Spain*, [7]*INP, Institute National du Patrimoine, Tunis, Tunisia*, [8]*Consell Balear d'Eivissa, Eivissa, Balearic Islands, Spain*, [9]*Departament de Prehistòria, Història Antiga i Arqueologia, Universitat de Barcelona, Barcelona, Spain*, [10]*UNIARQ, Centro de Arqueologia da Universidade de Lisboa, Faculdade de Letras da Universidade de Lisboa, Lisboa, Portugal*, [11]*LARC/DGPC, Laboratório de Arqueociências, Direcção Geral do Património Cultural, Lisboa, Portugal*, [12]*Unidade Estratégica de Investigação e Serviços de Biotecnologia e Recursos Genéticos, Instituto Nacional de Investigação Agrária e Veterinária, I.P, Oeiras, Portugal*, [13]*CE3C, Centre for Ecology, Evolution and Environmental Changes, Universidade de Lisboa, Lisboa, Portugal*, [14]*Faculdade de Medicina Veterinária, Universidade Lusófona, Lisboa, Portugal*, [15]*CSIC-IMF, Archaeology of Social Dynamics, Consejo Superior de Investigaciones Científicas-Institució Milà i Fontanals d'Humanitats, Barcelona, Spain*.

4:30 PM OP112 **ISAG Bursary Award: Temporal changes in genomic diversity of the northernmost cattle populations in Europe.**
M. Weldenegodguad*[1], M. Kjetså[2], A. Blauer[3], A. M. Johansson[4], C. Sarmento[5], S. Guimarães[5], C. Ginja[5], M. Honkatukia[2], and J. Kantanen[1], [1]*Natural Resources Institute Finland, Jokioinen, Finland*, [2]*NordGen–Nordic Genetic Resource Center, Ås, Norway*, [3]*University of Turku, Turku, Finland*, [4]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [5]*BIOPOLIS-CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal*.

4:45 PM OP113 **ISAG Bursary Award: Admixed ancestry or independent race: A phylogenetic meta-analysis on the phylogeography of Philippine chickens.**
C. Godinez*[1,2], J. Layos[2,3], Y. Yamamoto[2], T. Kunieda[4], and M. Nishibori[2,1], [1]*Department of Animal Science, College of Agriculture and Food Science, Visayas State University, Visca, Baybay City, Leyte, Philippines*, [2]*Laboratory of Animal Genetics, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*, [3]*College of Agriculture and Forestry, Capiz State University, Burias, Mambusao, Capiz, Philippines*, [4]*Faculty of Veterinary Medicine, Okayama University of Science, Imabari, Ehime, Japan*.

5:00 PM OP114 **ISAG Bursary Award: Multiple origins and genetic diversity of Philippine native pigs.**
J. B. Banayo*[1,2], K. L. V. Manese[2], K. O. Furusho[2], A. J. Salces[2], and T. Yamagata[1], [1]*Nagoya University, Chikusa, Nagoya, Japan*, [2]*University of the Philippines Los Baños, Laguna, Philippines*.

5:15 PM OP115 **ISAG Bursary Award: The first *Rangifer tarandus* Y chromosomal phylogeny.**
E. Bozlak*[1,2], K. Pokharel[3], M. Weldenegodguad[3], A. Paasivaara[3], J. Kantanen[3], and B. Wallner[1], [1]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [2]*Vienna Graduate School of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*.

5:30 PM OP116 **ISAG Bursary Award: Adipose gene expression profiles of four cattle breeds highlight selective pressures and tissue functions.**
D. Ruvinskiy*[1], K. Pokharel[1], A. Amaral[2], M. Weldenegodguad[1], M. Honkatukia[1,3], H. Lindberg[1], J. Peippo[1,3], P. Soppela[4], P. Uimari[5], C. Ginja[6], and J. Kantanen[1], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*CIISA–Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal*, [3]*Nordic Genetic Resources Center, Ås, Norway*, [4]*Arctic Centre, University of Lapland, Rovaniemi, Finland*, [5]*Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland*, [6]*BIOPOLIS-CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*.

5:45 PM OP117 **Reference genome of the native Finnhorse as a tool to study the adaptation of northern Eurasian horse breeds.**
K. Pokharel*[1], M. Honkatukia[1,2], C. Ginja[3], M. Weldenegodguad[1], J. Peippo[1,2], H. Lindeberg[4], T. Reilas[1], and J. Kantanen[1], [1]*Natural Resources Institute Finland, Jokioinen, Finland*, [2]*NordGen–Nordic Genetic Resource Center, Ås, Norway*, [3]*Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal*, [4]*Natural Resources Institute Finland, Maaninka, Finland*.

Animal Genetic Testing Standardization

Chair: **Leslie Lyons, University of Missouri - Columbia, United States**
Orchid
5:30 PM - 7:30 PM

5:30 PM **Discussion of new workshop.**

OTHER EVENTS

Illumina Workshop—Followed by cocktail reception in the exhibition hall (Hall 9)
Hall 8
6:00 PM - 8:00 PM

ISAG-FAO Advisory Group on Animal Genetic Diversity Business Meeting
Nerina
6:00 PM - 7:30 PM

Wednesday, July 5

SYMPOSIA AND ORAL SESSIONS

Words of Wisdom – Engaging with Future Generations Workshop

Chair: **Susan Lamont (1), & Japie Van der Westuizen (2),**
(1) Department of Animal Science, Iowa State University, (2) SA Stud book Association
Freesia
8:30 AM - 10:30 AM

8:30 AM **Welcome and introduction.**

8:40 AM **Experiences in poultry genetics and the development of the field during your career.**
Samuel Aggrey, Department of Poultry Science, University of Georgia.

9:00 AM **Experiences in running livestock genetic/genomics projects in different countries.**
Olivier Hanotte, International Livestock Research Institute (ILRI.

9:20 AM **How I found my passion for molecular genetics and lipid metabolism.**
Cynthia Bottema, School of Animal & Veterinary Sciences, University of Adelaide.

9:40 AM **Diversity in Science.**
Susan Lamont, Department of Animal Science, Iowa State University.

10:00 AM **Panel Discussion (Speakers & Moderators).**

Applied Genetics of Companion Animals

Chair: **Peter Dovc (1), Jiansheng Qiu (2), (1) University of Ljubljana, (2) Neogen Genomics**
Orchid
8:30 AM - 10:30 AM

8:30 AM OP118 **Invited Workshop Presentation: Using dog genomic resources in museomics: An assessment of dog introgression into the Iberian wolf genome.**
R. Godinho*, *CIBIO-InBIO, Universidade do Porto, Campus de Vairao, Vairao, Portugal*.

9:00 AM OP119 **Obligatory testing in dogs: Input from breeders and organizations.**
E. Beckers*, N. Buys, and S. Janssens, *Center for Animal Breeding and Genetics, KU Leuven, Leuven, Belgium*.

9:15 AM OP120 **AgriseqPI 1.0: Reporting utility for SNP-based parentage determination with targeted genotyping by sequencing panels.**
S. Chadaram*[1], A. Burrell[1], K. R. Gujjula[1], C. Carrasco[1], S. Daly[3], S. Udumudi[2], N. Anjuri[2], V. H. Kema[2], and A. Udumudi[2], [1]*Thermo Fisher Scientific, Austin, TX*, [2]*ATS GeneTech Pvt, Ltd, Hyderabad, Telangana, India*, [3]*Thermo Fisher Scientific, Lissieu, Lyon, France*.

9:30 AM **Cat Comparison Test.**

9:55 AM **Dog Comparison Test.**

10:20 AM **Workshop Business Meeting and Elections.**

Comparative MHC Genetics

Chair: **Jun Heon Lee, Chungnam National University**

Daisy

8:30 AM - 10:30 AM

8:30 AM OP121 **MHC haplotype diversity in the main equine breeds of the Iberian Peninsula.**
M. García-Martínez[1], A. Cequier[1,2], E. Bernad[1], B. Serrano[1], A. Romero[2,1], F. Vázquez[2,1], A. Vitoria[2,1], S. Fuente[2,1], C. Cons[1], C. Rodellar*[1], and L. Barrachina[1,2], [1]*Laboratorio de Genética Bioquímica LAGENBIO–Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA)–Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

8:45 AM OP122 **Successful reduction of proviral load by a novel bovine leukemia virus vaccine targeting cattle carrying susceptible bovine leukocyte antigen (BoLA)-*DRB3* allele.**
Y. Aida*[1,2], S.-N. Takeshima[2,3], L. Bai[2,4], J. Kim[2], Y. Matsumoto[2], R. Matsuura[1,2], and J. Kohara[5], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Viral Infectious Diseases Unit, RIKEN, Saitama, Japan*, [3]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*, [4]*Graduate School of Science and Engineering, Iwate University, Iwate, Japan*, [5]*Animal Health Group, Animal Research Center, Hokkaido Research Organization, Hokkaido, Japan*.

9:00 AM OP123 **A multi-omics approach to provide complete genomic information on long-debated genes in birds.**
Q.-S. Zhao*[1], F. Zhu[1], Z.-T. Yin[1], Y.-X. Sun[1], Y.-C. Jie[1], J. Smith[2], L.-W. Shao[1], N. Yang[1], and Z.-C. Hou[1], [1]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, MARA; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*The Roslin Institute & R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK*.

9:15 AM OP124 **Analysis of the genetic diversity of swine leukocyte antigen 1-linked olfactory receptor genes and analysis of correlation with reported porcine testicular expression levels.**
M. Kang*, B. Ahn, S. Youk, and C. Park, *Department of Stem Cell And Regenerative Biotechnology Graduate School of Konkuk University, Seoul, Republic of Korea*.

9:30 AM OP125 **Association of the *IRAK1* gene polymorphism with health, milk and exterior traits in cattle.**
L. Tichý*[1,2], V. Šteiger[1], L. Zavadilová[2], D. Schröffelová[1], J. Kyselová[2], M. Pribánová[1], L. Vostrý[2], J. Kucera[1], and Z. Sztankóová[2], [1]*Czech Moravian Breeders' Corporation, Hradištko, Czech Republic, Czech Republic*, [2]*Institute of Animal Science, Prague-Uhríneves, Czech Republic, Czech Republic*.

9:45 AM OP126 **Integration of information from multiple gene expression and genome-wide association studies on host resistance of cattle to infestation with *Rhipicephalus microplus* ticks.**
K. Chooyoung*, B. Mable, and N. Jonsson, *School of Biodiversity, One Health and Veterinary Medicine College of Medical, Veterinary and Life Sciences University of Glasgow, Glasgow, United Kingdom*.

10:00 AM OP127 **Investigating the role of β-globin in the response to mycotoxin exposure in sheep.**
K. McRae[1], E. Willems[2], A. Thomas[2], R. Clarke[1], J. Plowman[2], E. Maes[2], S. Clarke*[1], and P. Johnson[1], [1]*AgResearch Ltd, Mosgiel, New Zealand*, [2]*AgResearch Ltd, Lincoln, New Zealand*.

10:15 AM **General Discussion.**

Genome Edited Animals

Chair: **Peter Kalds, International Joint Agriculture Research Center for Animal Bio-Breeding, Ministry of Agriculture and Rural Affairs/Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China**

Hall 8

8:30 AM - 10:15 AM

8:30 AM OP128 **Evaluation of the resistance of Liang Guang Small Spotted pigs with partial deletion of the CD163 SRCR5 domain to porcine reproductive and respiratory syndrome virus 2 infection.**
Y. Wu*, X. Liu, Y. Chen, and Z. He, *School of Life Sciences, Sun Yat-sen University, Guangzhou, Guangdong, China*.

OP129 **Withdrawn**

8:45 AM OP130 **Rethinking the genetic basis of pregnancy recognition in ruminants: Pregnancy in type I interferon receptor (*IFNAR2*) knockout sheep.**
C. J. Davies*[1,2], E. K. Peterson[1,2], M. J. Brothers[1,2], A. J. Thomas[1,2], H. M. Rutigliano[1], Y.-M. Lee[1], and I. A. Polejaeva[1], [1]*Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, UT*, [2]*Center for Integrated Biosystems, Utah State University, Logan, UT*.

9:00 AM OP131 **Validation of the *PDGFD* gene function in sheep tail formation using base editing-induced start codon silencing.**
P. Kalds*[1,2], S. Zhou[1,3], S. Huang[1], K. Sun[1], Y. Gao[1], J. Han[4,5], Y. Chen[1], and X. Wang[1], [1]*Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China*, [2]*Department of Animal and Poultry Production, Faculty of Environmental Agricultural Sciences, Arish University, El-Arish, Egypt*, [3]*College of Veterinary Medicine, Northwest A&F University, Yangling, China*, [4]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [5]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Nairobi, Kenya*.

9:15 AM OP132 **ISAG Bursary Award: Field-deployable nucleic acid detection with RAVI-CRISPR.**
D. Tao[1], B. Xu[1], S. Li[1], C. Zhao[1], S. Zhao[1,3], X. Li[1,2], and S. Xie*[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China*.

9:30 AM OP133 **ISAG Bursary Award: sgRNAcas9-AI: A program for prediction of CRISPR/Cas9 and its variant sgRNA activity using deep learning.**
S. Li[1], X. Zhang*[2], S. Zhao[1,3], C. Zhao[1,4], and S. Xie[1,4], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, China*, [2]*Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany*, [3]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, China*, [4]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China*.

9:45 AM **Business Meeting.**

Small Ruminant Genetics and Genomics

Chair: **Meng-Hua Li (1), Rebecca Simon (2), Institute of Zoology, Chinese Academy of Sciences, Beijing, China (1); Justus-Liebig-Universitat Giessen, Germany**

Nerina

8:30 AM - 10:45 AM

8:30 AM OP134 **Gene expression profiling of the abomasum, duodenum, jejunum and ileum of resistant and susceptible Dohne Merino sheep naturally infected with *Haemonchus contortus*.**
T. M. Ramantswana*[1,2], D. P. Malatji[2], R. E. Pierneef[1], P. Soma[3], M. Van Der Nest[4], and F. C. Muchadeyi[1], [1]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, South Africa*, [2]*University of South Africa, Florida, Gauteng, South Africa*, [3]*Agricultural Research Council, Animal Production Institute, Irene, Pretoria, South Africa*, [4]*University of Pretoria, Hatfield, Pretoria, South Africa*.

8:45 AM OP135 **Identification of genetic regions associated with resistance to gastrointestinal nematodes in Comisana sheep using a genome-wide association study based on EBV ranking.**
C. Persichilli[1], S. Biffani[2], G. Senczuk[1], M. Di Civita*[1], M. K. Bitew[1], A. Bosco[3], S. Grande[4], and F. Pilla[1], [1]*Department of Agricultural, Environmental and Food Science, University of Molise, Campobasso, CB, Italy*, [2]*National Council of Research, Institute for Agriculture Biology and Biotechnology, Milan, MI, Italy*, [3]*University of Naples Federico II, Department of Veterinary Medicine and Animal Production, CREMOPAR, Naples, NA, Italy*, [4]*National Sheep and Goat Breeders Association, Rome, RM, Italy*.

9:00 AM OP136 **Positional candidate genes involved in the response to heat stress in sheep.**
M. Ramon*[1], C. Diaz[2], M. Serrano[2], and M. J. Carabaño[2], [1]*CERSYRA-IRIAF*, *Valdepeñas, Ciudad Real, Spain*, [2]*INIA-CSIC*, *Madrid, Spain*.

9:15 AM OP137 **ISAG Bursary Award: First look into the genetic architecture influencing liver copper concentration in Merinoland sheep.**
O. O. Adeniyi* and G. Lühken, *Institute of Animal Breeding and Genetics, Justus Liebig University*, *Giessen, Hessen, Germany*.

9:30 AM OP138 **DNA-based vaccine design against *Toxoplasma gondii* in ovines using rhoptry protein antigens through immunoinformatics approach.**
T. Madlala*[1], M. Adeleke[1], M. Okpeku[1], and S. Tshilwane[2], [1]*University of KwaZulu Natal*, *Durban, KwaZulu Natal, South Africa*, [2]*University of Pretoria*, *Onderstepoort, Pretoria, South Africa*.

9:45 AM OP139 **The benefit of genomic information for enhancing genetic prediction of production and reproduction traits in South African Merino sheep.**
C. Nel*[1,2], P. Gurman[3], A. Swan[3], J. van der Werf[4], M. Snyman[5], K. Dzama[2], W. Olivier[5], A. Scholtz[1], and S. Cloete[2], [1]*Directorate: Animal Sciences, Western Cape Department of Agriculture*, *Elsenburg, Western Cape, South Africa*, [2]*Department of Animal Sciences, Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*, [3]*Animal Genetics & Breeding Unit, University of New England*, *Armidale, New South Wales, Australia*, [4]*School of Environmental and Rural Science, University of New England*, *Armidale, New South Wales, Australia*, [5]*Grootfontein Agricultural Development Institute, Department of Agriculture, Land Reform and Rural Development*, *Middelburg, Eastern Cape, South Africa*.

10:00 AM OP140 **Goat milk oligosaccharide composition determined by genes with a large effect.**
R. Gonzalez-Prendes*[1,2], H. Bovenhuis[2], L. Pellis[1], and R. P. M. A. Crooijmans[2], [1]*Ausnutria BV*, *Zwolle, the Netherlands*, [2]*Animal Breeding and Genomics, Wageningen University & Research*, *Wageningen, the Netherlands*.

10:15 AM OP141 **Rumen microbial composition in sheep supplemented with *Acacia mearnsii* tannin extract for methane reduction.**
I. Lawal, E. van Marle-Koster*, and A. Hassen, *University of Pretoria*, *Pretoria, Gauteng, South Africa*.

10:30 AM OP142 **Modulation of innate immune memory and systemic effects of Gum Arabica in goats.**
Y. Ahmed and M. Worku*, *North Carolina A&T State University*, *Greensboro, NC*.

OTHER EVENTS

Tea/Coffee Break, Exhibition and Poster Viewing
Hall 9 - Exhibition Hall
10:30 AM - 11:00 AM

Thursday, July 6

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions

Plenary Session III: Functional Genomics (FAANG)
Chair: **Talk 1: Dr P Boettcher & Dr F Muchadeyi; Talk 2: Dr J Heon & Dr B Nkhane**
Hall 8
8:30 AM - 10:30 AM

8:30 AM OP143 **Using functional annotation and individual omics in genomic prediction.**
M. P. L. Calus*[1], B. C. Perez[2], J. de Vos[1], O. Madsen[1], L. Ayres[2], H. Bovenhuis[1], M. Ballester[3], M. J. Mercat[4], and M. C. A. M. Bink[2], [1]*Wageningen University & Research Animal Breeding and Genomics, Wageningen, the Netherlands*, [2]*Hendrix Genetics B.V., Research and Technology Center, Boxmeer, the Netherlands*, [3]*IRTA, Animal Breeding and Genetics Program, Caldes de Montbui, Spain*, [4]*IFIP-Institut du Porc and Alliance R&D, Le Rheu, France*.

9:30 AM OP144 **Aquaculture genetics, genomics and breeding to drive production growth, efficiency and sustainability.**
J. Kijas*, *CSIRO, Brisbane, Queensland, Australia*.

OTHER EVENTS

Tea/Coffee Break, Exhibition and Poster Viewing
Hall 9 - Exhibition Hall
10:30 AM - 10:30 AM

SYMPOSIA AND ORAL SESSIONS

Animal Forensic Genetics

Chair: **Guillermo Giovambattista, Universidad Nacional De La Plata, Argentina**
Orchid
11:00 AM - 12:45 PM

11:00 AM OP145 **ISAG Bursary Award: Can DNA help trace the local trade of pangolins? Conservation genetics of white-bellied pangolins from the Dahomey Gap (West Africa).**
S. Zanvo*[1], C. A. M. S. Djagoun[1], F. A. Azihou[1], B. Sinsin[1], and P. Gaubert[2], [1]*Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin*, [2]*Laboratoire Evolution et Diversité Biologique, Université Paul Sabatier, Toulouse, France*.

11:15 AM OP146 **ISAG Bursary Award: A new approach to the molecular differentiation of the wolf and the domestic dog in wildlife forensics.**
A. E. Hrebianchuk*[1] and I. S. Tsybovsky[2], [1]*State Forensic Examination Committee of the Republic of Belarus, Minsk, Republic of Belarus*, [2]*Republican Unitary Service Enterprise "BelJurZabespechenne," QQMinsk, Republic of Belarus*.

OP147 **Withdrawn**

11:30 AM OP148 **Identification of animal and plant species in foodstuffs using Target GBS assay.**
L. Forlani, D. M. Posik, M. C. Bruno, L. H. Olinera, M. E. Zappa, N. S. Castillo, G. Barbisan, E. E. Villegas Castagnasso, J. A. Crespi, P. Peral García, M. E. Fernandez, and G. Giovambattista*, *Instituto de Genética Veterinaria (IGEVET), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata–CONICET, La Plata, Buenos Aires, Argentina*.

11:45 PM **Results of 2022-2023 Comparison Test.**

12:00 PM **Election of committee members.**

12:15 PM **Design of the 2024-2025 CT. Other business.**

Companion Animal Genetics and Genomics

Chair: **Tosso Leeb (1), Rob Grahn (2), University of Bern, Switzerland (1), University of California Davis, California, United States**
Hall 8
11:00 AM - 1:00 PM

11:00 AM OP149 **Invited Workshop Presentation: On the origin of our companion animals: A palaeogenomics perspective.**
L. Frantz*[1,2], [1]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilians University of Munich, Munich, Germany*, [2]*School of Biological and Behavioural Sciences, Queen Mary University of London, London, UK*.

11:45 AM OP150 **ISAG Bursary Award: *RETREG1* variant causes canine acral mutilation syndrome (AMS) in purebred German spitz.**
A. Letko*[1,2], J. Plassais[1], P. Quignon[1], and C. André[1], [1]*Institut de Génétique et Développement de Rennes (IGDR), University Rennes, Rennes, France*, [2]*Institute of Genetics, University of Bern, Bern, Switzerland*.

11:58 AM OP151 **ISAG Bursary Award: Genomic and transcriptomic characterisation of hypertrophic cardiomyopathy in British Shorthair and Birman cats.**
T. Smedley*, L. Wilkie, V. Fuentes, D. Connolly, and A. Psifidi, *Royal Veterinary College, London, United Kingdom*.

12:11 PM OP152 **Comparative genomics of the natural killer cell receptor genes in felids.**
J. Futas[1,2], A. Jelinek[1], M. Plasil[2], J. Bubenikova[2], P. Burger[3], and P. Horin*[1,2], [1]*Department of Animal Genetics, Faculty of Veterinary Medicine, University of Veterinary Sciences Brno, Brno, Czech Republic*, [2]*Ceitec Vetuni, RG Animal Immunogenomics, University of Veterinary Sciences Brno, Brno, Czech Republic*, [3]*Research Institute of Wildlife Ecology, University of Veterinary Medicine, Vienna, Austria*.

12:24 PM OP153 **Genomic resources for the domestic cat.**
L. Lyons*[1], G. Habacher[2], R. Malik[3], L. Coghill[4], and 99 Lives Consortium[5], [1]*Department of Veterinary Medicine & Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO*, [2]*Raddenstiles Veterinary Surgery, CVS UK Ltd, Exmouth, UK*, [3]*Centre for Veterinary Education, The University of Sydney, Sydney, NSW, Australia*, [4]*Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO*, [5]*99 Lives Cat Genome Consortium*.

12:37 PM OP154 **ISAG Bursary Award: *PCYT2* missense variant in Saarloos Wolfhounds with neurodegeneration.**
M. Christen*[1], M. K. Hytönen[2], H. Lohi[2], A. Kehl[3], V. Jagannathan[1], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Department of Medical and Clinical Genetics, University of Helsinki, and Folkhälsan Research Center, Helsinki, Finland*, [3]*Laboklin GmbH & Co. KG, Bad Kissingen, Germany*.

12:50 PM **Business Meeting.**

FAANG Workshop

Chair: **Chris Tuggle, Department of Animal Science, Iowa State University**
Daisy
11:00 AM - 1:00 PM

11:00 AM	OP155	**FAANG 2023: Community input on FAANG Task Force activities and future priorities.** C. Tuggle*[1], H. Zhou[2], E. Clark[3], and E. Giuffra[4], [1]*Iowa State University, Ames, IA*, [2]*University of California–Davis, Davis, CA*, [3]*The Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK*, [4]*Paris-Saclay University, INRAE, Jouy-en-Josas, France*.
11:20 AM		**Breakout group formation (Breakout room is Freesia).**
11:25 AM		**Breakout group discussions- focus on TF.**
12:25 PM		**Report back and full group discussions.**
12:50 PM		**Wrap up and follow-up organizations.**

OTHER EVENTS

Animal Genetics Journal Editorial Meeting (By invite only)
Nerina
11:00 AM - 1:00 PM

Lunch Break, Exhibition and Poster Viewing
Hall 9 - Exhibition Hall
1:00 PM - 1:00 PM

SYMPOSIA AND ORAL SESSIONS

Avian Genetics and Genomics

Chair: **Susan Lamont, Iowa State University, Ames, Iowa, United States**

Orchid

2:00 PM - 5:30 PM

2:00 PM OP156 **ISAG Bursary Award: Invited Workshop Presentation: Chicken2K: A panel for global chicken genomic diversity and evolutionary inference.**
C. Ma*[1], M.-S. Peng[1,12], J. Smith[2], X. Huang[3], S. Zhang[1], X. Li[4], A. Esmailizadeh[1,5], S. C. Ommeh[6], D. W. Burt[7], A. C. Adeola[1,12], M.-S. Wang[1,12], O. Hanotte[8,9], J. Han[10,11], Y. Dong[4], Y.-P. Zhang[1,13], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, UK*, [3]*Guangdong Provincial Key Laboratory of Conservation and Precision Utilization of Characteristic Agricultural Resources in Mountainous Areas, School of Life Science, Jiaying University, Meizhou, Guangdong, China*, [4]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Kunming, Yunnan, China*, [5]*Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, Kerman, Iran*, [6]*Institute for Biotechnology Research (IBR), Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi, Kenya*, [7]*UQ Genomics, The University of Queensland, Brisbane, Australia*, [8]*Cells, Organisms and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, UK*, [9]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [10]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [11]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Nairobi, Kenya*, [12]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, Yunnan, China*, [13]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan University, Kunming, Yunnan, China*.

2:45 PM OP157 **ISAG Bursary Award: A lncRNA gene-enriched atlas for GRCg7b chicken genome and its functional annotation across 47 tissues.**
F. Degalez*[1,2], M. Charles[2], S. Foissac[2], H. Zhou[3], D. Guan[3], C. Alain[1,2], L. Fang[4], C. Klopp[2], L. Lagoutte[1,2], B. Lebez[1,2], F. Lecerf[1,2], F. Pitel[2], B. Vourc'h[1,2], T. Zerjal[2], S. Lagarrigue[1,2], [1]*Institut Agro, France*, [2]*INRAE, France*, [3]*University of California–Davis, Davis, CA*, [4]*Aarhus University, Denmark*.

3:00 PM OP158 **ISAG Bursary Award: Genetic diversity and relationship between Nigerian Muscovy duck populations using the mitochondria cytochrome *b* gene.**
O. Yusuf*[1], F. Sola-Ojo[1], and C. Adeola[2], [1]*Faculty of Agriculture, Department of Animal Production, University of Ilorin, Kwara state, Nigeria*, [2]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*.

3:15 PM OP159 **ISAG Bursary Award: Potential of a chicken AIL population to decipher the genetic mechanisms of complex traits in the integrative omics era.**
X. Zhu*[1], C. Li[1], C. Luo[2], H. Zhou[3], L. Fang[4], H. Qu[2], Y. Wang[1], and X. Hu[1], [1]*State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China*, [2]*State Key Laboratory of Livestock and Poultry Breeding, Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China*, [3]*Department of Animal Science, University of California, Davis, CA*, [4]*Center for Quantitative Genetics and Genomics (QGG), Aarhus University, Aarhus, Denmark*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP160 **The Chicken Genomic Diversity Consortium: Tracking immune diversity from ancient chickens to the present day.**
S. Fiddaman*[1], A. Smith[1], and L. Frantz[3,2], [1]*University of Oxford, Oxford, UK*, [2]*QMUL, London, UK*, [3]*LMU, Munich, Germany*.

4:15 PM OP161 **Accumulated variations in the promoter regions play an important role for complex traits during duck domestication.**
Z.-T. Yin*[1], X.-Q. Li[1], Y.-X. Sun[1], J. Smith[2], N. Yang[1], and Z.-C. Hou[1], [1]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, MARA; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*The Roslin Institute & R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK*.

4:30 PM OP162 **Allele-specific expression in the jejunal transcriptome profiles of two laying hen strains over the entire production period.**
S. Ponsuksili*, F. Hadlich, M. A. Iqbal, H. Reyer, M. Oster, N. Trakooljul, E. Murani, and K. Wimmers, *Research Institute for Farm Animal Biology, Dummerstorf, Germany*.

4:45 PM OP163 **Different stress response strategies of an Arctic breeding bird (*Calcarius lapponicus*) under inclement weather conditions revealed by the genome and RNA-seq analyses.**
Z. Wu*[1], M. M. Hindle[1], A. M. A. Reid[1], J. H. Pérez[2,3], J. S. Krause[2,4], J. C. Wingfield[2], S. L. Meddle[1], and J. Smith[1], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies R(D)SVS, University of Edinburgh, United Kingdom*, [2]*Department of Neurobiology Physiology Behavior, University of California, Davis, CA*, [3]*Department of Biology, University of South Alabama, Mobile, AL*, [4]*Department of Biology, University of Nevada–Reno, Reno, NV*.

5:00 PM OP164 **Genome-wide association study of nucleotide and peptide contents of breast meat in Korean native chickens.**
M. Kim*[1], E. Cho[1], J. Munyaneza[1], A. Jang[2], H. Choo[3], and J. Lee[1], [1]*Chungnam National University, Daejeon, Korea*, [2]*Kangwon National University, Chuncheon, Gangwon-do, Korea*, [3]*National Institute of Animal Science, Rural Development Administration, Pyeongchang, Gangwon-do, Korea*.

5:15 PM **Business meeting.**

Equine Genetics and Thoroughbred Parentage Testing

Chair: **Marcela Martinez, Laboratorio De Genetica Aplicada Sociedad Rural Argentina, Buenos Aires, Argentina**
Nerina
2:00 PM - 5:30 PM

2:00 PM **Welcoming Remarks.**

2:10 PM **Horse Comparison Test.**

2:30 PM **Donkey Comparison Test.**

2:50 PM OP165 **Contribution of STR genotyping to animal clinical cytogenetics.**
T. Raudsepp*, J. Kjöllerström, and R. Juras, *School of Veterinary Medicine, Texas A&M University, College Station, TX*.

3:10 PM **Election of CT Duty Labs, Election of Committee and Any Other Business.**

3:30 PM **Lunch Break, Exhibition and Poster Viewing.**

4:00 PM OP167 **Development of a robust across breed equine parentage SNP panel for ISAG approval.**
R. R. Bellone*[1,2], T. A. Mansour[2,3], E. Esdaile[1], B. Wallner[4], T. Raudsepp[5], B. Till[1], A. Kallenberg[1], S. Hughes[1], S. Chadaram[6], S. Shrestha[6], R. A. Grahn[1], Equine ISAG SNP Panel Consortium[9], F. Avila[1], M. McCue[7], P. Flynn[8], [1]*Veterinary Genetics Laboratory, School of Veterinary Medicine, UC Davis, Davis, CA*, [2]*Department of Population Health and Reproduction, School of Veterinary Medicine, UC Davis, Davis, CA*, [3]*Department of Clinical Pathology, School of Medicine, Mansoura University, Mansoura, Egypt*, [4]*Institute of Animal Breeding and Genetics, Veterinary University of Vienna, Wien, Austria*, [5]*Veterinary Integrative Biosciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX*, [6]*Thermo Fisher Scientific, Austin, TX*, [7]*Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, MN*, [8]*Weatherbys Scientific, Kildare, Ireland*, [9]*Various Affiliations*.

4:20 PM OP166 **Invited Workshop Presentation: Improving parentage verification, transiting from STR to SNP and beyond from a bovine perspective.**
M. McClure*, *ABS-Global*, *Deforest, WI*.

4:40 PM **Open Panel to discuss several aspects of SNPs in horses (Panel and next CT, transition between techniques, others).**

Genetics and Genomics of Aquaculture Species

Chair: **Francesca Bertolini (1), Maria Saura (2), University of Bologna, Italy (1); INIA, Madrid, Spain (2)**
Freesia
2:00 PM - 5:30 PM

2:00 PM OP168 **Invited Workshop Presentation: Epigenomic and microbiome signatures of early rearing conditions in aquaculture.**
S. Consuegra*, *Department of Biosciences, School of Biosciences, Geography, and Physics, Swansea University, Wales, UK*.

2:30 PM OP169 **ISAG Bursary Award: A high-density genetic linkage map and QTL mapping for growth traits in South African abalone (*Haliotis midae*).**
T. Tshilate*[1], E. Ishengoma[2], and C. Rhode[1], [1]*Department of Genetics, Stellenbosch University, Stellenbosch, South Africa*, [2]*Mkwawa University College of Education, University of Dar es Salaam, Iringa, Tanzania*.

2:45 PM OP170 **A technology for producing all-female progenies of the Flathead grey mullet by selecting sex-reversed males.**
L. David*[1], G. Hirsch[1], I. Oz[1], D. Agiv[1], E. Marcos-Hadad[1], A. Bennet-Perlberg[2], A. Naor[2], and B. Ginzbourg[3], [1]*The Hebrew University of Jerusalem, Rehovot, Israel*, [2]*Israel Ministry of Agriculture and Rural Development, Dor, Israel*, [3]*Dagon Fish Hatchery, Kibbutz Maagan-Michael, Israel*.

3:00 PM OP171 **Atlantic salmon miRNAs associated with smolitification and sea-water adaptation.**
R. Andreassen*[1], A. Shwe[1], S. Ramberg[1], A. Krasnov[2], and T. Østbye[2], [1]*Oslo Metropolitan University, Oslo, Norway*, [2]*Nofima (Norwegian Institute of Food, Fisheries and Aquaculture Research), Ås, Norway*.

3:15 PM OP172 **ISAG Bursary Award: Construction of a high-density genetic linkage map using 2b-RAD sequencing in dusky kob (*Argurosomus japonicus*).**
T. Jackson and C. Rhode*, *Stellenbosch University, Stellenbosch, South Africa*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP173 **Population genetics of two critically endangered rhino rays from the Southwest Indian Ocean region.**
M. Groeneveld*[1], J. Klein[1], R. Bennett[2], M. Bond[3], D. Ebert[4,5], K. Gledhill[6], S. Jaquemet[7], J. Kiszka[3], A. Macdonald[8], B. Mann[9], J. Nevill[10], A. Price[1], M. van Staden[1], B. Wueringer[11,12], A. Bester-van der Merwe[1], [1]*Department of Genetics, Stellenbosch University, Stellenbosch, South Africa*, [2]*Wildlife Conservation Society*, [3]*Institute of Environment, Department of Biological Sciences, Florida International University, Miami, FL*, [4]*Pacific Shark Research Center, Moss Landing Marine Laboratories, Moss Landing, CA*, [5]*South African Institute for Aquatic Biodiversity, Grahamstown, South Africa*, [6]*Fish Ecology Lab, University of Technology Sydney, Broadway, Sydney, Australia*, [7]*UMR Entropie, Université de La Réunion, La Réunion, France*, [8]*School of Life Sciences, University of KwaZulu-Natal, Westville, South Africa*, [9]*Oceanographic Research Institute, Durban, South Africa*, [10]*Environment Seychelles, Mahé, Seychelles*, [11]*Sharks And Rays Australia, Bungalow, Queensland, Australia*, [12]*Department of Biological Sciences, Faculty of Science and Engineering, Macquarie University, Macquarie Park, New South Wales, Australia*.

