



ISAG 2017

36th International Society for
Animal Genetics Conference

16th - 21st July 2017

University College Dublin | Ireland

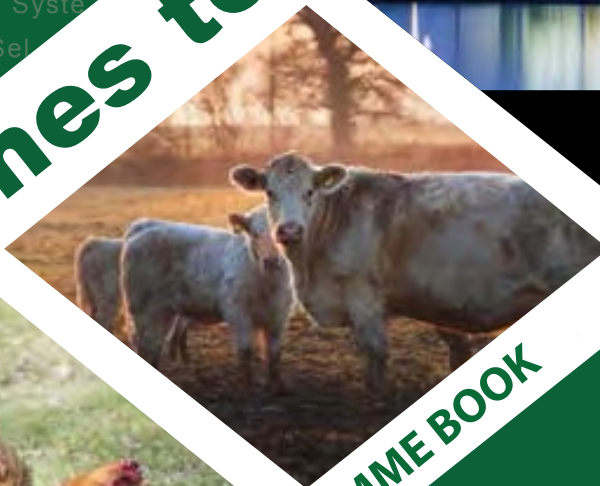


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Genomes to Phenomes



O'Brien Centre for Science
and O'Reilly Hall,
University College Dublin,
Dublin, Ireland



PROGRAMME BOOK

www.isag.us/2017



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17 July, 13:30–14:15
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Contents

Committees	2
ISAG 2017 Sponsors and Exhibitors.....	4
Schedule of Events.....	6
Social Programme	8
Poster Schedule	9
Scientific Program	11
Sunday/Monday	11
Tuesday.....	18
Wednesday.....	33
Thursday.....	34
Friday.....	40
Poster Session I: Monday and Tuesday	41
Poster Session II: Wednesday, Thursday, Friday	74
Author Index	83



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37th International Society for
Animal Genetics Conference

July 7 - 12, 2019 - Lleida, Spain



Committees

ISAG 2017 Local Organising Committee

Brian Wickham (co-chair), ConsultWickham
Romy Morrin-O'Donnell (co-chair), Weatherbys Ireland Ltd.
John Flynn, Weatherbys Ireland Ltd. (retired)
Donagh Berry, Teagasc
Martin Burke, ICAR
Michael Mullen, Athlone IT
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Sinead Waters, Teagasc
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ISAG Executive Committee

James Kijas, CSIRO, Australia (President)
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Clare Gill, Texas A&M University, USA
Martien A. M. Groenen, Wageningen University, Netherlands
Stephen S. Moore, University of Queensland, Australia
Hans Lenstra, Utrecht University, Netherlands (ex officio)
Romy Morrin-O'Donnell, Weatherbys Ireland Ltd. (ex officio)
Hein van Haeringen, Netherlands (Financial Administrator)

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David MacHugh (co-chair), UCD
Sinead Waters (co-chair), Teagasc
Adrian Allen, AFBI-Northern Ireland
Donagh Berry, Teagasc
Romy Morrin-O'Donnell, Weatherbys Ireland Ltd.
Michael Mullen, Athlone IT

ISAG 2017 Workshop Chairs

Avian Genetics and Genomics

Richard Crooijmans, Wageningen University & Research

Animal Epigenetics

Stephanie McKay, University of Vermont

Animal Forensic Genetics Workshop

Guillermo Giovambattista, Universidad Nacional De La Plata

Applied Genetics and Genomics in Other Species of Economic Importance

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

Applied Genetics of Companion Animals

Sofia Mikko, Swedish University of Agricultural Sciences

Applied Sheep and Goat Genetics

Gesine Luehken, University of Giessen

Cattle Molecular Markers and Parentage Testing

Romy Morrin-O'Donnell, Weatherbys Ireland Ltd.

Companion Animal Genetics and Genomics

Leslie Lyons, University of Missouri, and Tomas Bergstrom, Swedish University of Agricultural Sciences

Comparative and Functional Genomics

Fiona McCarthy, The University of Arizona

Comparative MHC Genetics: Populations and Polymorphism

Keith Ballingall, Moredun Research Institute

Domestic Animal Sequencing and Annotation

James Reecy, Iowa State University

Equine Genetics and Thoroughbred Parentage Testing Workshop

Cecilia Penedo, University of California at Davis

Genetics and Genomics of Aquaculture Species

Ross Houston, The Roslin Institute, and Francesca Bertolini, Iowa State University

Genetics of Immune Response and Disease Resistance

Huaijun Zhou, University of California, Davis

Genome Edited Animals

Bruce Whitelaw, University of Edinburgh

Horse Genetics and Genomics

Teruaki Tozaki, Laboratory of Racing Chemistry, and Tomas Bergström, Swedish University of Agricultural Sciences

ISAG-FAO Genetic Diversity

Catarina Ginja, CIBIO-InBIO, Universidade do Porto, PT

Livestock Genomics for Developing Countries

Ntanganedzeni Mapholi, University of South Africa, South Africa

Microbiomes

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

Pig Genetics and Genomics

Romi Pena I Subira, University of Lleida, and Kyle Schachtschneider, University of Illinois at Chicago

Ruminant Genetics and Genomics

Laercio Porto-Neto, CSIRO Agriculture

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Exhibitors



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United States Department of Agriculture
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Schedule of Events

Monday, July 17, 2017

08:00	Registration Desk Open	Atrium, O'Brien Science Building
08:00	Exhibition Open	Atrium, O'Brien Science Building
08:00	Poster Session I Setup	Atrium, O'Brien Science Building
09:00	Poster Session I Open	Atrium, O'Brien Science Building
09:15	Welcome and Opening	O'Reilly Hall
09:30	Plenary Session: The 200 Mammals Project: A resource for animal and human health	O'Reilly Hall
10:30	Plenary Session: Big data in biology: Challenges and opportunities	O'Reilly Hall
11:30	Coffee/Tea Break	Atrium, O'Brien Science Building
12:00	Plenary Session: Cut and paste genetic improvement: Changing direction and selection with advanced breeding methods	O'Reilly Hall
13:00	Lunch	Atrium, O'Brien Science Building
13:30	Thermo Fisher Scientific Vendor Presentation	George Moore Auditorium, O'Brien Science Building
14:30	Animal Forensic Genetics Workshop	Intel Theatre, O'Brien Science Building
14:30	Applied Genetics and Genomics in Other Species of Economic Importance	Lynch Theatre, O'Brien Science Building
14:30	Domestic Animal Sequencing and Annotation	Elan Theatre, O'Brien Science Building
14:30	Genome Edited Animals	George Moore Auditorium, O'Brien Science Building
14:30	Horse Genetics and Genomics	Icon Theatre, O'Brien Science Building
16:00	Coffee/Tea Break	Atrium, O'Brien Science Building
18:00	Welcome Reception	Atrium, O'Brien Science Building

Tuesday, July 18, 2017

07:45	Registration Desk Open	Atrium, O'Brien Science Building
08:00	Exhibition Open	Atrium, O'Brien Science Building
08:00	Poster Session I Open (continued)	Atrium, O'Brien Science Building
08:00	Illumina Vendor Seminar	George Moore Auditorium, O'Brien Science Building
09:00	Avian Genetics and Genomics	H1.51 Breakout, O'Brien Science Building
09:00	Comparative MHC Genetics: Populations and Polymorphism	Icon Theatre, O'Brien Science Building
09:00	Equine Genetics and Thoroughbred Parentage Testing Workshop	Lynch Theatre, O'Brien Science Building
09:00	Genetics of Immune Response and Disease Resistance	Intel Theatre, O'Brien Science Building
09:00	ISAG-FAO Genetic Diversity	Elan Theatre, O'Brien Science Building
09:00	Ruminant Genetics and Genomics	George Moore Auditorium, O'Brien Science Building
11:00	Coffee/Tea Break	Atrium, O'Brien Science Building
13:00	Lunch	Atrium, O'Brien Science Building
13:30	Weatherbys Vendor Presentation	George Moore Auditorium, O'Brien Science Building
14:30	Animal Epigenetics	Elan Theatre, O'Brien Science Building
14:30	Cattle Molecular Markers and Parentage Testing	Intel Theatre, O'Brien Science Building
14:30	Companion Animal Genetics and Genomics	Lynch Theatre, O'Brien Science Building
14:30	Microbiomes	Icon Theatre, O'Brien Science Building
14:30	Pig Genetics and Genomics	George Moore Auditorium, O'Brien Science Building
16:00	Coffee/Tea Break	Atrium, O'Brien Science Building
18:00	Irish Evening at Taylors Three Rock	Meet at registration desk

Wednesday, July 19, 2017

07:45	Registration Desk Open	Atrium, O'Brien Science Building
08:00	Exhibition Open	Atrium, O'Brien Science Building
08:00	Poster Session II Setup	Atrium, O'Brien Science Building
08:00	Poster Session II Open	Atrium, O'Brien Science Building
08:00	Pac Bio Vendor Seminar	George Moore Auditorium, O'Brien Science Building
09:00	Plenary Session: The role of enhancers in mammalian disease and development: Stories from more than thirty mouse knockouts	O'Reilly Hall
10:00	Plenary Session: How animal genomic research contributes to basic biology	O'Reilly Hall
11:00	Coffee/Tea Break	Atrium, O'Brien Science Building
11:30	Plenary Session: Filling the gap until the FAANG data comes in: Comparative annotation of sheep reveals selection has acted on the proximal regulatory machinery	O'Reilly Hall
13:00	Tours (preregistration mandatory)	Meet at registration desk

Thursday, July 20, 2017

08:00	Registration Desk Open	Atrium, O'Brien Science Building
08:00	Exhibition Open	Atrium, O'Brien Science Building
08:00	Poster Session II Open (continued)	Atrium, O'Brien Science Building
09:00	Plenary Session: Will animal genetics innovations be embraced or eschewed? The #Scicomm challenge facing agricultural biotechnology	O'Reilly Hall
10:00	Plenary Session: Molecular regulation of pregnancy establishment in cattle	O'Reilly Hall
11:00	Coffee/Tea Break	Atrium, O'Brien Science Building
11:30	Plenary Session: Is it time to change the paradigm? Mammals are not just genes interacting with their environment	O'Reilly Hall
12:30	Novel, Groundbreaking Research/Methodology Presentation: Sheep parchment as a genetic resource	O'Reilly Hall
13:00	Lunch	Atrium, O'Brien Science Building
13:30	Neogen Vendor Presentation	George Moore Auditorium, O'Brien Science Building
14:30	Applied Genetics of Companion Animals	Lynch Theatre, O'Brien Science Building
14:30	Applied Sheep and Goat Genetics	George Moore Auditorium, O'Brien Science Building
14:30	Comparative and Functional Genomics	Elan Theatre, O'Brien Science Building
14:30	Genetics and Genomics of Aquaculture Species	Intel Theatre, O'Brien Science Building
14:30	Livestock Genomics for Developing Countries	Icon Theatre, O'Brien Science Building
16:00	Coffee/Tea Break	Atrium, O'Brien Science Building
19:00	Gala Dinner	O'Reilly Hall

Friday, July 21, 2017

08:00	Registration Desk Open	Atrium, O'Brien Science Building
08:00	Exhibition Open	Atrium, O'Brien Science Building
08:00	Poster Session II Open (continued)	Atrium, O'Brien Science Building
09:00	Plenary Session: GBLUPs Me, GBLUPs Me Not: Marrying molecular biology and statistical genomics	O'Reilly Hall
10:00	Plenary Session: Picking the bones out: Ancient animal genomics of the fertile crescent	O'Reilly Hall
11:00	Coffee/Tea Break	Atrium, O'Brien Science Building
11:30	ISAG Business Meeting and Awards	O'Reilly Hall Atrium, O'Brien Science Building
11:30	Clear Exhibition and Posters	Atrium, O'Brien Science Building

Social Programme

Welcome Reception—Monday, July 17

The welcome reception will take place in the O'Brien Science Building on Monday, July 17. This kick-off event will include drinks and canapés and provides a relaxed environment for participants to network. The cost for the welcome reception is included in your registration.

Irish Evening—Tuesday, July 18

The Irish night will take place in Taylors Three Rock on Tuesday, July 18 (additional registration required). Showcasing the best of Irish hospitality, from entertainment to food, Taylors Three Rock is one of Ireland's most loved entertainment venues, offering captivating evenings of traditional Irish song and dance accompanied by a great selection of quality Irish food to delight your palate.

Delegates who attend the Irish Night can expect to be served a delicious three-course meal complete with traditional Irish coffee under the highest thatched roof in Europe, after which they will be entertained by world champion Irish dancers and famous Irish musicians, capturing the famous Irish spirit.

Audience participation is a must, so be prepared to take part in singing and dancing! You can expect to be singing classic Irish Ballads like Danny Boy, Fields of Athenry, and Whiskey in the Jar!

Cost: €85

Tours—Wednesday, July 19

All tours will take place on the afternoon of Wednesday, July 19. Preregistration for each tour is mandatory. Meet at registration desk for 13:15 departure.

Tour 1: The Irish Equine Centre/Weatherbys and the Irish National Stud

Tour 2: Irish Beef Data and Genomics Programme

Tour 3: Book of Kells and St. Patrick's Cathedral

Tour 4: Powerscourt House and Gardens

Gala Dinner—Thursday, July 20

The 36th International Society for Animal Genetics (ISAG) Conference Gala Dinner will take place on Thursday, July 20, at the famed O'Reilly Hall in University College Dublin (UCD), one of Ireland's largest and most prestigious venues, designed by famed architects Scott Tallon Walker.

Guests will arrive to a drinks reception in the conservatory, which overlooks the beautiful campus lake. Ten specially commissioned paintings line and complement the majestic yet modern walls of the venue, highlighting the work of local Irish artists.

The sit-down, three-course dinner will showcase the best of locally sourced Irish ingredients and will be paired with wine. The after-dinner entertainment will include Irish entertainment—an all-encompassing musical experience and a night sure to be remembered!

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

Poster Schedule

POSTER SESSION I: Monday and Tuesday Atrium, O'Brien Science Building

Posters on Monday/Tuesday should be mounted on their boards on Monday morning between 08:00 and 09:00. They should be removed on Tuesday afternoon once the afternoon coffee/tea break ends. Poster presenters should make themselves available to discuss their poster during tea/coffee breaks and lunch.

Poster Numbers	Topic
MT1–MT6	Animal Epigenetics
MT17	Animal Forensic Genetics
MT18–MT29	Applied Genetics and Genomics in Other Species of Economic Importance
MT30–MT68	Avian Genetics and Genomics
MT69–MT86	Cattle Molecular Markers and Parentage Testing
MT87–MT105	Companion Animal Genetics and Genomics
MT106–MT117	Comparative MHC Genetics: Populations and Polymorphism
MT118–MT129	Domestic Animal Sequencing and Annotation
MT130–MT135	Equine Genetics and Thoroughbred Parentage Testing
MT136–MT173	Genetics of Immune Response and Disease Resistance
MT174–MT177	Genome Edited Animals
MT178–MT221	Horse Genetics and Genomics
MT222–MT236	ISAG-FAO Genetic Diversity
MT237–MT242	Microbiomes
MT243–MT294	Pig Genetics and Genomics
MT295–MT374	Ruminant Genetics and Genomics

POSTER SESSION II: Wednesday, Thursday, Friday Atrium, O'Brien Science Building

Posters on Wednesday/Thursday should be mounted on their boards on Tuesday evening once the conference programme ends or on Wednesday morning between 8:00 and 9:00. They should be removed on Friday between 11:30 and 13:00. Poster presenters should make themselves available to discuss their poster during tea/coffee breaks and lunch.

Poster Numbers	Topic
WT1–WT6	Applied Genetics of Companion Animals
WT7–WT33	Applied Sheep and Goat Genetics
WT34–WT63	Comparative and Functional Genomics
WT64–WT70	Gene Function
WT71–WT86	Genetics and Genomics of Aquaculture Species
WT87–WT105	Livestock Genomics for Developing Countries

NOTES

Sunday, July 16

Registration Desk Open	Atrium, O'Brien Science Building	14:00 – 18:00
Exhibition Setup and Poster Board Setup	Atrium, O'Brien Science Building	14:00 – 18:00
ISAG Executive Committee Meeting (Private Invitation)	Boardroom H1.48, O'Brien Science Building	08:30 – 18:00

Monday, July 17

Registration Desk Open	Atrium, O'Brien Science Building	08:00 – 18:00
Poster Setup	Atrium, O'Brien Science Building	08:00 – 09:00
Exhibition Open	Atrium, O'Brien Science Building	08:00 – 18:00
Posters Open	Atrium, O'Brien Science Building	09:00 – 18:00
Welcome and Opening	O'Reilly Hall	09:15 – 09:30

ORAL SESSIONS

Plenary Session I

Chairs: **Romy Morrin-O'Donnell, Weatherbys Ireland Ltd.,
and Brian Wickham, ConsultWickham**
O'Reilly Hall

09:30 **The 200 Mammals Project: A resource for animal and human health.**
Kerstin Lindblad-Toh, *Uppsala University, Broad Institute of Harvard and MIT.*

10:30 **Big data in biology: Challenges and opportunities.**
Ewan Birney, *The European Bioinformatics Institute.*

Coffee/Tea break	Atrium, O'Brien Science Building	11:30 – 12:00
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12:00 **Cut and paste genetic improvement: Changing direction and selection with advanced breeding methods.**
Tad Sonstegard, *USDA, ARS, AGIL.*

Lunch	Atrium, O'Brien Science Building	13:00 – 14:00
Meeting of Board with Chairs (Private Invitation)	Boardroom H1.47, O'Brien Science Building	13:15 – 14:30
Thermo Fisher Scientific Vendor Presentation:	George Moore Auditorium, O'Brien Science Building	13:30 – 14:15

Thermo Fisher Scientific Vendor Presentation: Next-Generation Solutions for Animal Breeding and Parentage

Advances in genotyping and genomic technologies such as next-generation sequencing and microarray technologies are making it easier and more affordable than ever to genotype large populations of animals. Genomic evaluations provide insight into parentage, pedigrees, and other genetic effects that have both economic and animal health implications. Sequencing-based technologies like AgriSeq targeted genotyping by sequencing (GBS), and a microarray system such as Axiom microarrays, allow up to hundreds of thousands of markers to be interrogated simultaneously, improving selection accuracy and trait monitoring in animals. Attend this workshop and hear about how two genotyping labs have implemented AgriSeq targeted GBS and Axiom custom high-density microarrays in their genetic evaluation programs to improve lab efficiency, throughput, and cost per genotype for canine, feline, and ovine species.

Introduction to genotyping technologies

Ravi Ramadhar, Product Manager Leader Agrigenomics, Thermo Fisher Scientific

Ovine genotyping by numbers

Donagh Berry, Quantitative Genetics, Teagasc

Implementation of an AgriSeq genotyping workflow to improve efficiency of canine and feline genetic testing in a service lab

Maarten de Groot, Chief Financial Officer, VHLGenetics

WORKSHOPS AND ORAL SESSIONS

Bold font denotes presenter

Animal Forensic Genetics Workshop

Chair: **Guillermo Giovambattista, Universidad Nacional De La Plata**
Intel Theatre, O'Brien Science Building

14:30	1	<i>De novo</i> genome assembly of <i>Agapornis roseicollis</i> and SNP discovery for parentage verification. H. van der Zwan* ¹ , R. van der Sluis ¹ , and C. Visser ² , ¹ North-West University, Potchefstroom, North-West, South Africa; ² University of Pretoria, Pretoria, Gauteng, South Africa.
14:45	3	Effectiveness of SNPs genotyping assay as a tool for genetic traceability of cattle production chain. A. Pozzi* ¹ , C. Previtali ¹ , R. Capoferri ¹ , S. Arabi ¹ , A. Galli ² , and G. Bongioni* ¹ , ¹ Istituto Sperimentale Italiano L. Spallanzani, Rivolta d'Adda, Cremona, Italy; ² Centro di ricerca per le produzioni foraggere e lattiero-casearie CREA, Lodi, Italy.
15:00	4	The population and landscape genetics of the European badger (<i>Meles meles</i>) in Ireland. A. Allen* ¹ , J. Guerrero ² , A. Byrne ^{1,3} , J. Lavery ¹ , E. Presho ¹ , G. Kelly ¹ , E. Courcier ⁴ , J. O'Keefe ⁵ , U. Fogarty ⁶ , D. O'Meara ⁷ , G. Wilson ⁸ , D. Ensing ¹ , C. McCormick ¹ , R. Biek ⁹ , R. Skuce ^{1,3} , ¹ Agri Food and Biosciences Institute, Belfast, Northern Ireland; ² CEFE-CNRS, Centre D'Ecologie Fonctionnelle et Evolutive, Montpellier, France; ³ School of Biological Sciences, Queen's University Belfast, Belfast, Northern Ireland; ⁴ Department of Agriculture, Environment and Rural Affairs, Belfast, Northern Ireland; ⁵ Department of Agriculture Food and the Marine, Dublin, Ireland; ⁶ Irish Equine Centre, Johnstown, Republic of Ireland; ⁷ Waterford Institute of Technology, Waterford, Ireland; ⁸ Animal and Plant Health Agency (APHA), Stonehouse, Gloucestershire, England; ⁹ University of Glasgow, Glasgow, Scotland.
15:15	5	Comparison of the effectiveness of 19 STR and 22 STR panels for forensic DNA analysis of canine in Poland. A. Radko* , A. Podbielska, and M. Miszczak, Department of Animal Genomics and Molecular Biology, National Research Institute of Animal Production, Balice, Poland.

- 15:30 6 **Can-ID: The genetic Identification system for canine samples based on SNPs.**
O. Ramirez*¹, A. Cuscó¹, A. Sánchez², O. Francino², and L. Altet¹, ¹*Vetgenomics, Barcelona, Spain*; ²*Molecular Genetics Veterinary Service (SVGMM), Barcelona, Spain.*
- 15:45 7 **Application of multiplex microsatellite panel in *Felidae* family.**
A. Podbielska*¹, A. Radko¹, W. Nizanski², J. Kochan³, A. Nowak³, and M. Bugno-Poniewierska¹, ¹*Department of Animal Genomics and Molecular Biology, National Research Institute of Animal Production, Balice, Cracow, Poland*; ²*Department of Reproduction and Clinic of Farm Animals, Faculty of Veterinary Medicine, Wrocław University of Environmental and Life Sciences, Wrocław, Poland*; ³*Faculty of Animal Sciences, Institute of Veterinary Science, University of Agriculture in Krakow, Cracow, Poland.*
- Coffee/Tea break Atrium, O'Brien Science Building 16:00 – 16:30
- 16:30 8 **Plains bison triallelic SNPs for determining parentage, estimating cattle introgression, and inbreeding.**
T. Kalbfleisch*¹, J. Tait², V. Basnayake², B. Simpson², T. Smith³, and M. Heaton³, ¹*University of Louisville, Louisville, KY, USA*; ²*GeneSeek, Lincoln, NE, USA*; ³*USMARC, USDA, Clay Center, NE, USA.*
- 16:45 9 **Discrimination of native chicken breeds using SNP marker combination.**
 S. Jin¹, N.-R. Choi¹, D. Seo¹, P. Manjula¹, H.-Y. Kim², S. H. Lee¹, and **J. H. Lee***¹, ¹*Chungnam National University, Daejeon, Republic of Korea*; ²*Insilicogen, Inc, Yongin, Republic of Korea.*
- 17:00 **Results of the 2016-2017 Comparison Test.**
 Dr. Luis Cancela, Duty Lab.
- 17:15 **Election of new chairperson and committee members.**
- 17:30 **Other Business: Membership approval of Standing Committee Goals*.**
- 17:45 **Meeting ends.**