4:15 PM OP174 **Genetic variation in disease resistance traits in hybrid striped bass.**
J. Abernathy*[1], M. Lange[1], B. Farmer[2], M. McEntire[2], and S. Rawles[2], [1]*United States Department of Agriculture, Agricultural Research Service, Auburn, AL*, [2]*United States Department of Agriculture, Agricultural Research Service, Stuttgart, AR*.

4:30 PM OP175 **Multi-functional genomic analyses identify causal gene and variants modulating viral nervous necrosis resistance in European seabass.**
R. Mukiibi*[1], L. Peruzza[2], C. Penaloza[3], M. Babbucci[2], R. Franch[2], M. Freguglia[5], S. Laureau[5], G. Dalla Rovere[2], D. Bertotto[2], S. Ferraresso[2], C. Tsigenopoulos[4], R. D. Houston[3], L. Bargelloni[2], and D. Robledo[1], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, United Kingdom*, [2]*Department of Comparative Biomedicine and Food Science, University of Padova, Padova, Italy*, [3]*Benchmark Genetics, Edinburgh Technopole, Edinburgh, United Kingdom*, [4]*Institute of Marine Biology, Biotechnology and Aquaculture (IMBBC), Hellenic Centre for Marine Research (H.C.M.R.) Crete, Gournes Pediados Heraklion, Crete, Greece*, [5]*Valle Cà Zuliani Società Agricola s.r.l., Conselice (RA), Italy, Rovigo, Italy*.

4:45 PM OP176 **Utilizing of genetic evaluation system using genomic information of the Korean flatfish population.**
D. Lee*[1], J. Kang[1], Y. Chung[1], S. Lee[1], Y. Kim[2], J. Park[3,1], D. Lee[3], J. Kim[3], H. Yang[3], J. Lee[3], and S. Lee[1], [1]*Chungnam National University, Yuseong-gu, Daejeon, Republic of Korea*, [2]*Quantomic Research & Solution, Yuseong-gu, Daejeon, Republic of Korea*, [3]*Fish Genetics and Breeding Research Center, Geoje, Republic of Korea*.

5:00 PM OP177 **Whole-genome sequencing data provide a landscape picture of genetic variability in sea cucumber species.**
F. Bertolini*[1], A. Ribani[1], V. Taurisano[1], A. Rakaj[2], A. Fianchini[2], F. Capoccioni[3], D. Pulcini[3], S. Bovo[1], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Department of Biology, University of Rome Tor Vergata, Rome, Italy*, [3]*Centro di Ricerca "Zootecnia e Acquacoltura," Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria (CREA), Monterotondo (Rome), Italy*.

5:15 PM **Workshop Business Meeting.**

Livestock Genomics for Developing Countries

Chair: **Abdulfatai Tijjani, The Jackson Laboratory Bar Harbor, Maine, United States**

Daisy

2:00 PM - 5:15 PM

2:00 PM OP178 **The history and future of African cattle diversity and adaptation: The known and the possible.**
O. Hanotte*[1,2], [1]*ILRI, Ethiopia*, [2]*The University of Nottingham, Nottingham, United Kingdom*.

2:15 PM OP179 **Whole-genome diversity of dromedary camels from the entire geographic distribution range.**
G. Senczuk*[1], S. Bruno[2], M. Di Civita[1], V. Landi[3], S. Brooks[4], F. Almathen[5,6], B. Faye[7], S. B. S. Gaouar[8], M. Piro[9], K. S. Kim[10], H. Dadi[11], C. Iglesias Pastrana[12], H. Al-Haddad[13], M. Al-Abri[14], C. Persichilli[1], F. Pilla[1], P. Burger[15], and E. Ciani[2], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Department of Biosciences, Biotechnologies and Environment, University of Bari "Aldo Moro," QQBari, Italy*, [3]*Department of Veterinary Medicine, University of Bari "Aldo Moro," QQBari, Italy*, [4]*Department of Animal Sciences, University of Florida, Gainesville, FL*, [5]*Department of Public Health, College of Veterinary Medicine, King Faisal University, Al-Ahsa, Saudi Arabia*, [6]*Camel Research Center, King Faisal University, Al-Ahsa, Saudi Arabia*, [7]*CIRAD-ES, UMR SELMET, Montpellier, France*, [8]*Department of Biology, Abou Bakr Belkaid University of Tlemcen, Tlemcen, Algeria*, [9]*Department of Medicine, Surgery and Reproduction, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco*, [10]*Department of Animal Sciences, Chungbuk National University, Chungbuk, Korea*, [11]*Ethiopian Biotechnology Institute (EBTi), Addis Ababa, Ethiopia*, [12]*Department of Genetics, Faculty of Veterinary Sciences, University of Córdoba, Córdoba, Spain*, [13]*Department of Biological Sciences, Kuwait University, Kuwait City, Kuwait*, [14]*Department of Animal and Veterinary Sciences, Sultan Qaboos University, Muscat, Oman*, [15]*Research Institute of Wildlife Ecology, Vetmeduni, Vienna, Austria.*

2:30 PM OP180 **ISAG Bursary Award: Genome-wide scan for selection signatures in South African indigenous goat ecotypes.**
A. M. Magoro*[1,2], A. Zwane[2], K. Hadebe[3], and B. Mtileni[2], [1]*Tshwane University of Technology, Pretoria, South Africa*, [2]*Agricultural Research Council-Animal Production, Pretoria, South Africa*, [3]*Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa*.

2:45 PM OP181 **ISAG Bursary Award: Differential proteomics revealed the impact of heat stress on milk whey proteins in indigenous Deoni (*Bos indicus*) and Holstein Friesian (*Bos taurus*) crossbred cows.**
E. Rana*[1,4], K. P. Ramesha[1], N. Azharuddin[1], M. A. Najar[2], M. K. Sinha[1], S. Jeyakumar[1], L. Gopalakrishnan[2,3], P. Nag[1], S. Mall[1], M. Ashokan[1], M. Dasgupta[1], A. Kumaresan[1], D. N. Das[1], and T. S. K. Prasad[2], [1]*Southern Regional Station, ICAR-National Dairy Research Institute, Bangalore, India*, [2]*Center for Systems Biology and Molecular Medicine, Yenepoya Research Centre, Yenepoya (Deemed to be University), Mangalore, India*, [3]*Institute of Bioinformatics, International Technology Park, Bangalore, India*, [4]*Livestock Development Department, Government of Chhattisgarh, Chhattisgarh, India*.

3:00 PM OP182 **ISAG Bursary Award: Whole genome sequencing of Landim pigs of Mozambique reveals a close relationship with Angola native pigs and suggests selection for immune response.**
F. Teixeira*[1,2], P. Sá[1], D. Santos[1], C. Garrine[3], R. Zimba[4], L. Souza[3], H. Chiaia[2], A. Leitão[1], J. M. Cordeiro[2], L. T. Gama[1], and A. J. Amaral[1,5], [1]*Centre for Interdisciplinary Research in Animal Health and Associate Laboratory for Animal and Veterinary Sciences, Faculty of Veterinary Medicine, University of Lisbon, Alto da Ajuda, Lisbon, Portugal*, [2]*Faculty of Veterinary Medicine, University José Eduardo dos Santos, Huambo, Angola*, [3]*Faculty of Veterinary Medicine, University Eduardo Mondlane, Maputo, Mozambique*, [4]*Escola Superior de Desenvolvimento Rural de Vilankulo, University Eduardo Mondlane, Mozambique*, [5]*Escola de Ciências e Tecnologia Universidade de Évora, Évora, Portugal*.

3:15 PM OP183 **Structural variant calling using ONT long-read whole genome sequencing of indigenous Zulu sheep.**
N. Nxumalo*[1], A. Molotsi[1], C. Rhode[1], and N. Kunene[2], [1]*Stellenbosch University, Stellenbosch, Matieland, South Africa*, [2]*University of Zululand, Empangeni, Kwadlangezwa, South Africa*.

3:30 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP184 **Studying cattle structural variation and pangenome using whole genome sequencing.**
G. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD*.

4:15 PM OP185 **Poultry genomics within the Centre for Tropical Livestock Genetics and Health.**
J. Smith*[1], A. Gheyas[1], A. Trujillo[1,2], A. Kebede[3], G. Gebru[4,5], N. Seboka[5,6], M. Rachman[2], T. Dessie[7], and O. Hanotte[2,7], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [2]*University of Nottingham, Nottingham, UK*, [3]*Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia*, [4]*Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia*, [5]*Addis Ababa University, Addis Ababa, Ethiopia*, [6]*Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia*, [7]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*.

4:30 PM OP186 **Tracking the adaptive history of African cattle using low-coverage genomes.**
S. I. Ng'ang'a*[1,2], J. A. Ward[3], G. V. Smith[4], S. Rossiter[2], C. Faulkes[2], D. G. Bradley[5], O. Hanotte[6,7], D. E. MacHugh[8], and L. A. F. Frantz[1,2], [1]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilian University, Munich, Germany*, [2]*School of Biological and Chemical Sciences, Queen Mary University of London, London, United Kingdom*, [3]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*, [4]*SilverStreet Capital, London, United Kingdom*, [5]*Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland*, [6]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [7]*School of Life Sciences, University of Nottingham, Nottingham, United Kingdom*, [8]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland*.

4:45 PM OP187 **Virginia Tech research education programs: Models for increasing STEM participation in middle- and low-income countries.**
E. Smith*, *Virginia Tech, Blacksburg, VA*.

5:00 PM **Business meeting and election of committee.**

Ruminant Genetics and Genomics

Chair: **Shannon Clarke, AgResearch Mosgiel, New Zealand**
Hall 8
2:00 PM - 5:30 PM

2:00 PM OP193 **Analysis of differential isoform usage in production relevant tissues across pre- and post-natal development in sheep.**
S. A. Woolley[1], J. G. D. Prendergast[1], M. Salavati[1,2], and E. L. Clark*[1], [1]*The Roslin Institute, Edinburgh, Midlothian, UK*, [2]*SRUC, Edinburgh, Midlothian, UK*.

2:20 PM OP189 **Identification the genetic resistance genes and biosynthesis pathways to gastrointestinal nematodes infection in goat using RNA-sequencing.**
A. A. Bhuiyan[1], A. Bhuyan*[2], A. S. Afsana[3], S. Zhao[4], and X. Du[4], [1]*Bangladesh Agricultural Research Council, Dhaka, Dhaka, Bangladesh*, [2]*National Institute of Biotechnology, Savar, Dhaka, Bangladesh*, [3]*Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh*, [4]*Huazhong Agricultural University, Wuhan, Hubei, China*, [5]*Huazhong Agricultural University, Wuhan, Hubei, China*.

2:40 PM OP190 **A continent-wide genomic resource for African buffalo (*Syncerus caffer*).**
L. Morrison*[1,2], [1]*Roslin Institute, University of Edinburgh, Edinburgh, UK*, [2]*Centre for Tropical Livestock Genetics and Health, University of Edinburgh, Edinburgh, UK*.

2:55 PM OP191 **A time-resolved multi-omics atlas of transcriptional regulation in response to high-altitude hypoxia across the whole-body tissues.**
Z. Yan* and M. Li, *China Agricultural University, Beijing, China*.

3:10 PM OP192 **Copy number variation mapping and copy number variation contribution to genetic variance of complex traits in dairy cattle.**
G. Ladeira[1], P. Pinedo[2], J. Santos[1], W. Thatcher[1], and F. Rezende*[1], [1]*University of Florida, Gainesville, FL*, [2]*Colorado State University, Fort Collins, CO*.

3:25 PM **Tea/Coffee Break, Exhibition and Poster Viewing.**

4:00 PM OP188 **Living in two extremes: Convergent nucleotide evolution and parallel selection in cold- and heat-resistant cattle breeds and wild animals.**
G. Romashov[1], N. Yudin[1], J. Prendergast[2], A. Talenti[2], J. Powell[2], and D. Larkin*[3], [1]*Institute of Cytology and Genetics, Novosibirsk, Siberia, Russia*, [2]*Roslin Institute, Edinbough, Scotland, UK*, [3]*Royal Veterinary College, London, Greater London, UK*.

4:20 PM OP194 **Functional mapping of alternative polyadenylation in cattle.**
Z. Jiang[1], H. Wang[1], X. Zhou[1], J. J. Michal[1], S. A. Carrion[1], S. Zhang[1], Y. Zhang[1], M. J. Stotts[1], S. He[1], Y. Zhang[1], X. Zhang[1], X. Han[1], W. Wang[1], L. Qu[1], R. Li[1], M. Maquivar[1], M. Du[1], L. K. Fox[1], M. L. Bernhardt[2], Y. Wang[3], J. Velez[4], B. Hans[4], B. M. Murdoch[5], C. Gill[6], H. Jiang[7], H. Zhou[8], J. E. Koltes[9], J. Reecy[9], M. Rijnkels[10], P. J. Ross[8], S. McKay[11], T. P. L. Smith[12], W. Liu[13], K. Ren[14], L. Low[14], J. Yang[15], and S. P. Miller[16], *[1]Department of Animal Sciences and Center for Reproductive Biology, Washington State University, Pullman, WA, [2]Animal Production Core, Center for Reproductive Biology, Washington State University, Pullman, WA, [3]Department of Mathematics and Statistics, Washington State University, Pullman, WA, [4]Aurora Organic Farms, Platteville, CO, [5]Department of Animal and Veterinary Science, University of Idaho, Moscow, ID, [6]Department of Animal Science, Texas A&M University, College Station, TX, [7]Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA, [8]Department of Animal Science, University of California Davis, Davis CA, [9]Department of Animal Science, Iowa State University, Ames, IA, [10]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, [11]Department of Animal and Veterinary Science, University of Vermont, Burlington, VT, [12]Roman L. Hruska U.S. Meat Animal Research Center, USDA-ARS-PA-MARC, Clay Center, NE, [13]Department of Animal Science, The Pennsylvania State University, University Park, PA, [14]School of Animal and Veterinary Science, University of Adelaide, Adelaide, SA, Australia,[15]Department of Human Nutrition, Food and Animal Sciences, University of Hawaii at Manoa, Honolulu, HI, [16]Animal Genetics and Breeding Unit, University of New England, Armidale NSW 2351, Australia.*

4:35 PM OP195 **Insights into the genetic variation, gene-flow and demographic history of African cattle breeds.**
M. Malima[1,2], K. Nxumalo[1], A. Tijjani[3,4], M. Makgahlela*[1], F. Joubert[2], and A. Zwane[1], *[1]Department of Animal Breeding and Genetics, Agricultural Research Council-Animal Production Irene, Pretoria, South Africa, [2]Centre for Bioinformatics and Computational Biology, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa, [3]International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, [4]The Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, The University of Edinburgh, Midlothian, UK.*

4:50 PM OP196 **ISAG Bursary Award: Size and composition of haplotype reference panels impact the accuracy of imputation from low-pass sequencing in cattle.**
A. Lloret-Villas*, H. Pausch, and A. Leonard, *ETH Zürich, Universitätstrasse 2, 8092, Zürich, Switzerland.*

5:05 PM OP197 **ISAG Bursary Award: Pangenomes of haplotype-resolved assemblies enable population-scale genotyping of cattle structural variation for eQTL mapping.**
A. Leonard*, X. Mapel, and H. Pausch, *ETH Zurich, Zurich, Switzerland.*

5:20 PM **Business Meeting.**

OTHER EVENTS

Gala Dinner & Awards Ceremony
Gold Restaurant
7:00 PM - 11:00 PM

Friday, July 7

SYMPOSIA AND ORAL SESSIONS

Plenary Sessions

Plenary Session IV: Genomics for SA livestock and wildlife

Chair: **Talk 1: Dr EM Ibeagha-Awemu & Prof E Van Marle-Köster; Talk 2: Dr S Mikko & Prof C Banga**
Hall 8
9:00 AM - 10:50 AM

9:00 AM OP198 **The African BioGenome Project: An African initiative to conserve and document Africa's biodiversity.**
A. W. Muigai*[1,2], J. Kuja[3], N. Mapholi[4], T. Ebenezer[5], and A. Djikeng[6], [1]*Jomo Kenyatta University of Agriculture and Technology, Kiambu, Kenya*, [2]*National Defence University-Kenya, Nakuru, Kenya*, [3]*University of Copenhagen, Denmark*, [4]*University of South Africa, Pretoria, South Africa*, [5]*5European Bioinformatics Institute (EMBL), Hinxton, United Kingdom*, [6]*International Livestock Research Institute, Nairobi, Kenya*.

9:55 AM OP199 **Genetic biodiversity in southern Africa: Implications for wildlife conservation.**
P. Bloomer*[1], A. van Wyk[1], A. Klopper[1], D. de Jager[2], and I.-R. Russo[3,1], [1]*Molecular Ecology and Evolution Programme, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa*, [2]*Section of Molecular Ecology and Evolution, Globe Institute, University of Copenhagen, Copenhagen, Denmark*, [3]*School of Biosciences, Cardiff University, Cardiff, UK*.

OTHER EVENTS

Tea/Coffee Break
Hall 8 Foyer
10:50 AM - 11:30 AM

Business Meeting
Hall 8
11:30 AM - 12:30 PM

Closing Ceremony
Hall 8
12:30 PM - 1:00 PM

POSTER PRESENTATIONS

Animal Epigenetics

P1 **Gene orthology detection for long noncoding RNA (lncRNA).**
F. Degalez*[1,2], C. Allain[1,2], L. Lagoutte[1,2], and S. Lagarrigue[1,2], [1]*Institut Agro*, *France*, [2]*INRAE*, *France*.

P2 **Long-term selection impacts the rewiring of chromatin structure in chickens.**
D. Guan[1], Y. Wang[1], S. Aggrey[2], R. Okimoto[3], R. Hawken[3], and H. Zhou*[1], [1]*University of California, Davis*, *Davis, CA*, [2]*University of Georgia*, *Athens, GA*, [3]*Cobb-Vantress Inc*, *Siloam Springs, AR*.

P3 **Super-accessible chromatin regions are associated with increased gene transcription and regulation of cell differentiation in mammals.**
M. Hu*[1], Y. Zhao[1], X. Qi[1], H. Zhou[1], Y. Guo[1], L. Li[1], R. Kuang[1], R. Ma[1], G. Sun[4], L. Li[4], M. Zhu[1,3], X. Li[1,3], and S. Zhao[1,2], [1]*Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University*, *Wuhan, Hubei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production*, *Wuhan, Hubei, China*, [4]*College of Biomedicine and Health, Huazhong Agricultural University*, *Wuhan, Hubei, China*.

P4 **Annotation of functional variations in four livestock genomes utilizing cis-regulatory elements datasets.**
R. Ma*[1], R. Kuang[1], M. Hu[1], Y. Guo[1], D. Wang[1], H. Zhou[1], Z. Han[1], L. Li[1], Z. Xu[1], Y. Zhang[1], Y. Zhao[1], X. Li[1,2], and S. Zhao[1,2], [1]*Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University*, *Wuhan, China*.

P5 **DNA methylation alteration patterns in repeat elements are similar during subclinical mastitis caused by *Staphylococcus chromogenes* and *Staphylococcus aureus*.**
M. Wang[1,2], N. Bissonnette[1], M. Laterrière[3], D. Gagné[3], and E. M. Ibeagha-Awemu*[1], [1]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, Québec, Canada*, [2]*Département des Sciences Animales, Université Laval*, *Québec, Québec, Canada*, [3]*3Quebec Research and Development Centre, Agriculture and Agri-Food Canada*, *Québec, Québec, Canada*.

P6 **Genome-wide acetylation modification of H3K27ac in bovine rumen cell following butyrate exposure.**
X. Kang[1,2], C. Li[2], R. L. Baldwin[1], G. Liu[1], and C. Li*[1], [1]*ARS, USDA*, *Beltsville, MD*, [2]*Ningxia University*, *Yinchuan, Ningxia, China*.

P7 **M6A demethylase ALKBH5 regulates PRRSV replication by manipulating host immune response.**
Q. Su*[1], X. Meng[1], B. Liu[1,2], and X. Zhou[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University*, *Wuhan, China*, [2]*Hubei Hongshan Laboratory*, *Wuhan, China*.

P8 **ISAG Bursary Award: Relationship between spleen and uterus gene expression and DNA methylation according to developmental stages of pigs.**
B. Ahn*[1], M. Kang[1], M. Choi[1,2], L. Rund[3], L. Shook[3], and C. Park[1], [1]*Department of Stem Cell and Regenerative Biotechnology, Konkuk University*, *Seoul, Korea*, [2]*Living Systems Institute, University of Exeter*, *Exeter, United Kingdom*, [3]*Department of Animal Sciences, University of Illinois at Urbana-Champaign*, *Urbana, IL*.

P9 **Extending Ensembl regulatory annotation to farmed animals.**
G. R. Ilsley*, G. A. Merino, P. R. Branco Lins, M. Perry, D. Urbina-Gomez, and P. Harrison, *European Molecular Biology Laboratory, European Bioinformatics Institute*, *Hinxton, Cambridge, UK*.

P10 **Beyond the genome: Establishing molecular phenotypes to accelerate adaptation to a changing environment.**
A. Caulton*[1], R. Brauning[1], K. M. McRae[1], K. G. Dodds[1], C. Couldrey[2], P. L. Johnson[1], and S. M. Clarke[1], [1]*AgResearch, Invermay Agricultural Centre*, *Mosgiel, Otago, New Zealand*, [2]*Livestock Improvement Corporation*, *Hamilton, New Zealand*.

P11 **RNA methylation as a mechanistic link between epigenotype and phenotype.**
S. Xie[1], B. Murdoch[1], and S. McKay*[2,3], [1]*University of Idaho*, *Moscow, ID*, [2]*University of Vermont*, *Burlington, VT*, [3]*University of Missouri*, *Columbia, MO*.

Animal Forensic Genetics

P12 **Withdrawn**

P13 **Withdrawn**

P14 **Equine DNA sex identification using DDX3 gene X- and Y-chromosome polymorphisms.**
L. Rickords*, J. Felts, and M. Laker, *Utah State University, Logan, UT.*

P15 **DNA barcoding in South Africa: Progress, challenges and future plans.**
M. Mwale*, M. T. Sethusa, and J. R. Baxter, *Foundational Biodiversity Science, South African National Biodiversity Institute (SANBI), National Zoological Gardens, Pretoria, South Africa.*

P16 **Identification of animal and plant species in foodstuffs using target GBS assay.**
L. Forlani, D. M. Posik, M. C. Bruno, L. H. Olinera, M. E. Zappa, N. S. Castillo, G. Barbisan, E. E. Villegas Castagnasso, J. A. Crespi, P. Peral García, M. E. Fernandez, and G. Giovambattista*, *Instituto de Genética Veterinaria (IGEVET), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata—CONICET, La Plata, Buenos Aires, Argentina.*

P17 **Withdrawn**

P18 **ISAG Bursary Award: A new approach to the molecular differentiation of the wolf and the domestic dog in wildlife forensics.**
A. E. Hrebianchuk*[1] and I. S. Tsybovsky[2], [1]*State Forensic Examination Committee of the Republic of Belarus, Minsk, Republic of Belarus*, [2]*Republican Unitary Service Enterprise «BelJurZabespechenne», Minsk, Republic of Belarus.*

P19 **ISAG Bursary Award: *Can DNA help trace the local trade of pangolins? Conservation genetics of white-bellied pangolins from the Dahomey Gap (West Africa)*.**
S. Zanvo*[1], C. A. M. S. Djagoun[1], F. A. Azihou[1], B. Sinsin[1], and P. Gaubert[2], [1]*Laboratory of Applied Ecology, University of Abomey-Calavi, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin*, [2]*Laboratoire Evolution et Diversité Biologique, Université Paul Sabatier, Toulouse, France.*

Applied Genetics of Companion Animals

P20 **Circulating exosomes and microRNAs as biomarkers for canine idiopathic epilepsy.**
M. García-Gracia[1], S. Usón[1], L. Moreno-Martínez[1,2], J. Moral[3], D. Sanz-Rubio[4], A. Hernaiz[1], R. Osta[1,2], P. Zaragoza[1,2], B. Rosado[3], S. García-Belenguer[3], and I. Martín-Burriel*[1,2], [1]*Laboratorio de Genética Bioquímica (LAGENBIO), Facultad de Veterinaria, Universidad de Zaragoza, Instituto de Investigación Sanitaria de Aragón, Zaragoza, Spain*, [2]*Centro de Investigación Biomédica en Red de Enfermedades Neurodegenerativas (CIBERNED), Instituto de Salud Carlos III, Madrid, Spain*, [3]*Departamento de Patología Animal, Facultad de Veterinaria, Universidad de Zaragoza, Zaragoza, Spain*, [4]*Translational Research Unit, Instituto de Investigación Sanitaria de Aragón (IISAragón), Hospital Universitario Miguel Servet, Zaragoza, Spain.*

P21 **Candidate gene analysis of primary ciliary dyskinesia in the English cocker spaniel.**
R. T. Cheng[1], L. Hambrook[2], and C. M. Wade*[1], [1]*The University of Sydney, Camperdown, NSW, Australia*, [2]*Advanced Vet Care, Kensington, VIC, Australia.*

P22 **Obligatory testing in dogs: Input from breeders and organizations.**
E. Beckers*, N. Buys, and S. Janssens, *Center for Animal Breeding and Genetics, KU Leuven, Leuven, Belgium.*

Avian Genetics and Genomics

P24 **ISAG Bursary Award: Combined effect of microbially-derived caecal SCFA and host genetics on feed efficiency in broiler chickens.**
Z. He*[1,2], R. Liu[1], Q. Wang[1], J. Zheng[1], J. Ding[1], J. Wen[1], A. Fahey[2], and G. Zhao[1], [1]*Institution of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland.*

P25 **Production performance of four lines of Japanese Quail reared under tropical climatic conditions of Tamil Nadu, India.**
K. Vishal Arunrao[1], D. Kannan[1], R. Amutha[1], A. K. Thiruvenkadan[2], A. Yakubu[3], and S. O. Peters*[4], [1]*Department of Poultry Science, Veterinary College and Research Institute, Namakkal, Tamil Nadu, India*, *Namakkal, Tamil Nadu, India*, [2]*Department of Animal Genetics and Breeding, Veterinary College and Research Institute, Salem, Tamil Nadu, India*, *Salem, Tamil Nadu, India*, [3]*Centre for Sustainable Agriculture and Rural Development, Department of Animal Science, Faculty of Agriculture, Nasarawa State University, Keffi, Shabu-Lafia Campus, Nigeria*, *Nigeria*, [4]*Department of Animal Sciences, Berry College*, *Rome, GA*.

P26 **mRNA expression of the *GDF9* gene in ovarian follicles of South African Potchefstroom Koekoek chickens.**
T. Tyasi* and V. Hlokoe, *University of Limpopo*, *South Africa*.

P27 **Occurrence and genetic diversity of *Haemoproteus* and *Leucocytozoon* parasites in selected captive birds in South Africa.**
R. Gaorekwe*[1,2], V. Phetla[2], D. Malatji[2], and M. Chaisi[1,3], [1]*South African National Biodiversity Institute*, *Pretoria, South Africa*, [2]*University of South Africa*, *Florida, Roodepoort, South Africa*, [3]*University of Pretoria*, *Onderstepoort, South Africa*.

P28 **ISAG Bursary Award: Characterization of chicken strains in Isin local government based on phenotypic parameters, blood polymorphism, and 18s mitochondria genes.**
P. A. Owolabi*, F. E. Sola-Ojo, R. Y. Eseyin, A. G. Aremu, F. T. Sa'ad, E. O. Omidiji, A. O. Adeyanju, A. T. Fakayode, N. T. Fadairo, S. O. Oni, A. A. Odumade, K. A. Ganiyu, A. O. Muhammad-Nasir, S. D. Aniyi, S. D. Lawal, *University of Ilorin*, *Ilorin, Kwara, Nigeria*.

P29 **ISAG Bursary Award: Estimation of genetic diversity and population structure of Korean domestic chickens by comparison with SYNBREED data.**
E. Cho*, M. Kim, and J. Lee, *Chungnam National University*, *Daejeon, Republic of Korea*.

P30 **Genomic analysis of long-tailed chicken (Onagadori) offers insight into the evolution of avian molting.**
C. Ma[1,2], M.-S. Wang[1,2], F.-J. Wang[1,2], K. Kinoshita[3,4], Z.-F. Cai[1,5], K. Srikulnath[6], J.-L. Han[7,8], L. Zeng[1], F. Wu[1,2], H.-J. Wei[3,4], Y.-P. Zhang[1,5], and M.-S. Peng*[1,2], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, Yunnan, China*, [2]*Kunming College of Life Science, University of Chinese Academy of Sciences*, *Kunming, Yunnan, China*, [3]*State Key Laboratory for Conservation and Utilization of Bio-resources in Yunnan, Yunnan Agricultural University*, *Kunming, Yunnan, China*, [4]*Key Laboratory of Animal Gene Editing and Animal Cloning in Yunnan Province*, *Kunming, Yunnan, China*, [5]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan University*, *Kunming, Yunnan, China*, [6]*Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University*, *Bangkok, Thailand*, [7]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS)*, *Beijing, China*, [8]*Livestock Genetics Program, International Livestock Research Institute (ILRI)*, *Nairobi, Kenya*.

P31 **Metabolomic approach to investigate the effect of β-alanine and L-histidine supplementation on carnosine synthesis in slow-growing Korat chicken jejunum tissue.**
K. Promkhun*[1], C. Suwanvichanee[1], K. Thumanu[2], W. Molee[1], S. Kubota[1], P. Uimari[3], and A. Molee[1], [1]*School of Animal Technology and Innovation, Institute of Agricultural Technology, Suranaree University of Technology*, *Nakhon Ratchasima, Thailand*, [2]*Synchrotron Light Research Institute (Public Organization)*, *Nakhon Ratchasima, Thailand*, [3]*Department of Agricultural Sciences, Faculty of Agriculture and Forestry, University of Helsinki*, *Helsinki, Finland*.

P32 **ISAG Bursary Award: Genetic diversity in Nigeria laughing dove population using the mitochondria cytochrome C oxidase gene.**
I. A. Abubakar*[1], F. E. Sola-Ojo[1], C. A. Adeola[2], and M. O. Adesina[3], [1]*University of Ilorin*, *Ilorin, Kwara, Nigeria*, [2]*Chinese Academy of Sciences*, *Kunming, China*, [3]*Kwara State University*, *Malete, Kwara State, Nigeria*.

P33 **ISAG Bursary Award: Transcriptome analysis of pre-hierarchical follicles highlights dominance as the major mode of gene expression that underpins heterosis for egg number and clutch size in crossbred laying hens.**
A. M. Isa*[1,2], Y. Sun[1], and J. Chen[1], [1]*Key Laboratory of Animal (Poultry) Genetics Breeding and Reproduction, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*Department of Animal Science, Usmanu Danfodiyo University*, *Sokoto, Sokoto State, Nigeria*.

P34 **Comparative proteomics reveal the chicken sperm freezability.**
Y. Li*, Y. Zong, Y. Sun, J. Yuan, H. Ma, and J. Chen, *Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

P35 **Effects of single-nucleotide polymorphisms in histamine n-methyl transferase (hnmt) gene on anserine and carnosine contents in Korean native chickens.**
J. Munyaneza*[1], M. Kim[1], E. Cho[1], A. Jang[2], H. Choo[3], and J. Lee[1], [1]*Chungnam National University*, *Daejeon, Republic of Korea*, [2]*Kangwon National University*, *Chuncheon, Republic of Korea*, [3]*National Institute of Animal Science*, *Pyeongchang, Republic of Korea*.

P36 **Identification of core promoter region of polyunsaturated fatty acid synthesis-related gene family in chicken.**
Y.-T. Liu*, D.-D. Sun, X.-Q. Li, M.-Q. Ge, and Z.-C. Hou, *National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, MARA; College of Animal Science and Technology, China Agricultural University, Beijing, China*.

P37 **Assessment of incubation eggs quality of the local ducks crosses population.**
M. Saginbayeva*[1], R. Sharipov[2], A. Shamshidin[3], and G. Temirbekova[4], [1]*S. Seifullin Kazakh AgroTechnical Universit, Astana, Akmola Region, Kazakhstan*, [2]*Union of Poultry Breeders of Kazakhstan, Astana, Akmola Region, Kazakhstan*, [3]*Zhangir Khan University, Uralsk, Kazakhstan*, [4]*North-Kazakhstan Research Institute of Agriculture, Astana, Kazakhstan*.

P38 **Genome-wide association analysis (GWAS) and accuracy of genomic selection on growth traits in two duck lines using imputed genotypes.**
O. Matika*[1], E. Tarsani[1], S. Desire[1], K. McIntosh[1], A. Kranis[1], A. Rae[2], and K. Watson[1,3], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies University of Edinburgh, Edinburgh, Midlothian, United Kingdom*, [2]*Cherry Valley Farms (UK) Ltd, Grimsby, United Kingdom*, [3]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, United Kingdom*.

P40 **Genome-wide circular RNAs signatures involved in sexual maturation and its heterosis in chicken.**
Y. Wang, J. Yuan, Y. Sun, Y. Li, and J. Chen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing China*.

P41 **Profiling the diversity of the village chicken faecal microbiota using Amplicon and Shotgun metagenomic sequencing data.**
M. E. Nene*[1,2], N. W. Kunene[1], R. Pierneef[3], and K. Hadebe[2], [1]*University of Zululand, Mpangeni, KwaZulu Natal, South Africa*, [2]*Agricultural Research Council—Biotechnology Platform, Pretoria, Gauteng, South Africa*, [3]*University of Pretoria, Pretoria, Gauteng, South Africa*.

P42 **Identification of potential candidate genes for plumage color in Korean native duck based on whole-genome sequencing.**
E. Cho[1], M. Kim[1], H. Choo[2], and J. Lee*[1], [1]*Chungnam National University, Daejeon, Republic of Korea*, [2]*National Institute of Animal Science, Rural Development Administration, Pyeongchang, Gangwon-do, Republic of Korea*.

P43 **Using selection population revealed the mechanism of intramuscular fat formation in chicken.**
Y. Wang, L. Liu, H. Cui, and J. Wen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

P44 **Assessment of the usefulness of an additional set of six pigeon microsatellite markers for parentage testing and genetic diversity.**
A. Masior*, A. Szumiec, A. Radko, and K. Ropka-Molik, *Department of Animal Molecular Biology, National Research Institute of Animal Production, Krakowska, Balice, Poland*.

P45 **Landscape genomic approach to estimate the environmental suitability of village-based indigenous chickens in South African major production regions.**
R. R. Mogano*[1,2], T. J. Mpofu[1], B. J. Mtileni[1], K. Madlala[2], and T. Chokoe[3], [1]*Tshwane University Technology, Tshwane University Technology, Pretoria, Gauteng, South Africa*, [2]*Agricultural Research Council, Biotechnology Platform, Pretoria, Gauteng, South Africa*, [3]*Department of Agriculture, Land Reform and Rural Development, Pretoria, Gauteng, South Africa*.

P46 **ISAG Bursary Award: Complex genetic architecture of the chicken genome. An example of *Growth1* QTL region.**
J.-H. Ou*, T. Rönneburg, and C.-J. Rubin, *Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*.