Applied Genetics and Genomics in Other Species of Economic Importance

Chair: **Leanne Van de Goor, Dr. van Haeringen Laboratorium B.V**
Lynch Theatre, O'Brien Science Building

- 14:30 **Welcoming Remarks.**
- 14:45 **Results 2016-2017 Pig CT and future of Pig CT.**
 Amparo Martinez.
- 15:15 **Duty lab for next Dromedary/Alpaca CT.**
- 15:30 **Duty lab for next Pigeon CT.**
- 15:45 10 **An evaluation of the ISAG recommended parentage and identification panel for the domestic pigeon (*Columba livia domestica*).**
M. de Groot*, *VHLGenetics, Wageningen, the Netherlands.*

Coffee/Tea break Atrium, O'Brien Science Building 16:00 – 16:30

- 16:30 11 **Selection of SNP markers for a dromedary camel genotyping array.**
M. Al Abri*¹, H. M. Holl², D. Miller³, S. Abdalla⁴, B. Shykind⁴, J. Malek⁴, Y. Mohamoud⁴, K. Pasha⁵, A. Khalili⁵, D. F. Antczak³, and S. Brooks¹, ¹*Sultan Qaboos University, Department of Animal and Veterinary Sciences, Muscat, Sultanate of Oman*; ²*University of Florida, Department of Animal Sciences, Gainesville, Florida, USA*; ³*Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA*; ⁴*Weill Cornell Medical College in Qatar, Cornell University, Doha, Qatar*; ⁵*Tharb Veterinary Hospital, Doha, Qatar.*

- 16:45 12 **Characterisation of a family of alpacas exhibiting disproportionate dwarfism.**
K. A. Munyard* and T. Y. K. Tan, *School of Biomedical Sciences, Curtin Health Innovation Research Institute, Curtin University, Perth, WA, Australia.*
- 17:00 13 **Withdrawn**
- 17:15 14 **Genomic selection for performance and reproduction traits in American mink.**
K. Karimi*¹, M. Sargolzaei^{2,3}, and Y. Miar¹, ¹*Department of Animal Science and Aquaculture, Dalhousie University, Nova Scotia, Canada;* ²*Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada;* ³*Semex Alliance, 5653 Highway 6 North, Ontario, Canada.*
- 17:30 15 **SNP genotyping of reindeer (*Rangifer tarandus*) using BovineHD BeadChips.**
V. Kharzinova*¹, A. Dotsev¹, V. Fedorov², G. Brem^{1,3}, K. Wimmers⁴, H. Reyer⁴, and N. Zinovieva¹, ¹*L.K. Ernst Institute of Animal Husbandry, Moscow, Russia;* ²*Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russia;* ³*Institute of Animal Breeding and Genetics, VMU, Vienna, Austria;* ⁴*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.*
- 17:45 **Election of committee and any other business.**
- 18:00 **Meeting ends.**

Domestic Animal Sequencing and Annotation

Chair: **James Reecy, Iowa State University**
 Elan Theatre, O'Brien Science Building

- 14:30 16 **Combining transcriptome and epigenetic analysis of H3K36me3 and H3K4me3 marks to explore mechanisms of liver-specific gene expression in pigs.**
 J. Huang, M. Schroyen, N. Gabler, J. Dekkers, and **C. Tuggle***, *Department of Animal Science, Iowa State University, Ames, IA, USA.*
- 14:45 17 **Genome-wide analysis of H3K4me3 and H3K27me3 in three tissues in pigs.**
C. Kern*¹, Y. Wang¹, P. Saelao¹, K. Chanthavixay¹, I. Korf¹, C. K. Tuggle², C. Ernst³, P. Ross¹, and H. Zhou¹, ¹*University of California, Davis, Davis, CA, USA;* ²*Iowa State University, Ames, IA, USA;* ³*Michigan State University, East Lansing, MI, USA.*
- 15:00 18 **Effects of maternal nutrition on the transcriptome and epigenome of the offspring.**
 H. Namous¹, F. Peñagaricano², M. Del Corvo³, E. Capra⁴, A. Stella⁴, J. Williams⁵, P. A. Marsan³, and **H. Khatib***¹, ¹*University of Wisconsin, Madison, Wisconsin, USA;* ²*University of Florida, Gainesville, Florida, USA;* ³*Università Cattolica del S. Cuore, Piacenza, Italy;* ⁴*Istituto di Biologia e Biotecnologia Agraria, Lodi, Italy;* ⁵*University of Adelaide, Roseworthy, Australia.*
- 15:15 19 **Profiling the landscape of transcription, chromatin accessibility and chromosome conformation of cattle, pig, chicken and goat genomes [FAANG pilot project "FR-AgENCODE"].**
 S. Foissac¹, **S. Djebali***¹, H. Acloque¹, FR-AgENCODE Consortium², M. H. Pinard-Van der Laan², S. Lagarrigue³, and E. Giuffra², ¹*GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Toulouse, France;* ²*GABI, AgroParisTech, INRA, Université Paris Saclay, Paris, France;* ³*PEGASE, INRA, Agrocampus Ouest, Rennes, France.*
- 15:30 20 **Long-non coding RNAs repertoires in liver and two T lymphocyte cell types in four livestock species [FAANG pilot project "FR-AgENCODE"].**
K. Muret*¹, S. Djebali², T. Derrien³, C. Cabau², C. Klopp⁴, D. Esquerré^{2,5}, K. Munyard⁶, G. Tosser-Klopp², H. Acloque², E. Giuffra⁷, S. Foissac², and S. Lagarrigue¹, ¹*UMR PEGASE INRA, Agrocampus Ouest UMR PEGASE, Rennes, France;* ²*UMR GenPhySE, INRA, INPT, ENVT, Université de Toulouse, Castanet-Tolosan, France;* ³*IGDR, CNRS-University Rennes 1, Rennes, France;* ⁴*SIGENAE, INRA, Castanet-Tolosan, France;* ⁵*Plateforme GENOTOUL, INRA, Castanet-Tolosan, France;* ⁶*School of Biomedical Sciences, Curtin Health Innovation Research Institute, Western Australian Biomedical Research Institute, Curtin University, Perth, Western Australia, Australia;* ⁷*UMR GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France.*

15:45 **Workshop Business Meeting.**

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 21 **Genome-wide CRISPR knockout screening for host factors involved in bovine herpes virus type 1 infection.**
W. Tan^{*1}, I. Dry¹, S. Lilloco², C. B. A. Whitelaw², and B. Dalziel¹, ¹*Division of Infection and Immunity, the Roslin Institute, University of Edinburgh, Edinburgh, Scotland;* ²*Division of Developmental Biology, the Roslin Institute, University of Edinburgh, Edinburgh, Scotland.*
- 16:45 22 **Beyond sequencing: Assigning function to novel ncRNAs.**
F. McCarthy^{*1}, A. Cooksey¹, C. Gresham², and B. Nanduri², ¹*University of Arizona, Tucson, AZ, USA;* ²*Mississippi State University, Starkville, MS, USA.*
- 17:00 23 **Haplotype resolution of leukocyte receptor complex in cattle through targeted enrichment and SMRT sequencing.**
D. Heimeier^{*1}, J. Schwartz¹, D. Bickhart², T. Smith³, and J. Hammond¹, ¹*The Pirbright Institute, Woking, Surrey, England;* ²*Cell Wall Biology and Utilization Research, USDA-ARS, Madison, WI, USA;* ³*Meat Animal Research Center, USDA-ARS, Clay Center, NE, USA.*
- 17:15 24 **The ruminant biology and evolution revealed by a flock of ruminant *de novo* genomes.**
 W. Wang¹, Q. Q. Qiu¹, G. Zhang^{3,4}, R. Heller³, H. R. Siegismund³, and **Y. Jiang**^{*2}, ¹*Northwestern Polytechnical University, Xi'an, Shaanxi, China;* ²*Northwest A&F University, Yangling, Shaanxi, China;* ³*University of Copenhagen, Copenhagen, Denmark;* ⁴*Beijing Genomics Institute at Shenzhen, Shenzheng, Guangdong, China.*
- 17:30 25 **SheepGenomesDB: Towards 1000 Genomes.**
S. McWilliam^{*1}, R. Brauning², S. Clarke², A. McCulloch², N. Cockett³, G. Saunders⁴, M. Naval Sanchez¹, H. Daetwyler^{5,6}, and J. Kijas¹, ¹*CSIRO, St Lucia, Queensland, Australia;* ²*AgResearch Ltd, Invermay, Mosgiel, New Zealand;* ³*Utah State University, Logan, UT, USA;* ⁴*EMBL-EBI, Cambridge, United Kingdom;* ⁵*Department of Economic Development, Jobs, Transport and Resources, Bundoora, Victoria, Australia;* ⁶*La Trobe University, Bundoora, Victoria, Australia.*
- 17:45 26 **A novel approach for mapping of animal genome assemblies to a chromosomal level applied to avian genomes.**
 J. Damas¹, R. E. O'Connor², M. Farre¹, H. Martell², E. A. Slack¹, E. Allanson¹, L. Kiazim², R. Jennings², A. Mandawala³, S. Joseph², K. E. Fowler³, D. K. Griffin², and **D. M. Larkin**^{*1}, ¹*Department of Comparative Biomedical Sciences, Royal Veterinary College, University of London, London, UK;* ²*School of Biosciences, University of Kent, Canterbury, UK;* ³*Canterbury Christchurch University, Canterbury, UK.*
- 18:00 **Meeting ends.**

Genome Edited Animals

Chair: **Bruce Whitelaw, University of Edinburgh**
George Moore Auditorium, O'Brien Science Building

14:30 **Introduction to Session and Update on Genome Editing Regulatory Position.**
 Bruce Whitelaw, *University of Edinburgh.*

14:45 27 **Invited Workshop Speaker: Pest-off: Could gene drive help drive out Australia's invasive pest animals?**
M. Tizard^{*}, *CSIRO Health & Biosecurity, Australian Animal Health Laboratory, Geelong, Victoria, Australia.*

15:15 28 **Editing the future of the domestic pig.**
S. Lilloco^{*1}, C. Proudfoot¹, C. Burkard¹, F. Urnov², J. Oatley³, B. Telugu⁴, A. Mileham⁵, and B. Whitelaw¹, ¹*The Roslin Institute, Roslin, Midlothian, Scotland;* ²*Sangamo Biosciences, Richmond, CA, USA;* ³*Washington State University, Pullman, WA, USA;* ⁴*University of Maryland, Beltsville, MD, USA;* ⁵*Genus Plc, DeForest, WI, USA.*

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 29 **The role of leptin in nonalcoholic obesity, diabetes and hepatic fibrosis.**
T. Tan*^{1,2}, Z. Song¹, Y. Xing^{1,2}, X. Hu^{1,2}, and N. Li^{1,2}, ¹College of Biological Sciences, China Agricultural University, Beijing, China; ²State Key Laboratory for Agro-Biotechnology, Beijing, China.
- 17:00 30 **Developing and exploiting new technologies to advance understanding of the avian immune system.**
A. Balic*, H. Sang, and M. McGrew, *The Roslin Institute, University of Edinburgh, Edinburgh, Scotland.*
- 17:30 **Discussion on role of genome editing as a functional genomics platform.**
Bruce Whitelaw, *University of Edinburgh.*
- 18:00 **Meeting ends.**

Horse Genetics and Genomics

Chair: **Teruaki Tozaki, Laboratory of Racing Chemistry and Tomas Bergström, Swedish University of Agricultural Sciences**
Icon Theatre, O'Brien Science Building

- 14:30 **Welcome remarks.**
- 14:30 31 **Genetic diversity, evolution and selection in the major histocompatibility complex *DRB* and *DQB* genes in the family Equidae.**
M. Klumplerova¹, P. Splichalova¹, J. Oppelt², P. Musilova³, S. Kubickova³, R. Vodicka⁴, J. Vahala⁵, L. Orlando⁶, and P. Horin*¹, ¹Ceitec VFU, University of Veterinary and Pharmaceutical Sciences, Dept. of Animal Genetics, Brno, Czech Republic; ²Ceitec MU, Masaryk University, National Centre for Biomolecular Research, Faculty of Science, Brno, Czech Republic; ³Veterinary Research Institute, Dept. of Reproduction and Genetics, Brno, Czech Republic; ⁴Zoo Prague, Prague, Czech Republic; ⁵Zoo Dvur Kralove nad Labem, Dvur Kralove nad Labem, Czech Republic; ⁶Centre for GeoGenetics Natural History Museum of Denmark University of Copenhagen, Copenhagen, Denmark.
- 14:45 32 **The potential of Y-chromosomal markers for individual lineage tracking in horses.**
S. Felkel¹, D. Rigler¹, C. Vogl¹, M. Neuditschko², S. Rieder², V. Jagannathan³, T. Leeb³, T. Rattei⁴, C. Schlotterer⁵, G. Brem¹, and B. Wallner*¹, ¹Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria; ²Agroscope, Swiss National Stud Farm, Avenches, Switzerland; ³Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland; ⁴Department of Microbiology and Ecosystems Science, Division of Computational Systems Biology, University of Vienna, Vienna, Austria; ⁵Institute of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria.
- 15:00 33 **Zooming in on chronic progressive lymphedema using a high-density array in the Belgian draught horse.**
L. François*¹, A. Schurink², B. Velie³, A. Stinckens¹, S. Blott⁴, B. Ducro², C. Lamberigts⁵, S. Tinel¹, K. De Keyser¹, M. Oostlerlinck⁶, G. Lindgren³, S. Janssens¹, and N. Buys¹, ¹Research Group Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium; ²Animal Breeding and Genomics Centre, Wageningen University & Research, Wageningen, the Netherlands; ³Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁴School of Veterinary Medicine & Science, University of Nottingham, Leicestershire, United Kingdom; ⁵Research Group Livestock Physiology, Department of Biosystems, KU Leuven, Leuven, Belgium; ⁶Department of Surgery and Anesthesiology of Domestic Animals, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium.
- 15:15 34 **Genetic contributions to measured speed in Thoroughbred racehorses during early training.**
G. Farries*, B. A. McGivney, K. F. Gough, L. M. Katz, and E. W. Hill, *University College Dublin, Belfield, Dublin, Ireland.*
- 15:30 35 **Whole-genome sequencing reveals two Shetland pony specific variants affecting body size and shape.**
J. Metzger*, F. Naccache, A. Christmann, and O. Distl, *Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover Foundation, Hannover, Niedersachsen, Germany.*

15:45 36 **Epigenetic characterization of centromeric chromatin in equids.**
S. G. Nergadze¹, R. Gamba¹, F. M. Piras¹, E. Cappelletti¹, M. Corbo¹, F. Gozzo¹, D. Miller², D. Antczak², E. Raimondi¹, K. Sullivan³, and **E. Giulotto**^{*1}, ¹University of Pavia, Department of Biology and Biotechnology, Pavia, Italy; ²Cornell University, College of Veterinary Medicine, Ithaca, NY, USA; ³National University of Ireland, Centre for Chromosome Biology, Galway, Ireland.

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

16:30 37 **Unraveling gene function using co-expression networks in the domestic horse.**
R. Schaefer^{*1}, E. Norton¹, J. Mickelson², and M. McCue¹, ¹Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA; ²Department of Veterinary and Biomedical Science, University of Minnesota, St Paul, MN, USA.

16:45 38 **Invited Workshop Speaker: Mapping transcriptional regulation at multiple layers using ChRO-seq.**
C. Danko^{*1,2}, ¹Baker Institute for Animal Health, Ithaca, NY, USA; ²Cornell University, Ithaca, NY, USA.

17:15 39 **EquCab3.**
T. Kalbfleisch^{*1}, M. DePriest¹, L. Orlando², and J. MacLeod³, ¹University of Louisville, Louisville, KY, USA; ²University of Copenhagen, Copenhagen, Denmark; ³University of Kentucky, Lexington, KY, USA.

17:30 40 **Protein-coding gene and transcript sequences quantify progress toward the new equine reference genome assembly.**
M. S. DePriest^{*1,2}, J. N. MacLeod², and T. S. Kalbfleisch¹, ¹University of Louisville, Louisville, KY, USA; ²University of Kentucky, Lexington, KY, USA.

17:45 41 **Progress toward functional annotation of the equine genome.**
J. Petersen^{*1}, E. Burns², M. Bordbari², E. Scott², B. Ming-Whitfield², V. Affolter², C. Ramirez Alanis², M. Barro², M. Mack², G. Gianino², F. Gianino², E. Giulotto³, K. Hilburger², T. Kalbfleisch⁴, J. MacLeod⁵, M. Mienaltowski², S. Katzman², T. Leeb⁶, T. Raudsep⁷, P. Saelao², S. Vig², H. Zhou², R. Bellone², and C. Finno², ¹University of Nebraska-Lincoln, Lincoln, NE, USA; ²University of California-Davis, Davis, CA, USA; ³University of Pavia, Pavia, Italy; ⁴University of Louisville, Louisville, KY, USA; ⁵University of Kentucky, Lexington, KY, USA; ⁶University of Bern, Bern, Switzerland; ⁷Texas A&M, College Station, TX, USA.

18:00 **Business Meeting.**

18:05 **Meeting ends.**

Welcome Reception

Atrium, O'Brien Science Building

18:00 – 19:00

Tuesday, July 18

Registration Desk Open	Atrium, O'Brien Science Building	07:45 – 18:00
Exhibition and Posters Open	Atrium, O'Brien Science Building	08:00 – 18:00
Illumina Vendor Seminar	George Moore Auditorium, O'Brien Science Building	08:00 – 08:45

Illumina Vendor Seminar: Accelerating animal genomic breakthroughs

Advances in high quality de novo genome assemblies

Ryan Rapp, Associate Director, Agrigenomics, Illumina

Ultra-high-throughput genotyping with Infinium XT

Andre Eggen, Sr Market Development Manager, Illumina

Introducing TruSeq Genotype Ne – genotyping by sequencing solution

Jason Goode, Market Manager, New Ag Markets, Illumina

WORKSHOPS

Bold font denotes presenter

Avian Genetics and Genomics

Chair: **Richard Crooijmans, Wageningen University & Research**
H1.51 Breakout, O'Brien Science Building

09:00		Introduction. Richard Crooijmans, <i>Wageningen University & Research.</i>
09:05	42	The evolving chicken genome reference. W. Warren * ¹ , L. Hillier ¹ , C. Tomlinson ¹ , P. Minx ¹ , M. Kremitski ¹ , T. Graves ¹ , S. Sullivan ² , I. Liachko ² , M. Delaney ³ , J. Fulton ⁴ , M. Abrahamsen ⁵ , R. Hawken ⁵ , M. Miller ⁶ , and H. Cheng ⁷ , ¹ <i>Washington University School of Medicine, St Louis, MO, USA;</i> ² <i>Phase Genomics Inc, Seattle, WA, USA;</i> ³ <i>University of California-Davis, Davis, CA, USA;</i> ⁴ <i>Hy-Line International, Dallas Center, IA, USA;</i> ⁵ <i>Cobb-Vantress Inc, Siloam Springs, AR, USA;</i> ⁶ <i>Beckman Research Institute, Duarte, CA, USA;</i> ⁷ <i>USDA-ARS, East Lansing, MI, USA.</i>
09:25	43	Low number of mitochondrial DNA sequences inserted into the turkey (<i>Meleagris gallopavo</i>) nuclear genome: implications for evolutionary inferences. G. Schiavo ¹ , M. G. Strillacci ² , S. Bovo ^{1,3} , A. Ribani ¹ , S. I. Roman-Ponce ⁴ , S. Cerolini ² , F. Bertolini ^{1,5} , A. Bagnato ² , and L. Fontanesi* ¹ , ¹ <i>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy;</i> ² <i>Department of Veterinary Medicine, University of Milan, Milano, Italy;</i> ³ <i>Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy;</i> ⁴ <i>Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agrícola y Pecuarias (INIFAP), Col. Centro Veracruz, Mexico;</i> ⁵ <i>Department of Animal Science, Iowa State University, Ames, IA, USA.</i>
09:40	44	In situ and in silico improvement of the Japanese quail genome assembly. S. Galkina * ¹ , M. Kulak ¹ , A. Saifitdinova ¹ , A. Komissarov ¹ , A. Dyomin ¹ , V. Volodkina ¹ , J. Damas ² , M. Farre ² , D. Griffin ³ , D. Larkin ² , and E. Gaginskaya ¹ , ¹ <i>Saint-Petersburg State University, Saint-Petersburg, Russia;</i> ² <i>Royal Veterinary College, University of London, London, UK;</i> ³ <i>University of Kent, Kent, UK.</i>
09:55	45	The broiler chicken transcriptome. C. Schmidt * ¹ and S. Lamont ² , ¹ <i>University of Delaware, Newark, DE, USA,</i> ² <i>Iowa State University, Ames, IA, USA.</i>
10:15	46	The not-so-missing genes in birds. T. Hron * ¹ , H. Farkasova, P. Pajer, J. Paces, P. Bartunek, and D. Elleder, <i>Institute of Molecular Genetics of the AV CR, v.v.i., Videnská, Prague, Czech Republic.</i>

10:30	49	Evaluation of semen characteristic of the high and low sperm motility groups in two different strains of chicken. M. Farahi, A. A. Masoudi* , and A. Ehsani, <i>Tarbiat Modares University, Tehran, Tehran, Iran.</i>
10:45	51	Goose transcriptome provides insights into novel mechanisms of adipogenesis. G. Wang* ^{2,1} , Y. Liu ¹ , L. Jin ¹ , D. Shang ¹ , C. Gill ² , M. Li ¹ , and J. Wang ¹ , ¹ <i>Sichuan Agricultural University, Chengdu, Sichuan, China;</i> ² <i>Texas A&M University, College Station, TX, USA.</i>
Coffee/Tea break Atrium, O'Brien Science Building 11:00 – 11:30		
11:30	52	Integrating genome and transcriptome profiling for dissection of the mechanism of muscle growth and lipid deposition in ducks. L. Wang* , X. Li, J. Ma, Y. Zhang, and H. Zhang, <i>Lab of Animal Genetic Resource and Molecular Breeding, China Agricultural University, Beijing, China.</i>
11:45	53	Liver and whole blood transcriptome response to chronic heat exposure in laying hens. F. Jehl ¹ , A. Rau ¹ , C. Désert ^{2,3} , M. Boutin ^{2,3} , K. Muret ^{2,3} , S. Leroux ⁴ , D. Esquerré ⁵ , C. Klopp ⁶ , D. Gourichon ⁷ , F. Pitel ⁴ , A. Collin ⁸ , S. Lagarrigue ^{2,3} , and T. Zerjal* ¹ , ¹ <i>GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;</i> ² <i>INRA, UMR1348 Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'élevage, Saint-Gilles, France;</i> ³ <i>Agrocampus-Ouest, UMR1348, Rennes, France;</i> ⁴ <i>UMR INRA/INPT ENSAT/INPT ENVT-GenPhySE, Castanet Tolosan, France;</i> ⁵ <i>INRA, Plateforme GENOTOL, Castanet-Tolosan, France;</i> ⁶ <i>INRA, SIGENAE, Castanet-Tolosan, France;</i> ⁷ <i>INRA-PEAT, Nouzilly, France;</i> ⁸ <i>URA, INRA, Nouzilly, France.</i>
12:00	54	Mapping QTLs affecting Marek's disease by selective DNA pooling in eight lines across 15 generations. E. Lipkin* ¹ , J. Smith ² , D. Burt ² , M. Soller ¹ , and J. Fulton ³ , ¹ <i>Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel;</i> ² <i>The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK;</i> ³ <i>Hy-Line International, Dallas Center, IA, USA.</i>
12:15	55	Genome-wide association study of complex traits in response to Newcastle disease virus in chickens. K. Rowland* ¹ , H. Zhou ² , R. Gallardo ³ , T. Kelly ^{2,3} , A. Wolc ^{1,4} , and S. J. Lamont ¹ , ¹ <i>Iowa State University, Department of Animal Science, Ames, IA, USA;</i> ² <i>University of California-Davis, Department of Animal Science, Davis, CA, USA;</i> ³ <i>University of California-Davis, School of Veterinary Medicine, Davis, CA, USA;</i> ⁴ <i>Hy-Line International, Dallas Center, IA, USA.</i>
12:30		Concluding Remarks. Richard Crooijmans, <i>Wageningen University & Research.</i>
12:35		Workshop Business Meeting.
13:00		Meeting ends.