P47 **Identification of runs of homozygosity in a commercial laying hen population.**
M. Neuditschko*[1], B. Makanjuola[3], C. Baes[2,3], and M. Toscano[2], [1]*Agroscope, Posieux, Fribourg, Switzerland*, [2]*University of Bern, Bern, Bern, Switzerland*, [3]*University of Guelph, Guelph, Ontario, Canada*.

P48 **Genome wide association study to investigate shank skin colour of indigenous village chickens from Limpopo and KwaZulu-Natal.**
M. G. Segakoeng* and K. Hadebe, *Agricultural Research Council—Biotechnology Platform, Onderstepoort, Pretoria, South Africa*.

P49 **The TuBaVi project: An example of biodiversity management in Italian local chicken breeds.**
D. Soglia[1], F. Perini[2], N. Stoppani[1], A. Schiavone[1], and E. Lasagna*[3], [1]*Department of Veterinary Sciences, University of Turin, Grugliasco, Italy*, [2]*Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Legnaro, Italy*, [3]*Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy*.

P50 **Some genetic factors controlling water intake in meat-type chickens.**
S. E. Aggrey*[1], A. F. A. Ghareeb[1], M. C. Milfort[1], A. L. Fuller[1], M. I. El-Sabry[2], F. K. R. Stino[2], and R. Rekaya[1], [1]*University of Georgia, Athens, GA*, [2]*Cairo University, Giza, Egypt*.

P51 **lncRNA analysis in response to diet changes in broiler chickens.**
F. Degalez[1], L. Lagoutte[1], C. Allain[2], and S. Lagarrigue*[2], [1]*INRAE, Saint-Gilles, France*, [2]*Institut Agro, Rennes, France*.

P52 **One Health Poultry Hub: A multidisciplinary project that aims to increase poultry sustainability in Southeast Asia.**
A. Hinsu[1], M. Hay[1], P. Koringa[2], M. A. Hoque[3], H. T. T. Pham[4], A. Conan[5], G. Fournie[1], D. Blake[1], F. Tomley[1], and A. Psifidi*[1], [1]*Royal Veterinary College, United Kingdom*, [2]*Anand Agricultural University, Anand, India*, [3]*Chattogram Veterinary and Animal Sciences University, Chattogram, Bangladesh*, [4]*CIRAD, Hanoi, Vietnam*, [5]*City University of Hong Kong, Hong Kong SAR, China*.

P53 **Potential of a chicken AIL population to decipher the genetic mechanisms of complex traits in the integrative omics era.**
X. Zhu[1], C. Li[1], C. Luo[2], Z. Pan[2], L. Fang[2], H. Qu[2], Y. Wang*[1], and Z. Hu[1], [1]*State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China*, [2]*Guangdong Key Laboratory of Animal Breeding and Nutrition, Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhong, China*.

P54 **The Chicken Genomic Diversity Consortium: Tracking immune diversity from ancient chickens to the present day.**
S. Fiddaman*[1], A. Smith[1], and L. Frantz[3,2], [1]*University of Oxford, Oxford, UK*, [2]*QMUL, London, UK*, [3]*LMU, Munich, Germany*.

P55 **Genome-wide association study of nucleotide and peptide contents of breast meat in Korean native chickens.**
M. Kim*[1], E. Cho[1], J. Munyaneza[1], A. Jang[2], H. Choo[3], and J. Lee[1], [1]*Chungnam National University, Daejeon, Korea*, [2]*Kangwon National University, Chuncheon, Gangwon-do, Korea*, [3]*National Institute of Animal Science, Rural Development Administration, Pyeongchang, Gangwon-do, Korea*.

P56 **ISAG Bursary Award: Invited Workshop Presentation: Chicken2K: A panel for global chicken genomic diversity and evolutionary inference.**
C. Ma*[1], M.-S. Peng[1,12], J. Smith[2], X. Huang[3], S. Zhang[1], X. Li[4], A. Esmailizadeh[1,5], S. C. Ommeh[6], D. W. Burt[7], A. C. Adeola[1,12], M.-S. Wang[1,12], O. Hanotte[8,9], J. Han[10,11], Y. Dong[4], Y.-P. Zhang[1,13], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*The Roslin Institute and R(D)SVS, University of Edinburgh, Midlothian, UK*, [3]*Guangdong Provincial Key Laboratory of Conservation and Precision Utilization of Characteristic Agricultural Resources in Mountainous Areas, School of Life Science, Jiaying University, Meizhou, Guangdong, China*, [4]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Kunming, Yunnan, China*, [5]*Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, Kerman, Iran*, [6]*Institute for Biotechnology Research (IBR), Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi, Kenya*, [7]*UQ Genomics, The University of Queensland, Brisbane, Australia*, [8]*Cells, Organisms and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, UK*, [9]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [10]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [11]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Nairobi, Kenya*, [12]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, Yunnan, China*, [13]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan University, Kunming, Yunnan, China*.

P57 **A multi-omics approach to provide complete genomic information on long-debated genes in birds.**
Q.-S. Zhao*[1], F. Zhu[1], Z.-T. Yin[1], Y.-X. Sun[1], Y.-C. Jie[1], J. Smith[2], L.-W. Shao[1], N. Yang[1], and Z.-C. Hou[1], [1]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, MARA; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*The Roslin Institute & R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK*.

P58 **Allele-specific expression in the jejunal transcriptome profiles of two laying hen strains over the entire production period.**
S. Ponsuksili*, F. Hadlich, M. A. Iqbal, H. Reyer, M. Oster, N. Trakooljul, E. Murani, and K. Wimmers, *Research Institute for Farm Animal Biology, Dummerstorf, Germany*.

P59 **Accumulated variations in the promoter regions play an important role for complex traits during duck domestication.**
Z.-T. Yin*[1], X.-Q. Li[1], Y.-X. Sun[1], J. Smith[2], N. Yang[1], and Z.-C. Hou[1], [1]*National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, MARA; College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*The Roslin Institute & R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK*.

P60 **ISAG Bursary Award: Genetic diversity and relationship between Nigerian Muscovy duck populations using the mitochondria cytochrome b gene.**
O. Yusuf*[1], F. Sola-Ojo[1], and C. Adeola[2], [1]*Faculty of Agriculture, Department of Animal Production, University of Ilorin, Kwara state, Nigeria*, [2]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*.

P61 **Different stress response strategies of an arctic breeding bird (*Calcarius lapponicus*) under inclement weather conditions revealed by the genome and RNA-seq analyses.**
Z. Wu*[1], M. M. Hindle[1], A. M. A. Reid[1], J. H. Pérez[2,3], J. S. Krause[2,4], J. C. Wingfield[2], S. L. Meddle[1], and J. Smith[1], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies R(D)SVS, University of Edinburgh, United Kingdom*, [2]*Department of Neurobiology Physiology Behavior, University of California, Davis, CA*, [3]*Department of Biology, University of South Alabama, Mobile, AL*, [4]*Department of Biology, University of Nevada Reno, Reno, NV*.

P62 **ISAG Bursary Award: Potential of a chicken AIL population to decipher the genetic mechanisms of complex traits in the integrative omics era.**
X. Zhu*[1], C. Li[1], C. Luo[2], H. Zhou[3], L. Fang[4], H. Qu[2], Y. Wang[1], and X. Hu[1], [1]*State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China*, [2]*State Key Laboratory of Livestock and Poultry Breeding, Institute of Animal Science, Guangdong Academy of Agricultural Sciences, Guangzhou, China*, [3]*Department of Animal Science, University of California, Davis, CA*, [4]*Center for Quantitative Genetics and Genomics (QGG), Aarhus University, Aarhus, Denmark*.

P63 **ISAG Bursary Award: A lncRNA gene-enriched atlas for GRCg7b chicken genome and its functional annotation across 47 tissues.**
F. Degalez*[1,2], M. Charles[2], S. Foissac[2], H. Zhou[3], D. Guan[3], C. Alain[1,2], L. Fang[4], C. Klopp[2], L. Lagoutte[1,2], B. Lebez[1,2], F. Lecerf[1,2], F. Pitel[2], B. Vourc'h[1,2], T. Zerjal[2], S. Lagarrigue[1,2], [1]*Institut Agro, France*, [2]*INRAE, France*, [3]*University of California Davis, Davis, CA*, [4]*Aarhus University, Denmark*.

P64 **High-throughput detection of single nucleotide polymorphisms with flexible content panels.**
S. Camiolo[1], J. Yeakley[1], E. Clark[2], B. Seligmann[1], and J. McComb*[1], [1]*BioSpyder Technologies Inc, Carlsbad, CA*, [2]*Zoetis Inc, Kalamazoo, MI*.

Cattle Molecular Markers and Parentage Testing

P66 **Genetic diversity and population structure of Zambian indigenous cattle.**
E. Musimuko*[1,3], K. S. Nalumamba[1], V. C. Zulu[1], K. I. Odubote[2], and W. Muleya[1], [1]*University of Zambia, School of Veterinary Medicine, Lusaka Zambia*, [2]*University of Zambia, School of Agricultural Sciences, Lusaka Zambia*, [3]*Ministry of Fisheries and Livestock, Department of Livestock Research and Development, Lusaka Zambia*.

P67 **Effects of training population sizes in detecting genomic markers for low heritability traits in beef cattle.**
J. K. Macharia*, J. H. Lee, and S. H. Lee, *Chungnam National University, Division of Animal and Dairy Sciences, Republic of Korea*.

P68 **Association of copy number variants with coat colour in Nguni cattle investigated using BovineHD SNP and Bionano optical mapping data.**
N. M. Dlamini*[1,2], E. F. Dzomba[2], M. Magawana[3], S. Ngcamu[3], and F. C. Muchadeyi[1], [1]*Agricultural Research Council-Biotechnology Platform, Onderstepoort, Pretoria, South Africa*, [2]*University of KwaZulu-Natal, Scottsville, Pietermaritzburg, South Africa*, [3]*KwaZulu-Natal (KZN) Department of Agriculture & Rural Development, Pietermaritzburg, South Africa*.

P69 **Genomic assessment of inbreeding and identification of markers associated with carcass weight gain in Portuguese Preta cattle using a medium-density SNP-chip.**
M. C. Feliciano[1,2], A. J. Amaral*[3,4], F. Teixeira[3,5], F. Ferreira[6], E. Bettencourt[1], and L. T. Gama[3], [1]*Instituto Mediterrâneo para Agricultura Ambiente e Desenvolvimento, University of Évora, Polo da Mitra, Évora, Portugal*, [2]*University Lusófona, Campo Grande, Lisboa, Portugal*, [3]*Centre for Interdisciplinary Research in Animal Health and Associate Laboratory for Animal and Veterinary Sciences, Faculty of Veterinary Medicine, University of Lisbon, Lisboa, Portugal*, [4]*Escola de Ciências e Tecnologia University of Évora, Largo dos Colegiais, Évora, Portugal*, [5]*Faculty of Veterinary Medicine, University José Eduardo dos Santos, Huambo, Angola*, [6]*Associação de Criadores de Bovinos da Raça Preta, Samora Correia, Portugal*.

P70 **Low-density genotype panels performance for parentage verification in South African beef cattle breeds.**
Y. Sanarana*[1,2], D. Berry[1,3], A. Maiwashe[2], C. Banga[2,4], and E. Van Marle-Köster[1], [1]*University of Pretoria, Hatfield, Pretoria, Gauteng, South Africa*, [2]*Agricultural Research Council, Irene, Pretoria, Gauteng, South Africa*, [3]*Teagasc, Fermoy, County Cork, Ireland*, [4]*Botswana University of Agriculture and Natural Resources, Gaborone, Botswana*.

P71 **Genetic diagnosis of sex chromosome aberrations in cattle based on parentage test by microsatellite DNA, X- and Y-linked markers.**
L. Borreguero*[1], M. R. Maya[2], A. Trigo[2], I. Bonet[2], and J. A. Bouzada[1], [1]*Laboratorio Central de Veterinaria, Algete, Madrid, Spain*, [2]*Tecnologias y Servicios Agrarios S.A, Madrid, Spain*.

Companion Animal Genetics and Genomics

P72 **Independent *COL17A1* variants in cats with junctional epidermolysis bullosa (JEB).**
S. Kiener[1,2], H. Troyer[3], D. Ruvolo[3], A. Rostaher[4], P. Grest[5], S. Soto[2,6], E. A. Mauldin[7], C. Yang[7], V. Jagannathan[1,2], and T. Leeb*[1,2], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Dermfocus, University of Bern, Bern, Switzerland*, [3]*Oradell Animal Hospital, Paramus, NJ*, [4]*Clinic for Small Animal Internal Medicine, Vetsuisse Faculty University of Zurich, Zurich, Switzerland*, [5]*Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*, [6]*Institute of Animal Pathology, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [7]*University of Pennsylvania, School of Veterinary Medicine, Philadelphia, PA*.

P73 **AgriseqRI 1.0: Reporting utility for canine traits and disorders panel.**
S. Chadaram*[1], A. Burrell[1], K. R. Gujjula[1], N. Anjuri[2], A. Udumudi[2], and S. Udumudi[2], [1]*Thermo Fisher Scientific, Austin, TX*, [2]*ATS GeneTech Pvt, Ltd, Hyderabad, Telangana, India*.

P74 **Design and validation of high density SNP array for Indian dog populations.**
R. Kolandanoor Nachiappan*, R. Arora, S. Ahlawat, U. Sharma, M. Raheja, M. Maggon, A. K. Mishra, and R. K. Vijh, *ICAR-National Bureau of Animal Genetic Resources, Karnal, Haryana, India*.

P75 **Genetic parameters and genome wide association studies for feed efficiency-related traits in F2 Nguni × Angus cattle.**
L. Nesengani*[1], N. Nemukondeni[1], N. Mkize[2], B. Dube[2], T. Masebe[1], and N. Mapholi[1], [1]*University of South Africa, Florida, South Africa*, [2]*Agricultural Research Council, Irene, South Africa*.

P76 **Are the rules of World Union of German Shepherd Clubs (WUSV) enough for the maintenance of genetic diversity of the breed in Brazil?**
F. M. de Andrade*[1], I. A. Scabello[1], A. V. L. Pereira[2], A. G. Sedrez[3], and J. A. Cobuci[1], [1]*Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil*, [2]*Universidade Federal da Bahia, Salvador, BA, Brazil*, [3]*Universidade Federal de Pelotas, Pelotas, RS, Brazil*.

P77 **AgriseqPI 1.0: Reporting utility for SNP based parentage determination with targeted genotyping by sequencing panels.**
S. Chadaram*[1], A. Burrell[1], K. R. Gujjula[1], C. Carrasco[1], S. Daly[3], S. Udumudi[2], N. Anjuri[2], V. H. Kema[2], and A. Udumudi[2], [1]*Thermo Fisher Scientific, Austin, TX*, [2]*ATS GeneTech Pvt, Ltd, Hyderabad, Telangana, India*, [3]*Thermo Fisher Scientific, Lissieu, Lyon, France*.

P78 **ISAG Bursary Award: *RETREG1* variant causes canine acral mutilation syndrome (AMS) in purebred German spitz.**
A. Letko*[1,2], J. Plassais[1], P. Quignon[1], and C. André[1], [1]*Institut de Génétique et Développement de Rennes (IGDR), University Rennes, Rennes, France*, [2]*Institute of Genetics, University of Bern, Bern, Switzerland*.

P79 **Comparative genomics of the natural killer cell receptor genes in felids.**
J. Futas[1,2], A. Jelinek[1], M. Plasil[2], J. Bubenikova[2], P. Burger[3], and P. Horin*[1,2], [1]*Department of Animal Genetics, Faculty of Veterinary Medicine, University of Veterinary Sciences Brno, Brno, Czech Republic*, [2]*Ceitec Vetuni, RG Animal Immunogenomics, University of Veterinary Sciences Brno, Brno, Czech Republic*, [3]*Research Institute of Wildlife Ecology, University of Veterinary Medicine, Vienna, Austria*.

P80 **ISAG Bursary Award: *PCYT2* missense variant in Saarloos Wolfhounds with neurodegeneration.**
M. Christen*[1], M. K. Hytönen[2], H. Lohi[2], A. Kehl[3], V. Jagannathan[1], and T. Leeb[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*, [2]*Department of Medical and Clinical Genetics, University of Helsinki, and Folkhälsan Research Center, Helsinki, Finland*, [3]*Laboklin GmbH & Co. KG, Steubenstraße 4, Bad Kissingen, Germany*.

P81 **Genomic resources for the domestic cat.**
L. Lyons*[1], G. Habacher[2], R. Malik[3], L. Coghill[4], and 99 Lives Cat Genome Sequencing Consortium[5], [1]*Department of Veterinary Medicine & Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO*, [2]*Raddenstiles Veterinary Surgery, CVS UK Ltd, Exmouth, UK*, [3]*Centre for Veterinary Education, The University of Sydney, Sydney, NSW, Australia*, [4]*Department of Veterinary Pathobiology, College of Veterinary Medicine, University of Missouri, Columbia, MO*, [5]*99 Lives Cat Genome Sequencing Consortium*.

P82 **ISAG Bursary Award: Genomic and transcriptomic characterisation of hypertrophic cardiomyopathy in British Shorthair and Birman cats.**
T. Smedley*, L. Wilkie, V. Fuentes, D. Connolly, and A. Psifidi, *Royal Veterinary College, London, United Kingdom*.

Comparative and Functional Genomics

P83 **Long-term effect of dietary antioxidants supplementation to pregnant sows on early ovarian functionality in gilt progeny.**
Y. Núñez*[1], G. Gómez[2], H. Laviano[3], F. García[1], M. Muñoz[1], J. García Casco[1], R. Benítez[1], F. Sánchez-Esquiliche[4], A. González-Bulnes[5], A. Rey[3], C. López-Bote[3], and C. Ovilo[1], [1]*Instituto Nacional Investigacion y Tecnologia Agraria y Alimentaria—Consejo Superior de Investigaciones Cientificas, Madrid, Spain*, [2]*Instituto Regional de Investigacion y Desarrollo Agroalimentario y Forestal, Oropesa, Toledo, Spain*, [3]*Facultad de Veterinaria, Universidad Complutense, Madrid, Spain*, [4]*Sanchez Romero Carvajal, Jabugo, Huelva, Spain*, [5]*Facultad de Medicina Veterinaria, Universidad Cardenal Herrera—CEU, Valencia, Spain*.

P84 **ISAG Bursary Award: Functional variants associated with male fertility in reproductive tissues of Brown Swiss bulls.**
X. Mapel*, N. Kadri, Q. He, A. Leonard, A. Lloret-Villas, and H. Pausch, *ETH Zürich, Zürich, Switzerland*.

P85 **Identification of consensus homozygous regions and their associations with growth and feed efficiency traits in American mink.**
P. Davoudi*[1], D. Ngoc Do[1], S. Colombo[1], B. Rathgeber[1], M. Sargolzaei[2,3], G. Plastow[4], Z. Wang[4], and Y. Miar[1], [1]*Department of Animal Science and Aquaculture, Dalhousie University, Truro, NS, Canada*, [2]*Department of Pathobiology, University of Guelph, Guelph, ON, Canada*, [3]*Select Sires Inc, Plain City, OH*, [4]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

P86 **Single-cell RNA sequencing reveals thoracolumbar vertebra heterogeneity and rib-genesis in pigs.**
J. Li*[1], L. Wang[2], D. Yu[3], H. Xie[4], and Y. Zhang[5], [1]*State Key Laboratory of Genetic Resources and Evolution, Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*, [3]*State Key Laboratory of Stem Cell and Reproductive Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing China*, [4]*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*, [5]*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*.

P87 **Online Mendelian Inheritance in Animals—Introducing OMIA variant IDs and the Vertebrate Breed Ontology.**
I. Tammen*[1], M. Mather[1], S. Toro[2], K. R. Mullen[2], H. M. Rondo[2], N. Vasilevsky[2], N. Matentzoglu[3], M. Haendel[2], Z.-L. Hu[4], C. A. Park[4], G. Leroy[5], and F. W. Nicholas[1], [1]*The University of Sydney, Sydney, NSW, Australia*, [2]*University of Colorado Anschutz Medical Campus, Aurora, CO*, [3]*Semanticly, Athens, Greece*, [4]*Department of Animal Science, Ames, IA*, [5]*Food and Agricultural Organization of the United Nations, Rome, Italy*.

P88 **Is a combination of biomarkers a good strategy to assign animals to stress categories when studying differences in transcriptomic profiles?**
C. Diaz*[1], J. Rosa[1], R. Peiro[1], C. Meneses[1], J. de la Fuente[2], C. Gonzalez-Verdejo[1], M. Ramon[3], and M. Carabaño[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*UCM, Madrid, Spain*, [3]*CERSYRA-IRIAF, Valdepeñas, Spain*.

P89 **Genome-wide association studies and pathway enrichment analyses for growth curve parameters in American mink.**
D. N. Do[1], M. Sargolzaei[2,3], G. Plastow[4], Z. Wang[4], and Y. Miar*[1], [1]*Department of Animal Science and Aquaculture, Dalhousie University, Truro, NS, Canada*, [2]*Department of Pathobiology, University of Guelph, Guelph, ON, Canada*, [3]*Select Sires Inc, Plain City, OH*, [4]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

P90 **Incidence of stillbirth across fourteen generations in South African Holstein dairy cattle.**
M. Mamakoko*, O. Tada, and T. Tyasi, *University of Limpopo, Polokwane, Limpopo, South Africa*.

P91 **Phenotypic and genotypic identification of hard ticks (Acari: Ixodidae) species infesting cattle in South Africa.**
T. Makwarela*[1], N. Mapholi[1], T. Masebe[1], L. Nesengani[1], R. Smith[1], N. Nyangiwe[2], and D. Appolinaire[3], [1]*University of South Africa, Florida, Gauteng, South Africa*, [2]*Döhne Agricultural Development Institute, Stutterheim, Eastern Cape, South Africa*, [3]*University of Edinburgh, Edinburgh, UK*.

P92 **Phylogenetic analysis of bacterial tick-borne pathogen species found in South Africa.**
N. Mametja* and T. Masebe, *University of South Africa, Florida, Johannesburg, South Africa*.

P93 **Explore of major adipogenic regulation factors and genes for pork belly parameters using the AWM-PCIT network analysis.**
J.-M. Kim*, *Department of Animal Science and Technology, Chung-Ang University, Gyeonggi-do, Anseong-si, Republic of Korea*.

P94 **Genetic resources and biodiversity biobanks: A win-win situation.**
K. Labuschagne*, *South African National Biodiversity Institute, Pretoria, Gauteng, South Africa*.

P95 **Global phylogeography and population genomics of the commercially exploited smoothhound shark, *Mustelus mustelus*.**
J. C. Winn*[1], A. E. Bester Van der Merwe[1], and S. N. Maduna[2], [1]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [2]*Norwegian Institute of Bioeconomy Research, Svanhovd Research Station, Svanvik, Norway*.

P96 **ISAG Bursary Award: Ribosome profiling reveals stage-specific translational regulation during muscle differentiation.**
A. Goldkamp*[1], L. Okamoto[2], K. Thornton[2], and D. Hagen[1], [1]*Oklahoma State University, Stillwater, OK*, [2]*Utah State University, Logan, UT*.

P97 **ISAG Bursary Award: Adipose gene expression profiles of four cattle breeds highlight selective pressures and tissue functions.**
D. Ruvinskiy*[1], K. Pokharel[1], A. Amaral[2], M. Weldenegodguad[1], M. Honkatukia[1,3], H. Lindberg[1], J. Peippo[1,3], P. Soppela[4], P. Uimari[5], C. Ginja[6], and J. Kantanen[1], [1]*Natural Resources Institute Finland (Luke), Jokioinen, Finland*, [2]*CIISA—Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal*, [3]*Nordic Genetic Resources Center, Ås, Norway*, [4]*Arctic Centre, University of Lapland, Rovaniemi, Finland*, [5]*Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland*, [6]*BIOPOLIS-CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*.

P98 **Transcriptome and histological analysis of skin Brangus cattle under heat stress conditions.**
P. Alvarez Cecco*[1], M. Balbi[1], M. Bonamy[1], A. Rogberg-Muñoz[2], L. H. Olivera[1], G. Giovambattista[1], and M. E. Fernández[1], [1]*Intituto de Genética Veterinaria (IGEVET), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*Instituto de Investigaciones en Producción Animal (INPA), Universidad de Buenos Aires, CONICET, Buenos Aires, Buenos Aires, Argentina*.

P99 **Chromosome conformation comparison in Piedmontese × Gaur F1 fetal muscle tissue.**
M. R. Stegemiller*[1], K. L. Kuhn[2], T. P. Smith[2], B. D. Rosen[3], and B. M. Murdoch[1], [1]*Department of Animal, Veterinary, and Food Sciences, University of Idaho QQMoscow, ID*, [2]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE*, [3]*USDA, ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD*.

P100 **Exploring tissue-specificity in the regulatory landscape of bovine genome.**
G. Costa Monteiro Moreira*[1], C. Yuan[1], S. Dupont[1], L. Tang[1], Y. Lee[1], D. Becker[2], M. Salavati[3], R. Clark[4], E. Clark[3], G. Plastow[5], C. Kühn[2,6], C. Charlier[1], and BovReg consortium[7], [1]*Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium*, [2]*Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany*, [3]*The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [4]*Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK*, [5]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, [6]*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [7]*https://www.bovreg.eu/project/consortium/*.

P101 **A multi-omic approach to understanding genetic and phenotypic variation in mass reared black soldier flies (*Hermetia illucens*).**
C. Rhode*, K. Hull, and M. Greenwood, *Stellenbosch University, Stellenbosch, Western Cape, South Africa*.

P102 **ISAG Bursary Award: DNA methylation dynamics regulating embryonic development in pig.**
J. de Vos*[1], M. Derks[1], H. Acloque[2], S. Djebali[3], S. Foissac[4], C. Guyomar[4], C. Kurylo[4], E. Giuffra[2], M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University, Wageningen, the Netherland*, [2]*Paris-Saclay University, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [3]*IRSD, Université de Toulouse, INSERM, INRA, ENVT, UPS, Toulouse, France*, [4]*GenPhySE, Université de Toulouse, INRAE, ENVT, Toulouse, France*.

P103 **Genomic and functional characterization of frequently used bovine cell lines.**
D. Becker*[1], G. C. M. Moreira[2], C. Mörke[1], M. Charles[3], F. Hadlich[1], C. Lopez-Roques[10], M. Schmicke[4], V. Blanchet[5], H. Taniguchi[6], E. Clark[7], C. Pfarrer[8], J. Vanselow[1], C. Charlier[2], D. Rocha[3], C. Kuehn[1,11], [1]*Research Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [2]*Unit of Animal Genomics, GIGA, Liege, Belgium*, [3]*INRAE, Jouy-en-Josas, France*, [4]*Veterinary Endocrinology and Laboratory Diagnostics, University of Veterinary Medicine Hannover, Foundation, Hannover, Germany*, [5]*Unité de Génétique Moléculaire Animale (UGMA), University of Limoges, Limoges, France*, [6]*Institute of Genetics & Animal Biotechnology, Polish Academy of Sciences, Magdalenka, Poland*, [7]*The Roslin Institute, Edinburgh, UK*, [8]*Institute of Anatomy, University of Veterinary Medicine Hannover, Foundation, Hannover, Germany*, [9]*Agricultural and Environmental Faculty, University Rostock, Rostock, Germany*, [10]*INRAE, US 1426, GeT-PlaGe, Genotoul, Castanet-Tolosan, France*, [11]*Agricultural and Environmental Faculty, University Rostock, Rostock, Germany*.

P104 **ISAG Bursary Award: Single cell atlas of developing ovine tail tissue reveals multi cellular origins contributing to fat deposition.**
J. Han*[1,2], [1]*Institute of Animal Science, Chinese Academy of Agriculture Science, Beijing, China*, [2]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*.

P105 **A multi-tissue porcine single-cell immune atlas: Resources for comparative and systems immunology.**
C. Tuggle*[1,2], L. Daharsh[1], M. Kapoor[1,2], P. BK[2], S. Sivasankaran[3], K. Byrne[3], J. Herrera-Uribe[1], and C. Loving[3], [1]*Department of Animal Science, Iowa State University, Ames, IA*, [2]*Bioinformatics and Computation Biology, Iowa State University, Ames, IA*, [3]*USDA-Agriculture Research Service, National Animal Disease Center, Food Safety and Enteric Pathogens Research Unit, Ames, IA*.

P106 **Genome-wide association study between copy number variations and economically important traits in American mink.**
P. Davoudi*[1], D. Ngoc Do[1], B. Rathgeber[1], S. Colombo[1], M. Sargolzaei[2,3], G. Plastow[4], Z. Wang[4], G. Hu[1], S. Valipour[1], and Y. Miar[1], [1]*Department of Animal Science and Aquaculture, Dalhousie University, Truro, NS, Canada*, [2]*Department of Pathobiology, University of Guelph, Guelph, ON, Canada*, [3]*Select Sires Inc, Plain City, OH*, [4]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

Comparative MHC Genetics

P107 **Successful reduction of proviral load by a novel bovine leukemia virus vaccine targeting cattle carrying susceptible bovine leukocyte antigen (BoLA)-*DRB3* allele.**
Y. Aida*[1,2], S.-N. Takeshima[2,3], L. Bai[2,4], J. Kim[2], Y. Matsumoto[2], R. Matsuura[1,2], and J. Kohara[5], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Viral Infectious Diseases Unit, RIKEN, Saitama, Japan*, [3]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*, [4]*Graduate School of Science and Engineering, Iwate University, Iwate, Japan*, [5]*Animal Health Group, Animal Research Center, Hokkaido Research Organization, Hokkaido, Japan*.

P108 **MHC haplotype diversity in the main equine breeds of the Iberian Peninsula.**
M. García-Martínez[1], A. Cequier[1,2], E. Bernad[1], B. Serrano[1], A. Romero[1,2], F. Vázquez[1,2], A. Vitoria[1,2], S. Fuente[1,2], C. Cons[1], C. Rodellar*[1], and L. Barrachina[1,2], [1]*Laboratorio de Genética Bioquímica LAGENBIO-Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA)—Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

Domestic Animal Sequencing and Annotation

P109 **ISAG Bursary Award: Comparative genomics reveals common diversity and signature of selection in Saudi Arabian indigenous chickens.**
A. Assiri*[1,2], [1]*University Of Nottingham, Nottingham, United Kingdom*, [2]*King Faisal University, Al-Hufuf, Saudi Arabia*.

P110 **AgriSeqSV: A solution to genotype structural variants on AgriSeq™.**
K. R. Gujjula[1], A. Burrell[1], S. Daly[2], M. Lelievre[2], and S. Chadaram*[1], [1]*Thermo Fisher Scientific, Austin, TX*, [2]*Thermo Fisher Scientific, Lissieu, Lyon, France*.

P111 **Growth and development of Kazakh white-head breed bulls of different genotypes depending on the type of temperaments.**
R. Uskenov*, S. Bostanova, and B. Akkair, *Saken Seifullin Kazakh Agrotechnical Research University, Astana, Kazakhstan*.

P112 **Identification of characteristic aroma substances and their metabolic precursors in chickens.**
Y. Wang, Y. Jin, X. Liu, H. Cui, and J. Wen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

P113 **Development of genomic tools for American mink (*Neogale vison*).**
Y. Miar*, *Dalhousie University, Truro, Nova Scotia, Canada*.

P114 **ISAG Bursary Award: An organism-wide ATAC-Seq peak catalogue for the bovine and its use to identify regulatory variants.**
C. Yuan*[1], L. Tang[1], T. Lopdell[2], C. Oget-Ebrad[1], G. Costa Monteiro Moreira[1], J. L. Gualdron[1], Z. Cheng[3], M. Salavati[3], D. C. Wathes[3], M. A. Crowe[4], W. Coppieters[1], C. Charlier[1], T. Druet[1], M. Georges[1], H. Takeda[1], [1]*GIGA Institute, University of Liège, Liège, Belgium*, [2]*Livestock Improvement Corporation, Hamilton, New Zealand*, [3]*Royal Veterinary College, Herts, UK*, [4]*School of Veterinary Medicine, University College Dublin, Dublin, Ireland*.

P115 **Discovery of deleterious genetic variants in farmed animals.**
X. R. Arias[1], J. L. Petersen[2], B. M. Murdoch[3], F. M. McCarthy[4], and T. S. Kalbfleisch*[1], [1]*University of Kentucky, Lexington, KY*, [2]*University of Nebraska–Lincoln, Lincoln, NE*, [3]*University of Idaho, Moscow, ID*, [4]*University of Arizona, Tucson, AZ*.

P116 **ISAG Bursary Award: Identification and comparison of plant-derived miRNAs based on massive public data.**
H. Liu*[1], P. Xu[1], Y. Liao[1], C. Li[1], J. Dou[1], Y. Wang[1], Z. Tang[1], J. Xu[1], D. Yin[1], S. Zhu[1], L. Yin[1,2], M. Yu[1], S. Zhao[1,2], X. Liu[1,2], Y. Fu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, China*.

P117 **Overview of Ruminant T2T Consortium.**
B. M. Murdoch*[1], S. D. McKay[2], B. D. Rosen[3], and T. P. L. Smith[4], [1]*University of Idaho, Moscow, ID*, [2]*University of Missouri, Columbia, MO*, [3]*USDA, Agricultural Research Service, USDA, Animal Genomics and Improvement Laboratory, Beltsville Agricultural Research Center, Beltsville, MD*, [4]*USDA, Agricultural Research Service, USDA, Genetics and Animal Breeding, Clay Center, NE*.

P118 **Discovering the missing structural variation in the bovine genome.**
A. Chamberlain*[1,2], T. Nguyen[1], J. Wang[1], and I. Macleod[1,2], [1]*Agriculture Victoria, Bundoora, Victoria, Australia*, [2]*La Trobe University, Bundoora, Victoria, Australia*.

Equine Genetics and Thoroughbred Parentage Testing

P119 **Characterization of genetic variants of equine cathelicidin.**
T. Ishige*, M. Kikuchi, H. Kakoi, K.-I. Hirota, A. Ohnuma, T. Tozaki, and S.-I. Nagata, *Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*.

P120 **Overlapping allelic ranges in equine STR panel for parentage verification—Technical notes.**
A. Bieniek* and A. Piestrzynska-Kajtoch, *National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland*.

P121 **ISAG Bursary Award: Investigating the effect of chromosome 20 on lordosis in Saddlebred horses.**
N. Yousefi-Mashouf*, K. Graves, T. Kalbfleisch, and E. Bailey, *University of Kentucky, Lexington, KY*.

P122 **Developmental validation of 36 plex equine profiling kit.**
S. Zeinali*, *Genetek Biopharma, Berlin, Germany*.

P123 **Contribution of STR genotyping to animal clinical cytogenetics.**
T. Raudsepp*, J. Kjöllerström, and R. Juras, *School of Veterinary Medicine, Texas A&M University, College Station, TX*.

P124 **Development of a robust across breed equine parentage SNP panel for ISAG approval.**
R. R. Bellone*[1,2], T. A. Mansour[2,3], E. Esdaile[1], B. Wallner[4], T. Raudsepp[5], B. Till[1], A. Kallenberg[1], S. Hughes[1], S. Chadaram[6], S. Shrestha[6], R. A. Grahn[1], Equine ISAG SNP Panel Consortium[1], F. Avila[1], M. McCue[7], P. Flynn[8], [1]*Veterinary Genetics Laboratory, School of Veterinary Medicine, UC Davis, Davis, CA*, [2]*Department of Population Health and Reproduction, School of Veterinary Medicine, UC Davis, Davis, CA*, [3]*Department of Clinical Pathology, School of Medicine, Mansoura University, Mansoura, Egypt*, [4]*Institute of Animal Breeding and Genetics, Veterinary University of Vienna, Vienna, Austria*, [5]*Veterinary Integrative Biosciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX*, [6]*Thermo Fisher Scientific, Austin, TX*, [7]*Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, MN*, [8]*Weatherbys Scientific, Kildare, Ireland*.