Comparative MHC Genetics: Populations and Polymorphism

Chair: **Keith Ballingall**, *Moredun Research Institute*
Icon Theatre, O'Brien Science Building

09:00		Introductory Remarks.
09:00	56	IPD-MHC 2.0: An improved interspecies database for the study of the major histocompatibility complex. G. Maccari* ^{1,2} , J. Robinson ^{2,3} , K. Ballingal ⁴ , L. Guethlein ⁵ , U. Grimholt ⁶ , J. Kaufman ⁷ , C. Ho ⁸ , N. de Groot ⁹ , R. Bontrop ⁹ , P. Flicek ¹⁰ , J. Hammond ¹ , and S. Marsh ^{2,3} , ¹ <i>The Pirbright Institute, Pirbright, Woking, Surrey, UK;</i> ² <i>Anthony Nolan Research Institute, Royal Free Hospital, London, UK;</i> ³ <i>UCL Cancer Institute, Royal Free Campus, London, UK;</i> ⁴ <i>Moredun Research Institute, Pentlands Science Park, Scotland, UK;</i> ⁵ <i>Stanford University, Stanford, CA, USA;</i> ⁶ <i>Norwegian Veterinary Institute, Oslo, Norway;</i> ⁷ <i>University of Cambridge, Cambridge, UK;</i> ⁸ <i>Gift of Life Michigan, Michigan, USA;</i> ⁹ <i>Biomedical Primate Research Centre, Rijswijk, Netherlands;</i> ¹⁰ <i>European Molecular Biology Laboratory, Wellcome Genome Campus, Hinxton, UK.</i>

- 09:15 57 **Major update to the Swine Leukocyte Antigen (SLA) Nomenclature System of the International Society for Animal Genetics (ISAG) and the International Union of Immunological Societies (IUIS).**
S. Ho*¹, J. Lunney², A. Ando³, C. Rogel-Gaillard⁴, J.-H. Lee⁵, L. Schook⁶, and S. Hammer⁷, ¹*Gift of Life Michigan, Ann Arbor, MI, USA;* ²*USDA, Beltsville, MD, USA;* ³*Tokai University School of Medicine, Isehara, Kanagawa, Japan;* ⁴*INRA, Jouy-en-Josas, France;* ⁵*Chungnam National University, Daejeon, Korea;* ⁶*University of Illinois, Urbana, IL, USA;* ⁷*University of Veterinary Medicine Vienna, Vienna, Austria.*
- 09:30 58 **Studies of MHC class II content in three common Arabian horse haplotypes.**
D. Miller*¹, A. Case¹, L. Younger¹, J. Tseng¹, H. Holl², Y. A. Mohamoud³, A. Ahmed³, J. Malek³, S. Brooks², and D. Antczak¹, ¹*Cornell University, Ithaca, NY, USA;* ²*University of Florida, Gainesville, FL, USA;* ³*Weill Cornell Medicine, Doha, Qatar.*
- 09:45 59 **A rapid, direct sequencing-based MHC genotyping system for populations with insufficient information on allelic variation.**
J. Buitkamp* and J. Semmer, *Bavarian State Research Center for Agriculture Institute of Animal Breeding, Grub, Bavaria, Germany.*
- 10:00 60 **Molecular characterisation of Ovar-MHC class II region reveals novel alleles in the Djallonke and Sahelian sheep breeds of Ghana.**
M. Yaro*¹, K. Munyard¹, E. Morgan¹, M. Stear², and D. Groth¹, ¹*Curtin University, Perth, WA, Australia;* ²*La Trobe University, Melbourne, Victoria, Australia.*
- 10:15 61 **Withdrawn**
- 10:30 63 **Invited Workshop Speaker: Large-scale analysis of the specificities of livestock MHC class I and II molecules.**
S. Buus*, *Laboratory of Experimental Immunology, University of Copenhagen, Copenhagen, Denmark.*

Coffee/Tea break

Atrium, O'Brien Science Building

11:00 – 11:30

- 11:30 64 **The ligands and polymorphic residues of chicken MHC YF class I-like molecules.**
 R. M. Goto¹, G. Gugiu¹, B. M. Stadtmueller², P. J. Bjorkman², and **M. M. Miller***¹, ¹*Beckman Research Institute, City of Hope, Duarte, CA, USA;* ²*California Institute of Technology, Pasadena, CA USA.*
- 12:00 65 **Evolution by gene duplication of the horse major histocompatibility complex class II structure.**
A. Viluma*, S. Mikko, G. Andersson, and T. F. Bergström, *Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences (SLU), Sweden.*
- 12:15 66 **Chicken MHC-B diversity detected by a high-density SNP panel.**
J. E. Fulton*¹, B. Bed'Hom², and M. M. Miller³, ¹*Hy-Line International, Dallas Center, IA, USA;* ²*GABI, INRA, AgroParis-Tech, Jouy-en-Josas, France;* ³*Department of Molecular and Cellular Biology, Duarte, CA, USA.*
- 12:30 **Workshop Business Meeting.**
- 13:00 **Meeting ends.**

Equine Genetics and Thoroughbred Parentage Testing Workshop

Chair: **Cecilia Penedo, University of California at Davis**
Lynch Theatre, O'Brien Science Building

- 09:00 **Welcoming Remarks.**
- 09:10 **Horse Comparison Test.**
- 10:00 **Donkey Comparison Test.**
- 10:30 **Horse SNP Comparison Test.**

Coffee/Tea break

Atrium, O'Brien Science Building

11:00 – 11:30

- 11:30 67 **Genetic diagnosis of sex chromosome aberrations in horses based on analysis of microsatellite and X- and Y-linked markers.**
J. A. Bouzada*, J. M. Lozano, M. R. Maya, A. Trigo, I. Bonet, F. Castillo, J. Fernández-León, T. Mayoral, E. Anadón, and L. B. Pitarch, *Laboratorio de Genética y Control, Algete, Madrid, Spain.*
- 11:45 68 **Rate of sex reversal cases in horses of Argentina.**
M. Martinez*, M. Costa, B. Elguero, and C. Ratti, *Laboratorio de Genética Aplicada, Sociedad Rural Argentina, Buenos Aires, Argentina.*
- 12:00 69 **Characterization of equine STR panel “15 TKY system” by imputation from dense SNP genotypes in a Thoroughbred population.**
M. Kikuchi*, H. Kakoi, T. Tozaki, K. Hirota, and S. Nagata, *Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan.*
- 12:15 70 **Preliminary results of genetic monitoring of the occurrence of three genetic diseases (CA, SCID, LFS) in Arabian horses from Poland.**
M. Bugno-Poniewierska*¹, M. Stefaniuk-Szmukier², A. Piestrzynska-Kajtoch¹, A. Fornal¹, and K. Ropka-Molik¹, ¹*National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice n. Krakow, Poland;* ²*University of Agriculture, Department of Horse Breeding, Kraków, Poland.*
- 12:30 Election of Committee Members and Any Other Business.
- 13:00 Meeting ends.

Genetics of Immune Response and Disease Resistance

Chair: **Huaijun Zhou, University of California, Davis**
Intel Theatre, O'Brien Science Building

- 09:00 71 **Enhanced genetic disease control with selection for low susceptibility and infectivity.**
S. Tsairidou*, O. Anacleto, J. A. Woolliams, and A. Doeschl-Wilson, *Roslin Institute, Edinburgh, UK.*
- 09:15 73 **Genetic basis for resistance to avian influenza in commercial egg layer chicken lines.**
W. Drobik-Czwaro*¹, A. Wolc^{2,3}, J. Fulton³, T. Jankowski⁴, J. Arango³, P. Settar³, N. O'Sullivan³, and J. Dekkers², ¹*Department of Animal Genetics and Breeding, Faculty of Animal Science, Warsaw University of Life Sciences, Warsaw, Poland;* ²*Department of Animal Science, Iowa State University, Ames, IA, USA;* ³*Hy-Line International, West Des Moines, IA, USA;* ⁴*NutriBiogen, Poznan, Poland.*
- 09:30 74 **Integrated network analysis for mRNAs and miRNAs expressed in PRRSV vaccinated peripheral blood mononuclear cells of pigs.**
M. A. Islam¹, C. Neuhoﬀ*¹, S. Rony¹, C. Große-Brinkhaus¹, M. J. Uddin², M. Hölker¹, D. Tesfaye¹, E. Tholen¹, M. J. Pröll¹, and K. Schellander¹, ¹*Institute of Animal Science, Animal Breeding and Husbandry group, University of Bonn, Endenicher Allee 15, Bonn, Germany;* ²*School of Veterinary Science, The University of Queensland, Gatton campus, QLD, Australia.*
- 09:45 75 **Mammary epithelial cells, rather than professional immune cells dictate the pathogen species-specific immune reaction of the udder.**
J. Hehl*¹, M. Koy², A. Berthold¹, H.-J. Schuberth², M. Weinert³, S. Engelmann³, C. Kühn¹, H.-M. Seyfert¹, and J. Günther¹, ¹*Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany;* ²*Immunology Unit, University of Veterinary Medicine Foundation, Hannover, Germany;* ³*Institute of Microbiology, Technical University Braunschweig, Braunschweig, Germany.*

- 10:00 76 **Integrative network genomics of the bovine host response to infection with *Mycobacterium bovis*.**
T. J. Hall*¹, K. E. Killick^{1,2}, M. P. Mullen³, K. E. McLoughlin¹, N. C. Nalpas⁴, I. W. Richardson⁵, D. A. Magee¹, C. N. Correia¹, J. A. Browne¹, H. M. Vordermeier⁶, B. Villarreal-Ramos⁶, D. P. Berry⁷, E. Gormley⁸, S. V. Gordon^{2,8}, D. E. MacHugh^{1,2},
¹Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland; ²UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland; ³Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland; ⁴Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany; ⁵IdentiGEN Ltd., Blackrock Business Park, Blackrock, Dublin, Ireland; ⁶Animal and Plant Health Agency (APHA), Weybridge, Addlestone, United Kingdom.; ⁷Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland; ⁸UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland.
- 10:15 77 **Identification of putative key transcription factors in canine macrophages after infection with *Leishmania infantum* and stimulation with a toll-like receptor-2 agonist.**
 L. Solano-Gallego², S. Montserrat², F. Mayer¹, A. Castello¹, L. Alborch², S. Heath³, A. Esteve-Codina³, J. Gomez-Garrido³, R. A. Cigliano⁴, and **A. Clop***¹, ¹Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Valles, Catalonia, Spain; ²Universitat Autònoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain; ³Centre Nacional d'Anàlisi Genòmica CNAG-CRG, Barcelona, Catalonia, Spain; ⁴Sequentia Biotech, Barcelona, Catalonia, Spain.
- 10:30 78 **Analysis of the genomic regions associated to response to coccidiosis caused by *Eimeria maxima* in broiler chickens.**
B. Bed'Hom*¹, M. H. Pinard-Van der Laan¹, R. Hawken², and H. Edin¹, ¹INRA, Jouy-en-Josas, France; ²Cobb-Vantress Inc, Siloam Springs, AR, USA.
- 10:45 79 **Genetic individual variability of vaccine responses in pigs.**
F. Blanc*¹, G. Lemonnier¹, J. Leplat^{1,2}, E. Bouguyon³, Y. Billon⁴, J. Estelle¹, and C. Rogel-Gaillard¹, ¹GABI, INRA, AgroParis-Tech, Université Paris-Saclay, Jouy-en-Josas, France; ²CEA, DRF/IRCM/SREIT/LREG, Jouy-en-Josas, France; ³VIM-INRA-Université Paris-Saclay, Jouy-en-Josas, France; ⁴GenESI, INRA, Surgères, France.
- Coffee/Tea break Atrium, O'Brien Science Building 11:00 – 11:30
- 11:30 80 **QTLs associated with resistance to MAP infection in Holstein-Friesian cattle.**
S. Mallikarjunappa*^{1,3}, M. Sargolzaei⁴, K. Meade², N. Karrow³, and S. Pant¹, ¹Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW, Australia; ²Teagasc Animal and Bioscience Research Department, Grange, Co. Meath, Ireland; ³Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada; ⁴The Semex Alliance, Guelph, ON, Canada.
- 11:45 81 **The association of copy number variations with tick count in South African Nguni cattle.**
L. Pickering*¹, K. Dzama¹, F. Muchadeyi², and M. Wang², ¹Animal Science Department, University of Stellenbosch, Stellenbosch, Western Cape, South Africa; ²Agriculture Research Council Biotechnology Platform, Pretoria, Gauteng, South Africa.
- 12:00 82 **Investigating genetic control of resistance to avian pathogenic *Escherichia coli* colonization in chickens.**
M. Monson*¹, M. Kaiser¹, A. Wolc^{1,2}, and S. Lamont¹, ¹Iowa State University, Ames, IA, USA; ²Hy-Line International, Dallas Center, IA, USA.
- 12:15 84 **Lightning Talk: Genome-wide association study for monocyte count at day 7 post-challenge with bovine viral diarrhoea virus in F₂ and F₃ Nellore-Angus halfblood steers.**
K. M. S. Davila*¹, A. D. Herring¹, J. E. Sawyer¹, J. F. Ridpath^{2,3}, and C. A. Gill¹, ¹Texas A&M University, College Station, TX, USA; ²National Animal Disease Center, Ames, IA, USA; ³Ridpath Consulting, Ames, IA, USA.
- 12:19 85 **Lightning Talk: Polymorphism in TLR2 in different dairy cattle breeds suggests immune functional modulation.**
M. Bartens*¹, K. Tombacz, A. Gibson, and D. Werling, Department of Pathobiology and Population Sciences, Royal Veterinary College, University of London, Hatfield, UK.
- 12:23 86 **Lightning Talk: Delineating Indian native cattle-specific allelic variants and haplotypes in lactoferrin gene: A potential candidate for disease resistance.**
A. Sharma*^{1,2}, M. Sodhi², P. Jain¹, M. Kumar², and M. Mukesh², ¹University Institute of Engineering & Technology, Kurukshetra, Haryana, India; ²National Bureau of Animal Genetics Resources, Karnal, Haryana, India.
- 12:27 **Workshop Business Meeting.**
- 13:00 **Meeting ends.**

ISAG-FAO Genetic Diversity

Chair: Catarina Ginja, CIBIO-InBIO, Universidade do Porto, Portugal
Elan Theatre, O'Brien Science Building

09:00	87	Invited Workshop Speaker: An ancient genomic perspective on the horse domestication process. L. Orlando ^{*1,2} , ¹ <i>University of Copenhagen, Centre for GeoGenetics, Natural History Museum of Denmark, Copenhagen, Denmark;</i> ² <i>Université de Toulouse, University Paul Sabatier (UPS), Laboratoire AMIS, CNRS UMR 5288, Toulouse, France.</i>
09:30	88	Withdrawn
09:45	89	When <i>taurus</i> met <i>indicus</i>. Exploring admixture events in ancient cattle. M. Verdugo [*] , <i>Trinity College Dublin, Dublin, Ireland.</i>
10:00	90	Genetic continuity of maternal lineages in Iberian cattle populations since Roman times. L. Simões ¹ , A. E. Pires ^{2,3} , C. Detry ⁴ , I. Ureña ² , E. Svensson ¹ , J. Matos ⁵ , C. Rodriguez-Fernández ⁶ , A. M. Arruda ⁴ , I. Fernandes ⁷ , S. Davis ³ , A. Götherström ⁸ , and C. Ginja ^{*2} , ¹ <i>Department of Organismal Biology, Uppsala University, Uppsala, Sweden;</i> ² <i>CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, Vairão, Portugal;</i> ³ <i>Laboratório de Arqueociências-InBIO, DGCP, Lisboa, Portugal;</i> ⁴ <i>UNUARQ, Centro de Arqueologia da Universidade de Lisboa, Faculdade de Letras, Universidade de Lisboa, Lisboa, Portugal;</i> ⁵ <i>Grupo de Biologia Molecular, Instituto Nacional de Investigação Agrária e Veterinária, Oeiras, Portugal;</i> ⁶ <i>Departamento de História, Facultad de Filosofía y Letras, Universidad de León, León, Spain;</i> ⁷ <i>Câmara Municipal de Palmela, Palmela, Portugal;</i> ⁸ <i>Archaeological Research Laboratory, Department of Archaeology and Ancient History, Stockholm University, Stockholm, Sweden.</i>
10:15	91	Comparative genome-wide characterisation of five rare British Isles cattle breeds. P. Flynn ^{*1,2} , J. Carlsson ² , and D. Berry ³ , ¹ <i>Weatherbys DNA Laboratory, Johnstown, Naas, Co. Kildare, Ireland;</i> ² <i>University College Dublin, School of Biology & Environmental Science, UCD, Belfield, Dublin, Ireland;</i> ³ <i>Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.</i>
10:30	92	Diversity of sheep breeds in Russia based on SNP analysis. T. Deniskova ^{*1} , A. Dotsev ¹ , M. Selionova ² , K. Wimmers ³ , H. Reyer ³ , V. Kharzinova ¹ , E. Gladyr ¹ , G. Brem ^{1,4} , and N. Zinovieva ¹ , ¹ <i>L.K. Ernst Institute of Animal Husbandry, Podolsk, Moscow region, Russia;</i> ² <i>All-Russian Research Institute of Sheep and Goat, Stavropol, Stavropol region, Russia;</i> ³ <i>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany;</i> ⁴ <i>Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.</i>
10:45	93	Ancient whole mitochondrial genomes and insights into the prehistory of goats. K. Daly [*] , <i>Smurfit Institute of Genetics, Trinity College, Dublin, Ireland.</i>
Coffee/Tea break		
Atrium, O'Brien Science Building		11:00 – 11:30
11:30	94	Genome-wide analysis for signature of selection in domestic chicken and red jungle fowl. R. A. Lawal ^{*1} and O. Hanotte ^{1,2} , ¹ <i>The University of Nottingham, Nottingham, Nottinghamshire, UK;</i> ² <i>International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.</i>
11:45	95	Genome-wide assessment of genetic diversity in the Synbreed Chicken Diversity Panel. S. Weigend ^{*1} , A. Weigend ¹ , D. Malomane ² , and H. Simianer ² , ¹ <i>Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt-Mariensee, Höltystraße 10, Germany;</i> ² <i>University of Göttingen, Animal Breeding and Genetics Group, Göttingen, Albrecht-Thaer-Weg 3, Germany.</i>
12:00	97	Detection of selection signals between Merino and Churra sheep breeds. B. Gutierrez-Gil ^{*1} , P. K. Chitneedi ¹ , A. Suarez-Vega ¹ , P. Wiener ² , C. Esteban-Blanco ¹ , and J. J. Arranz ¹ , ¹ <i>Department of Animal Production, Faculty of Veterinary Sciences, University of León, León, Spain;</i> ² <i>Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush Campus, Midlothian, United Kingdom.</i>
12:15	98	Distribution of polymorphisms in major and candidate genes for productive and domestication-related traits in European local pig breeds. A. Fernández ¹ , M. Muñoz ¹ , F. García ¹ , Y. Núñez ¹ , C. Geraci ² , A. Crovetto ³ , J. García-Casco ¹ , E. Alves ¹ , M. Skrlep ⁴ , J. Riquet ⁵ , M. Mercat ⁶ , R. Bozzi ³ , M. Candek-Potokar ⁴ , L. Fontanesi ² , C. Óvilo ^{*1} , ¹ <i>INIA, Madrid, Spain;</i> ² <i>UNIBO, Bologna, Italy;</i> ³ <i>UNIFI, Firenze, Italy;</i> ⁴ <i>KIS, Ljubljana, Slovenia;</i> ⁵ <i>INRA, Toulouse, France;</i> ⁶ <i>IFIP, Paris, France.</i>

12:30 188 **Genetic diversity among domestic goats (*Capra hircus*) and wild goats (*Capra aegagrus*) in Turkey.**
 I. S. Yildirim¹, M. Nizamlioglu¹, M. D. Oncu², E. K. Bastanlar², and **Z. Bulut***^{1, 1}*Selcuk University, Faculty of Veterinary Medicine, Departments of Biochemistry, Konya, Turkey;* ²*TUBITAK-MAM, Genetic Engineering and Biotechnology Institute, Gebze, Kocaeli, Turkey.*

12:40 **Workshop Committee Business Meeting—Challenges for FAnGr in the Era of the ‘omics’.**

13:25 **Meeting ends.**

Ruminant Genetics and Genomics

Chair: **Laercio Porto-Neto, CSIRO Agriculture**
George Moore Auditorium, O'Brien Science Building

09:00 99 **Evidence from the bovine of major differences between individuals in the rate of *de novo* single nucleotide mutation and transposon mobilization in the germline.**
 C. Harland^{1,2}, K. Durkin¹, M. Artesi¹, L. Karim^{1,3}, N. Cambisano^{1,3}, M. Deckers^{1,3}, N. Tamma^{1,3}, E. Mullaart⁴, W. Coppie-
 ters^{1,3}, M. Georges¹, and **C. Charlier***¹, ¹*Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Belgium;* ²*Livestock Improvement Corporation, Research & Development, Hamilton, New Zealand;* ³*GIGA-Genomics Platform, University of Liège, Liège, Belgium;* ⁴*CRV, Research & Development, Arnhem, Netherlands.*

09:15 100 **Pinpointing causal mutations among imputed sequence variant genotypes in three cattle breeds.**
H. Pausch*^{1,2}, I. MacLeod¹, P. Bowman^{1,3}, R. Emmerling⁴, R. Fries⁵, B. Gredler-Grandl⁶, H. Daetwyler^{1,3}, and M. God-
 dard^{1,7}, ¹*Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, VIC, Australia;* ²*Animal Genomics, Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland;* ³*School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia;* ⁴*Institute of Animal Breeding, Bavarian State Research Centre for Agriculture, Poing-Grub, Germany;* ⁵*Chair of Animal Breeding, Technische Universitaet Muenchen, Freising, Germany;* ⁶*Qualitas AG, Zug, Switzerland;* ⁷*Faculty of Veterinary and Agricultural Science, University of Melbourne, Melbourne, VIC, Australia.*

09:30 **Invited Workshop Speaker: Cytoplasmic inheritance on farm animals and biotechnologies for selection.**
Flavio V. Meirelles*, *University of Sao Paulo.*