Genetics and Genomics of Aquaculture Species

P125 **ISAG Bursary Award: Introgressive hybridization levels of tilapiines species in Lake Victoria basin, Kenya, inferred from microsatellite and mitochondrial DNA genotyping based on next-generation sequencing.**
G. Kwikiriza*[1,2], T. Vijayan[1], P. D. Tibihika[3], M. Curto[1,4], G. Winkler[5], J. K. Nattabi[2], J. Kariuki[6], and H. Meimberg[1], [1]*Institute for Integrative Nature Conservation Research, University of Natural Resources and Life Sciences Vienna (BOKU), Vienna, Austria*, [2]*Makerere University Kampala, Kampala, Uganda*, [3]*National Fisheries Resources Research Institute, Aquaculture Research and Development Center, Kampala, Uganda*, [4]*MARE-Marine and Environmental Sciences Centre, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, Lisbon, Portugal*, [5]*Institute of Hydrobiology and Water Management, University of Natural Resources and Life Sciences Vienna (BOKU), Vienna, Austria*, [6]*Department of Biochemistry, University of Nairobi, Nairobi, Kenya*.

P126 **ISAG Bursary Award: Phylogenetic status and origin of monogenean gill parasites of *Synodontis* spp. (Actinopterygii, Siluroidei) from Cameroon: Influence of the ichthyological province.**
J. A. Mbondo*[1], D. N. D. Bahanak[1], E. D. Bayiha[2], and C. F. Bilong Bilong[2], [1]*Institute of Agricultural Research for Development, Yaounde, Centre, Cameroon*, [2]*University of Yaounde I, Yaounde, Centre, Cameroon*.

P127 **Comparative gene expression and regulation of the response of head kidney immune-related cells of turbot (*Scophthalmus maximus*) to common virus (Poly I:C) and bacteria (*Vibrio*) triggers after in vitro and in vivo challenges.**
O. Aramburu[1], B. G. Pardo[1], P. R. Villamayor[1], J. Lamas[1], P. S. Dewari[2], D. Perojil[2], D. J. Macqueen[2], C. Bouza[1], and P. Martínez*[1], [1]*Universidade de Santiago de Compostela, Lugo, Spain*, [2]*University of Edinburgh, Midlothian, United Kingdom*.

P128 **ISAG Bursary Award: Metagenomics analysis of salt-fermented hilsa (*Tenualosa ilisha*) at different processing stages.**
H. Muhammad Shahdat*[1] and S. Islam Sarkar[2], [1]*National Institute of Biotechnology, Savar, Dhaka, Bangladesh*, [2]*Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh*.

P129 **Digital phenotyping of omega-3 fatty acid content in Atlantic salmon (*Salmo salar*) using Raman spectroscopy.**
G. F. Difford*[1,2], J. Park[1,2], S. S. Horn[2], B. Ruyter[2], B. Hillestad[3], A. Sonesson[2], and N. K. Afseth[2], [1]*Norwegian University of Life Sciences (NMBU), Ås, Norway*, [2]*Norwegian Insitute of Food, Fisheries and Aquaculture (NOFIMA), Tromsø, Norway*, [3]*Benchmark Genetics AS, Bergen, Norway*.

P130 **Metabolomics analysis of select sea cucumber species from Southern Africa.**
C. Upton*[1], M. Okpeku[1], G. Prinsloo[2], and O. Bodede[3], [1]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa*, [2]*Department of Agriculture and Animal Health, UNISA, Pretoria, South Africa*, [3]*Department of Chemistry, University of Pretoria, Hatfield Campus, South Africa*.

P131 **ISAG Bursary Award: A high-density genetic linkage map and QTL mapping for growth traits in South African abalone (*Haliotis midae*).**
T. Tshilate*[1], E. Ishengoma[2], and C. Rhode[1], [1]*Department of Genetics, Stellenbosch University, Stellenbosch, South Africa*, [2]*Mkwawa University College of Education, University of Dar es Salaam, Iringa, Tanzania*.

P132 **Utilizing of genetic evaluation system using genomic information of the Korean flatfish population.**
D. Lee*[1], J. Kang[1], Y. Chung[1], S. Lee[1], Y. Kim[2], J. Park[3,1], D. Lee[3], J. Kim[3], H. Yang[3], J. Lee[3], and S. Lee[1], [1]*Chungnam National University, Yuseong-gu, Daejeon, Republic of Korea*, [2]*Quantomic research & solution, Yuseong-gu, Daejeon, Republic of Korea*, [3]*Fish Genetics and Breeding Research Center, Geoje, Republic of Korea*.

P133 **Multi-functional genomic analyses identify causal gene and variants modulating viral nervous necrosis resistance in European seabass.**
R. Mukiibi*[1], L. Peruzza[2], C. Penaloza[3], M. Babbucci[2], R. Franch[2], M. Freguglia[4], S. Laureau[4], G. Dalla Rovere[2], D. Bertotto[2], S. Ferraresso[2], C. Tsigenopoulos[5], R. D. Houston[3], L. Bargelloni[2], and D. Robledo[1], [1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, United Kingdom*, [2]*Department of Comparative Biomedicine and Food Science, University of Padova, Padova, Italy*, [3]*Benchmark Genetics, Edinburgh, United Kingdom*, [4]*Valle Cà Zuliani Società Agricola s.r.l., Conselice (RA), Italy, Rovigo, Italy*, [5]*Institute of Marine Biology, Biotechnology and Aquaculture (IMBBC), Hellenic Centre for Marine Research (HCMR) Crete, Heraklion, Greece*.

P134 **Atlantic salmon miRNAs associated with smolitification and sea-water adaptation.**
R. Andreassen*[1], A. Shwe[1], S. Ramberg[1], A. Krasnov[2], and T. Østbye[2], [1]*Oslo Metropolitan University, Oslo, Norway*, [2]*Nofima (Norwegian Institute of Food, Fisheries and Aquaculture Research), Ås, Norway*.

P135 **Whole-genome sequencing data provide a landscape picture of genetic variability in sea cucumber species.**
F. Bertolini*[1], A. Ribani[1], V. Taurisano[1], A. Rakaj[2], A. Fianchini[2], F. Capoccioni[3], D. Pulcini[3], S. Bovo[1], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Department of Biology, University of Rome Tor Vergata, Rome, Italy*, [3]*Centro di ricerca "Zootecnia e Acquacoltura," Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria (CREA), Monterotondo (Rome), Italy*.

P136 **ISAG Bursary Award: Construction of a high-density genetic linkage map using 2b-RAD sequencing in dusky kob (*Argurosomus japonicus*).**
T. Jackson and C. Rhode*, *Stellenbosch University, Stellenbosch, South Africa*.

P137 **Competing endogenous RNA (ceRNA) in a non-model animal: Non-coding RNAs respond to heat stress in rainbow trout (*Oncorhynchus mykiss*) through ceRNA-regulated mechanisms.**
J. Quan*, *Gansu Agricultural University, Lanzhou, China*.

P138 **Genetic variation in disease resistance traits in hybrid striped bass.**
J. Abernathy*[1], M. Lange[1], B. Farmer[2], M. McEntire[2], and S. Rawles[2], [1]*United States Department of Agriculture, Agricultural Research Service, Auburn, AL*, [2]*United States Department of Agriculture, Agricultural Research Service, Stuttgart, AR*.

P139 **A technology for producing all-female progenies of the flathead grey mullet by selecting sex-reversed males.**
L. David*[1], G. Hirsch[1], I. Oz[1], D. Agiv[1], E. Marcos-Hadad[1], A. Bennet-Perlberg[2], A. Naor[2], and B. Ginzbourg[3], [1]*The Hebrew University of Jerusalem, Rehovot, Israel*, [2]*Israel Ministry of Agriculture and Rural Development, Dor, Israel*, [3]*Dagon Fish Hatchery, Kibbutz Maagan-Michael, Israel*.

P140 **Population genetics of two critically endangered rhino rays from the Southwest Indian Ocean region.**
M. Groeneveld*[1], J. Klein[1], R. Bennett[2], M. Bond[3], D. Ebert[4,5], K. Gledhill[6], S. Jaquemet[7], J. Kiszka[3], A. Macdonald[8], B. Mann[9], J. Nevill[10], A. Price[1], M. van Staden[1], B. Wueringer[11,12], A. Bester-van der Merwe[1], [1]*Department of Genetics, Stellenbosch University, Stellenbosch, South Africa*, [2]*Wildlife Conservation Society, New York, NY*, [3]*Institute of Environment, Department of Biological Sciences, Florida International University, University Park, FL*, [4]*Pacific Shark Research Center, Moss Landing Marine Laboratories, Moss Landing, CA*, [5]*South African Institute for Aquatic Biodiversity, Grahamstown, South Africa*, [6]*Fish Ecology Lab, University of Technology Sydney, Broadway, Sydney, Australia*, [7]*UMR Entropie, Université de La Réunion, La Réunion, France*, [8]*School of Life Sciences, University of KwaZulu-Natal, Westville, South Africa*, [9]*Oceanographic Research Institute, Durban, South Africa*, [10]*Environment Seychelles, Mahé, Seychelles*, [11]*Sharks and Rays Australia, Bungalow, Queensland, Australia*, [12]*Department of Biological Sciences, Faculty of Science and Engineering, Macquarie University, Macquarie Park, New South Wales, Australia*.

Genetics of Immune Response and Disease Resistance

P141 **A genome-wide association study for genetic susceptibility to *Corynebacterium pseudotuberculosis* infection in sheep.**
J. Kyselová*[1], L. Tichý[1], J. Marková[2], K. Kavanová[2], M. Beinhauerová[2], A. Gurgul[3], T. Szmatola[3,4], and Z. Sztankóová[1], [1]*Institute of Animal Science, Prague, Czechia*, [2]*Veterinary Research Institute, Brno, Czechia*, [3]*University of Agriculture in Krakow, Centre for Experimental and Innovative Medicine, Krakow, Poland*, [4]*National Research Institute of Animal Production, Balice, Poland*.

P142 **A sensitive and specific exonuclease III–assisted recombinase-aided amplification colorimetric assay for rapid detection of nucleic acids.**
C. Zhao*[1], Y. Zhou[1], J. Zhang[1], S. Zhao[1,2], and S. Xie[1,2], [1]*Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, China*.

P143 **Identification and discovering the role of hub genes and their molecular mechanisms in the immune response of mice vaccinated with glycosylated HA of H5N1 influenza virus.**
S. Golpasand*, S. Ghovvati, and Z. Pezeshkian, *Department of Animal Sciences, Faculty of Agriculture, University of Guilan, Rasht, Guilan, Iran*.

P145 **Porcine epidemic diarrhea virus induces upregulation of kruppel-like factor 4 to promote its replication in porcine intestinal epithelial cells.**
H. Wang*, S. Wu, and W. Bao, *Yangzhou University, Yangzhou, Jiangsu Province, China*.

P146 **ISAG Bursary Award: Characterization of the host-specific glycan responding to African swine fever virus infections.**
K. Han*[1], L. Sun[2,3], S. Wan[1], C. Cao[1], M. Lu[1], J. Yan[4], G. Peng[2,3], S. Zhao[1], and M. Yu[1], [1]*Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China*, [3]*Key Laboratory of Preventive Veterinary Medicine in Hubei Province, The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China*, [4]*Key Laboratory of Separation Science for Analytical Chemistry, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian, China*.

P147 **Functional verification of key miR-223 for *Staphylococcus aureus*–induced bovine mastitis.**
X. Liu*[1,2], G. Dari[1], S. Mi[1], D. E. MacHugh[2,3], and Y. Yu[1], [1]*College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*UCD School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*, [3]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland*.

P148 **Investigation on the interference effect of CRISPR-Cas13d system against porcine epidemic diarrhea virus.**
C. Zhao, X. Hu, and R. Zhang*, *China Agricultural University, Beijing, China*.

P149 **Identification of porcine genes against pseudorabies virus infection by genome-wide CRISPR activation screening.**
A. Shangguan*, Y. Sun, Z. Liu, J. Jiang, and S. Zhang, *Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Education Ministry of China, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei Province, China*.

P150 **A forty-year analysis of literature on *Babesia* infection (1982–2022): A systematic bibliometric approach.**
S. A. Malgwi*[1], R. E. Ogunsakin[2], M. A. Adeleke[1], and M. Okpeku[1], [1]*Discipline of Genetics, School of Life Sciences, University of Kwa-Zulu Natal, Westville, Durban, South Africa*, [2]*Biostatistics Unit, Discipline of Public Health Medicine, School of Nursing & Public Health, College of Health Sciences, University of Kwa-Zulu Natal, Durban, South Africa*.

P151 **ISAG Bursary Award: Functional diversity of toll signaling pathway in Czech Simmental cattle with respect to health and resilience traits.**
K. Samake*[1], T. Valcikova[2], M. Bjelka[3], and K. Novak[4], [1]*Charles University, Prague, Czech Republic*, [2]*Czech University of Life Sciences, Prague, Czech Republic*, [3]*Breeding Company CHD Impuls, Bohdalec, Czech Republic*, [4]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*.

P152 **Superior survivability of *GBP1* and *GBP5* heterozygous pigs undergoing porcine respiratory syndrome outbreaks.**
R. Pena*[1], K. Keutgens[2], and L. Fraile[1], [1]*Universitat de Lleida-AGROTECNIO Centre, Lleida, Spain*, [2]*PXL University of Applied Sciences and Arts, Hasselt, Belgium*.

P153 **IUIS-VIC Travel Award 2: Due to their improved immunity, disease-resistant common carp fish are also less infective.**
B. Dorfman*, E. Marcos-Hadad, R. Tadmor-Levi, and L. David, *Department of Animal Sciences, R. H. Smith Faculty of Agriculture, Food and Environment, Hebrew University of Jerusalem, Rehovot, Israel*.

P154 **Association of the *IRAK1* gene polymorphism with health, milk and exterior traits in cattle.**
L. Tichý*[1,2], V. Šteiger[1], L. Zavadilová[2], D. Schröffelová[1], J. Kyselová[2], M. Pribánová[1], L. Vostrý[2], J. Kucera[1], and Z. Sztankóová[2], [1]*Czech Moravian Breeders' Corporation, Hradištko, Czech Republic*, [2]*Institute of Animal Science, Prague-Uhríneves, Czech Republic*.

P155 **ISAG Bursary Award: IUIS-VIC Travel Award 1: Transcriptomic signatures of peripheral immune cells associated with immune competence traits in Australian Angus cattle.**
A. Wilson*[1], P. Alexandre[2], T. Legrand[2], S. Denman[2], T. Reverter[2], C. Stewart[1], and R. Farr[1], [1]*Commonwealth Scientific and Industrial Research Organization, East Geelong, VIC, Australia*, [2]*Commonwealth Scientific and Industrial Research Organization, St Lucia, QLD, Australia*.

P156 **ISAG Bursary Award: Assessment of haemagglutination titre and serum lysozyme concentration in Nigerian indigenous chicken genotypes.**
U. Akpan*, A. S. Adenaike, M. I. Takeet, A. A. Bello-Ibiyemi, and C. O. N. Ikeobi, *Federal University of Agriculture, Abeokuta, Ogun state, Nigeria*.

P157 **ISAG Bursary Award: CRISPR-SpRY-mediated base-editing screening identifies TMEM41B amino acids that are critical for transmissible gastroenteritis virus replication in pig.**
Y. Zhou*[1], J. Zhang[1], Y. Zhang[1], X. Li[1,3], S. Xie[1,2], C. Zhao[1,2], and S. Zhao[1,3], [1]*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, Hu Bei, China*, [2]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hu Bei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hu Bei, China*.

P158 **Exploring, evaluating, and quantifying the mammalian alveolar macrophage response to intracellular mycobacterial pathogens using an integrative multi-omics approach.**
T. J. Hall[1], M. Mittermite[2], J. A. Browne[1], G. P. McHugo[1], J. F. O'Grady[1], E. L. Clark[3], M. Salavati[3,4], S. V. Gordon[2,5], and D. E. MacHugh*[1,5], [1]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*, [2]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*, [3]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, United Kingdom*, [4]*Dairy Research and Innovation Centre, SRUC South and West Faculty, Barony Campus, Parkgate, Dumfries, Scotland, United Kingdom*, [5]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*.

P159 **ISAG Bursary Award: Multi-omics integration analysis deciphering genetic basis of host resistance to PRRSV.**
Q. Wu*[1], T. Zhang[1], X. Wu[1], X. Zhou[1,2], and B. Liu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*Hubei Hongshan Laboratory, Wuhan, China*.

P160 **Genome-scale CRISPR screen identifies TRIM2 and SLC35A1 associated with porcine epidemic diarrhea virus infection.**
H. Liu[1], J. Wang[2], Z. Guo[1], X. Zeng[2], Y. Yang[1], S. Li[1], X. Li[1,3], S. Zhao[1,4], C. Wang[2], and S. Xie*[1,4], [1]*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, Hubei, P. R. China*, [2]*Key Laboratory of Pig Molecular Quantitative Genetics of Anhui Academy of Agricultural Sciences, Livestock and Poultry Epidemic Diseases Research Center of Anhui Province, Anhui Provincial Key Laboratory of Livestock and Poultry Product Safety Engineering, Hefei, Anhui, P. R. China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hubei, P. R. China*, [4]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, P. R. China*.

P161 **ISAG Bursary Award: LncRNA446 regulates tight junctions by inhibiting the ubiquitinated degradation of Alix after porcine epidemic diarrhea virus infection.**
Y. Xiao*, W. Qin, H. Wang, and W. Bao, *Yangzhou University, Yangzhou, Jiangsu, China*.

P162 **Association of variants in antibacterial *TLR* genes with reproductive traits in Czech Simmental cattle.**
K. Novak*[1], K. Samake[2], and M. Bjelka[3], [1]*Institute of Animal Science, Prague-Uhrineves, Czech Republic*, [2]*Charles University, Prague, Czech Republic*, [3]*Breeding Company CHD Impuls, Bohdalec, Czech Republic*.

P163 **ISAG Bursary Award: Genomic markers associated with immune traits in Sasso chickens raised in Ethiopia.**
M. Girma*[1,2], M. Katrina[3], S. Kate[3], W. Esatu[2], B. Solomon[2], T. Dessie[2], P. Andronikі[3,4], V. Lonneke[3], H. Olivier[2,5], B. Georgios[3,6], and M. Dikeledi[1], [1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Florida, South Africa*, [2]*CTLGH-LiveGene, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [3]*Centre for Tropical Livestock Genetics and Health, The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK*, [4]*The Royal Veterinary College, Hawkshead Lane, Hatfield, Hertfordshire, UK*, [5]*Cells, Organisms and Molecular Genetics, School of Life Sciences, University of Nottingham, Nottingham, UK*, [6]*Scotland's Rural College (SRUC), Animal and Veterinary Sciences, Easter Bush, Midlothian, UK*.

P164 **Integration of information from multiple gene expression and genome-wide association studies on host resistance of cattle to infestation with *Rhipicephalus microplus* ticks.**
K. Chooyoung*, B. Mable, and N. Jonsson, *School of Biodiversity, One Health and Veterinary Medicine College of Medical, Veterinary and Life Sciences University of Glasgow, Glasgow, United Kingdom*.

Genome Edited Animals

P165 ***Drosophila melanogaster* (fruit fly): A platform for anticancer drug discovery and development.**
S. Malindisa* and M. Ntwasa, *University of South Africa, Florida, Johannesburg, South Africa*.

P166 **Genome editing of VNN gene in Sparidae and Moronidae cell lines.**
L. Sanchez*, A. Arana, and D. Robledo, *University of Santiago de Compostela, Lugo, Spain*.

P167 **Withdrawn**

P168 **Evaluation of the resistance of Liang Guang Small Spotted pigs with partial deletion of the CD163 SRCR5 domain to porcine reproductive and respiratory syndrome virus 2 infection.**
Y. Wu*, X. Liu, Y. Chen, and Z. He, *School of Life Sciences, Sun Yat-sen University, Guangzhou, Guangdong, China*.

P169 **ISAG Bursary Award: Field-deployable nucleic acid detection with RAVI-CRISPR.**
D. Tao[1], B. Xu[1], S. Li[1], C. Zhao[1], S. Zhao[1,2], X. Li[1,3], and S. Xie*[1,3], [1]*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*, [2]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China*, [3]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, China*.

P170 **Rethinking the genetic basis of pregnancy recognition in ruminants: Pregnancy in type I interferon receptor (*IFNAR2*) knockout sheep.**
C. J. Davies*[1,2], E. K. Peterson[1,2], M. J. Brothers[1,2], A. J. Thomas[1,2], H. M. Rutigliano[1], Y.-M. Lee[1], and I. A. Polejaeva[1], [1]*Department of Animal, Dairy & Veterinary Sciences, Utah State University, Logan, UT*, [2]*Center for Integrated Biosystems, Utah State University, Logan, UT*.

P171 **ISAG Bursary Award: sgRNAcas9-AI: A program for prediction of CRISPR/Cas9 and its variant sgRNA activity using deep learning.**
S. Li[1], X. Zhang*[2], S. Zhao[1,3], C. Zhao[1,4], and S. Xie[1,4], [1]*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*, [2]*Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany*, [3]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, China*, [4]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China*.

P172 **Validation of the *PDGFD* gene function in sheep tail formation using base editing-induced start codon silencing.**
P. Kalds*[1,2], S. Zhou[1,3], S. Huang[1], K. Sun[1], Y. Gao[1], J. Han[4,5], Y. Chen[1], and X. Wang[1], [1]*Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China*, [2]*Department of Animal and Poultry Production, Faculty of Environmental Agricultural Sciences, Arish University, El-Arish, Egypt*, [3]*College of Veterinary Medicine, Northwest A&F University, Yangling, China*, [4]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [5]*Livestock Genetics Program, International Livestock Research Institute (ILRI), Nairobi, Kenya*.

Horse Genetics and Genomics

P173 **A genome scan for homozygous haplotype deficiency in the Thoroughbred horse identifies variants for normal embryogenesis.**
J. F. O'Grady[1,2], B. A. McGivney[1], D. E. MacHugh[2], and E. W. Hill*[1,2], [1]*Plusvital Ltd, Dun Laoghaire, Dublin, Ireland*, [2]*University College Dublin, Belfield, Dublin, Ireland*.

P174 **ISAG Bursary Award: Introgression within the horse genome.**
L. Johnson*[1], T. Kalbfleisch[1], E. Bailey[1], and K. de Silva[2], [1]*University of Kentucky, Lexington, KY*, [2]*University of Louisville, Louisville, KY*.

P175 **Identification of genetic variants frequency from RNAseq datasets and its use as a filtration tool to identify rare diseases in Arabian horse species.**
T. Szmatola[1,2], M. Stefaniuk-Szmukier[2], K. Piorkowska[2], T. Zabek*[2], and K. Ropka-Molik[2], [1]*University Centre of Veterinary Medicine, University of Agriculture in Krakow, Krakow, Poland*, [2]*National Research Institute of Animal Production, Department of Animal Molecular Biology, Balice, Poland*.

P176 **Is the Argentinean Polo Pony a horse breed? Genomic characterization and comparison with Thoroughbreds using SNP-array data.**
F. Azcona[1,2], A. Karlau[1,3], P. Trigo[1,2], R. Alvarez[1], and S. Demyda-Peyrás*[1,3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*IGEVET, CONICET, La Plata, Buenos Aires, Argentina*, [3]*CONICET, La Plata, Buenos Aires, Argentina*.

P177 **ISAG Bursary Award: Genomic analysis using massive sequencing data reveals genetic signatures that underlie breed features.**
Y. Wang[1], X. Chai[1], H. Liu*[1], J. Dou[1], Y. Liao[1], Z. Tang[1], J. Xu[1], S. Zhu[1], Y. Liu[1], X. Shen[1], D. Yin[1], L. Yin[1,2], X. Liu[1,2], M. Yu[1], Y. Fu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, PR China*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, PR China*.

P178 **Association of the *mypn* gene with structural muscle fiber traits in the Purebred Spanish Horse by genome-wide association analysis.**
R. Álvarez-Quiñonez[1], M. Macri[2,3], A. Martinez[2,3], J. Rivero[1], and J. Vega-Pla*[4], [1]*Laboratory of Muscular Biopathology, Department of Comparative Anatomy and Pathology, School of Veterinary Medicine, University of Cordoba, Cordoba, Spain*, [2]*Department of Genetics, University of Cordoba, Cordoba, Spain*, [3]*Animal Breeding Consulting S.L, Cordoba, Spain*, [4]*Laboratorio de Investigación Aplicada, Cría Caballar de las Fuerzas Armadas, Cordoba, Spain*.

P179 **A de novo large ECAX partial deletion in a fertile Pura Raza Española mare detected using genomic data.**
Y. Pirosanto[1,2], A. Encina[3], G. Anaya[4], M. Valera[3], and S. Demyda-Peyrás*[1,5], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*IGEVET, CONICET, La Plata, Buenos Aires, Argentina*, [3]*Departamento de Agronomía, ETSIA, Universidad de Sevilla, Sevilla, España*, [4]*Departamento de Genética, Universidad de Córdoba, Córdoba, España*, [5]*CONICET, La Plata, Buenos Aires, Argentina*.

P180 **Exterior features and DNA quality of the Kazakh horse of Zhabe type for 16S sequencing.**
S. Kassymbekova*[1], T. Assanbayev[2], A. Khamzina[1], and A. Ibadullayeva[1], [1]*Kazakh National Agrarian Research University, Almaty, Kazakhstan*, [2]*Toraighyrov University, Pavlodar, Kazakhstan*.

P181 **Genome-wide association study for microphthalmia in Warmblood horses.**
L. Chapard[1], N. Aerts[1], B. Van Mol[1,2], R. Meyermans[1], W. Gorssen[1], K. Hooyberghs[1], F. Pille[2], S. Janssens[1], and N. Buys*[1], [1]*KU Leuven, Center for Animal Breeding and Genetics, Department of Biosystems, Leuven, Belgium*, [2]*Department of Surgery and Anesthesiology of Domestic Animals, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium*.

P182 **Dissecting the genetic cause of myotonic dystrophy in horses.**
T. Simon*[1], D. Vélez-Irizarry[2], R. Naboulsi[1], A. Niazi[1], E. Bongcam-Rudloff[1], S. Valberg[2], and G. Lindgren[1,3], [1]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*, [2]*Department of Large Animal Clinical Science, College of Veterinary Medicine, Michigan State University, East Lansing, MI*, [3]*Center for Animal Breeding and Genetics, Department of Biosystems, Leuven, Belgium*.

P183 **SNP-based genomic characterization of a top-performance population of Peruano de Paso horses.**
A. Karlau[1,2], F. Azcona[1,2], P. Trigo[1,2], A. Antonini[1], A. Molina[3], and S. Demyda-Peyrás*[1,2], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina*, [2]*CONICET, La Plata, Buenos Aires, Argentina*, [3]*Universidad de Córdoba, Córdoba, España*.

P184 **Evaluation of single nucleotide polymorphisms (SNPs) for parentage control in horse breeds in Korea.**
S. Y. Lee* and G.-J. Cho, *Korea Racing Authority, Racing Laboratory, Gwqcheon Si, Gyeonggi-do, South Korea*.

P185 **ISAG Bursary Award: Single-step genomic model improved reliability in conformation traits in the Pura Raza Español horse.**
C. Ziadi*[1], D. Perdomo-González[2], M. Valera[2], A. Encina[3], N. Laseca[1], S. Demyda-Peyrás[1], and A. Molina[1], [1]*Department of Genetics, University of Córdoba, Córdoba, Spain*, [2]*Department of Agronomy, ETSIA, University of Sevilla, Sevilla, Spain*, [3]*Asociación Nacional de Criadores de Caballos de Pura Raza Española (ANCCE), Sevilla, Spain*.

P186 **ISAG Bursary Award: Molecular inbreeding negatively affects the reproductive life of Pura Raza Española mares.**
N. Laseca*[1], D. Perdomo-González[2], M. Valera[2], A. Molina[1], P. Azor[3], and S. Demyda-Peyrás[1], [1]*Department of Genetics, University of Cordoba, Córdoba, Spain*, [2]*Department of Agronomy, ETSIA, University of Seville, Seville, Spain*, [3]*Asociación Nacional de Criadores de Caballo de Pura Raza Española, ANCCE, Seville, Spain*.

P187 **Reference genome of the native Finnhorse as a tool to study the adaptation of northern Eurasian horse breeds.**
K. Pokharel*[1], M. Honkatukia[1,2], C. Ginja[3], M. Weldenegodguad[1], J. Peippo[1,2], H. Lindeberg[4], T. Reilas[1], and J. Kantanen[1], [1]*Natural Resources Institute Finland, Jokioinen, Finland*, [2]*NordGen - Nordic Genetic Resource Center, Ås, Norway*, [3]*Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal*, [4]*Natural Resources Institute Finland, Maaninka, Finland*.

P188 **ISAG Bursary Award: Identification of personality-related genes associated with tractability of handling in Thoroughbred horses.**
T. Yokomori*[1], A. Ohnuma[2], T. Tozaki[2], M. Ishimaru[3], F. Sato[3], Y. Hori[4], T. Segawa[1], and I. Takuya[1], [1]*Nihon University, Fujisawa, Kanagawa, Japan*, [2]*Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [3]*Japan Racing Association, Urakawa, Hokkaido, Japan*, [4]*The University of Tokyo, Meguro, Tokyo, Japan*.

P189 **Changes in the gene expression profile of equine mesenchymal stem cells (MSC) after their allogeneic administration in horses matched or mismatched for the major histocompatibility complex (MHC).**
A. Cequier[1,2], E. Bernad[1], M. García-Martínez[1], B. Serrano[1], F. Vázquez[1,2], A. Romero[1,2], A. Vitoria[1,2], L. Barrachina[1,2], and C. Rodellar*[1], [1]*Laboratorio de Genética Bioquímica LAGENBIO, Instituto Agroalimentario de Aragón–IA2 (Universidad de Zaragoza-CITA), Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*, [2]*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain*.

P190 **Whole-genome trio sequencing to reveal the genetics of equine microphthalmia.**
I. Shutava[1], B. Ekesten[1], C.-J. Rubin[2], S. Mäkeläinen[2], T. Bergström[1], J. Tetens[3], and S. Mikko*[1], [1]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [2]*Uppsala University, Uppsala, Sweden*, [3]*University of Göttingen, Göttingen, Germany*.

P191 **ISAG Bursary Award: The epigenetic landscape of the satellite-free centromere of horse chromosome 11.**
E. Cappelletti*[1], F. Piras[1], L. Sola[1], S. Peng[2], A. Barber[3], M. Santagostino[1], J. Petersen[3], R. Bellone[2,4], C. Finno[2], T. Kalbfleisch[5], E. Bailey[5], S. Nergadze[1], and E. Giulotto[1], [1]*Department of Biology and Biotechnology, University of Pavia, Pavia, Italy*, [2]*University of California-Davis, School of Veterinary Medicine, Department of Population Health and Reproduction, Davis, CA*, [3]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE*, [4]*University of California-Davis, School of Veterinary Medicine, Veterinary Genetics Laboratory, Davis, CA*, [5]*University of Kentucky, Gluck Equine Research Center, Lexington, KY*.

P192 **A missense mutation of BCHE promotes the butyrylcholinesterase activity in Chinese horses.**
Y. Zhang*[1], X. Liu[1,2], and L. Jiang[1], [1]*Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [2]*Centre d'Anthropobiologie et de Génomique de Toulouse, Toulouse, France*.

P193 **Construction of genome-wide INDEL database, application to a parentage-test using INDELs for horse registration, and a gene-editing test for doping control.**
T. Tozaki*, A. Ohnuma, M. Kikuchi, T. Ishige, H. Kakoi, K.-i. Hirota, and S.-I. Nagata, *Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*.

P194 **Genomics of gaits in Icelandic horses is more complex than DMRT3.**
H. Sigurdardottir*[1,2], E. Albertsdottir[3], T. Kristjansson[3], M. Rhodin[4], G. Lindgren[1,5], and S. Eriksson[1], [1]*Swedish University of Agricultural Sciences, Dept. of Animal Breeding and Genetics, Uppsala, Sweden*, [2]*Agricultural University of Iceland, Faculty of Agricultural Sciences, Hvanneyri, Borgarbyggð, Iceland*, [3]*The Icelandic Agricultural Advisory Centre, Reykjavik, Iceland*, [4]*Swedish University of Agricultural Sciences, Dept. of Anatomy, Physiology and Biochemistry, Uppsala, Sweden*, [5]*KU Leuven, Livestock Genetics, Department of Biosystems, Leuven, Belgium*.

P195 **A resource for documenting and tracking genetic diversity in US Thoroughbred horses.**
J. L. Petersen*[1], T. S. Kalbfleisch[2], J. N. Cullen[3], and E. F. Bailey[2], [1]*University of Nebraska–Lincoln, Lincoln, NE*, [2]*University of Kentucky, Lexinton, KY*, [3]*University of Minnesota, Minneapolis, MN*.

P196 **Genomics of Thoroughbred stallion subfertility.**
C. Castaneda, R. Juras, B. W. Davis, and T. Raudsepp*, *School of Veterinary Medicine, Texas A&M University, College Station, TX*.

ISAG-FAO Genetic Diversity

P198 **ISAG Bursary Award: Updated perspective on the genetic diversity, phylogeography and population dynamics of domestic pigs in Southeast Asia.**
J. K. Layos*[1], C. J. Godinez[2], and M. Nishibori[3], [1]*College of Agriculture and Forestry, Capiz State University, Mambusao, Capiz, Philippines*, [2]*Department of Animal Science, Visayas State University, Baybay City, Leyte, Philippines*, [3]*Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan*.

P199 **Using microsatellite markers to study the population structure and genetic diversity of the native Pulawska and three commercial pig breeds in Poland.**
A. Radko, A. Koseniuk, and G. Smolucha*, *National Research Institute of Animal Production, Balice, Poland*.

P200 **History and genetic diversity of African sheep: Perpendicular contrasts of phenotypes and genomic diversity.**
A. Da Silva[1], A. Ahbara[2], S. Ben Jemaa[3], Y. Cao[4], E. Ciani[5], E. Dzomba[6], O. Hanotte[7], S. Mastrangelo[8], A. Missohou[9], A. Molotsi[10], A. Muchadeyi[11], J. Mwacharo[12], M.-L. Li[4], S. Hall[13], J. Lenstra*[14], [1]*PEREINE/E2LIM, Faculty of Science and Technics, Limoges, France*, [2]*Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya*, [3]*Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Université de Carthage, Ariana, Tunisia*, [4]*CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing, China*, [5]*Department of Biosciences, Biotechnologies and Biopharmaceutics, University of Bari "Aldo Moro," QQBari, Italy*, [6]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa*, [7]*School of Life Sciences, University of Nottingham, Nottingham, UK*, [8]*Dipartimento Scienze Agrarie, Alimentari e Forestali, University of Palermo, Palermo, Italy*, [9]*Animal Production and Nutrition Unit, Inter-State School of Veterinary Science and Medicine (EISMV), Dakar, Senegal*, [10]*Department of Animal Sciences, University of Stellenbosch, Matieland, Stellenbosch, South Africa*, [11]*Agricultural Research Council, Biotechnology, Platform, Onderstepoort, South Africa*, [12]*International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [13]*Department of Environmental Protection and Landscape, Estonian University of Life Sciences, Tartu, Estonia*, [14]*Faculty of Veterinary Medicine, Utrecht University, Utrecht, Utrecht, The Netherlands*.