10:00 101 **Genotyping by sequencing for genomic selection in dairy goats (*Capra hircus*).**
S. Clarke*¹, K. Dodds¹, R. Brauning¹, T. Van Stijn¹, R. Anderson¹, M. Wheeler², B. Foote³, A. Cameron⁴, and J. McEwan¹,
¹*AgResearch, Mosgiel, Dunedin, New Zealand;* ²*AgResearch, Ruakura, Hamilton, New Zealand;* ³*Foote Dairy, Hikurangi, Northland, New Zealand;* ⁴*Meredith Dairy, Meredith, Victoria, Australia.*

10:15 102 **Identification of polymorphisms modifying gene expression regulation in cattle.**
G. Guillocheau* and D. Rocha, *GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France.*

10:30 103 **GWAS for response to vaccination in Angus calves.**
L. Kramer*¹, M. Mayes¹, J. Williams¹, E. Fritz-Waters¹, E. Downey², R. Tait Jr.³, A. Woolums⁴, C. Chase⁵, J. Ridpath⁶,
 and J. Reecy¹, ¹*Iowa State University, Ames, IA, USA;* ²*Elanco Animal Health, Larchwood, IA, USA;* ³*Neogen GeneSeek Operations, Lincoln, NE, USA;* ⁴*Mississippi State University, Mississippi State, MS, USA;* ⁵*South Dakota State University, Brookings, SD, USA;* ⁶*Ridpath Consulting, Gilbert, IA, USA.*

10:45 104 **The water buffalo gene expression atlas.**
R. Young*¹, L. Lefevre¹, S. Bush¹, J. Williams², S. Gokhale³, S. Kumar⁴, A. Archibald¹, and D. Hume¹, ¹*The Roslin Institute and Royal (Dick) School of Veterinary Studies (RDSVS), Easter Bush, Midlothian, UK;* ²*School of Animal and Veterinary Sciences, The University of Adelaide, Adelaide, South Australia, Australia;* ³*BAIF Development Research Foundation, Central Research Station, Pune, Maharashtra, India;* ⁴*Centre for Cellular and Molecular Biology, Hyderabad, Telangana, India.*

Coffee/Tea break

Atrium, O'Brien Science Building

11:00 – 11:30

11:30	105	Origin and evolutionary history of the European bison unraveled through ancient DNA. T. Grange* , D. Massilani, S. Guimaraes, and E.-M. Giegl, <i>Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France.</i>
11:45	106	Signals of adaptive introgression between European taurine and indicine cattle revealed by local ancestry inference. M. Barbato* ¹ , M. Del Corvo ¹ , T. Sonstegard ² , and P. Ajmone-Marsan ¹ , ¹ <i>Istituto di Zootechnica, Università Cattolica del Sacro Cuore, Piacenza, Italy;</i> ² <i>Recombinetics Inc., St. Paul, MN, USA.</i>
12:00	107	Cattle on the Western Atlantic edge of Europe: A time series of ancient cattle genomes through Ireland and Britain. V. Mullin* , <i>Trinity College Dublin, Dublin, Ireland.</i>
12:15	108	Whole genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry. G. Spangler* ¹ , B. Rosen ¹ , O. Hanotte ² , T. Sonstegard ³ , and C. Van Tassell ¹ , ¹ <i>USDA/ARS/AGIL, Beltsville, MD, USA;</i> ² <i>U of Nottingham/School of Life Sciences, Nottingham, UK;</i> ³ <i>Acceligen of Recombinetics, St Paul, MN.</i>
12:30	109	A worldwide investigation of the effects of climate selection on goat genomes. F. Bertolini* ¹ , E. Rochat ² , S. Joost ² , B. Servin ³ , P. Crepaldi ⁴ , A. Stella ⁵ , and M. F. Rothschild ¹ , ¹ <i>Department of Animal Science, Iowa State University, Ames, IA, USA;</i> ² <i>LASIG, EPFL, Lausanne, Switzerland;</i> ³ <i>INRA, Castanet-Tolosan, France;</i> ⁴ <i>DIMEVET, University of Milan, Milan, Italy;</i> ⁵ <i>PTP, Lodi, Italy.</i>
12:45		Workshop Business Meeting.
13:00		Meeting ends.

Lunch	Atrium, O'Brien Science Building	13:00 – 14:00
Weatherbys Vendor Presentation	George Moore Auditorium, O'Brien Science Building	13:30 – 14:15
Weatherbys Vendor Presentations:		
The Irish Beef Genomics Scheme: Applying the latest DNA technology to address global challenges around GHG emissions and food security <i>Andrew Cromie, The Irish Cattle Breeding Federation</i>		
SNP parentage and identification: Making the transition from microsatellites <i>Paul Flynn, Research and Development, Weatherbys DNA Laboratory</i>		
Animal Genetics Editorial Board Meeting (Private Invitation)	Boardroom H1.47, O'Brien Science Building	13:30 – 14:30

Animal Epigenetics

Chair: **Stephanie McKay, University of Vermont**
Elan Theatre, O'Brien Science Building

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| 14:30 | | Invited Workshop Speaker: Dynamics of 4D Nucleome during differentiation of mouse hematopoietic stem cells.
Keji Zhao* , <i>National Heart, Lung, and Blood Institute.</i> |
| 15:15 | 110 | DNA methylation and microRNA modifications in scrapie.
J. Toivonen ¹ , A. Sanz ¹ , O. López-Pérez ^{1,2} , D. Sanz-Rubio ¹ , M. Salinas-Pena ¹ , J. Alejo ¹ , R. Bolea ² , J. Espinosa ³ , J. Badiola ² , P. Zaragoza ¹ , J. Torres ³ , and I. Martín-Burriel* ^{1,2} , ¹ <i>Laboratorio de Genética Bioquímica, IIS Aragón, IA2, Universidad de Zaragoza, Zaragoza, Spain;</i> ² <i>Centro de Investigación en Encefalopatías y Enfermedades Transmisibles Emergentes, IIS Aragón, IA2, Universidad de Zaragoza, Zaragoza, Spain;</i> ³ <i>Centro de Investigación en Sanidad Animal, CISA-INIA, Valdeolmos, Madrid, Spain.</i> |
| 15:35 | 111 | Evaluating the role of epigenomic modifications in host-pathogen interaction for bovine alveolar macrophages infected with <i>Mycobacterium bovis</i>.
A. O'Doherty* ¹ , K. Rue-Albrecht ² , J. Browne ¹ , T. Hall ¹ , N. Nalpas ³ , D. Magee ¹ , S. Gordon ^{1,4} , D. Vernimmen ⁵ , and D. MacHugh ^{1,6} , ¹ <i>Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland;</i> ² <i>NDM Research Building, University of Oxford, Oxford, UK;</i> ³ <i>Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany;</i> ⁴ <i>UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland;</i> ⁵ <i>The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK;</i> ⁶ <i>UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.</i> |
| Coffee/Tea break | | |
| Atrium, O'Brien Science Building | | |
| 15:55 – 16:30 | | |
| 16:30 | 112 | Maternal nutrition during the first 50 days of gestation alters expression of histone and histone modifying genes in bovine fetal liver.
M. S. Crouse* ¹ , J. S. Caton ¹ , R. A. Cushman ³ , K. J. McLean ² , C. R. Dahlen ¹ , P. P. Borowicz ¹ , L. P. Reynolds ¹ , and A. K. Ward ¹ , ¹ <i>Department of Animal Sciences, North Dakota State University, Fargo, ND, USA;</i> ² <i>Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, USA;</i> ³ <i>USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA.</i> |
| 16:50 | 113 | Transgenerational phenotypic and epigenetic inheritance across three generations in layers induced by Poly(I:C).
L. Liu* , D. Wang, Z. Y. Duan, S. Yang, G. Y. Xu, N. Yang, and Y. Yu, <i>China Agricultural University, Beijing, China.</i> |
| 17:10 | 114 | Update on DNA methylation datasets of FAANG reference samples for the chicken and pig.
N. Trakooljul* ¹ , H. Zhou ² , P. Ross ² , I. Korf ³ , M. E. Delany ² , H. H. Cheng ⁴ , C. Ernst ⁵ , C. Kern ² , F. Hadlich ¹ , S. Ponsuksili ¹ , and K. Wimmers ¹ , ¹ <i>Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;</i> ² <i>Department of Animal Science, University of California, Davis, CA, USA;</i> ³ <i>Genome Center, University of California, Davis, CA, USA;</i> ⁴ <i>USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA;</i> ⁵ <i>Department of Animal Science, Michigan State University, East Lansing, MI, USA.</i> |
| 17:30 | 115 | Genome-wide identification of imprinted genes and its methylation statuses in various tissues of Hanwoo.
K.-T. Lee* , K.-S. Lim, B.-H. Choi, H.-H. Chai, J.-E. Park, E.-W. Park, G.-W. Jang, and D. Lim, <i>National Institute of Animal Science, RDA, Wanju, Jeonbuk, South Korea.</i> |
| 17:50 | | Meeting ends. |

Cattle Molecular Markers and Parentage Testing

Chair: **Romy Morrin-O'Donnell, Weatherbys Ireland Ltd.**
Intel Theatre, O'Brien Science Building

14:30	Welcoming Remarks.
14:35	Cattle STR/SNP Comparison Test 2016-2017.
14:40	Presentation by Duty Lab.
14:55	Presentation of STR results.
15:10	Presentation of SNP results.
15:25	Evaluation of the results by the chair.
15:40	Next Comparison Test (2018-2019).

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

16:30	116	Next-generation targeted sequencing panel for verification of bovine parentage. A. Burrell* ¹ , P. Siddavatam ¹ , A. Allred ¹ , C. Willis ¹ , R. Ferretti ² , and A. Raeber ¹ , ¹ <i>Thermo Fisher Scientific</i> ; ² <i>Neogen GeneSeek Operations</i> .
16:50	117	SNP data quality control in a national beef and dairy cattle system and highly accurate SNP-based parentage verification and identification. M. McClure* ¹ , J. McCarthy ¹ , R. Weld ² , P. Flynn ² , M. Kean ¹ , K. O'Connell ¹ , and J. Kearney ¹ , ¹ <i>Irish Cattle Breeding Federation, Bandon, Cork, Ireland</i> ; ² <i>Weatherbys Ireland, Johnstown, Kildare, Ireland</i> .
17:10	118	High cross-platform genotyping concordance of Axiom high-density microarrays and Eureka low-density targeted NGS assays. M. A. Patil* and A. Pirani, <i>Thermo Fisher Scientific, Santa Clara, CA, USA</i> .
17:30		Election of Committee.
17:40		Any Other Business.
18:00		Meeting ends.