P201 **ISAG Bursary Award: The first *Rangifer tarandus* Y chromosomal phylogeny.**
E. Bozlak*[1,2], K. Pokharel[3], M. Weldenegodguad[3], A. Paasivaara[3], J. Kantanen[3], and B. Wallner[1], [1]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [2]*Vienna Graduate School of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*, [3]*Natural Resources Institute Finland, Jokioinen, Finland*.

P202 **ISAG Bursary Award: Temporal changes in genomic diversity of the northernmost cattle populations in Europe.**
M. Weldenegodguad*[1], M. Kjetså[2], A. Blauer[3], A. M. Johansson[4], C. Sarmento[5], S. Guimarães[5], C. Ginja[5], M. Honkatukia[2], and J. Kantanen[1], [1]*Natural Resources Institute Finland, Jokioinen, Finland*, [2]*NordGen—Nordic Genetic Resource Center, Ås, Norway*, [3]*University of Turku, Turku, Finland*, [4]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [5]*BIOPOLIS-CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal*.

P203 **An archaeogenomics study of Iron Age cattle from Althiburos, Tunisia.**
C. Ginja*[1], S. Guimarães[1], R. da Fonseca[2], R. Rasteiro[3], R. Rodríguez-Varela[4], L. G. Simões[5], C. Sarmento[1], M. Carme Belarte[6], N. Kallala[7], J. Ramon Torres[8], J. Sanmartí[9], A. M. Arruda[10], C. Detry[10], S. Davis[11], J. Matos[12,13], A. Götherström[4], A. E. Pires[1,14], S. Valenzuela-Lamas[10,15], [1]*BIOPOLIS/CIBIO/InBIO, Universidade do Porto, Vairão, Portugal*, [2]*GLOBE Institute, University of Copenhagen, Copenhagen, Denmark*, [3]*Bristol Medical School, University of Bristol, Bristol, UK*, [4]*CPG—Centre for Palaeogenetics, Stockholm University, Stockholm, Sweden*, [5]*Human Evolution, Department of Organismal Biology, Uppsala University, Uppsala, Sweden*, [6]*ICREA-ICAC, Institut Català de Recerca i Estudis Avançats i d'Arqueologia Clàssica, Barcelona, Spain*, [7]*INP, Institute National du Patrimoine, Tunis, Tunisia*, [8]*Consell Balear d'Eivissa, Eivissa, Balearic Islands, Spain*, [9]*Departament de Prehistòria, Història Antiga i Arqueologia, Universitat de Barcelona, Barcelona, Spain*, [10]*UNIARQ, Centro de Arqueologia da Universidade de Lisboa, Faculdade de Letras da Universidade de Lisboa, Lisboa, Portugal*, [11]*LARC/DGPC, Laboratório de Arqueociências, Direcção Geral do Património Cultural, Lisboa, Portugal*, [12]*Unidade Estratégica de Investigação e Serviços de Biotecnologia e Recursos Genéticos, Instituto Nacional de Investigação Agrária e Veterinária, I.P, Oeiras, Portugal*, [13]*CE3C, Centre for Ecology, Evolution and Environmental Changes, Universidade de Lisboa, Lisboa, Portugal*, [14]*Faculdadede Medicina Veterinária, Universidade Lusófona, Lisboa, Portugal*, [15]*CSIC-IMF, Archaeology of Social Dynamics, Consejo Superior de Investigaciones Científicas-Institució Milà i Fontanals d'Humanitats, Barcelona, Spain.*

P204 **Genetic structure of Criollo sheep populations with Iberian and African breeds.**
J. Cappello[1,2], M. Revidatti*[1,2], S. De la Rosa[1,2], V. Morales[1,2], E. Tejerina[1,2], BiOvis Consortium[2], and A. Martínez[2,3], [1]*Facultad de Ciencias Veterinarias, Universidad Nacional del Nordeste, Corrientes, Argentina*, [2]*Red CONBIAND, Córdoba, España*, [3]*Facultad de Veterinaria, Universidad de Córdoba, Córdoba, España*.

P205 **Genetic diversity of Clydesdale and Shire draft horses with implications for management.**
J. L. Petersen*, A. M. Barber, A. M. Fuller, and I. Grazian, *University of Nebraska-Lincoln, Lincoln, NE*.

P206 **Genetic characterization of deleterious alleles in traditional cattle populations in Europe and Africa.**
R. Crooijmans*[1], R. Gonzalez-Prendes[1], M. Derks[1], N. Ghanem[2], C. Ginja[3], D. Kugonza[4], L. Makgahlela[5], and K. Juha[6], [1]*Wageningen University and Research, Animal Breeding and Genomics, Wageningen, The Netherlands*, [2]*University of Cairo, Animal Reproduction Department, Cairo, Egypt*, [3]*University of Porto, Centro de Investigacão em Biodiversidade e Resursos Genéticos, Vairão, Portugal*, [4]*Makerere University, Animal Breeding and Genetics, Kampala, Uganda*, [5]*Agricultural Research Council, Animal Breeding and Genetics, Pretoria, South Africa*, [6]*Natural Resources Institute Finland, Jokioinen, Finland*.

P207 **ISAG Bursary Award: Admixed ancestry or independent race: A phylogenetic meta-analysis on the phylogeography of Philippine chickens.**
C. Godinez*[1,2], J. Layos[2,3], Y. Yamamoto[2], T. Kunieda[4], and M. Nishibori[2,1], [1]*Department of Animal Science, College of Agriculture and Food Science, Visayas State University, Visca, Baybay City, Leyte, Philippines*, [2]*Laboratory of Animal Genetics, Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan*, [3]*College of Agriculture and Forestry, Capiz State University, Burias, Mambusao, Capiz, Philippines*, [4]*Faculty of Veterinary Medicine, Okayama University of Science, Imabari, Ehime, Japan*.

P208 **Genomic tools for the monitoring of genetic diversity.**
P. Boettcher*[1], R. Baumung[1], P. Burger[2], L. Colli[3], I. Curik[4], G. Leroy[1], C. Looft[5], A. Manunza[6], G. Mészáros[7], D. Ouedraogo[8], B. Rosen[9], A. Stella[6], Y. Utsunomiya[10], J. Windig[11], J. Soelkner[7], [1]*Food and Agriculture Organization of the UN, Rome, Italy*, [2]*University of Veterinary Medicine Vienna, Vienna, Austria*, [3]*Università Cattolica del Sacro Cuore, Piacenza, Italy*, [4]*University of Zagreb, Zagreb, Croatia*, [5]*University of Applied Science Neubrandenburg, Neubrandenburg, Germany*, [6]*IBBA-CNR, Milan, Italy*, [7]*BOKU, Vienna, Austria*, [8]*Joseph KI-ZERBO University, Ouagadougou, Burkina Faso*, [9]*United States Department of Agriculture, Beltsville, MD*, [10]*São Paulo State University, São Paulo, Brazil*, [11]*Wageningen University and Research, Wageningen, The Netherlands*.

P209 **ISAG Bursary Award: An insight into whole-genome resequencing data of Indian native goats with global breeds reveals high within-breed genetic diversity and distinct population structure.**
N. Balasubramaniam*[1,2], S. Dixit[2], S. Singh[2], S. Koloi[1,2], and I. Ganguly[2], [1]*ICAR-National Dairy Research Institute, Karnal, Haryana, India*, [2]*ICAR-National Bureau of Animal Genetic Resources, Karnal, Haryana, India*.

P210 **Differences in effective population sizes and breed contributions to genetic variation in Estonian farm animal breeds.**
E. Sild*, S. Värv, T. Põlluäär, H. Viinalass, and T. Kaart, *Estonian University of Life Sciences, Institute of Veterinary Medicine and Animal Sciences, Tartu, Estonia*.

P211 **ISAG Bursary Award: Multiple origins and genetic diversity of Philippine native pigs.**
J. B. Banayo*[1,2], K. L. V. Manese[2], K. O. Furusho[2], A. J. Salces[2], and T. Yamagata[1], [1]*Nagoya University, Chikusa, Nagoya, Japan*, [2]*University of the Philippines Los Baños, Laguna, Philippines*.

Livestock Genomics for Developing Countries

P212 **ISAG Bursary Award: History and unique evolutionary adaptation of indicine cattle.**
N. Chen*[1], X. Xia[1], Q. Hanif[2,3], T. Hussain[4], N. A. Gorkhali[5], E. Terefe[6,7], G. Belay[6], A. Tijjani[7], T. Zegeye[8], M. G. Gebre[9], J. A. Lenstra[10], J. Han[3,11], O. Hanotte[11,12], Y. Jiang[1], C. Lei[1], [1]*Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China*, [2]*National Institute for Biotechnology and Genetic Engineering, Faisalabad, Pakistan*, [3]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [4]*Department of Molecular Biology, Virtual University of Pakistan, Rawalpindi, Punjab, Pakistan*, [5]*National Animal Breeding and Genetics Centre, National Animal Science Research Institute, Nepal Agriculture Research Council, Khumaltar, Lalitpur, Nepal*, [6]*College of Natural and Computational Sciences, Addis Ababa University, Addis Ababa, Ethiopia*, [7]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [8]*Mekelle Agricultural Research Center, Tigray, Ethiopia*, [9]*College of Agriculture, Haramaya University, Haramaya, Oromia, Ethiopia*, [10]*Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands*, [11]*International Livestock Research Institute (ILRI), Nairobi, Kenya*, [12]*School of Life Sciences, University of Nottingham, Nottingham, UK*.

P213 **Journeying to a sustainable dairy breeding program in Tanzania.**
G. Gebreyohanes*[1], J. Ojango[1], L. Eliamoni[1], N. Kelay[1], K. Suzan[2], K. Daniel[3], C. Ekine[1], M. Raphael[1], and O. Mwai[1], [1]*International Livestock Research Institute, Nairobi, Kenya*, [2]*Green Dreams Tech, Nairobi, Kenya*, [3]*Tanzania Agriculture and Livestock Research Institute, Dodoma, Tanzania*.

P214 **ISAG Bursary Award: A genomic characterization of the SA Bonsmara breed using the BovineHD 777K array.**
D. Alberts*, S. F. Lashmar, and E. van Marle-Köster, *University of Pretoria, Pretoria, Gauteng, South Africa*.

P215 **ISAG Bursary Award: Genotyping-by-sequencing: A powerful tool to reveal genomic relatedness and admixture in local Tunisian sheep breeds.**
I. Baazaoui*[1], S. Bedhiaf-Romdhani[1], K. G. Dodds[2], R. Brauning[2], R. Anderson[2], T. Van Stijn[2], A. McCulloch[2], and J. McEwan[2], [1]*National Agricultural Research Institute of Tunisia, Ariana, Tunisia*, [2]*AgResearch Limited Invermay Agricultural Centre, New Zealand*.

P216 **ISAG Bursary Award: Genomic analysis reveals low level of inbreeding in Ugandan goat breeds.**
R. B. Onzima*[1], H. P. Doekes[2], R. Mukiibi[3], and R. P. M. G. Crooijmans[2], [1]*Faculty of Agriculture and Environmental Science, Muni University, Arua, Uganda*, [2]*Animal Breeding and Genomics, Wageningen University and Research, Wageningen, The Netherlands*, [3]*Roslin Institute, University of Edinburgh, Edinburgh, Scotland, United Kingdom*.

P217 **ISAG Bursary Award: Anthropological events and environmental stress are shaping the genomes of Ethiopian indigenous goats.**
S. Belay*[1,2], G. Belay[2], H. Nigussie[2], A. Tijjani[3,4], A. M. Ahbara[3,5], T. Dessie[4], G. M. Tarekegn[6,7], H. Jian-Lin[8,9], S. Mor[4,10], H. S. Woldekiros[11], K. Dobney[12,13], O. Lebrasseur[4], O. Hanotte[3,4], and J. M. Mwacharo[14,15], [1]*Tigray Agricultural Research Institute, Mekelle, Ethiopia*, [2]*Addis Ababa University, Department of Microbial, Cellular and Molecular Biology, Addis Ababa, Ethiopia*, [3]*School of Life Sciences, University of Nottingham, Nottingham, UK*, [4]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [5]*Department of Zoology, Misurata University, Misurata, Libya*, [6]*Animal and Veterinary Sciences, Scotland's Rural College (SRUC) Staff Group, Roslin Institute Building, Easter Bush Campus, University of Edinburgh, Edinburgh, UK*, [7]*Institute of Biotechnology (IoB), Addis Ababa University, Addis Ababa, Ethiopia*, [8]*CAAS-ILRI Joint Laboratory on Livestock and Forage Genetic Resources, Beijing, China*, [9]*Institute of Animal Science, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China*, [10]*University of Liverpool, Institute of Infection, Veterinary and Ecological Sciences, Liverpool, UK*, [11]*Department of Anthropology Washington University in St. Louis, St. Louis, MO*, [12]*University of Liverpool, Department of Archaeology, Classics and Egyptology, Liverpool, UK*, [13]*University of Sydney, Sydney, Australia*, [14]*Small Ruminant Genomics, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [15]*SRUC, Animal and Veterinary Sciences and Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Edinburgh, UK*.

P218 **Post-GWAS functional annotation for tick count, growth traits, and skin thickness in F_2 Angus × Nguni crossbred cattle.**
N. Mkize*[1,2], A. N. Maiwashe[1], B. Dube[1], K. Dzama[2], and N. O. Mapholi[3], [1]*Agricultural Research Council, Centurion, Gauteng, South Africa*, [2]*Stellenbosch University, Stellenbosch, Western Cape, South Africa*, [3]*University of South Africa, Florida, Gauteng, South Africa*.

P219 **ISAG Bursary Award: Low genetic diversity and population structuring of *Amblyomma hebraeum* and *Rickettsia africae* from coastal and inland regions in the Eastern Cape Province of South Africa.**
A. Pillay*[1], N. Nyangiwe[2], and S. Mukaratirwa[1,3], [1]*University of KwaZulu-Natal, Durban, KwaZulu-Natal, South Africa*, [2]*Döhne Agricultural Development Institute, Stutterheim, South Africa*, [3]*Ross University School of Veterinary Medicine, Basseterre, St. Kitts & Nevis*.

P220 **ISAG Bursary Award: Building genomic resources for cattle breeds at risk of extinction in Nigeria.**
O. Opoola*[1], M. Wheto[2], R. Mukiibi[3], R. Mrode[4,5,6], and A. Djikeng[1,5], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Easter Bush Campus, Edinburgh, UK*, [2]*College of Animal Science and Livestock Production, Federal University of Agriculture, Abeokuta (FUNAAB), Abeokuta, Ogun State, Nigeria*, [3]*The Roslin Institute, University of Edinburgh, Easter Bush Campus, Edinburgh, UK*, [4]*Scotland's Rural College (SRUC), Edinburgh, UK*, [5]*International Livestock Research Institute (ILRI), Nairobi, Kenya*, [6]*The University Edinburgh, Scotland.*

P221 **Associations between transformation growth factor beta (TGF-β) gene polymorphism with growth performance of Nigerian improved local chicken and exotic ones.**
N. J. Chukwuka*[1], U. E. Ogundu[1], B. O. Agaviezor[2], F. Ajayi[2], and V. M. O. Okoro[1], [1]*Department of Animal Science and Tech., Federal University of Technology, Owerri, Imo, Nigeria*, [2]*Department of Animal Science, University of PortHarcourt, Choba, PortHarcourt, Nigeria*.

P223 **ISAG Bursary Award: Molecular detection and phylogenetic analysis of lumpy skin disease virus (LSDV) from 2019 to 2022 outbreak in Bangladesh.**
A. Bhuyan*[1], J. Khanom[1], A. Bhuiyan[2], R. Rubaya[1], and J. Alam[1], [1]*National Institute of Biotechnology, Ashulia, Bangladesh*, [2]*Bangladesh Agricultural Research Council, Faridpur, Bangladesh*.

P224 **Genome-wide association study screens candidate genes for semen quality traits in selected Chinese and South African beef cattle bulls.**
M. Modiba*[1], K. Nephawe[1], J. Wang[2], C. Yuan[2], K. Mdladla[3], L. Wenfa[2], and B. Mtileni[1], [1]*Tshwane University of Technology, Department of Animal Sciences, Pretoria, Gauteng, South Africa*, [2]*Jilin Agricultural University, College of Animal Sciences and Technology, Changchun, Jilin, China*, [3]*Agricultural Research Council, Biotechnology Platform, Pretoria, Gauteng, South Africa*.

P225 **ISAG Bursary Award: Low-coverage whole-genome genomic characterization of indigenous chicken ecotypes of Tigray, Ethiopia.**
G. G. Berhe*[1,2], G. B. Woldemichael[2], and M. Z. Kelkay[1], [1]*Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia*, [2]*Addis Ababa University, College of Natural resource; Department of Microbial, Cellular and Molecular Biology, Addis Ababa, Addis Ababa, Ethiopia*.

P226 **ISAG Bursary Award: Population structure and admixture patterns in indigenous African cattle.**
M. K. Bitew*[1], G. Senczuk[1], M. Di Civita[1], C. Persichilli[1], S. Ben Jemaa[2], E. Ciani[3], J. M. Mwacharo[4,5], O. Hanotte[6,7], and F. Pilla[1], [1]*Department of Agriculture Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Laboratoire des Productions Animales et Fourragères, Institut National de la Recherche Agronomique de Tunisie, Université de Carthage, Ariana, Tunisia*, [3]*Department of Biosciences, Biotechnologies & Environment, University of Bari Aldo Moro, Bari, Italy*, [4]*Small Ruminant Genomics, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [5]*Animal and Veterinary Sciences, Scotland's Rural College (SRUC) and Centre for Tropical Livestock Genetics and Health (CTLGH), Edinburgh, United Kingdom*, [6]*School of Life Sciences, University of Nottingham, Nottingham, United Kingdom*, [7]*LiveGene, International Livestock Research Institute, Addis Ababa, Ethiopia*.

P228 **Indigenous Veld Goat breed-informative SNPs: Towards establishing optimal genomics tools for improved animals in community-based improvement initiatives in South Africa.**
K. Hadebe* and L. Rashijane, *Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, Gauteng, South Africa*.

P229 **Identification of recombination hotspots in selected South African indigenous beef cattle.**
N. A. Magagula*[1,2], A. A. Zwane[2], K. T. Ncube[3], and B. J. Mtileni[1], [1]*Tshwane University of Technology, Pretoria, Gauteng, South Africa*, [2]*Agricultural Research Council, Centurion, Gauteng, South Africa*, [3]*ZooOmics Indaba Biotechnical Industries, Pretoria, Gauteng, South Africa*.

P230 **ISAG Bursary Award: Autozygous regions, inbreeding, and effective population size in South African Afrikaner cattle.**
S. Lashmar*[1,2] and E. van Marle-Köster[1], [1]*University of Pretoria, Pretoria, Gauteng, South Africa*, [2]*Agricultural Research Council, Animal Production, Pretoria, Gauteng, South Africa*.

P231 **Genomic characterization of the South African Nguni and F_2 Angus × Nguni cattle.**
S. Mdyogolo*[1], N. Mkize[2], G. Hutang[3], and N. O. Mapholi[1], [1]*UNISA, Johannesburg, Gauteng, South Africa*, [2]*ARC–AP, Pretoria, Gauteng, South Africa*, [3]*CSIR, Pretoria, Gauteng, South Africa*.

P234 **Structural variations and wild introgression in East Asian cattle genomes confer adaptation to local environments.**
X. Xia, F. Zhang, S. Li, X. Luo, L. Peng, W. Pang, C. Lei, and N. Chen*, *Northwest A&F Unversity, Yangling, Shaanxi, China*.

P235 **Recent selection and adaptive introgression facilitated adaptation to high altitude in QTP cattle.**
Y. Lyu, X. Xia, F. Wang, N. Chen*, and C. Lei, *Northwest A&F University, Yangling, Shaanxi, China*.

P237 **Molecular and serological prevalence of corridor disease (buffalo-associated *Theileria parva*) in cattle populations at the livestock/game interface of KwaZulu-Natal province, South Africa.**
S. Mbizeni*[1,2], B. J. Mans[1,3], and A. A. Latif[2], [1]*University of South Africa, Johannesburg, Gauteng, South Africa*, [2]*University of KwaZulu-Natal, Durban, KwaZulu-Natal, South Africa*, [3]*Agricultural Research Council, Pretoria, Gauteng, South Africa*.

P238 **ISAG Bursary Award: The development of a 61K Illumina SNP chip for dromedaries under the frame of the 2019 Agricultural Greater Good (AGG) initiative.**
M. Di Civita*[1], G. Senczuk[1], S. Bruno[2], V. Landi[3], S. Brooks[4], F. Almathen[5,6], B. Faye[7], S. B. S. Gaouar[8], M. Piro[9], K. S. Kim[10], H. Dadi[11], P. C. Iglesias[12], H. Al-Haddad[13], M. Al-Abri[14], F. Pilla[1], X. David[15], A. Eggen[15], P. Burger[16], and E. Ciani[2], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Department of Biosciences, Biotechnologies and Environment, University of Bari "Aldo Moro," QQBari, Italy*, [3]*Department of Veterinary Medicine, University of Bari "Aldo Moro," QQValenzano, Bari, Italy*, [4]*Department of Animal Sciences, University of Florida, Gainesville, FL*, [5]*Department of Public Health, College of Veterinary Medicine, King Faisal University, Al-Ahsa, Saudi Arabia*, [6]*Camel Research Center, King Faisal University, Al-Ahsa, Saudi Arabia*, [7]*CIRAD-ES, UMR SELMET, Montpellier, France*, [8]*Department of Biology, Abou Bakr Belkaid University of Tlemcen, Tlemcen, Algeria*, [9]*Department of Medicine, Surgery and Reproduction, Institut Agronomique et Vétérinaire Hassan II, Rabat BP, Morocco*, [10]*Department of Animal Sciences, Chungbuk National University, Chungbuk, Korea*, [11]*Ethiopian Biotechnology Institute (EBTi), Addis Ababa, Etiopia*, [12]*Department of Genetics, Faculty of Veterinary Sciences, University of Córdoba, Córdoba, Spain*, [13]*Department of Biological Sciences, Kuwait University, Kuwait City, Kuwait*, [14]*Department of Animal and Veterinary Sciences, Sultan Qaboos University, Muscat, Oman*[15] *Illumina, Agrigenomics, Evry, France,* [16] *Research Institute of Wildlife Ecology, Vetmeduni, Vienna, Austria.*

P239 **ISAG Bursary Award: Genome-wide scan for selection signatures in South African indigenous goat ecotypes.**
A. M. Magoro*[1,2], A. Zwane[2], K. Hadebe[3], and B. Mtileni[2], [1]*Tshwane University of Technology, Pretoria, South Africa*, [2]*Agricultural Research Council-Animal Production, Pretoria, South Africa*, [3]*Agricultural Research Council-Biotechnology Platform, Pretoria, South Africa*.

P240 **The history and future of African cattle diversity and adaptation: The known and the possible.**
O. Hanotte*[1,2], [1]*International Livestock Research Institute, Addis Ababa, Ehtiopia*, [2]*The University of Nottingham, Nottingham, United Kingdom*, [3]*Centre for Tropical Livestock Genetics and Health, Edinburgh, United Kingdom*.

P241 **Virginia Tech research education programs: Models for increasing STEM participation in middle- and low-income countries.**
E. Smith*, *Virginia Tech, Blacksburg, VA*.

P242 **ISAG Bursary Award: Population genomics of indigenous African cattle inferred from 537 whole-genome sequencing.**
A. Tijjani[1,2], S. Kambal*[3,4], K. Marshall[5], O. Hanotte[1,3,6], and on behalf of the African Cattle Genomics Consortium[1], [1]*Centre for Livestock Genetics and Health (CTLGH), International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [2]*The Jackson Laboratory, Bar Harbor, ME*, [3]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [4]*University of Khartoum, Khartoum, Sudan*, [5]*International Livestock Research Institute (ILRI), Nairobi, Kenya*, [6]*School of Life Sciences, University of Nottingham, University Park Campus, Nottingham, UK.*

P243 **Structural variant calling using ONT long-read whole-genome sequencing of indigenous Zulu sheep.**
N. Nxumalo*[1], A. Molotsi[1], C. Rhode[1], and N. Kunene[2], [1]*Stellenbosch University, Stellenbosch, Matieland, South Africa*, [2]*University of Zululand, Empangeni, Kwadlangezwa, South Africa*.

P244 **ISAG Bursary Award: Whole-genome sequencing of Landim pigs of Mozambique reveals a close relationship with Angolan native pigs and suggests selection for immune response.**
F. Teixeira*[1,2], P. Sá[1], D. Santos[1], C. Garrine[3], R. Zimba[4], L. Souza[3], H. Chiaia[2], A. Leitão[1], J. M. Cordeiro[2], L. T. Gama[1], and A. J. Amaral[1,5], [1]*Centre for Interdisciplinary Research in Animal Health and Associate Laboratory for Animal and Veterinary Sciences, Faculty of Veterinary Medicine, University of Lisbon, Alto da Ajuda, Lisbon, Portugal*, [2]*Faculty of Veterinary Medicine, University José Eduardo dos Santos, Huambo, Angola*, [3]*Faculty of Veterinary Medicine, University Eduardo Mondlane, Maputo, Mozambique*, [4]*Escola Superior de Desenvolvimento Rural de Vilankulo, University Eduardo Mondlane, Maputo, Mozambique*, [5]*Escola de Ciências e Tecnologia Universidade de Évora, Évora, Portugal*.

P245 **Genetic differentiation of *Camelus bactrianus* from Kazakhstan.**
K. Dossybayev*[1,2], D. Ualiyeva[1], M. Amandykova[1,2], T. Kapasuly[1,2], A. Mussayeva[1], Z. Orazymbetova[1], G. Shaltenbay[1,2], and B. Bekmanov[1,2], [1]*Laboratory of Genetics and Cytogenetics, Institute of Genetics and Physiology, CS MSHE RK, Almaty, Kazakhstan*, [2]*Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan*.

P246 **Whole-genome diversity of dromedary camels from the entire geographic distribution range.**
G. Senczuk*[1], S. Bruno[2], M. Di Civita[1], V. Landi[3], S. Brooks[4], F. Almathen[5,6], B. Faye[7], S. B. S. Gaouar[8], M. Piro[9], K. S. Kim[10], H. Dadi[11], C. Iglesias Pastrana[12], H. Al-Haddad[13], M. Al-Abri[14], C. Persichilli[1], F. Pilla[1], P. Burger[15], and E. Ciani[2], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Department of Biosciences, Biotechnologies and Environment, University of Bari "Aldo Moro," QQBari, Italy*, [3]*Department of Veterinary Medicine, University of Bari "Aldo Moro," QQBari, Italy*, [4]*Department of Animal Sciences, University of Florida, Gainesville, FL*, [5]*Department of Public Health, College of Veterinary Medicine, King Faisal University, Al-Ahsa, Saudi Arabia*, [6]*Camel Research Center, King Faisal University, Al-Ahsa, Saudi Arabia*, [7]*CIRAD-ES, UMR SELMET, Montpellier, France*, [8]*Department of Biology, Abou Bakr Belkaid University of Tlemcen, Tlemcen, Algeria*, [9]*Department of Medicine, Surgery and Reproduction, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco*, [10]*Department of Animal Sciences, Chungbuk National University, Chungbuk, Korea*, [11]*Ethiopian Biotechnology Institute (EBTi), Addis Ababa, Ethiopia*, [12]*Department of Genetics, Faculty of Veterinary Sciences, University of Córdoba, Córdoba, Spain*, [13]*Department of Biological Sciences, Kuwait University, Kuwait City, Kuwait*, [14]*Department of Animal and Veterinary Sciences, Sultan Qaboos University, Muscat, Oman*, [15]*Research Institute of Wildlife Ecology, Vetmeduni, Vienna, Austria.*

P247 **ISAG Bursary Award: Differential proteomics revealed the impact of heat stress on milk whey proteins in indigenous Deoni (*Bos indicus*) and Holstein Friesian (*Bos taurus*) crossbred cows.**
E. Rana*[1,2], K. P. Ramesha[1], N. Azharuddin[1], M. A. Najar[3], M. K. Sinha[1], S. Jeyakumar[1], L. Gopalakrishnan[3,4], P. Nag[1], S. Mall[1], M. Ashokan[1], M. Dasgupta[1], A. Kumaresan[1], D. N. Das[1], and T. S. K. Prasad[3], [1]*Southern Regional Station, ICAR—National Dairy Research Institute, Bangalore, India*, [2]*Livestock Development Department, Government of Chhattisgarh, Chhattisgarh, India*, [3]*Center for Systems Biology and Molecular Medicine, Yenepoya Research Centre, Yenepoya (Deemed to be University), Mangalore, India*, [4]*Institute of Bioinformatics, International Technology Park, Bangalore, India*.

P248 **Tracking the adaptive history of African cattle using low-coverage genomes.**
S. I. Ng'ang'a*[1,2], J. A. Ward[3], G. V. Smith[4], S. Rossiter[2], C. Faulkes[2], D. G. Bradley[5], O. Hanotte[6,7], D. E. MacHugh[8], and L. A. F. Frantz[1,2], [1]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilian University, Munich, Germany*, [2]*School of Biological and Chemical Sciences, Queen Mary University of London, London, United Kingdom*, [3]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Dublin, Ireland*, [4]*SilverStreet Capital, London, United Kingdom*, [5]*Smurfit Institute of Genetics, Trinity College Dublin, Dublin, Ireland*, [6]*International Livestock Research Institute, Addis Ababa, Ethiopia*, [7]*School of Life Sciences, University of Nottingham, Nottingham, United Kingdom*, [8]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland*.

P249 **Poultry genomics within the Centre for Tropical Livestock Genetics and Health.**
J. Smith*[1], A. Gheyas[1], A. Trujillo[1,2], A. Kebede[3], G. Gebru[4,5], N. Seboka[5,6], M. Rachman[2], T. Dessie[7], and O. Hanotte[2,7], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, University of Edinburgh, Edinburgh, UK*, [2]*University of Nottingham, Nottingham, UK*, [3]*Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia*, [4]*Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia*, [5]*Addis Ababa University, Addis Ababa, Ethiopia*, [6]*Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia*, [7]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*.

Microbiomes

P250 **Comparison of rumen microbial analysis pipelines based on 16S rRNA gene sequencing.**
X. Ye*, Z. Cai, and M. Lund, *Center for Quantitative Genetics and Genomics, Aarhus University, Aarhus, Denmark*.

P251 **High-throughput metagenomic characterization of the fecal microbiota of peste des petits ruminants–infected West African Dwarf goats.**
I. Muritala*[1], B. O. Sodimu[1], M. N. Bemji[1], M. A. Busari[1], G. F. Farayola[1], S. Saleem[2], N. Kumari[3], S. Jaiswal[3], M. A. Iquebal[3], S. M. Ahmad[2], A. O. Sonibare[4], M. Wheto[1], and E. M. Ibeagha-Awemu[5], [1]*Department of Animal Breeding and Genetics, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [2]*Division of Animal Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Faculty of Veterinary Sciences and Animal Husbandry, Shuhama, Jammu and Kashmir, India*, [3]*Division of Agricultural Bioinformatics, ICAR—Indian Agricultural Statistics Research Institute, New Delhi, India*, [4]*Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [5]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*.

P252 **ISAG Bursary Award: Nasal microbiome diversity in West African Dwarf goats with peste des petits ruminants viral infection.**
I. Muritala*[1], M. N. Bemji[1], M. A. Busari[1], B. O. Sodimu[1], S. M. Ahmad[2], A. Negi[3], S. Jaiswal[3], M. A. Iquebal[3], B. Bhat[2], M. O. Ozoje[1], O. L. Ajayi[4], and E. M. Ibeagha-Awemu[5], [1]*Department of Animal Breeding and Genetics, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [2]*Division of Animal Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Faculty of Veterinary Sciences and Animal Husbandry, Shuhama, Jammu and Kashmir, India*, [3]*Division of Agricultural Bioinformatics, ICAR—Indian Agricultural Statistics Research Institute, New Delhi, India*, [4]*Department of Pathology, College of Veterinary Medicine, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria*, [5]*Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*.

P253 **Links between gut microbiome functions and feed efficiency in growing pigs fed a conventional or a high-fiber diet.**
A. Cazals[1], O. Zemb[2], V. Déru[2,3], J. Bidanel[4], H. Gilbert[2], and J. Estellé*[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [3]*France Génétique Porc, Le Rheu, France*, [4]*IFIP-Institut du Porc, Le Rheu, France*.

P254 **Comparative metagenomic along the gut biogeography of indigenous chicken.**
A. Tangomo Ngnintedem*[1,2], E. Machuka[3], B. Waweru[3], J.-B. Domelevo Entfellner[3], M. Gitau Gicheha[4], J. Maina Kagira[4], R. Pelle[3], A. Djikeng[5], and C. Keambou Tiambo[6], [1]*Biotechnology and Bioinformatics Research and Training Unit, Department of Animal Science, FASA, University of Dschang, Dschang, Cameroon*, [2]*Department of Molecular Biology and Biotechnology, Pan-African University Institute of Basic Sciences, Technology and Innovation, Nairobi, Kenya*, [3]*Biosciences Eastern and Central Africa–International Livestock Research Institute (BecA–ILRI) Hub, Nairobi, Kenya*, [4]*Department of Animal Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya*, [5]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush Campus, Edingburgh, UK*, [6]*Centre for Tropical Livestock Genetics and Health (CTLGH), ILRI Kenya, Nairobi, Kenya*.

P255 **Preliminary results: Bacterial abundance in the microbiome from South African beef fecal samples through 16s rRNA targeted sequencing.**
O. P. Monchusi[1,2], K. P. Montso[2], C. N. Ateba[2], A. A. Zwane[1], and M. M. Makgahlela*[1], [1]*Agricultural Research Council, Irene, Centurion, Gauteng, South Africa*, [2]*North-West University, Mahikeng, South Africa*.

P256 **Impact of the vaginal microbiota on the pregnancy rate by artificial insemination in three Spanish sheep breeds.**
E. L. Reinoso[1,2], F. Puente-Sánchez[3], C. González[1], J. H. Calvo[4], M. Serrano[1], and M. Saura*[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*ETSIAAB Universidad Politécnica de Madrid, Madrid, Spain*, [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [4]*CITA-IA2, Zaragoza, Spain*.

P257 **Using a Snakemake workflow for metagenomic analysis of sheep rumen microbiome divergently selected for methane emissions.**
B. Perry, A. Kim, H. Henry, T. Bilton, A. McCulloch, K. McRae, S. Clarke*, P. Janssen, J. McEwan, and S. Rowe, *AgResearch Limited, Lincoln, Canterbury, New Zealand*.

P258 **Bacterial diversity associated with feeding Boschveld chicken with the South African red sorghum variety.**
N. Nemukondeni*[1], C. A. Mbajiorgu[1], A. N. Sebola[1], O. M. Letsoalo[1], T. Mafuna[2], and M. Mabelebele[1], [1]*University of South Africa, Florida, South Africa*, [2]*University of Johannesburg, Auckland Park, South Africa*.

P259 **Analysis of the gut microbiome sheds insights into breed resilience to challenges of antimicrobial resistance in Dohne Merino sheep.**
A. Khwela*[1,2], E. F. Dzomba[2], R. Pierneef[1], and F. C. Muchadeyi[1], [1]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Gauteng, South Africa*, [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, KwaZulu-Natal, South Africa*.

P260 **Exploring links between porcine genome copy number variants and the diversity and composition of pig gut eukaryote and prokaryote microbial communities.**
M. Ballester*[1], D. Crespo-Piazuelo[1], J. Morata[2], L. Ramírez[1], O. González-Rodríguez[1], C. Sebastià[3,4], A. Castelló[3,4], A. Dalmau[5], S. E. Ramos-Onsins[3], K. Alexiou[3], J. M. Folch[3,4], R. Quintanilla[1], and Y. Ramayo-Caldas[1], [1]*IRTA, Caldes de Montbui, Spain*, [2]*CNAG-CRG, Barcelona, Spain*, [3]*CRAG, Campus UAB, Bellaterra, Spain*, [4]*UAB, Bellaterra, Spain*, [5]*IRTA, Girona, Spain*.

P261 **Possible coevolution of balanced polymorphisms in the pig host and its intestinal microbiome.**
C. Hupperts*[1], M. Mni[1], W. Coppieters[1,2], C. Charlier[1], and M. Georges[1], [1]*Unit of Animal Genomics, GIGA-R and Faculty of Veterinary Medicine, Liège, Belgium*, [2]*GIGA—Genomics Platform, University of Liège, Liège, Belgium*.

P262 **Bacterial metagenomics sequencing of chickens fed tannins.**
T. Manyelo*, E. Malematja, N. Sebola, S. Kolobe, and M. Mabelebele, *University of South Africa, Gauteng, South Africa*.

P263 **Genetic selection of the host drives gut microbiota enterotypes across generations.**
J. Estellé*[1], C. Larzul[2], M. Borey[1], F. Blanc[1], G. Lemonnier[1], Y. Billon[3], M. Thiam[4], B. Quinquis[4], N. Galleron[4], D. Jardet[3], J. Lecardonnel[3], F. Plaza-Oñate[4], and C. Rogel-Gaillard[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France*, [3]*INRAE, GenESI, Surgères, France*, [4]*Université Paris-Saclay, INRAE, MGP, Jouy-en-Josas, France*.

P264 **Differential miRNA profile in response to dietary treatment and their possible impact in the host-microbiota genetic regulation.**
T. Porto[1], T. Cardoso[2], J. Bruscadin[1], L. Conteville[2], P. Oliveira[1], G. Mourao[3], L. Coutinho[3], A. Zerlotini[4], J. Reecy[5], and L. Regitano*[2], [1]*Post-Graduation Program of Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, São Carlos, SP, Brazil*, [2]*Embrapa Southeast Livestock Research Center, São Carlos, SP, Brazil*, [3]*Department of Animal Science, University of São Paulo, Piracicaba, SP, Brazil*, [4]*Embrapa Digital Agriculture, Campinas, SP, Brazil*, [5]*Department of Animal Science, Iowa State University, Ames, IA*.

P265 **ISAG Bursary Award: Study of gut microbes and body metabolism function between Dorper and Tan sheep.**
Y. Ma*[1], X. Yang[1], G. Hua[1], G. Cai[1], X. Li[2], D. Feng[2], and X. Deng[1], [1]*Key Laboratory of Animal Genetics, Breeding, and Reproduction of the Ministry of Agriculture and Beijing Key Laboratory of Animal Genetic Improvement, China Agricultural University, Beijing, China*, [2]*Department of Animal Science and college of Agriculture, Ningxia University, Ningxia Hui Autonomous Region, China*.

P266 **Optimizing metagenomic sequencing: A comparative study of ONT adaptive sampling strategies to improve microbial DNA recovery.**
E. L. Reinoso-Peláez*[1,2], M. Saura[1], C. González[1], F. Puente-Sánchez[3], and M. Serrano[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*ETSIAAB, Universidad Politécnica de Madrid, Madrid, Spain*, [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden*.

P267 **Host genomic regions associated with ewes' vaginal microbiota.**
M. Ramon*[1], E. Reinoso-Pelaez[2], M. Saura[2], O. González-Recio[2], C. Gonzalez[2], R. Arias[1], M. Pérez-Guzman[1], I. Beltrán de Heredia[3], J. Calvo[4], and M. Serrano[2], [1]*CERSYRA-IRIAF, Valdepeñas, Ciudad Real, Spain*, [2]*INIA-CSIC, Madrid, Spain*, [3]*NEIKER, Arkaute, Spain*, [4]*CITA-ARAID-IA2, Zaragoza, Aragón, Spain*.

Pig Genetics and Genomics

P268 **Study on BMPR1B gene affecting endometrial cell growth and development to regulate high reproductive performance in Taihu pigs.**
Z. Liu[1,2], H. Zhang[1,2], D. Wang[1,2], J. Wang[1,2], T. Zeng[1,2], and K. Wu*[1,2], [1]*Department of Animal Genetics and Breeding, National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*Key Laboratory of Animal Genetics, Breeding and Reproduction of the Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing, China*.

P269 **GWAS analyses identify strong novel candidate genes influencing the fatty acid composition in porcine muscle.**
I.-C. Cho*[1], Y.-J. Kang[2], S.-G. Kim[3], and H.-A. Kim[4], [1]*Subtropical Livestock Research Institute, National Institute of Animal Science, Rural Development Administration, Jeju-si, Jeju-do, Republic of Korea*, [2]*Subtropical Livestock Research Institute, National Institute of Animal Science, Rural Development Administration, Jeju-si, Jeju-do, Republic of Korea*, [3]*Subtropical Livestock Research Institute, National Institute of Animal Science, Rural Development Administration, Jeju-si, Jeju-do, Republic of Korea*, [4]*Subtropical Livestock Research Institute, National Institute of Animal Science, Rural Development Administration, Jeju-si, Jeju-do, Republic of Korea*.

P270 **Effects of genetic markers on yield and meat quality traits is influenced by diet energy content in Iberian pigs.**
C. Óvilo*[1], L. Calvo[2], Y. Núñez[1], D. Menoyo[3], A. Rodríguez[2], C. López-Bote[4], and M. Muñoz[1], [1]*Departamento Mejora Genética Animal, INIA-CSIC, Madrid, Spain*, [2]*Incarlopsa, Tarancón, Cuenca, Spain*, [3]*Departamento de Producción Agraria, ETSIAAB, UPM, Madrid, Spain*, [4]*Departamento de Producción animal, Facultad de Veterinaria, UCM, Madrid, Spain*.

P271 **Research on the classification model of selective sweep for different lines of Yorkshire pigs based on genome information.**
Y. Ma*, H. Song, S. Zhang, X. Li, and S. Zhao, *Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of the Ministry of Education & Key Laboratory of Swine Genetics and Breeding of the Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei, China*.

P272 **ISAG Bursary Award: Genome selection based on multiple artificial intelligence approaches boosting prediction accuracy.**
L. Wei*, D. Zhu, X. Hu, and Y. Wang, *State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China*.

P273 **Genome-wide analysis of allele-specific circular RNAs in pigs and their role in cell proliferation.**
Y.-J. Li[1,2], H. Liu[1,3], Y.-D. Zhang[1,2], A. Li[4], L.-X. Pu[5], S.-R. Zhang[1], N. O. Otecko[1,3], M.-S. Peng[1], D. M. Irwin[6], W. Xie[7], Y. Qin[8,9], Z. Wang[9,10], H.-J. Wei[11,12], Z.-Y. Zhou*[1], Y.-P. Zhang[1], [1]*State Key Laboratory of Genetic Resources and Evolution, and Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*State Key Laboratory for Conservation and Utilization of Bio-resource in Yunnan, Yunnan University, Kunming, Yunnan, China*, [3]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan, China*, [4]*Shaanxi Key Laboratory for Network Computing and Security Technology, School of Computer Science and Engineering, Xi'an University of Technology, Xi'an, Shanxi, China*, [5]*State Key Laboratory of Veterinary Etiological Biology, Key Laboratory of Veterinary Parasitology of Gansu Province, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China*, [6]*Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Canada*, [7]*Center for Stem Cell Biology and Regenerative Medicine, MOE Key Laboratory of Bioinformatics, THU-PKU Center for Life Sciences, School of Life Sciences, Tsinghua University, Beijing, China*, [8]*CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China*, [9]*University of Chinese Academy of Sciences, Chinese Academy of Sciences, Beijing, China*, [10]*CAS Key Laboratory of Computational Biology, CAS Center for Excellence in Molecular Cell Science, Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, Shanghai, China*, [11]*State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Kunming, Yunnan, China*, [12]*College of Veterinary Medicine, Yunnan Agricultural University, Kunming, Yunnan, China*.

P275 **Effects of maternal antioxidant supplementation on the gut health of the offspring.**
A. Heras-Molina*[1,2], H. Laviano[1], G. Gomez[3], Y. Nuñez[2], F. Sanchez-Esquiliche[4], A. Gonzalez-Bulnes[5], A. Rey[1], C. Lopez-Bote[1], M. Muñoz[2], and C. Óvilo[2], [1]*UCM, Madrid, Spain*, [2]*INIA-CSIC, Madrid, Spain*, [3]*IRIAF, Toledo, Spain*, [4]*Sánchez Romero Carvajal, Huelva, Spain*, [5]*UCH-CEU, Valencia, Spain*.

P276 **Exploring the genetic basis of fetal development in Iberian pigs using liver RNA-seq data.**
P. Vázquez-Ortego[1], A. López-García[1], Y. Núñez[1], C. García-Contreras[1], M. Vázquez-Gómez[2], S. Astiz[1], A. Heras-Monina[2], B. Isabel[2], A. González-Bulnes[1], C. Óvilo[1], and M. Muñoz*[1], [1]*INIA-CSIC, Madrid, Spain*, [2]*UCM, Madrid, Spain*.

P277 **Strategic decision-making within Iberian pig breeding programs through simulation approaches.**
M. Revilla*[1], B. Perez[1], E. Alcázar[2], A. González[2], J. Requejo-Puerto[1], J. Sánchez[2], and A. Huisman[1], [1]*Hendrix Genetics, 5830 AC Boxmeer, the Netherlands*, [2]*Ibéricos Vallehermoso S.L., Carretera la Solana a Villanueva de los Infantes, km. 9, 13248 Alhambra, Ciudad Real, Spain*.

P278 **Interactions of cortisol and sex-steroids in the regulation of porcine oviduct epithelium functions: insights from transcriptomic profiling.**
N. Trakooljul*[1], S. Du[2,1], E. Murani[1], J. Schoen[2,1], K. Wimmers[1], and S. Chen[2,1], [1]*Institute of Genome Biology, Research Institute for Farm Animal Biology (FBN), Dummerstorf, MV, Germany*, [2]*Department of Reproduction Biology, Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin, BE, Germany*.

P279 **Effect of chicory flour on inflammation and gut permeability in weaned piglets.**
T. Kulkarni[1,2], P. Siegien[1], P. Lemal[1], E. Arévalo Sureda[3], J. Wavreille[4], B. Cudennec[2], A. Lucau[2], N. Everaert[3], R. Ravallec[2], and M. Schroyen*[1], [1]*ULiège, Gembloux, Namur, Belgium*, [2]*ULille, Lille, Hauts-de-France, France*, [3]*KU Leuven, Leuven, Brabant, Belgium*, [4]*CRA-W, Gembloux, Namur, Belgium*.

P280 **Enhanced prime editor by prolonging its expression and affecting strands discrimination in mismatch repair via harnessing episomal element.**
X. Han*[1], G. Zhao[1], Y. Xiong[1], R. He[1], Y. Su[1], S. Li[1], Y. Liu[1], C. Zhao[1], X. Xi[1], X. Wang[1], H. Wang[1], S. Xie[1], X. Li[1,2], J. Ruan[1,3], S. Zhao[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, Hubei, China*.

P281 **Genetic improvement of litter size for dam line of Korean swine improvement network system.**
S. S. Lee*, S. M. Lee, and H. B. Yoon, *National Institute of Animal Science, Cheonan, Chungnam, South Korea*.

P282 **Estimation of variance components and GWAS for individual birth weight in Duroc pigs.**
S. M. Lee*, S. S. Lee, and H. B. Yoon, *Animal Genetics & Breeding Division, National Institute of Animal Science, Cheonan-si, Chungcheongnam-do, Republic of Korea*.

P283 **Individual and population diversity of 20 representative olfactory receptor genes in pigs.**
M. Kang, B. Ahn, S. Youk, and C. Park*, *Department of Stem Cell and Regenerative Biotechnology Graduate School of Konkuk University, Seoul, Republic of Korea*.

P284 **Comparison of the general co-expression landscapes in large-scale pig, human, and mouse populations.**
J. Dou[1], X. Huang[1], Y. Liao[1], Z. Tang[1], H. Liu[1], J. Xu[1], Y. Wang[1], Y. Liu[1], X. Shen[1], D. Yin[1], L. Yin[1], X. Li[1,2], X. Liu[1,2], Y. Fu[1,2], S. Zhao*[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei, China*, [3]*Hubei Hongshan Laboratory, Wuhan, Hubei, China*.

P285 **Wild boar and domestic pig distinguishing using SNP markers – preliminary studies.**
A. Piestrzynska-Kajtoch*, M. Natonek-Wisniewska, A. Koseniuk, A. Bieniek, B. Kleczek, J. Wolkowicz, P. Krzyscin, and A. Radko, *National Research Institute of Animal Production, Balice, Malopolska, Poland*.

P286 **Detection of porcine testicular cells using ATAC-Seq and gene expression profiles.**
Y. Lian[1], S. Lukassen[2], J. Liebig[2], A. Sanchez[1,3], E. Rodriguez-Sierra[4], C. Lewis[4], C. Conrad[2], and A. Clop*[1,5], [1]*Centre for Research in Agricultural Genomis CRAG (CSIC-IRTA-UAB-UB), Cerdanyola del Valles, Catalonia, Spain*, [2]*BIH at Charité-Universitatsmedizin Berlin, Berlin, Germany*, [3]*Autonomous University of Barcelona, Cerdanyola del Valles, Catalonia, Spain*, [4]*PIC Europe, Sant Cugat del Valles, Catalonia, Spain*, [5]*Consejo Superior de Investigaciones Cientificas, Barcelona, Catalonia, Spain*.

P287 **ISAG Bursary Award: A GWAS and RNA-Seq based analysis to shed light into the molecular and genetic basis of sperm cryo-tolerance in swine.**
Y. Lian*[1], M. Godia[1,2], J. E. Rodriguez-Gil[3], A. Castello[1], M. Yeste[4], S. Balasch[5], X. Barrera[6], C. Lewis[7], A. Sanchez[1,3], and A. Clop[1,8], [1]*Centre for Research in Agricultural Genomics, Cerdanyola del Vallès, Catalonia, Spain*, [2]*Wageningen University & Research, Wageningen, the Netherlands*, [3]*Autonomous University of Barcelona, Cerdanyola del Vallès, Catalonia, Spain*, [4]*University of Ginora, Girona, Catalonia, Spain*, [5]*Grup Gepork S.A, Les Masies de Rada, Catalonia, Spain*, [6]*Semen Cardona S.L, Cardona, Catalonia, Spain*, [7]*PIC Europe, Sant Cugat de Valles, Catalonia, Spain*, [8]*Consejo Superior de Investigaciones Cientificas, Barcelona, Catalonia, Spain*.

P288 **Genomic regions harboring signatures of selection associated with QTLs in South African pigs from different breeds and production environments.**
N. Hlongwane*[1,2], E. Dzomba[2], M. Van Der Nest[1], K. Hadebe[1], and F. Muchadeyi[1], [1]*Agricultural Research Council - Biotechnology Platform, Private Bag X5, Onderstepoort, 0110, South Africa*, [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Private Bag X01, Scottsville, 3209, South Africa*.

P289 **Analysis of the genetic variation in mitogenome sheds light on the ancestry of Tanzanian indigenous pigs.**
G. M. Msalya*[1], A. C. Adeola[2,3], L. Ajuma[2,3], Z. F. Cai[2], D. Mauki[4], T. T. Yin[2], M. S. Sheng[2,3], and Y. P. Zhang[2,3], [1]*Department of Animal, Aquaculture, and Range Sciences (DAARS), Sokoine University of Agriculture (SUA), Morogoro, Tanzania*, [2]*State Key Laboratory of Genetic Resources and Evolution and Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China*, [3]*Sino-Africa Joint Research Centre, Chinese Academy of Sciences, Kunming, China*, [4]*Center for Cancer Immunology, Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences (CAS), Shenzhen, China*.

P290 **Detecting copy number variation in a Korean composite pig breed, Woori-Heukdon populations.**
E. Cho[1], Y. Kim[1], H. Seong[1], S. Ha[2], H. Baek[2], J. Kim[2], S. Kwon[2], W. Park[1], D. Kim[3], D. Seo*[3], and J. Choi[2], [1]*Swine Science Division, National Institute of Animal Science, Rural Development Administration, Cheonan, South Korea*, [2]*Department of Animal Science, College of Animal Life Sciences, Kangwon National University, Chuncheon, South Korea*, [3]*TNT Research Institute, Jeonju, South Korea*.

P291 **PIG-PARADIGM Host Pillar: Toward elucidating the interactions between the intestinal microbiome and host factors to determine their separate and combined influence on intestinal health in pigs.**
P. Karlskov-Mortensen*, J. P. Nielsen, M. K. Morsing, B. Guldbrandtsen, C. B. Jørgensen, and M. Fredholm, *University of Copenhagen, Frederiksberg, Denmark*.

P292 **Copy number variation in porcine KIT locus affecting coat color detected with read depth analysis and digital PCR.**
M. Zorc*[1], M. Candek-Potokar[2], U. Sivka[3], N. Toplak[3], A. Tansek[1], and P. Dovc[1], [1]*University of Ljubljana, Biotechnical Faculty, Ljubljana, Slovenia*, [2]*Agricultural Institute of Slovenia, Ljubljana, Slovenia*, [3]*Omega d.o.o, Ljubljana, Slovenia*.

P293 **A deeper screening of Bazna pigs genome revealed a significant contribution of Mangalitza pigs to their genetic background.**
V. A. Balteanu*[1], T. Figueiredo Cardoso[2], A. Zsolnai[3], and M. Amills[2], [1]*University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Institute of Life Sciences, Cluj-Napoca, Cluj, Romania*, [2]*Center for Research in Agricultural Genomics (CSIC-IRTA-UAB-UB), Campus Universitat Autònoma de Barcelona, Bellaterra, Catalonia, Spain*, [3]*NARIC-Research Institute for Animal Breeding, Nutrition and Meat Science (ÁTHK), Herceghalom, Budapest, Hungary*.

P297 **Withdrawn**

P298 **Withdrawn**

P299 **ISAG Bursary Award: Enhancer-promoter interaction map in the maternal-fetal interface during implantation reveals important regulatory regions and variations in pigs.**
Y. Sun*[1,2], R. Liu[1,2], H. Liang[1,2], K. Han[1,2], F. Wang[1,2], J. Cao[1,2], and M. Yu[1,2], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China*.

P300 **Analysis of the genetic diversity of swine leukocyte antigen 1-linked olfactory receptor genes and analysis of correlation with reported porcine testicular expression levels.**
M. Kang*, B. Ahn, S. Youk, and C. Park, *Department of Stem Cell and Regenerative Biotechnology Graduate School of Konkuk University, Seoul, Republic of Korea*.

P301 **ISAG Bursary Award: Integrated analysis of genome-wide association studies and 3D epigenomic characteristics reveal the *BMP2* gene regulating loin muscle depth in Yorkshire pigs.**
S. Wan*[1], Y. Miao[2], Y. Zhao[1], S. Zhao[1], X. Xu[1], and T. Xiang[1], [1]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University, Wuhan 430070, Hubei Province, China*, [2]*Research Institute of Agricultural Biotechnology, Jingchu University of Technology, Jingmen 448000, Hubei Province, China*.

P302 **Methods to predict lameness in sows.**
G. A. Rohrer*[1], L. Ostrand[2], L. A. Rempel[1], T. Schmidt[2], and B. Mote[2], [1]*USDA-ARS US Meat Animal Research Center, Clay Center, NE*, [2]*University of Nebraska, Lincoln, NE*.

P303 **Identification of genomic regions associated with fatty acid metabolism across four tissues in pigs.**
J. Liu*[1,2], C. Sebastià[1,2], T. Jové-Juncà[3], R. Quintanilla[3], O. González-Rodríguez[3], M. Passols[1,2], A. Castelló[1,2], A. Sánchez[1,2], M. Ballester[3], and J. M. Folch[1,2], [1]*Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Spain*, [3]*Animal Breeding and Genetics Program, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Spain*.

P304 **Initiative for African indigenous pig genome project.**
A. C. Adeola*[1,2], X. Shi[1], X. Liu[3], O. F. Olaniyan[4], C. A. M. S. Djagoun[5], G. Msalya[6], D. H. Mauki[7], N. K. Wanzie[8], G. Niba[9], P. D. Luka[10], S. C. Olaogun[11], V. M. O. Okoro[12], J.-L. Han[13], M.-S. Peng[1,2], Y.-P. Zhang[1,2], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*, [2]*Sino-Africa Joint Research Centre, Chinese Academy of Sciences, Kunming, Yunnan, China*, [3]*Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [4]*West Africa Livestock Innovation Centre, Banjul, the Gambia*, [5]*Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin*, [6]*Sokoine University of Agriculture, Morogoro, Tanzania*, [7]*Center for Cancer Immunology, Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences (CAS), Shenzhen, China*, [8]*Department of Zoology, University of Douala, Douala, Cameroon*, [9]*National Centre for Animal Husbandry, Veterinary and Halieutic Training, Jakiri, Cameroon*, [10]*National Veterinary Research Institute, Vom, Nigeria*, [11]*Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria*, [12]*Department of Animal Science and Technology, School of Agriculture and Agricultural Technology, Federal University of Technology, Owerri, Nigeria*, [13]*International Livestock Research Institute, Nairobi, Kenya*.

P305 **Multi-breed, multi-tissue, and multi-omics aiding the quest for key porcine regulators.**
D. Crespo-Piazuelo[1], A. Reverter[2], Y. Ramayo-Caldas[1], R. Quintanilla[1], H. Acloque[3], M.-J. Mercat[4], M. C. A. M. Bink[5], A. E. Huisman[5], and M. Ballester*[1], [1]*Animal Breeding and Genetics Program, Institute of Agrifood Research and Technology (IRTA), Torre Marimon, Caldes de Montbui, E08140, Spain*, [2]*CSIRO Agriculture and Food, St. Lucia, Brisbane, Queensland 4067, Australia*, [3]*INRAE GABI, Domaine de Vilvert, 78350 Jouy-en-Josas, France*, [4]*IFIP-Institut du porc and Alliance R&D, La Motte au Vicomte, 35651 Le Rheu, France*, [5]*Hendrix Genetics, P.O. Box 114, 5830 AC Boxmeer, the Netherlands*.

P306 **Identification of new transcription factors using eGWAS in four porcine tissues.**
S. Hosseini[1], M. Gòdia[1], M. Derks[1], B. Harlizius[2], O. Madsen[1], and M. Groenen*[1], [1]*Wageningen University & Research, Wageningen, the Netherlands*, [2]*Topigs Norsvin Research Center, Beuningen, the Netherlands*.

P307 **ISAG Bursary Award: Sequence based GWAS identifies novel loci influencing growth and reproduction traits in pigs.**
A. Boshove*[1], M. F. L. Derks[1,2], B. Harlizius[1], E. F. Knol[1], M. S. Lopes[3], M. van Son[4], and C. A. Sevillano[1], [1]*Topigs Norsvin Research Center, Beuningen, the Netherlands*, [2]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands*, [3]*Topigs Norsvin, Curitiba, Brazil*, [4]*Norsvin SA, Hamar, Norway*.

P308 **ISAG Bursary Award: Allele-specific expression in pig genomic makeup and phenotypic implications.**
W.-y. Yao*[1,2], L. Bai[2], K. Li[2], L. Fang[3], M. A. M. Groenen[1], and O. Madsen[1], [1]*Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands*, [2]*Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China*, [3]*Center for Quantitative Genetics and Genomics (QGG), Aarhus University, Aarhus, Denmark*.

P309 **ISAG Bursary Award: Comprehensive identification of functional DNA elements and 3D chromatin interaction map in the pig genome.**
D. Wang*[1], M. Hu[1], Y. Guo[1], R. Kuang[1], H. Zhou[1], R. Ma[1], Z. Han[1], L. Li[1], H. Peng[1], Z. Xu[1], Y. Zhang[1], M. Zhu[1,3], C. K. Tuggle[4], Y. Zhao[1], S. Zhao[1,2], [1]*Key Lab of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China*, [2]*Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan, Hubei, China*, [3]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China*, [4]*Department of Animal Science, Iowa State University, Ames, IA*.

P310 **African swine fever infection enhances the host transcriptional regulation of membrane protein-encoding genes mediated by changes in chromatin state.**
X. Qi*[1], Y. Xiang[1], L. Sun[3,4], L. Xing[3], S. Zhang[1], Q. Zhao[1], L. Zhang[1], J. Li[1], P. Zhou[1], Z. Zheng[1], X. Li[1], L. Fu[1,2], G. Peng[3,4], and S. Zhao[1,2], [1]*Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China*, [2]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, China*, [3]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China*, [4]*State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, China*.

P311 **Toward identification of new genetic determinants for postweaning diarrhea in piglets.**
E. Ibragimov, E. Ø. Eriksen, J. P. Nielsen, C. B. Jørgensen, M. Fredholm, and P. Karlskov-Mortensen*, *University of Copenhagen, Frederiksberg, Denmark*.

P312 **Combined targeted and untargeted metabolomics in pigs coupled with genomic information: toward a comprehensive genetic characterization of the pig metabolome.**
S. Bovo[1], G. Schiavo[1], F. Fanelli[2], A. Ribani[1], F. Bertolini*[1], M. Gallo[3], G. Galimberti[4], S. Dall'Olio[1], P. Martelli[5], R. Casadio[5], U. Pagotto[2], and L. Fontanesi[1], [1]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy*, [2]*Department of Surgical and Medical Sciences, Endocrinology Unit, University of Bologna, Bologna, Italy*, [3]*Associazione Nazionale Allevatori Suini, Roma, Italy*, [4]*Department of Statistical Sciences "Paolo Fortunati," University of Bologna, Bologna, Italy*, [5]*Biocomputing Group, Department of Pharmacy and Biotechnology, University of Bologna, Bologna, Italy*.

P313 **ISAG Bursary Award: On the genetic basis of porcine semen traits: a large-scale genome-wide study on a synthetic line.**
P. Sá*[1], R. Godinho[2], M. Gòdia[1], C. Sevillano[2], B. Harlizius[2], O. Madsen[1], and H. Bovenhuis[1], [1]*Wageningen University and Research, Wageningen, the Netherlands*, [2]*Topigs Norsvin Research Center, Beuningen, the Netherlands*.

Ruminant Genetics and Genomics

P314 **ISAG Bursary Award: Association between host genetics of sheep and the rumen microbial composition.**
S. Mani*[1,3], O. Aiyegoro[2], and M. Adeleke[3], [1]*Agricultural Research Council – Anima Production, Agricultural Research Council – Anima Production, Pretoria, Gauteng, South Africa*, [2]*North West University, North West University, Potchefstroom, North West, South Africa*, [3]*University of KwaZulu Natal, University of KwaZulu Natal, Westville Campus, Durban, KwaZulu Natal, South Africa*.

P315 **Genome-wide association for functional longevity in Rubia Gallega beef cattle breed using a censored threshold model.**
M. Martínez-Castillero[1], D. López-Carbonell[1], H. Srihi[1], J. Altarriba[1], P. Martínez[2], M. Hermida[2], and L. Varona*[1], [1]*Universidad de Zaragoza, Zaragoza, Spain*, [2]*Universidad de Santiago, Lugo, Spain*.

P316 **Evaluation of Gal-3bp expression and modulation in cow blood and milk.**
M. Worku*[1] and B. Mulakala[2], [1]*North Carolina A&T State University, Greensboro, NC*, [2]*University of Vermont, Burlington, VT*.

P317 **The novel RNA-RNA activation of H19 on MyoD transcripts promoting myogenic differentiation of goat muscle satellite cells.**
L. Li*, C. Qin, Y. Chen, W. Zhao, Q. Zhu, D. Dai, S. Zhan, J. Guo, T. Zhong, L. Wang, J. Cao, and H. Zhang, *Farm Animal Genetic Resources Exploration and Innovation Key Laboratory of Sichuan Province, Sichuan Agricultural University, Chengdu, Sichuan, China*.

P318 **ISAG Bursary Award: eQTL mapping in beef cows to identify genetic variants underlying fertility.**
N. Kertz*[1], P. Banerjee[1], J. Afonso[2], P. Dyce[1], and W. Diniz[1], [1]*Auburn University, Auburn, AL*, [2]*Embrapa Pecuária Sudeste, São Carlos, SP, Brazil*.

P319 **Genome-wide estimation of ROH, linkage disequilibrium, haplotype block structure and past effective population size in Hanwoo cows.**
S. Oh* and D. Yoon, *Department of Animal Science and Biotechnology, Graduate School, Kyungpook National University, Sangju, Korea*.

P320 **CD44 gene regulation of bovine adipogenic differentiation and lipid metabolism.**
G. Li*, X. Fang, X. Lu, Y. Liu, and R. Yang, *Jilin University, Changchun, Jilin, China*.

P321 **Analysis of the impact of *DGAT1* p.M435L and p.K232A variants on pre-mRNA splicing in a full-length gene assay.**
N. Gaiani, L. Bourgeois-Brunel, D. Rocha, and A. Boulling*, *Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France*.

P322 **ISAG Bursary Award: Genomic differentiation within the South African Hereford reference population.**
C. Croucamp* and E. van Marle-Köster, *University of Pretoria, Pretoria, Gauteng, South Africa*.

P323 **ISAG Bursary Award: Genes near the Celtic POLLED variant are differentially expressed between horned and polled bovine fetuses at 58 days of development.**
J. Aldersey*[1], Y. Ren[1], W. Low[1], K. Petrovski[1], J. Williams[1,2], and C. Bottema[1], [1]*Davies Livestock Research Centre, University of Adelaide, Roseworthy, South Australia, Australia*, [2]*Department of Animal Science, Food and Technology, Università Cattolica del Sacro Cuore, Emilia Parmense, Piacenza, Italy*.

P324 **ISAG Bursary Award: Multiple-trait joint genetic evaluation improves accuracy of prediction in South-African and Kenyan Holstein cattle population.**
I. Houaga*[1,2], R. Mrode[3,4,11], O. Opoola[1], M. Chagunda[5], M. Okeyo[4], J. E. O. Rege[6], V. E. Olori[7], O. Nash[8], C. B. Banga[9], T. O. Okeno[10], and A. Djikeng[1], [1]*Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh, United Kingdom*, [2]*The Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh, United Kingdom*, [3]*Scotland Rural College (SRUC), Easter Bush, Edinburgh, United Kingdom*, [4]*International Livestock Research Institute (ILRI), Nairobi, Kenya*, [5]*University of Hohenheim, Hohenheim, Stuttgart, Germany*, [6]*Emerge Centre for Innovations-Africa (ECI-Africa), Nairobi, Kenya*, [7]*Aviagen Limited, Newbridge, EH28 8SZ, Edinburgh, United Kingdom*, [8]*Centre for Genomics Research and Innovation, National Biotechnology Development Agency, Abuja, Nigeria*, [9]*Agricultural Research Council (ARC), Pretoria, 0002, South Africa*, [10]*Department of Animal Sciences, Egerton University, Egerton, Kenya*, [11]*The University Edinburgh, Scotland.*

P325 **A two-stage F_{ST} prioritization approach in the presence of high-density marker panels: a simulation study.**
S. Toghiani*[1], S. Aggrey[2,3], and R. Rekaya[2,4], [1]*USDA, Agricultural Research Service, Animal Genomics and Improvement Laboratory, Beltsville, MD*, [2]*Institute of Bioinformatics, The University of Georgia, Athens, GA*, [3]*Department of Poultry Science, The University of Georgia, Athens, GA*, [4]*Department of Animal and Dairy Science, The University of Georgia, Athens, GA*.

P327 **ISAG Bursary Award: Molecular investigations on cryptorchidism in German Holsteins.**
F. Krull*[1], W. Wemheuer[1], T. Melbaum[2], and B. Brenig[1], [1]*University of Goettingen, Institute of Veterinary Medicine, 37077 Goettingen, Germany*, [2]*Bullseye-Genetics GmbH, 48341 Altenberge, Germany*.

P328 **ISAG Bursary Award: Genome-wide association analysis reveals polygenic regulation of ovine high-altitude adaptability.**
C. Li[1,2], B. C. Chen*[1], Y. J. Wu[3], J.-L. Han[4,5], Y. L. Chen[1], P. Zhou[6], H. Pausch[2], and X. L. Wang[1], [1]*Northwest A&F University, Yangling, Shaanxi, China*, [2]*ETH Zürich, Zürich, Switzerland*, [3]*Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, China*, [4]*Chinese Academy of Agricultural Sciences, Beijing, China*, [5]*International Livestock Research Institute, Nairobi, Kenya*, [6]*Xinjiang Academy of Agricultural and Reclamation Sciences, Shihezi, China*.

P330 **Search for new mutations in cattle by systematic whole genome resequencing.**
M. Boussaha[1], C. Eché[2], C. Escouflaire[3], C. Grohs[1], C. Iampietro[2], A. Capitan[1], D. Milan[2,4], C. Gaspin[5,6], S. Fritz[3], C. Donnadieu[2], and D. Boichard*[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France*, [2]*INRAE, US 1426, GeT-PlaGe, Genotoul, France Genomique, Université Fédérale de Toulouse, Castanet-Tolosan, France*, [3]*Eliance, 75012 Paris, France*, [4]*GenPhySE, Université de Toulouse, INRAE, INPT, ENVT, Castanet-Tolosan Cedex, F-31326, France*, [5]*Université Fédérale de Toulouse, INRAE, BioinfOmics, GenoToul Bioinformatics facility, 31326, Castanet-Tolosan, France*, [6]*Université Fédérale de Toulouse, INRAE, MIAT, 31326, Castanet-Tolosan, France*.

P331 **Genomic partitioning to identify hidden heritability using multi-omics data set in Hanwoo cattle.**
Y. Kim*[1], D. Lee[2], D. Lee[2], Y. Chung[2], J. Kang[2], S. Lee[2], and S. Lee[2], [1]*Quantomic Research & Solution, Yuseong-gu, 34134, Daejeon, Republic of Korea*, [2]*Chugnam National University, Yuseong-gu, 34134, Daejeon, Republic of Korea*.

P332 **ISAG Bursary Award: The first gapless complete T2T Y-chromosome assemblies of cattle and sheep uncover their genomic architectures.**
T. Olagunju[1], B. Rosen[2], T. Smith[3], T. Hadfield[4], S. Koren[5], H. Neibergs[6], N. Cockett[4], and B. Murdoch*[1], [1]*University of Idaho, Moscow, ID*, [2]*USDA, ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD*, [3]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*, [4]*Utah State University, Logan, UT*, [5]*National Human Genome Research Institute (NHGRI), NIH, Bethesda, MD*, [6]*Washington State University, Pullman, WA*.

P334 **Milk productivity of different selection Holstein cows at Ayna dairy farm.**
A. Daulet*, B. Saule, U. Rashit, and N. Dinara, *Saken Seyfullin Kazakh Agrotechnical Research University, Astana c., Republic of Kazakhstan*.

P335 **ISAG Bursary Award: Development of a rapid SNP genotyping assay for novel SNPs associated with BLV-induced lymphoma.**
S. Watanuki*[1], R. Matsuura[1], C.-W. Lo[1], S. Saito[1], Y. Miyazaki[2], Y. Matsumoto[1,3], S.-n. Takeshima[4], and Y. Aida[1], [1]*Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [2]*Livestock Improvement Association of Japan, Inc, Gunma, Japan*, [3]*Laboratory of Global Animal Resource Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan*, [4]*Department of Food and Nutrition, Jumonji University, Saitama, Japan*.

P336 **New loci for milk production traits in German Black Pied cattle (DSN) using whole-genome sequencing data.**
P. Korkuc*[1], G. B. Neumann[1], D. Arends[2], K. May[3], S. König[3], and G. A. Brockmann[1], [1]*Humboldt-Universität zu Berlin, Berlin, Germany*, [2]*Northumbria University, Newcastle upon Tyne, United Kingdom*, [3]*Justus-Liebig-Universität Gießen, Gießen, Germany*.

P338 **ISAG Bursary Award: A cell atlas across longissimus dorsi muscle from early embryo to aging goats and trajectories of myogenic progenitor/stem cells.**
Y. Chen*, C.-H. Huang, H.-P. Zhang, and L. Li, *Institute of Animal Genetics, Breeding and Reproduction, College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, Sichuan, China*.

P339 **MicroRNA levels in newborn calves before and after colostrum ingestion.**
H. T. Do[1,2], T. Chen[1], J. L. Williams[1,3], K. Petrovski[1], K. Ren[1], W. Y. Low[1], T. D. Van[1], and C. D. K. Bottema*[1], [1]*Davies Livestock Research Centre, School of Animal & Veterinary Sciences, University of Adelaide, Roseworthy Campus, Roseworthy, SA 5371, Australia*, [2]*Faculty of Animal Science, Vietnam National University of Agriculture, Trau Quy, Gia Lam, Hanoi, Vietnam*, [3]*Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del Sacro Cuore, via Emilia Parmense 84, 29122 Piacenza, Italy*.

P340 **Deep ancestral introgression in the *Ovis* genus shapes argali (*Ovis ammon*) and indirectly draws gene flow patterns in both domestic sheep and wild relatives.**
F.-H. Lv and M.-H. Li*, *China Agricultural University, Beijing, China*.

P341 **Population genomics of South American Creole cattle using high-resolution genome-scale SNP data.**
J. A. Ward*[1], S. I. Ng'ang'a[2,3], I. A. S. Randhawa[4], G. P. McHugo[1], J. F. O'Grady[1], J. A. Browne[1], A. M. Pérez O'Brien[5], T. S. Sonstegard[5], D. G. Bradley[6], L. A. F. Frantz[2,3], and D. E. MacHugh[1,7], [1]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Dublin, D04 V1W8, Ireland*, [2]*Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilian University, Munich, 80539, Germany*, [3]*School of Biological and Chemical Sciences, Queen Mary University of London, London, E1 4NS, United Kingdom*, [4]*Faculty of Science, The University of Queensland, Gatton, QLD 4343, Australia*, [5]*Acceligen, Eagan, MN*, [6]*Smurfit Institute of Genetics, Trinity College Dublin, Dublin, D02 PN40, Ireland*, [7]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, D04 V1W8, Ireland*.

P343 **Study on cattle genomic selection for low-carbon beef production.**
D. Shin*[1], J.-E. Park[2], J. Heo[1], H.-K. Lee[1], S. Son[1], and J.-M. Kim[3], [1]*Jeonbuk National University, Jeonju-si, Jeollabuk-do, Korea*, [2]*Jeju National University, Jeju-si, Jeju-do, Korea*, [3]*Chung-Ang University, Anseong-si, Gyeonggi-do, Korea*.

P344 **Identification of biomarkers for residual feed intake in dairy cows using targeted serum metabolomics.**
D. Hailemariam*[1], M. Hashemiranjbar[1], G. Manafiazar[1,2], P. Stothard[1], and G. Plastow[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*, [2]*Animal Science and Aquaculture Department, Faculty of Agriculture, Dalhousie University, NS, Canada*.

P345 **ISAG Bursary Award: A bovine GWAS reveals determinants of mobilization rate and dynamics of endogenous retroviruses.**
L. Tang*[1], B. J. Swedlund[1,2], C. Harland[1,3], K. Durkin[1,4], M. Artesi[1,4], G. C. M. Moreira[1], S. Dupont[1], J. Dejong[5], L. Karim[5], M. Deckers[5], E. Mullaart[6], W. Coppieters[1,5], M. Georges[1], and C. Charlier[1], [1]*Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Liège, Belgium*, [2]*Keck School of Medicine, University of Southern California, Los Angeles, CA*, [3]*Livestock Improvement Corporation, Research & Development, Hamilton, New Zealand*, [4]*Laboratory of Human Genetics, GIGA-R, Liège, Liège, Belgium*, [5]*GIGA-Genomics Platform, University of Liège, Liège, Liège, Belgium*, [6]*CRV, Research & Development, Arnhem, the Netherlands*.

P346 **High genetic diversity is maintained in the small endangered breed of German Black Pied cattle.**
G. A. Brockmann*[1], G. B. Neumann[1], P. Korkuc[1], M. J. Wolf[2], K. May[2], and S. König[2], [1]*Humboldt-Universität, Berlin, Germany*, [2]*Justus-Liebig Universität, Giessen, Germany*.

P347 **X-linked genes influence various complex traits in dairy cattle.**
M. Sanchez*[1], C. Escouflaire[2], A. Baur[2], F. Bottin[1], C. Hozé[2], M. Boussaha[1], S. Fritz[2], A. Capitan[1], and D. Boichard[1], [1]*Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France*, [2]*Eliance, Paris, France*.

P348 **Nanopore long read sequencing for genome-wide cattle sperm methylation profiling.**
M. Gòdia*, R. P. M. A. Crooijmans, A. C. Bouwman, M. P. L. Calus, and M. A. M. Groenen, *Wageningen University & Research, Wageningen, the Netherlands*.

P349 **Sequence-based GWAS meta-analyses for beef production traits.**
M. Sanchez*[1], T. Tribout[1], N. Kadri[2], P. Chitneedi[3], S. Maak[3], C. Hozé[4], M. Boussaha[1], R. Philippe[5], M. Spengeler[6], C. Kuehn[3], Y. Wang[7], C. Li[7,8], G. Plastow[8], H. Pausch[2], D. Boichard[1], [1]*Université Paris Saclay, INRAE, AgroParisTech, GABI, Jouy en Josas, France*, [2]*ETH, Zürich, Switzerland*, [3]*Research Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*, [4]*Eliance, Paris, France*, [5]*INRAE, USC1061 GAMAA, Université de Limoges, Limoges, France*, [6]*QualitasAG, Zug, Switzerland*, [7]*Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, Canada*, [8]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*.

P350 **ISAG Bursary Award: Size and composition of haplotype reference panels impact the accuracy of imputation from low-pass sequencing in cattle.**
A. Lloret-Villas*, H. Pausch, and A. Leonard, *ETH Zürich, Universitätstrasse 2, 8092, Zürich, Switzerland*.

P351 **Puberty changes the transcriptome of epiphyseal growth plates in *Bos indicus* heifers.**
M. Fortes*[1,2], T. Daro[1], J. Afonso[3], M. Tahir[4], and L. PN[5], [1]*The University of Queensland, School of Chemistry and Molecular Biosciences, Brisbane, Queensland 4072, Australia*, [2]*Queensland Alliance for Agriculture and Food Innovation, Brisbane, Queensland, Australia*, [3]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil*, [4]*Agriculture Victoria, AgriBio Center, Melbourne, Victoria, Australia*, [5]*CSIRO, Agriculture and Food, Queensland Bioscience Precinct, Brisbane, Queensland, Australia*.

P352 **International Sheep Genomics Consortium: providing underpinning resources for the sheep research community.**
S. M. Clarke*[1], R. Brauning[1], and International Sheep Genomics Consortium[2], [1]*AgResearch, Mosgiel, Otago, New Zealand*, [2]*sheephapmap.org, International Sheep Genomics Consortium*.

P353 **The automated genetic ability evaluation system based on genomic information using Hanwoo reference cattle.**
Y. Kim*[1], D. Seo[1], D. Kim[1], O. Kwon[1], E. Hong[1], S. Yu[2], S. Lee[3], J. Kim[4], and M. Park[1], [1]*TNT Research Co, Ltd, Jeonju, South Korea*, [2]*Korea Institute for Animal Products Quality Evaluation, Sejong, South Korea*, [3]*Chungnam National University, Daejeon, South Korea*, [4]*Yeungnam University, Gyeongsan, South Korea*.

P354 **ISAG Bursary Award: Long read based chromosome-level reference genome that encounters complex repetitive sequences in Alpaca (*Vicugna pacos*).**
M. Mendoza*[1], K. Munyard[2], T. Raudsepp[1], and B. Davis[1,3], [1]*Department of Veterinary Integrative Biosciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX*, [2]*Faculty of Health Sciences, Curtin Medical School, Curtin University, Perth, Australia*, [3]*Department of Small Animal Clinical Sciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX*.

P355 **Genomic selection for milk fatty acids from Canadian Holstein cows.**
S. Peters*[1], K. Kadir[2], E. Ibeagha-Awemu[3], and X. Zhao[4], [1]*Department of Animal Science, Berry College, Mount Berry, GA*, [2]*Department of Animal Science, Faculty of Agriculture, Aydin Adnan Menderes University, Aydin, Turkey*, [3]*Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, JIM 0C8 Canada*, [4]*Department of Animal Science, McGill University, Anne de Bellavue, QC H9X 3V9, Canada*.

P356 **TGF-β1 mediated Smad4-Bmf pathway to regulate ovarian granulosa cell apoptosis in small tail Han sheep.**
M. Li*, W. Liang, Y. Luo, J. Wang, X. Liu, S. Li, and Z. Hao, *Gansu Key Laboratory of Herbivorous Animal Biotechnology, College of Animal Science and Technology, Gansu Agricultural University, Lanzhou 730070, China*.

P357 **ISAG Bursary Award: Model comparison of genomic prediction for commercial population in Hanwoo (Korean cattle).**
S. Lee*[1], D. Lee[1], Y. Kim[2], J. Kang[1], D. Lee[1], H. Lee[1], and S. Lee[1], [1]*Chugnam National University, Yuseong-gu, Daejeon, South Korea*, [2]*Quantomic Research & Solution, Yuseong-gu, Daejeon, South Korea*.

P358 **Preliminary results: identification of genomic regions associating with wet carcass syndrome in sheep.**
B. Bhika Kooverjee*[1,2], P. Soma[1], M. van der Nest[3], F. W. C. Neser[2], and M. M. Scholtz[1,2], [1]*Agricultural Research Council, Irene, Pretoria, South Africa*, [2]*University of the Free State, Bloemfontein, South Africa*, [3]*University of Pretoria, Pretoria, South Africa*.

P359 **Genetic analysis of milking temperament and its association with daily milk yield and composition in South African Holstein cattle.**
T. T. Siwele[1,2], B. J. Mtileni[1], K. A. Nephawe[1], M. A. Madilindi[2], B. Dube[2], and C. B. Banga*[3,4], [1]*Department of Animal Science, Tshwane University of Technology, Pretoria, South Africa*, [2]*Agricultural Research Council, Animal Production, Irene, South Africa*, [3]*Department of Agriculture and Animal Health, University of South Africa, Florida, South Africa*, [4]*Department of Animal Sciences, Faculty of Animal and Veterinary Sciences, Botswana University of Agriculture and Natural Resources, Gaborone, Botswana*.

P360 **ISAG Bursary Award: Population fine structure analyses of the indigenous Croatian cattle populations.**
I. Drzaic*[1], I. Curik[1], V. Brajkovic[1], D. Novosel[1,2], and V. Cubric-Curik[1], [1]*University of Zagreb Faculty of Agriculture, Svetošimunska cesta 25, 10040 Zagreb, Croatia*, [2]*Croatian Veterinary Institute, Savska cesta 143, 10000 Zagreb, Croatia*.

P361 **Multibreed genomic prediction and detection of QTL for fertility traits of tropical bulls.**
L. R. Porto-Neto*[1], P. A. Alexandre[1], J. Dorji[1], M. R. Fortes[2], and A. Reverter[1], [1]*CSIRO Agriculture and Food, Brisbane, QLD, Australia*, [2]*The University of Queensland, School of Chemistry and Molecular Bioscience, Brisbane, QLD, Australia*.

P362 **The genetic structure and differentiation within and between smallholder and commercial beef cattle of South Africa.**
M. Ramoroka*[1,2], F. Neser[1], R. Grobler[2], S. F. Lashmar[2], and M. Makgahlela[1,2], [1]*Department of Animal Science, University of the Free State, Bloemfontein, Free State, South Africa*, [2]*Agricultural Research Council-Irene, Animal Production, Pretoria, Gauteng, South Africa*.

P363 **Genome-wide association study of footrot in Portuguese native Merino.**
D. Gaspar*[1,2], C. Ginja[2], C. Leão[1,3], H. Monteiro[4], L. Tábuas[4], S. Branco[3], L. Padre[3], P. Caetano[3], N. Carolino[5], C. Matos[4], A. Ramos[1,3], E. Bettencourt[3], and A. Usié[1,3], [1]*Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo (CEBAL)/ Instituto Politécnico de Beja (IPBeja), Beja, Portugal*, [2]*BIOPOLIS/CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Porto, Portugal*, [3]*MED - Mediterranean Institute for Agriculture, Environment and Development, University of Évora, Polo da Mitra, Évora, Portugal*, [4]*ACOS – Agricultores do Sul, Beja, Portugal*, [5]*Instituto Nacional de Investigação Agrária e Veterinária, I.P. (INIAV, I.P.), Quinta do Marquês, Oeiras, Portugal*.

P364 **ISAG Bursary Award: Genome-wide association studies reveal candidate genes associated with plasma and wool metabolites indicators of water deprivation tolerance in Rasa aragonesa sheep.**
S. Pérez-Redondo*[1], C. Calvete[1,2], M. Joy[1,2], A. Domínguez[1], S. Lobón[1,2], M. Serrano[3], and J. Calvo[1,4], [1]*Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Zaragoza, Spain*, [2]*Instituto Agroalimentario de Aragón (IA2), Zaragoza, Spain*, [3]*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA-CSIC), Madrid, Spain*, [4]*ARAID, Zaragoza, Spain*.

P365 **Meta-analysis of physiological responses to heat stress in Dorper and Ile de France sheep populations.**
P. Soma*[1], B. Kooverjee[1], and M. van der Nest[2], [1]*Agricultural Research Council, Irene, Gauteng, South Africa*, [2]*University of Pretoria, Pretoria, South Africa*.

P366 **Genetic analysis of hypospadias in Coburg fox sheep.**
G. Rudd Garces*[1], A. Letko[2], I. M. Häfliger[2], C. Drögemüller[2], and G. Lühken[1], [1]*Institute of Animal Breeding and Genetics, Giessen, Hessen, Germany*, [2]*Institute of Genetics, Bern, Bern, Switzerland*.

P367 **Transcriptome profiling and functional enrichment analysis of abscessed liver tissue in beef cattle.**
Y. Wang[1,2], J. Wang[3], Z. Pan[1], R. J. Gruninger[4], R. Zaheer[4], T. A. McAllister[4], and L. L. Guan*[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [2]*Institute of Animal Genetics and Breeding, College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, Sichuan, China*, [3]*State Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, College of Animal Science and Technology, Guangxi University, Nanning, Guangxi, China*, [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*.

P368 **Scalepopgen: a bioinformatics workflow resources for population genomic analyses.**
M. Upadhyay* and I. Medugorac, *LMU Munich, Population Genomics Group, Department of Veterinary Sciences, Lena-Christ-Str. 48, 82152 Martinsried, Germany*.

P369 **Assessment of different enrichment methods to characterize bovine circRNAs.**
Y. Wang[1,2], J. Wang[3], R. J. Gruninger[4], T. A. McAllister[4], and L. L. Guan*[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [2]*Institute of Animal Genetics and Breeding, College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, Sichuan, China*, [3]*State Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, College of Animal Science and Technology, Guangxi University, Nanning, Guangxi, China*, [4]*Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*.

P371 **Maternal demographic history of cattle and domestication.**
V. Cubric-Curik*[1], D. Novosel[1], V. Brajkovic[1], J. Soelkner[2], C. Vernesi[3], P. T. Miracle[4], I. Medugorac[5], and I. Curik[1], [1]*University of Zagreb Faculty of Agriculture, Department of Animal Science, Svetosimunska cesta 25, 10000 Zagreb, Croatia*, [2]*Division of Livestock Sciences, Department of Sustainable Agricultural Systems, BOKU-University of Natural Resources and Life Sciences Vienna, Vienna, Austria*, [3]*Department of Sustainable Agro-Ecosystems and Bioresources, Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all' Adige, Italy*, [4]*Department of Archaeology, University of Cambridge, Cambridge, United Kingdom*, [5]*Population Genomics Group, Faculty of Veterinary Medicine, Department of Veterinary Sciences, LMU Munich, Munich, Germany*.

P372 **ISAG Bursary Award: Ubiquitous impact of sex on gene expression across cattle tissues.**
M. Bhati*, J. Prendergast, and A. Tenesa, *The Roslin Institute, University of Edinburgh, Midlothian, Scotland, United Kingdom*.

P373 **Genome-wide association studies for resumption of postpartum ovarian cyclicity trait during seasonal anestrus in Spanish Merino sheep breed.**
J. Calvo*[1,2], J. Marti[3], K. Lakhssassi[1,4], M. García-Méndez[1], M. Sarto[1], B. Lahoz[1], J. Bravo[5], A. Domingo[5], and J. Alabart[1], [1]*Centro de Investigación y Tecnología agroalimentaria de Aragón (CITA)-IA2, Zaragoza, Spain*, [2]*ARAID, Zaragoza, Spain*, [3]*UNIZAR-IA2, Zaragoza, Spain*, [4]*INRA, Rabat, Morocco*, [5]*CENSYRA (Extremadura), Badajoz, Spain*.

P375 **Investigating neutral and functional genetic diversity in South African Bontebok (*Damaliscus pygargus pygargus*).**
M. Mogakala[1], R. Smith*[2,3], C. Mavimbela[1], and D. Dalton[4,2], [1]*Sefako Makgatho Health Sciences Univerty, Pretoria, Gauteng, South Africa*, [2]*South African National Biodiversity Institute, Pretoria, Gauteng, South Africa*, [3]*University of South Africa, Johannesburg, Gauteng, South Africa*, [4]*Teesside University, Middlesbrough, North Yorkshire, England, United Kingdom*.

P376 **Detection of QTL for global recombination rate in Fleckvieh cattle.**
N. Kadri* and H. Pausch, *ETH Zurich, Zurich, Switzerland*.

P377 **The genetic mechanisms of resistance to heartwater in goats from endemic and non-endemic regions of South Africa investigated using Illumina Goat SNP65K genotypes.**
X. Nuse*[1,2], M. A. Van Der Nest[3], E. F. Dzomba[1], F. C. Muchadeyi[2], and H. C. Steyn[4], [1]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scotsville, KwaZulu-Natal, South Africa*, [2]*Agricultural Research Council - Biotechnology Platform, Onderstepoort, Pretoria, Gauteng, South Africa*, [3]*Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, Gauteng, South Africa*, [4]*Molecular Biology Department, Agricultural Research Council - OVI, Onderstepoort, Gauteng, South Africa*.

P378 **Mapping moose short-read sequences on the bovine genome – a tool to investigate the white moose.**
D. Paul[1], T. Kalbfleisch[2], M. Baghdy Sar[1], B. Herlemont[1], T. Bergström[1], I. Shutava[1], and S. Mikko*[1], [1]*Swedish University of Agricultural Sciences, Uppsala, Sweden*, [2]*University of Kentucky, Lexington, KY*.

P379 **ISAG Bursary Award: Tail morphology and environmental adaptations of Ethiopian indigenous sheep: an ecological niche modelling and genomic approaches.**
A. Amane*[1,2], G. Belay[2], T. Dessie[3], A. M. Ahbara[4], E. Vila[5], and O. Hanotte[3,6], [1]*Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia*, [2]*Microbial, Cellular and Molecular Biology, Addis Ababa University, Addis Ababa, Ethiopia*, [3]*LiveGene, International Livestock Research Institute (ILRI), P.O. 5689, Addis Ababa, Ethiopia*, [4]*Department of Zoology, Misurata University, Misurata, Libya*, [5]*CNRS/Univ. Lyon 2, UMR 5133 Archéorient, Maison de l'Orient et de la Méditerranée, Lyon, France*, [6]*School of Life Sciences, University of Nottingham, University Park, Nottingham NG7 2RD, United Kingdom*, [7]*Centre for Tropical Livestock Genetics and Health, The Roslin Institute, Edinburgh EH25 9RG, United Kingdom*.

P380 **ISAG Bursary Award: Integration of reduced representation bisulphite sequencing with RNA sequencing data provides further insights in claw horn disruption lesions susceptibility in dairy cattle.**
E. Attree*[1], X. Dai[1], D. Xia[1], M. Barden[2], B. Griffiths[2], A. Anagnostopoulos[2], D. Werling[3], G. Oikonomou[2], G. Banos[4], and A. Psifidi[1], [1]*The Royal Veterinary College, Department of Clinical Science and Services, The Royal Veterinary College, Hatfield, United Kingdom*, [2]*Scotland's Rural College, Department of Animal and Veterinary Sciences, Scotland's Rural College, Midlothian, Scotland, United Kingdom*, [3]*University of Liverpool, Department of Livestock and One Health, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Neston, United Kingdom*, [4]*The Royal Veterinary College, Department of Pathobiology and Population Sciences, Royal Veterinary College, Hatfield, United Kingdom*.

P381 **Genomic breed composition information can optimize stratified randomization strategies in beef cattle experiments.**
O. Durunna*[1,2] and C. Ekine-Dzivenu[3], [1]*Lakeland College, Vermilion, Alberta, Canada*, [2]*University of Saskatchewan, Saskatoon, Saskatchewan, Canada*, [3]*International Livestock Research Institute, Nairobi, Kenya*.

P382 **DNA variant related to congenital adrenal hyperplasia in cattle.**
R. Hofmeyer, T. Chen, L. Hampton, W. Y. Low, W. S. Pitchford, K. Petrovski, and C. D. Rottema*, *Davies Livestock Research Centre, School of Animal and Veterinary Sciences, Roseworthy Campus, University of Adelaide, Roseworthy, Australia*.

P383 **Insights into the genetic variation, gene-flow and demographic history of African cattle breeds.**
M. Malima[1,2], K. Nxumalo[1], A. Tijjani[3,4], M. Makgahlela*[1], F. Joubert[2], and A. Zwane[1], [1]*Department of Animal Breeding and Genetics, Agricultural Research Council-Animal Production Irene, Pretoria, South Africa*, [2]*Centre for Bioinformatics and Computational Biology, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa*, [3]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*, [4]*The Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, The University of Edinburgh, Midlothian, United Kingdom*.

P384 **A continent-wide genomic resource for African buffalo (*Syncerus caffer*).**
L. Morrison*[1,2], [1]*Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom*, [2]*Centre for Tropical Livestock Genetics and Health, University of Edinburgh, Edinburgh, United Kingdom*.

P385 **Convergent selection of structural variations reveals genes associated with domestication and production traits in sheep and goats.**
J. Yang*[1], D.-F. Wang[1,2], Q.-H. Zhu[1,2], J.-H. Huang[1], L.-Y. Luo[1], R. Lu[1], X.-L. Xie[2,3], H. Salehian-Dehkordi[2,3], A. Esmailizadeh[4], G. E. Liu[5], and M.-H. Li[1], [1]*College of Animal Science and Technology, China Agricultural University, Beijing, China*, [2]*CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences (CAS), Beijing, China*, [3]*College of Life Sciences, University of Chinese Academy of Sciences (UCAS), Beijing, China*, [4]*Department of Animal Science, Shahid Bahonar University of Kerman, Kerman, Iran*, [5]*Animal Genomics and Improvement Laboratory, BARC, USDA-ARS, Beltsville, MD*.

P386 **ISAG Bursary Award: Pangenomes of haplotype-resolved assemblies enable population-scale genotyping of cattle structural variation for eQTL mapping.**
A. Leonard*, X. Mapel, and H. Pausch, *ETH Zurich, Zurich, Switzerland*.

P387 **Living in two extremes: convergent nucleotide evolution and parallel selection in cold- and heat-resistant cattle breeds and wild animals.**
G. Romashov[1], N. Yudin[1], J. Prendergast[2], A. Talenti[2], J. Powell[2], and D. Larkin*[3], [1]*Institute of Cytology and Genetics, Novosibirsk, Siberia, Russia*, [2]*Roslin Institute, Edinbough, Scotland, United Kingdom*, [3]*Royal Veterinary College, London, Greater London, United Kingdom*.

P388 **Identification the genetic resistance genes and biosynthesis pathways to gastrointestinal nematodes infection in goat using RNA-sequencing.**
A. A. Bhuiyan[1], A. Bhuyan*[2], A. S. Afsana[3], S. Zhao[4], and X. Du[5], [1]*Bangladesh Agricultural Research Council, Dhaka, Dhaka, Bangladesh*, [2]*National Institute of Biotechnology, Savar, Dhaka, Bangladesh*, [3]*Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh*, [4]*Huazhong Agricultural University, Wuhan, Hubei, China*, [5]*Huazhong Agricultural University, Wuhan, Hubei, China*.

P389 **Analysis of differential isoform usage in production relevant tissues across pre- and post-natal development in sheep.**
S. A. Woolley[1], J. G. D. Prendergast[1], M. Salavati[1,2], and E. L. Clark*[1], [1]*The Roslin Institute, Edinburgh, Midlothian, United Kingdom*, [2]*SRUC, Edinburgh, Midlothian, United Kingdom*.

P390 **Functional mapping of alternative polyadenylation in cattle.**
Z. Jiang[1], H. Wang[1], X. Zhou[1], J. J. Michal[1], S. A. Carrion[1], S. Zhang[1], Y. Zhang[1], M. J. Stotts[1], S. He[1], Y. Zhang[1], X. Zhang[1], X. Han[1], W. Wang[1], L. Qu[1], R. Li[1], M. Maquivar[1], M. Du[1], L. K. Fox[1], M. L. Bernhardt[2], Y. Wang[3], J. Velez[4], B. Hans[4], B. M. Murdoch[5], C. Gill[6], H. Jiang[7], H. Zhou[8], J. E. Koltes[9], J. Reecy[9], M. Rijnkels[10], P. J. Ross[8], S. McKay[11], T. P. L. Smith[12], W. Liu[13], K. Ren[14], L. Low[14], J. Yang[15], and S. P. Miller[16], [1]*Department of Animal Sciences and Center for Reproductive Biology, Washington State University, Pullman, WA,* [2]*Animal Production Core, Center for Reproductive Biology, Washington State University, Pullman, WA,* [3]*Department of Mathematics and Statistics, Washington State University, Pullman, WA,* [4]*Aurora Organic Farms, Platteville, CO,* [5]*Department of Animal and Veterinary Science, University of Idaho, Moscow, ID,* [6]*Department of Animal Science, Texas A&M University, College Station, TX,* [7]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA,* [8]*Department of Animal Science, University of California Davis, Davis CA,* [9]*Department of Animal Science, Iowa State University, Ames, IA,* [10]*Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX,* [11]*Department of Animal and Veterinary Science, University of Vermont, Burlington, VT,* [12]*Roman L. Hruska U.S. Meat Animal Research Center, USDA-ARS-PA-MARC, Clay Center, NE,* [13]*Department of Animal Science, The Pennsylvania State University, University Park, PA,* [14]*School of Animal and Veterinary Science, University of Adelaide, Adelaide, SA, Australia,*[15]*Department of Human Nutrition, Food and Animal Sciences, University of Hawaii at Manoa, Honolulu, HI,* [16]*Animal Genetics and Breeding Unit, University of New England, Armidale NSW 2351, Australia.*

P391 **Genetic diversity and population structure among Central European native sheep breeds using microsatellite markers.**
Z. Sztankoova, M. Milerski, M. Brzáková, J. Rychtárová, and J. Kyselova*, *Institute of Animal Science, Praha-Uhrineves, Czech Republic*.

P392 **A time-resolved multi-omics atlas of transcriptional regulation in response to high-altitude hypoxia across the whole-body tissues.**
Z. Yan* and M. Li, *China Agricultural University, Beijing, China*.

P393 **CNV mapping and CNV contribution to genetic variance of complex traits in dairy cattle.**
G. Ladeira[1], P. Pinedo[2], J. Santos[1], W. Thatcher[1], and F. Rezende*[1], [1]*University of Florida, University of Florida, Gainesville, FL*, [2]*Colorado State University, Colorado State University, Fort Collins, CO*.

P394 **Investigating the role of β-globin in the response to mycotoxin exposure in sheep.**
K. McRae[1], E. Willems[2], A. Thomas[2], R. Clarke[1], J. Plowman[2], E. Maes[2], S. Clarke*[1], and P. Johnson[1], [1]*AgResearch Ltd, Mosgiel, New Zealand*, [2]*AgResearch Ltd, Lincoln, New Zealand*.

P395 **Studying cattle structural variation and pangenome using whole genome sequencing.**
G. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD*.

Small Ruminant Genetics and Genomics

P396 **Investigating the association of the goat *CSN1S1* polymorphism with milk traits in Murciano-Granadina goats through the use of a KASP assay.**
A. Castello[1,2], T. F. Cardoso[1], M. Luigi[1], A. Martínez[3], J. V. Delgado[3], J. Jordana[2], G. Cosenza[4], and M. Amills*[1,2], [1]*Centre of Research in Agricultural Genomics, Bellaterra, Barcelona, Spain*, [2]*Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain*, [3]*Universidad de Cordoba, Cordoba, Spain*, [4]*University of Naples, Naples, Italy*.

P397 **ISAG Bursary Award: Identification of long non-coding RNAs differentially expressed in the mammary gland of lactating and dry goats.**
M. Wang*[1], E. Varela-Martínez[1], M. Luigi-Sierra[1], A. Noce[1], A. Martínez[2], J. Delgado[2], A. Salama[3], X. Such[3], J. Jordana[3], and M. Amills[1,3], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*, [2]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*, [3]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain*.

P398 **Genomic improvement in dairy goats using DNA sequencing.**
A. Caulton*[1], M. Wheeler[2], S. Clarke[1], R. Brauning[1], T. Van Stijn[1], H. Baird[1], R. Anderson[1], B. Foote[3], J. Foote[3], S. Cameron[4], T. Blichfeldt[5], J. Jakobsen[5], K. Dodds[1], and J. McEwan[1], [1]*AgResearch, Mosgiel, Otago, New Zealand*, [2]*AgResearch, Hamilton, Waikato, New Zealand*, [3]*Footes, Hikurangi, Northland, New Zealand*, [4]*Meredith Dairy, Meredith, Victoria, Australia*, [5]*NSG, As, Norway*.

P399 **Ascertaining the variability and demographic history of the Canarian goat breeds through the use of genome-wide SNPs data.**
G. Senczuk*[1], M. Macrì[2,3], S. Mastrangelo[4], M. Di Civita[1], M. del Rosario Fresno[5], J. Capote[5], F. Pilla[1], J. V. Delgado[3], M. Amills[6], and A. Martínez[3], [1]*Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy*, [2]*Animal Breeding Consulting S.L, Córdoba, Spain*, [3]*Universidad de Córdoba, Córdoba, Spain*, [4]*Department of Agricultural, Food and Forest Sciences, University of Palermo, Palermo, Italy*, [5]*Instituto Canario de Investigaciones Científicas, Tenerife, Spain*, [6]*CRAG, CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

P400 **Combining ATAC-Seq and RNA-Seq data to investigate the molecular basis of lactation in goats.**
A. Noce*[1], M. Luigi-Sierra[1], A. Martínez[2], M. Wang[1], M. Macri[2], J. Delgado[2], A. Salama[3], X. Such[3], J. Jordana[3], and M. Amills[1,3], [1]*Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra 08193, Spain*, [2]*Departamento de Genética, Universidad de Córdoba, Córdoba 14071, Spain*, [3]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra 08193, Spain*.

P401 **Heritability estimates of hematological, serological, morphological and productive traits in Murciano-Granadina goats, using a univariate animal model.**
M. Macrì[1,2], M. Amills[3,4], J. León Jurado[5], L. Gama[6], M. Luigi-Sierra[3], J. Delgado[2], J. Fernández[7], and A. Martínez Martínez*[2], [1]*Animal Breeding Consulting, 14014-Córdoba, Spain*, [2]*Universidad de Córdoba, 14071-Córdoba, Spain*, [3]*CRAG, CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, 08193-Bellaterra, Spain*, [4]*Universitat Autònoma de Barcelona, 08193-Bellaterra, Spain*, [5]*Diputación Provincial de Córdoba, 14071 Córdoba, Spain*, [6]*Universidad de Lisboa, 1649-004 Lisboa, Portugal*, [7]*Asociación Nacional de Criadores de Caprino de Raza Murciano-Granadina (CAPRIGRAN), 18340-Granada, Spain*.

P402 **A study of body weight and type traits recorded on Hairy goat in Punjab, Pakistan.**
A. Qayyum*, J. A. Baig, G. Bilal, H. M. Waheed, H. M. B. Akhtar, and F. Ahad, *Department of Animal Breeding and Genetics/National Center for Livestock Breeding Genetics and Genomics, PMAS-Arid Agriculture University Rawalpindi, Rawalpindi, Punjab, Pakistan*.

P405 **Genetic analysis of body weight of Mecheri sheep using robust model.**
A. K. Thiruvenkadan[1], K. Kizilkaya[2], S. O. Peters*[3], J. Muralidharan[4], and C. Bandeswaran[5], [1]*Department of Animal Genetics and Breeding, Veterinary College and Research Institute, Salem, Tamil Nadu, India*, [2]*Aydin Adnan Menderes University, Faculty of Agriculture, Department of Animal Science, Biometry and Genetics Unit, Aydin, Turkey*, [3]*Department of Animal Science, Berry College, Mount Berry, GA*, [4]*Mecheri Sheep Research Station, Pottaneri, Tamil Nadu, India*, [5]*Department of Animal Nutrition, Madras Veterinary College, Chennai, Tamil Nadu, India*.

P406 **Phenotypic and genomic variation in gastrointestinal nematode (GIN) infection in Tunisian indigenous sheep.**
J. Mwacharo*[1,2], M. Rouatbi[3], A. Ahbara[2], M. Gharbi[3], M. Rekik[1], A. Haile[1], and B. Rischkowsky[1], [1]*Small Ruminant Genomics, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia*, [2]*Animal and Veterinary Sciences, Scotland's Rural College (SRUC) and Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute, Midlothian, Scotland*, [3]*Laboratoire de Parasitologie, Université de la Manouba,École Nationale de Médecine Vétérinaire de Sidi Thabet, Sidi Thabet Tunisia*.

P407 **Withdrawn**

P409 **Association analysis of Foxn1 gene and Foxe1 gene polymorphisms with wool traits in Gansu Alpine Fine wool sheep.**
L. He, Y. Luo, F. Zhao*, J. Hu, J. Wang, X. Liu, Z. Zhao, M. Li, and S. Li, *Gansu Key Laboratory of Herbivorous Animal Biotechnology, Faculty of Animal Science and Technology, International Wool Research Institute, Gansu Agricultural University, Lanzhou, Gansu Province, China*.

P410 **Whole-genome diversity across Nubian, Old English, and Anglo-Nubian goat breeds.**
S. A. Rahmatalla*[1,2], D. Arends[3], G. B. Neumann[1], H. Abdel-Shafy[4], J. Conington[5], M. Reissmann[1], M. K. Nassar[1,4], and G. A. Brockmann[1], [1]*Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Humboldt-Universität zu Berlin, Berlin, Germany*, [2]*Faculty of Animal Production, University of Khartoum, Khartoum, Sudan*, [3]*Department of Applied Sciences, Northumbria University, Newcastle upon Tyne, UK*, [4]*Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt*, [5]*SRUC, W Mains, Rd, Edinburgh, Scotland, United Kingdom*.

P411 **ISAG Bursary Award: Investigation on already known variants and markers for horn phenotypes in Icelandic sheep.**
R. Simon*[1], K. Elísabetardóttir[2], and G. Lühken[1], [1]*Institute of Animal Breeding and Genetics, Justus Liebig University, 35390 Giessen, Germany*, [2]*Hvammshlíð, Iceland*.

P412 **Assessing runs of homozygosity Kazakh Edilbay sheep breed.**
A. Khamzina*[1], S. Darkhan[1], A. Shamshidin[1], and K. Khamzin[2], [1]*Zhangir Khan University, Uralsk, Kazakhstan*, [2]*Kazakh National Agrarian Research University, Almaty, Kazakhstan*.

P414 **Monitoring of genetic polymorphism at *CSN2* and *CSN3* loci in Czech goat population using primer extension analysis (PEA).**
Z. Sztankoova, L. Tichý, K. Novák, and J. Kyselová*, *Institute of Animal Science, Praha-Uhrineves, 104 00 Czech Republic*.

P415 **ISAG Bursary Award: Genetic diversity among Swakara sub-populations and their founders.**
A. Njilo*[1,2], F. Muchadeyi[1], and E. Dzomba[1], [1]*Agricultural Research Council, Pretoria, Gauteng, South Africa*, [2]*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*.

P416 **Genetic diversity of United States Rambouillet, Dorper, and Katahdin sheep.**
G. Becker*[1], J. Thorne[1,2], J. Burke[3], R. Lewis[4], D. Notter[5], J. Morgan[6], C. Schauer[7], W. Stewart[8], R. Redden[2], and B. Murdoch[1], [1]*Department of Animal, Veterinary and Food Science, University of Idaho, Moscow, ID*, [2]*Texas A&M AgriLife Extension, Texas A&M University, San Angelo, TX*, [3]*United States Department of Agriculture, Agricultural Research Service, Dale Bumpers Small Farms Research Center, Booneville, AR*, [4]*Department of Animal Science, University of Nebraska–Lincoln, Lincoln, NE*, [5]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, VA*, [6]*Round Mountain Consulting, Fayetteville, AR*, [7]*Hettinger Research Extension Center, North Dakota State University, Hettinger, ND*, [8]*Department of Animal Science, University of Wyoming, Laramie, WY*.

P417 **Unravelling of genes associated with coat color and coat color patterns in South African meat-type goats.**
S. Gcabashe*[1], F. Muchadeyi[2], and E. Dzomba[3], [1]*University of KwaZulu-Natal-School of Life Sciences, University of KwaZulu-Natal-School of Life Sciences, Pietermaritzburg, KwaZulu-Natal, South Africa*, [2]*Agricultural Research Council-Biotechnology Platform, Agricultural Research Council-Biotechnology Platform, Pretoria (Onderstepoort), Gauteng, South Africa*, [3]*University of KwaZulu-Natal-School of Life Sciences, University of KwaZulu-Natal-School of Life Sciences, Pietermaritzburg, KwaZulu-Natal, South Africa*.

P418 **Genome-wide association study of growth traits in Tswana goats of Botswana.**
A. B. Chalebgwa*[1], P. I. Monau[1], K. Raphaka[2], P. Kgwatalala[1], and S. J. Nsoso[1], [1]*Botswana University of Agriculture and Natural Resources, Gaborone, Botswana*, [2]*National Agricultural Research and Development Institute, Gaborone, Botswana*.

P419 **Differentiation of Indigenous Veld goats (IVG) breed in South Africa.**
L. Rashijane*[1,2], T. Tyasi[2], and K. Hadebe[1], [1]*Agricultural Research Council*, *Pretoria, Gauteng, South Africa*, [2]*University of Limpopo*, *Polokwane, Limpopo, South Africa*.

P420 **Polymorphism and association of growth hormone gene with growth traits in Dorper sheep.**
K. Molabe*[1], T. Tyasi[1], V. Mbazima[1], B. Gunya[1], and L. Bila[2], [1]*University of Limpopo*, *Polokwane, Limpopo, South Africa*, [2]*Potchefstroom College of Agriculture*, *Potchefstroom, North West, South Africa*.

P421 **Absolute quantification of growth differentiation factor-9 (GDF9) gene in ovarian tissues of high prolific and low prolific sheep breeds.**
J. Mamutse*[1], A. Molotsi[1], K. Dzama[1], and C. Urbano-Braz[2], [1]*Stellenbosch University*, *Capetown, Western Cape, South Africa*, [2]*University of Illinois*, *Champaign, IL*.

P422 **ISAG Bursary Award: Breed composition of South African sheep affected by wet carcass syndrome.**
R. Grobler*, P. Soma, B. B. Kooverjee, and M. M. Scholtz, *Agricultural Research Council – Animal Production Institute*, *Irene, Gauteng, South Africa*.

P424 **The benefit of genomic information for enhancing genetic prediction of production and reproduction traits in South African Merino sheep.**
C. Nel*[1,2], P. Gurman[3], A. Swan[3], J. van der Werf[4], M. Snyman[5], K. Dzama[2], W. Olivier[5], A. Scholtz[1], and S. Cloete[2], [1]*Directorate: Animal Sciences, Western Cape Department of Agriculture*, *Elsenburg, Western Cape, South Africa*, [2]*Department of Animal Sciences, Stellenbosch University*, *Stellenbosch, Western Cape, South Africa*, [3]*Animal Genetics & Breeding Unit, University of New England*, *Armidale, New South Wales, Australia*, [4]*School of Environmental and Rural Science, University of New England*, *Armidale, New South Wales, Australia*, [5]*Grootfontein Agricultural Development Institute, Department of Agriculture, Land Reform and Rural Development*, *Middelburg, Eastern Cape, South Africa*.

P425 **Rumen microbial composition in sheep supplemented with *Acacia mearnsii* Tannin extract for methane reduction.**
I. Lawal, E. van Marle-Koster*, and A. Hassen, *University of Pretoria*, *Pretoria, Gauteng, South Africa*.

P426 **DNA-based vaccine design against *Toxoplasma gondii* in ovines using rhoptry protein antigens through immunoinformatics approach.**
T. Madlala*[1], M. Adeleke[1], M. Okpeku[1], and S. Tshilwane[2], [1]*University of KwaZulu Natal*, *Durban, KwaZulu Natal, South Africa*, [2]*University of Pretoria*, *Onderstepoort, Pretoria, South Africa*.

P427 **Goat milk oligosaccharide composition determined by genes with a large effect.**
R. Gonzalez-Prendes*[1,2], H. Bovenhuis[2], L. Pellis[1], and R. P. M. A. Crooijmans[2], [1]*Ausnutria BV*, *Zwolle, the Netherlands*, [2]*Animal Breeding and Genomics, Wageningen University & Research, Animal Breeding and Genomics, Wageningen University & Research, Droevendaalsesteeg 1, 6708 PB*, *Wageningen, The Netherlands*.

P428 **Identification of genetic regions associated with resistance to gastrointestinal nematodes in Comisana sheep using a genome-wide association study based on EBV ranking.**
C. Persichilli[1], S. Biffani[2], G. Senczuk[1], M. Di Civita*[1], M. K. Bitew[1], A. Bosco[3], S. Grande[4], and F. Pilla[1], [1]*University of Molise, Department of Agricultural, Environmental and Food Science*, *Campobasso, CB, Italy*, [2]*National Council of Research, Institute for Agriculture Biology and Biotechnology*, *Milan, MI, Italy*, [3]*University of Naples Federico II, Department of Veterinary Medicine and Animal Production, CREMOPAR*, *Naples, NA, Italy*, [4]*National Sheep and Goat Breeders Association*, *Rome, RM, Italy*.

P429 **ISAG Bursary Award: First look into the genetic architecture influencing liver copper concentration in Merinoland sheep.**
O. O. Adeniyi* and G. Lühken, *Institute of Animal Breeding and Genetics, Justus Liebig University*, *Giessen, Hessen, Germany*.

P430 **The extreme genotypes of *CSN1S1* gene have a significant effect on milk composition and cheese yield in Carpathian goat.**
V. A. Balteanu*[1], R. K. Sigartau[2], D. Nadolu[3], and A. H. Anghel[4], [1]*University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Institute of Life Sciences*, *Cluj-Napoca, Cluj, Romania*, [2]*Babes-Bolyai University, Faculty of Mathematics and Computer Science*, *Cluj-Napoca, Cluj, Romania*, [3]*ICDCOC Palas*, *Constanta, Constanta, Romania*, [4]*Ovidius University*, *Constanta, Constanta, Romania*.

P431 **Positional candidate genes involved in the response to heat stress in sheep.**
M. Ramon*[1], C. Diaz[2], M. Serrano[2], and M. J. Carabaño[2], [1]*CERSYRA-IRIAF, Valdepeñas, Ciudad Real, Spain*, [2]*INIA-CSIC, Madrid, Spain*.

P432 **Selection of an ovine SNP parentage panel for consideration as the ISAG comparison test panel.**
R. Ferretti*[1], K. Schutt[2], M. Dowling[2], J. Qiu[1], and R. Tait[1], [1]*Neogen GeneSeek Operations*, *Lincoln, NE*, [2]*Neogen Australasia*, *Ipswitch, QLD 4304, Australia*.

P433 **Modulation of innate immune memory and systemic effects of Gum Arabica in goats.**
Y. Ahmed and M. Worku*, *North Carolina A&T State University*, *Greensboro, NC*.

P434 **Gene expression profiling of the abomasum, duodenum, jejunum and ileum of resistant and susceptible Dohne Merino sheep naturally infected with *Haemonchus contortus*.**
T. M. Ramantswana*[1,2], D. P. Malatji[2], R. E. Pierneef[1], P. Soma[3], M. Van Der Nest[4], and F. C. Muchadeyi[1], [1]*Agricultural Research Council, Biotechnology Platform, Biotechnology Platform*, *Onderstepoort, Pretoria, South Africa*, [2]*University of South Africa*, *Florida, Gauteng, South Africa*, [3]*Agricultural Research Council, Animal Production Institute*, *Irene, Pretoria, South Africa*, [4]*University of Pretoria*, *Hatfield, Pretoria, South Africa*.

Award Winners

International Union of Immunological Societies-Veterinary Immunology Committee Travel Award Winners

OP99 + P153
IUIS-VIC Travel Award 2: Due to their improved immunity, disease-resistant common carp fish are also less infective.
B. Dorfman, Department of Animal Sciences, R.H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Israel

OP92 + P155
IUIS-VIC Travel Award 1: Transcriptomic signatures of peripheral immune cells associated with immune competence traits in Australian Angus cattle.
A. Wilson, Commonwealth Scientific and Industrial Research Organization, East Geelong, VIC, Australia

ISAG/IFAG 2023 Travel Bursary Award Winners

P345
ISAG Bursary Award: A bovine GWAS reveals determinants of mobilization rate and dynamics of endogenous retroviruses.
L. Tang, Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Liège, Belgium

P338
ISAG Bursary Award: A cell atlas across longissimus dorsi muscle from early embryo to aging goats and trajectories of myogenic progenitor/stem cells.
Y. Chen, Institute of Animal Genetics, Breeding and Reproduction, College of Animal Science and Technology, Sichuan Agricultural University, Chengdu, Sichuan, China

P214
ISAG Bursary Award: A genomic characterization of the SA Bonsmara breed using the BovineHD 777K array.
D. Alberts, University of Pretoria, Pretoria, Gauteng, South Africa

P287
ISAG Bursary Award: A GWAS and RNA-Seq based analysis to shed light into the molecular and genetic basis of sperm cryo-tolerance in swine.
Y. Lian, Centre for Research in Agricultural Genomics, Cerdanyola del Vallès, Catalonia, Spain

OP169 + P131
ISAG Bursary Award: A high-density genetic linkage map and QTL mapping for growth traits in South African abalone (Haliotis midae).
T. Tshilate, Department of Genetics, Stellenbosch University, Stellenbosch, South Africa

OP157 + P63
ISAG Bursary Award: A lncRNA gene-enriched atlas for GRCg7b chicken genome and its functional annotation across 47 tissues.
F. Degalez, Institut Agro, France

OP146 + P18
ISAG Bursary Award: A new approach to the molecular differentiation of the wolf and the domestic dog in wildlife forensics.
A. E. Hrebianchuk, State Forensic Examination Committee of the Republic of Belarus, Minsk, Republic of Belarus

OP116 + P97
ISAG Bursary Award: Adipose gene expression profiles of four cattle breeds highlight selective pressures and tissue functions.
D. Ruvinskiy, Natural Resources Institute Finland (Luke), Jokioinen, Finland

OP113 + P207
ISAG Bursary Award: Admixed ancestry or independent race: A phylogenetic meta-analysis on the phylogeography of Philippine chickens.
C. Godinez, Department of Animal Science, College of Agriculture and Food Science, Visayas State University, Visca, Baybay City, Leyte, Philippines

OP49 + P308
ISAG Bursary Award: Allele-specific expression in pig genomic makeup and phenotypic implications.
W.-Y. Yao, Animal Breeding and Genomics, Wageningen University & Research, Wageningen, the Netherlands

OP107 + P209
ISAG Bursary Award: An insight into whole-genome resequencing data of Indian native goats with global breeds reveals high within-breed genetic diversity and distinct population structure.
N. Balasubramaniam, ICAR-National Dairy Research Institute, Karnal, Haryana, India

OP84 + P114
ISAG Bursary Award: An organism-wide ATAC-Seq peak catalogue for the bovine and its use to identify regulatory variants.
C. Yuan, GIGA Institute, University of Liège, Liège, Belgium

P217
ISAG Bursary Award: Anthropological events and environmental stress are shaping the genomes of Ethiopian indigenous goats.
S. Belay, Tigray Agricultural Research Institute, Mekelle, Ethiopia

OP102 + P156
ISAG Bursary Award: Assessment of haemagglutination titre and serum lysozyme concentration in Nigerian indigenous chicken genotypes.
U. Akpan, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria

P314
ISAG Bursary Award: Association between host genetics of sheep and the rumen microbial composition.
S. Mani, Agricultural Research Council – Anima Production, Agricultural Research Council – Anima Production, Pretoria, Gauteng, South Africa

P230
ISAG Bursary Award: Autozygous regions, inbreeding, and effective population size in South African Afrikaner cattle.
S. Lashmar, University of Pretoria, Pretoria, Gauteng, South Africa

P422
ISAG Bursary Award: Breed composition of South African sheep affected by wet carcass syndrome.
R. Grobler, Agricultural Research Council – Animal Production Institute, Irene, Gauteng, South Africa

P220
ISAG Bursary Award: Building genomic resources for cattle breeds at risk of extinction in Nigeria.
O. Opoola, Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Intitute, University of Edinburgh, Easter Bush Campus, Edinburgh, UK

P19
ISAG Bursary Award: Can DNA help trace the local trade of pangolins? Conservation genetics of white-bellied pangolins from the Dahomey Gap (West Africa).
S. Zanvo, Laboratory of Applied Ecology, University of Abomey-Calavi, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin

OP145
ISAG Bursary Award: Can DNA help trace the local trade of pangolins? Conservation genetics of white-bellied pangolins from the Dahomey Gap (West Africa).
S. Zanvo, Laboratory of Applied Ecology, Faculty of Agronomic Sciences, University of Abomey-Calavi, Cotonou, Benin

P28
ISAG Bursary Award: Characterization of chicken strains in Isin local government based on phenotypic parameters, blood polymorphism, and 18s mitochondria genes.
P. A. Owolabi, University of Ilorin, Ilorin, Kwara, Nigeria

P146
ISAG Bursary Award: Characterization of the host-specific glycan responding to African swine fever virus infections.
K. Han, Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China

P24
ISAG Bursary Award: Combined effect of microbially-derived caecal SCFA and host genetics on feed efficiency in broiler chickens.
Z. He, Institution of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

P109
ISAG Bursary Award: Comparative genomics reveals common diversity and signature of selection in Saudi Arabian indigenous chickens.
A. Assiri, University Of Nottingham, Nottingham, United Kingdom

P46
ISAG Bursary Award: Complex genetic architecture of the chicken genome. An example of Growth1 QTL region.
J.-H. Ou, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden

OP47 + P309
ISAG Bursary Award: Comprehensive identification of functional DNA elements and 3D chromatin interaction map in the pig genome.
D. Wang, Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China

OP172 + P136
ISAG Bursary Award: Construction of a high-density genetic linkage map using 2b-RAD sequencing in dusky kob (Argurosomus japonicus).
C. Rhode, Stellenbosch University, Stellenbosch, South Africa

OP94 + P157
ISAG Bursary Award: CRISPR-SpRY-mediated base-editing screening identifies TMEM41B amino acids that are critical for transmissible gastroenteritis virus replication in pig.
Y. Zhou, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, Hu Bei, China

P335
ISAG Bursary Award: Development of a rapid SNP genotyping assay for novel SNPs associated with BLV-induced lymphoma.
S. Watanuki, Laboratory of Global Infectious Diseases Control Science, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan

OP181 + P247
ISAG Bursary Award: Differential proteomics revealed the impact of heat stress on milk whey proteins in indigenous Deoni (Bos indicus) and Holstein Friesian (Bos taurus) crossbred cows.
E. Rana, Southern Regional Station, ICAR- National Dairy Research Institute, Bangalore, India

OP13 + P102
ISAG Bursary Award: DNA methylation dynamics regulating embryonic development in pig.
J. de Vos, Animal Breeding and Genomics, Wageningen University, Wageningen, the Netherlands

OP51 + P299
ISAG Bursary Award: Enhancer-promoter interaction map in the maternal-fetal interface during implantation reveals important regulatory regions and variations in pigs.
Y. Sun, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China

P318
ISAG Bursary Award: eQTL mapping in beef cows to identify genetic variants underlying fertility.
N. Kertz, Auburn University, Auburn, AL

P29
ISAG Bursary Award: Estimation of genetic diversity and population structure of Korean domestic chickens by comparison with SYNBREED data.
E. Cho, Chungnam National University, Daejeon, Republic of Korea

OP132 + P169
ISAG Bursary Award: Field-deployable nucleic acid detection with RAVI-CRISPR.
S. Xie, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture and Rural Affairs, Huazhong Agricultural University, Wuhan, China

OP137 + P429
ISAG Bursary Award: First look into the genetic architecture influencing liver copper concentration in Merinoland sheep.
O. O. Adeniyi, Institute of Animal Breeding and Genetics, Justus Liebig University, Giessen, Hessen, Germany

OP100 + P151
ISAG Bursary Award: Functional diversity of Toll signaling pathway in Czech Simmental cattle with respect to health and resilience traits.
K. Samake, Charles University, Prague, Czech Republic

OP16 + P84
ISAG Bursary Award: Functional variants associated with male fertility in reproductive tissues of Brown Swiss bulls.
X. Mapel, ETH Zürich, Zürich, Switzerland

P323
ISAG Bursary Award: Genes near the Celtic POLLED variant are differentially expressed between horned and polled bovine fetuses at 58 days of development.
J. Aldersey, Davies Livestock Research Centre, University of Adelaide, Roseworthy, South Australia, Australia

P415
ISAG Bursary Award: Genetic diversity among Swakara sub-populations and their founders.
A. Njilo, Agricultural Research Council, Pretoria, Gauteng, South Africa

OP158 + P60
ISAG Bursary Award: Genetic diversity and relationship between Nigerian Muscovy duck populations using the mitochondria cytochrome b gene.
O. Yusuf, Faculty of Agriculture, Department of Animal Production, University of Ilorin, Kwara state, Nigeria

P32
ISAG Bursary Award: Genetic diversity in Nigeria laughing dove population using the mitochondria cytochrome C oxidase gene.
I. A. Abubakar, University of Ilorin, Ilorin, Kwara, Nigeria

P272
ISAG Bursary Award: Genome selection based on multiple artificial intelligence approaches boosting prediction accuracy.
L. Wei, State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China

P328
ISAG Bursary Award: Genome-wide association analysis reveals polygenic regulation of ovine high-altitude adaptability.
B. C. Chen, Northwest A&F University, Yangling, Shaanxi, China

P364
ISAG Bursary Award: Genome-wide association studies reveal candidate genes associated with plasma and wool metabolites indicators of water deprivation tolerance in Rasa aragonesa sheep.
S. Pérez-Redondo, Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Zaragoza, Spain

OP180 + P239
ISAG Bursary Award: Genome-wide scan for selection signatures in South African indigenous goat ecotypes.
A. M. Magoro, Tshwane University of Technology, Pretoria, South Africa

P216
ISAG Bursary Award: Genomic analysis reveals low level of inbreeding in Ugandan goat breeds.
R. B. Onzima, Faculty of Agriculture and Environmental Science, Muni University, Arua, Uganda

P177
ISAG Bursary Award: Genomic analysis using massive sequencing data reveals genetic signatures that underlie breed features.
H. Liu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, PR China

OP151
ISAG Bursary Award: Genomic and transcriptomic characterisation of hypertrophic cardiomyopathy in British Shorthair and Birman cats.
T. Smedley, Royal Veterinary College, London, United Kingdom

P82
ISAG Bursary Award: Genomic and transcriptomic characterisation of hypertrophic cardiomyopathy in British Shorthair and Birman cats.
T. Smedley, Royal Veterinary College, London, United Kingdom

P322
ISAG Bursary Award: Genomic differentiation within the South African Hereford reference population.
C. Croucamp, University of Pretoria, Pretoria, Gauteng, South Africa

OP101 + P163
ISAG Bursary Award: Genomic markers associated with immune traits in Sasso chickens raised in Ethiopia.
M. Girma, Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Florida, South Africa

P215
ISAG Bursary Award: Genotyping-by-sequencing: A powerful tool to reveal genomic relatedness and admixture in local Tunisian sheep breeds.
I. Baazaoui, National Agricultural Research Institute of Tunisia, Ariana, Tunisia

P212
ISAG Bursary Award: History and unique evolutionary adaptation of indicine cattle.
N. Chen, Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling, China

OP86 + P116
ISAG Bursary Award: Identification and comparison of plant-derived miRNAs based on massive public data.
H. Liu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei, China

OP61 + P397
ISAG Bursary Award: Identification of long non-coding RNAs differentially expressed in the mammary gland of lactating and dry goats.
M. Wang, Centre de Recerca Agrigenòmica (CRAG), Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain

OP24 + P188
ISAG Bursary Award: Identification of personality-related genes associated with tractability of handling in Thoroughbred horses.
T. Yokomori, Nihon University, Fujisawa, Kanagawa, Japan

OP55 + P301
ISAG Bursary Award: Integrated analysis of genome-wide association studies and 3D epigenomic characteristics reveal the BMP2 gene regulating loin muscle depth in Yorkshire pigs.
S. Wan, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University, Wuhan, Hubei Province, China

P380
ISAG Bursary Award: Integration of reduced representation bisulphite sequencing with RNA sequencing data provides further insights in claw horn disruption lesions susceptibility in dairy cattle.
E. Attree, The Royal Veterinary College, Department of Clinical Science and Services, The Royal Veterinary College, Hatfield, United Kingdom

P174
ISAG Bursary Award: Introgression within the horse genome.
L. Johnson, University of Kentucky, Lexington, KY

P125
ISAG Bursary Award: Introgressive hybridization levels of tilapiines species in Lake Victoria basin, Kenya, inferred from microsatellite and mitochondrial DNA genotyping based on next-generation sequencing.
G. Kwikiriza, Institute for Integrative Nature Conservation Research, University of Natural Resources and Life Sciences Vienna (BOKU), Vienna, Austria

P121
ISAG Bursary Award: Investigating the effect of chromosome 20 on lordosis in Saddlebred horses.
N. Yousefi-Mashouf, University of Kentucky, Lexington, KY

P411
ISAG Bursary Award: Investigation on already known variants and markers for horn phenotypes in Icelandic sheep.
R. Simon, Institute of Animal Breeding and Genetics, Justus Liebig University, 35390 Giessen, Germany

P56
ISAG Bursary Award: Invited Workshop Presentation: Chicken2K: A panel for global chicken genomic diversity and evolutionary inference.
C. Ma, 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

OP96 + P161
ISAG Bursary Award: LncRNA446 regulates tight junctions by inhibiting the ubiquitinated degradation of Alix after porcine epidemic diarrhea virus infection.
Y. Xiao, Yangzhou University, Yangzhou, Jiangsu, China

P354
ISAG Bursary Award: Long read based chromosome-level reference genome that encounters complex repetitive sequences in Alpaca (Vicugna pacos).
M. Mendoza, Department of Veterinary Integrative Biosciences, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX

P219
ISAG Bursary Award: Low genetic diversity and population structuring of Amblyomma hebraeum and Rickettsia africae from coastal and inland regions in the Eastern Cape Province of South Africa.
A. Pillay, University of KwaZulu-Natal, Durban, KwaZulu-Natal, South Africa

P225
ISAG Bursary Award: Low-coverage whole-genome genomic characterization of indigenous chicken ecotypes of Tigray, Ethiopia.
G. G. Berhe, Tigray Agricultural Research Institute, Mekelle, Tigray, Ethiopia

P128
ISAG Bursary Award: Metagenomics analysis of salt-fermented hilsa (Tenualosa ilisha) at different processing stages.
H. Muhammad Shahdat, National Institute of Biotechnology, Savar, Dhaka, Bangladesh

P357
ISAG Bursary Award: Model comparison of genomic prediction for commercial population in Hanwoo (Korean cattle).
S. Lee, Chugnam National University, Yuseong-gu, Daejeon, South Korea

P223
ISAG Bursary Award: Molecular detection and phylogenetic analysis of lumpy skin disease virus (LSDV) from 2019 to 2022 outbreak in Bangladesh.
A. Bhuyan, National Institute of Biotechnology, Ashulia, Bangladesh

P186
ISAG Bursary Award: Molecular inbreeding negatively affects the reproductive life of Pura Raza Española mares.
N. Laseca, Department of Genetics, University of Cordoba, Córdoba, Spain

P327
ISAG Bursary Award: Molecular investigations on cryptorchidism in German Holsteins.
F. Krull, University of Goettingen, Institute of Veterinary Medicine, 37077 Goettingen, Germany

OP97
ISAG Bursary Award: Multi-omics integration analysis deciphering genetic basis of host resistance to PRRSV.
Q. Wu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China

P159
ISAG Bursary Award: Multi-omics integration analysis deciphering genetic basis of host resistance to PRRSV.
Q. Wu, Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China

OP114 + P211
ISAG Bursary Award: Multiple origins and genetic diversity of Philippine native pigs.
J. B. Banayo, Nagoya University, Chikusa, Nagoya, Japan

P324
ISAG Bursary Award: Multiple-trait joint genetic evaluation improves accuracy of prediction in South-African and Kenyan Holstein cattle population.
I. Houaga, Centre for Tropical Livestock Genetics and Health (CTLGH), Roslin Institute, University of Edinburgh, Easter Bush, Edinburgh, United Kingdom

OP34 + P252
ISAG Bursary Award: Nasal microbiome diversity in West African Dwarf goats with peste des petits ruminants viral infection.
I. Muritala, Department of Animal Breeding and Genetics, Federal University of Agriculture Abeokuta, Abeokuta, Ogun State, Nigeria

OP52 + P313
ISAG Bursary Award: On the genetic basis of porcine semen traits: A large-scale genome-wide study on a synthetic line.
P. Sá, Wageningen University and Research, Wageningen, the Netherlands

OP197 + P386
ISAG Bursary Award: Pangenomes of haplotype-resolved assemblies enable population-scale genotyping of cattle structural variation for eQTL mapping.
A. Leonard, ETH Zurich, Zurich, Switzerland

OP154 + P80
ISAG Bursary Award: PCYT2 missense variant in Saarloos Wolfhounds with neurodegeneration.
M. Christen, Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland

P126
ISAG Bursary Award: Phylogenetic status and origin of monogenean gill parasites of Synodontis spp. (Actinopterygii, Siluroidei) from Cameroon: Influence of the ichthyological province.
J. A. Mbondo, Institute of Agricultural Research for Development, Yaounde, Centre, Cameroon

P360
ISAG Bursary Award: Population fine structure analyses of the indigenous Croatian cattle populations.
I. Drzaic, University of Zagreb Faculty of Agriculture, Svetošimunska cesta 25, 10040 Zagreb, Croatia

OP4 + P242
ISAG Bursary Award: Population genomics of indigenous African cattle inferred from 537 whole-genome sequencing.
S. Kambal, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia

P226
ISAG Bursary Award: Population structure and admixture patterns in indigenous African cattle.
M. K. Bitew, Department of Agriculture Environmental and Food Sciences, University of Molise, Campobasso, Italy

OP159 + P62
ISAG Bursary Award: Potential of a chicken AIL population to decipher the genetic mechanisms of complex traits in the integrative omics era.
X. Zhu, State Key Laboratory for Agro-Biotechnology, China Agricultural University, Beijing, China

OP72 + P8
ISAG Bursary Award: Relationship between spleen and uterus gene expression and DNA methylation according to developmental stages of pigs.
B. Ahn, Department of Stem Cell and Regenerative Biotechnology, Konkuk University, Seoul, Korea

OP150 + P78
ISAG Bursary Award: RETREG1 variant causes canine acral mutilation syndrome (AMS) in purebred German spitz.
A. Letko, Institut de Génétique et Développement de Rennes (IGDR), University Rennes, Rennes, France

OP11 + P96
ISAG Bursary Award: Ribosome profiling reveals stage-specific translational regulation during muscle differentiation.
A. Goldkamp, Oklahoma State University, Stillwater, OK

P307
ISAG Bursary Award: Sequence based GWAS identifies novel loci influencing growth and reproduction traits in pigs.
A. Boshove, Topigs Norsvin Research Center, Beuningen, the Netherlands

OP56
ISAG Bursary Award: Sequence-based GWAS identifies novel loci influencing growth and reproduction traits in pigs.
A. Boshove, Topigs Norsvin Research Center, Beuningen, the Netherlands

OP133 + P171
ISAG Bursary Award: sgRNAcas9-AI: A program for prediction of CRISPR/Cas9 and its variant sgRNA activity using deep learning.
X. Zhang, Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany

OP9 + P104
ISAG Bursary Award: Single cell atlas of developing ovine tail tissue reveals multi-cellular origins contributing to fat deposition.
J. Han, Institute of Animal Science, Chinese Academy of Agriculture Science, Beijing, China

P185
ISAG Bursary Award: Single-step genomic model improved reliability in conformation traits in the Pura Raza Español horse.
C. Ziadi, Department of Genetics, University of Córdoba, Córdoba, Spain

OP196 + P350
ISAG Bursary Award: Size and composition of haplotype reference panels impact the accuracy of imputation from low-pass sequencing in cattle.
A. Lloret-Villas, ETH Zürich, Universitätstrasse 2, 8092, Zürich, Switzerland

OP29 + P265
ISAG Bursary Award: Study of gut microbes and body metabolism function between Dorper and Tan sheep.
Y. Ma, Key Laboratory of Animal Genetics, Breeding, and Reproduction of the Ministry of Agriculture and Beijing Key Laboratory of Animal Genetic Improvement, China Agricultural University, Beijing, China

P379
ISAG Bursary Award: Tail morphology and environmental adaptations of Ethiopian indigenous sheep: an ecological niche modelling and genomic approaches.
A. Amane, Amhara Regional Agricultural Research Institute, Bahir Dar, Ethiopia

OP112 + P202
ISAG Bursary Award: Temporal changes in genomic diversity of the northernmost cattle populations in Europe.
M. Weldenegodguad, Natural Resources Institute Finland, Jokioinen, Finland

OP77
ISAG Bursary Award: The development of a 61K Illumina SNP chip for dromedaries under the frame of the 2019 Agricultural Greater Good (AGG) initiative.
M. Di Civita, Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy

P238
ISAG Bursary Award: The development of a 61K Illumina SNP chip for dromedaries under the frame of the 2019 Agricultural Greater Good (AGG) initiative.
M. Di Civita, Department of Agricultural, Environmental and Food Sciences, University of Molise, Campobasso, Italy

OP18 + P191
ISAG Bursary Award: The epigenetic landscape of the satellite-free centromere of horse chromosome 11.
E. Cappelletti, Department of Biology and Biotechnology, University of Pavia, Pavia, Italy

P332
ISAG Bursary Award: The first gapless complete T2T Y-chromosome assemblies of cattle and sheep uncover their genomic architectures.
B. Murdoch, University of Idaho, Moscow, ID

OP115 + P201
ISAG Bursary Award: The first Rangifer tarandus Y chromosomal phylogeny.
E. Bozlak, Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria

P33
ISAG Bursary Award: Transcriptome analysis of pre-hierarchical follicles highlights dominance as the major mode of gene expression that underpins heterosis for egg number and clutch size in crossbred laying hens.
A. M. Isa, Key Laboratory of Animal (Poultry) Genetics Breeding and Reproduction, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

OP92 + P155
ISAG Bursary Award: Transcriptomic signatures of peripheral immune cells associated with immune competence traits in Australian Angus cattle.
A. Wilson, Commonwealth Scientific and Industrial Research Organization, East Geelong, VIC, Australia

P372
ISAG Bursary Award: Ubiquitous impact of sex on gene expression across cattle tissues.
M. Bhati, The Roslin Institute, University of Edinburgh, Midlothian, Scotland, United Kingdom

P198
ISAG Bursary Award: Updated perspective on the genetic diversity, phylogeography and population dynamics of domestic pigs in Southeast Asia.
J. K. Layos, College of Agriculture and Forestry, Capiz State University, Mambusao, Capiz, Philippines

OP182
ISAG Bursary Award: Whole genome sequencing of Landim pigs of Mozambique reveals a close relationship with Angola native pigs and suggests selection for immune response.
F. Teixeira, Centre for Interdisciplinary Research in Animal Health and Associate Laboratory for Animal and Veterinary Sciences, Faculty of Veterinary Medicine, University of Lisbon, Alto da Ajuda, Lisbon, Portugal

P244
ISAG Bursary Award: Whole-genome sequencing of Landim pigs of Mozambique reveals a close relationship with Angolan native pigs and suggests selection for immune response.
F. Teixeira, Centre for Interdisciplinary Research in Animal Health and Associate Laboratory for Animal and Veterinary Sciences, Faculty of Veterinary Medicine, University of Lisbon, Alto da Ajuda, Lisbon, Portugal

Author Index

Numbers following names refer to abstract numbers. A number preceded by OP indicates an oral presentation, and a number preceded by P indicates a poster. Orals are listed first, followed by posters in session and number order.

The author index is created directly and automatically from the submitted abstracts. If an author's name is entered differently on multiple abstracts, the entries in this index will reflect those discrepancies. Efforts have been made to make this index consistent; however, error from author entry contributes to inaccuracies.

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Q

R

S

T

U

V

W

X

Y

Z