Companion Animal Genetics and Genomics

Chair: **Leslie Lyons, University of Missouri, and Tomas Bergstrom, Swedish University of Agricultural Sciences**
Lynch Theatre, O'Brien Science Building

- 14:30 119 **Genetic variants in *ATP1B2* and *KCNJ10* in Belgian Shepherd dogs with ataxia.**
 N. Mauri¹, M. Kleiter², M. Leschnik², S. Högler³, E. Dietschi¹, C. Monney⁴, A. Oevermann⁴, D. Henke⁵, M. Wiedmer¹, J. Dietrich¹, F. Steffen⁶, S. Schuller⁷, C. Gurtner⁸, N. Stokar-Regenscheit⁸, D. O'Toole⁹, T. Bilzer¹⁰, C. Herden¹¹, V. Jagannathan¹, and **T. Leeb***¹, ¹*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland*; ²*University Clinic for Small Animals, Department for Companion Animals and Horses, University of Veterinary Medicine Vienna, Vienna, Austria*; ³*Institute of Pathology and Forensic Veterinary Medicine, Department of Pathobiology, University of Veterinary Medicine Vienna, Vienna, Austria*; ⁴*Division of Neurological Sciences, Department of Clinical Research and Veterinary Public Health, Vetsuisse Faculty, University of Bern, Bern, Switzerland*; ⁵*Division of Clinical Neurology, Department of Clinical Veterinary Medicine, Vetsuisse Faculty University of Bern, Bern, Switzerland*; ⁶*Section of Neurology, Department of Small Animals, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland*; ⁷*Division of Small Animal Internal Medicine, Department of Clinical Veterinary Medicine, Vetsuisse Faculty University of Bern, Bern, Switzerland*; ⁸*Institute of Animal Pathology, Department of Infectious Diseases and Pathobiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland*; ⁹*Wyoming State Veterinary Laboratory, University of Wyoming, Laramie, WY, USA*; ¹⁰*Institute of Neuropathology, University Hospital Düsseldorf, Düsseldorf, Germany*; ¹¹*Institute of Veterinary Pathology, Justus-Liebig-Universität, Gießen, Germany.*
- 14:45 120 **Phylogenetic analysis of Angora, Van, and stray cats of Anatolia.**
N. Bilgen*, B. C. Kul, M. Akkurt, O. Cildir, O. Ozmen, and O. Ertugrul, *Ankara University Faculty of Veterinary Medicine Department of Genetics, Ankara, Turkey.*
- 15:00 121 **Canine brachycephaly is associated with a retrotransposon-induced missplicing of *SMOC2*.**
 T. Marchant¹, E. Johnson¹, R. Harrington¹, L. McTier¹, C. Johnson¹, A. Gow¹, T. Liuti¹, D. Kuehn², K. Svenson³, M. Bermingham⁴, M. Drögemüller⁵, M. Nussbaumer⁶, M. Davey¹, D. Argyle¹, R. Powell⁷, S. Guilherme⁸, J. Lang⁹, G. Ter Haar¹, T. Leeb⁵, T. Schwarz¹, R. Mellanby¹, D. Clements¹, and **J. Schoenebeck***¹, ¹*Royal (Dick) School of Veterinary Studies and Roslin Institute, The University of Edinburgh, Midlothian, UK*; ²*Friendship Hospital for Animals, Washington, DC, USA*; ³*The Jackson Laboratory Bar Harbor, Bar Harbor, ME, USA*; ⁴*Institute of Genetics and Molecular Medicine, The University of Edinburgh, Edinburgh, UK*; ⁵*Institute of Genetics, University of Bern, Bern, Switzerland*; ⁶*Naturhistorisches Museum, Bern, Switzerland*; ⁷*Powell Torrance Diagnostic Services, Hertfordshire, UK*; ⁸*Davies Veterinary Specialists, Hertfordshire, UK*; ⁹*Department of Clinical Veterinary Medicine, University of Bern, Bern, Switzerland*; ¹⁰*Department of Clinical Sciences and Services, The Royal Veterinary College, Hertfordshire, UK.*
- 15:15 122 **Revealing the genetic basis of diabetes mellitus in Burmese cats.**
 G. Samaha¹, J. Beatty¹, L. Lyons², C. Wade³, and **B. Haase***¹, ¹*School of Veterinary Science, Faculty of Science, University of Sydney, Sydney, NSW, Australia*; ²*College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*; ³*School of Life and Environmental Sciences, Faculty of Science, University of Sydney, Sydney, NSW, Australia.*
- 15:30 123 **Localizing the regions of causative mutations in feline amyloidosis: a next-generation genomic approach.**
F. Genova*¹, B. Gandolfi², A. Thomas³, E. Creighton², L. Lyons², and M. Longeri¹, ¹*Department of Veterinary Medicine, Università degli Studi di Milano, Milan, Italy*; ²*Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA*; ³*Antagene, La tour de Salvagny, France.*
- 15:45 124 **Insights into 115 domestic cat and 17 wild felid genomes.**
L. Lyons*, *University of Missouri, Columbia, MO, USA.*

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 125 **Invited Workshop Speaker: Early events of cat domestication uncovered through ancient mitochondrial DNA analysis.**
E.-M. Geigl*, *Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France.*

- 17:00 126 **Characterization of Plakophilin-2 expression in canine skin and identification of differential gene expression in non-lesional skin from dogs affected by atopic dermatitis.**
G. Andersson*¹, K. Tengvall^{2,3}, B. Ardesjö-Lundgren^{1,2}, S. Kozyrev², M. Kierczak², M. Olsson^{2,3}, F. F. Farias², Å. Hedhammar⁴, K. Bergvall⁴, and K. Lindblad-Toh^{2,5}, ¹Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ²Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, BMC, Uppsala University, Uppsala, Sweden; ³Center for Molecular Medicine, Department of Medicine, Karolinska University Hospital, Karolinska Institutet, Stockholm, Sweden; ⁴Department of Clinical Sciences, Swedish University of Agricultural Sciences, Sweden; ⁵Broad Institute of MIT and Harvard, Cambridge, MA, USA.
- 17:15 127 **An analysis of canine caudal fossa morphology and its genetics.**
R. Harrington*, T. Marchant, D. Argyle, D. Clements, T. Liuti, T. Schwarz, K. Marioni-Henry, and J. Schoenebeck, *Royal (Dick) School of Veterinary Studies and Roslin Institute, The University of Edinburgh, Easter Bush, Midlothian, UK.*
- 17:30 128 **Detection and characterisation of a genetic association with Norwich terrier upper airway syndrome.**
T. Marchant*¹, E. Dietschi², R. Harrington¹, M. Drögemüller², U. Rytz³, T. Leeb², and J. Schoenebeck¹, ¹The Royal (Dick) School for Veterinary Studies and Roslin Institute, The University of Edinburgh, Edinburgh, Midlothian, UK; ²The Institute of Genetics, Vetsuisse Faculty, The University of Bern, Bern, Switzerland; ³Department of Clinical Veterinary Medicine, Division of Small Animal Surgery, Vetsuisse Faculty, The University of Bern, Bern, Switzerland.
- 17:45 129 **Canine diversity and disease: Genome analysis in Australian dogs.**
 S.-A. Mortlock, J. Marin-Cely, R. Booth, P. Soh, M.-S. Khatkar, and **P. Williamson***, *The University of Sydney, Sydney, NSW, Australia.*
- 18:00 **Concluding remarks and Business Meeting with election of committee members.**
- 18:00 **Meeting ends.**

Microbiomes

Chair: **Claire Rogel-Gaillard, GABI, INRA, AgroParisTech, Université Paris-Saclay
 Icon Theatre, O'Brien Science Building**

- 14:30 **Introduction.**
- 14:35 130 **Advanced bioinformatics and molecular analysis of whole-genome-shotgun metagenomics data from rumen microbiomes reveals remarkable diversity, structure and function.**
M. Watson*¹, R. Stewart¹, A. Warr¹, T. Snelling³, M. Auffret², A. Walker³, R. Wallace³, and R. Roehe², ¹The Roslin Institute, University of Edinburgh, Easter Bush, Scotland; ²SRUC, Easter Bush, Scotland; ³The Rowett Institute, University of Aberdeen, Aberdeen, Scotland.
- 14:55 131 **Bovine genes regulate the rumen microbial composition.**
O. Gonzalez-Recio*¹, I. Zubiria², A. García-Rodríguez², A. Hurtado³, and R. Atxaerandio², ¹Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain; ²Departamento de Producción Animal. NEIKER-Tecnalia, Granja Modelo de Arkaute, Vitoria-Gasteiz, Alava, Spain; ³Departamento de Salud Animal. NEIKER-Tecnalia, Derio, Bilbao, Spain.
- 15:15 132 **16SrRNA amplicon sequencing of mock microbial populations to investigate DNA extraction methodology, primer selection and PCR cycles.**
E. McGovern*^{1,2}, M. S. McCabe¹, A. K. Kelly², D. A. Kenny¹, P. Cormican¹, and S. M. Waters¹, ¹Teagasc, Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Grange, Dunsany, County Meath, Ireland; ²University College Dublin, School of Agriculture and Food Science, Belfield, Dublin, Ireland.
- 15:35 134 **Host genetics influences gut microbiota composition in pigs.**
J. Estellé*^{1,2}, N. Mach^{1,2}, Y. Ramayo-Caldas¹, F. Levenez², G. Lemonnier¹, C. Denis¹, M. Berris³, M.-J. Mercat⁴, Y. Billon⁵, J. Doré², C. Larzul^{1,6}, P. Lepage², and C. Rogel-Gaillard¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ²MICALIS, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ³ISP, INRA, Université de Tours, Nouzilly, France; ⁴IFIP-BIOPORC, Pôle génétique, Le Rheu, France; ⁵GENESI, INRA, Surgères, France; ⁶GenPhySe, INRA, INP, ENSAT, Université de Toulouse, Castanet-Tolosan, France.

Coffee/Tea break		Atrium, O'Brien Science Building	16:00 – 16:30
16:30	135	<p>The MetaPig project: Leveraging potentials in pig genomics and metagenomics to boost feed efficiency and gut health in modern pig production.</p> <p>P. Karlskov-Mortensen*¹, A. Ø. Pedersen¹, N. Canibe², P. Kiilerich³, K. Kristiansen³, and M. Fredholm¹, ¹<i>Department of Veterinary and Animal Science, Faculty of Health & Medical Sciences, University of Copenhagen, Frederiksberg, Denmark;</i> ²<i>Department of Animal Science, Aarhus University, Tjele, Denmark;</i> ³<i>Department of Biology, Faculty of Science, University of Copenhagen, Copenhagen, Denmark.</i></p>	
16:50	136	<p>Characterization of the gut microbiome along the digestive tract of Iberian pigs.</p> <p>D. Crespo-Piazuelo*^{1,2}, J. Estellé³, M. Revilla^{1,2}, L. Criado-Mesas^{1,2}, Y. Ramayo-Caldas³, C. Óvilo⁴, A. I. Fernández⁴, M. Ballester⁵, and J. M. Folch^{1,2}, ¹<i>Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Barcelona, Spain;</i> ²<i>Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain;</i> ³<i>Génétique Animale et Biologie Intégrative (GABI), Institut National de la Recherche Agronomique (INRA), AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;</i> ⁴<i>Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain;</i> ⁵<i>Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Caldes de Montbui, Barcelona, Spain.</i></p>	
17:10	137	<p>A metagenomics study on a non-metagenomics experiment: Mining next-generation sequencing datasets from porcine DNA identified unexpected viral sequences.</p> <p>S. Bovo^{1,2}, G. Mazzoni^{1,3}, A. Ribani¹, V. J. Utzeri¹, F. Bertolini^{1,4}, G. Schiavo¹, and L. Fontanesi*¹, ¹<i>Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy;</i> ²<i>Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy;</i> ³<i>Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, Copenhagen, Denmark;</i> ⁴<i>Department of Animal Science, Iowa State University, Ames, IA, USA.</i></p>	
17:30		Discussion.	
18:00		Meeting ends.	

Pig Genetics and Genomics

Chairs: Romi Pena I Subirà, University of Lleida, and Kyle Schachtschneider, University of Illinois at Chicago
George Moore Auditorium, O'Brien Science Building

14:30	138	<p>Expression of identical genetic mutations across Oncopig cell types results in distinct expression profiles recapitulating transcriptional hallmarks of human tumors.</p> <p>K. M. Schachtschneider*¹, R. M. Schwind¹, K. A. Darfour-Oduro², Y. Liu^{2,3}, S. Mäkeläinen^{4,5}, A. K. De², L. A. Rund², O. Madsen⁴, M. A. M. Groenen⁴, R. C. Gaba¹, and L. B. Schook^{1,2}, ¹<i>Department of Radiology, University of Illinois at Chicago, Chicago, IL, USA;</i> ²<i>Department of Animal Sciences, University of Illinois, Champaign-Urbana, IL, USA;</i> ³<i>Department of Animal Genetics and Breeding, Sichuan Agricultural University, Chengdu, China;</i> ⁴<i>Wageningen University & Research, Animal Breeding and Genomics, Wageningen, The Netherlands;</i> ⁵<i>Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.</i></p>	
14:45	139	<p>Genome-scale sgRNA library construction and use for CRISPR/Cas9-based genetic screens in the pig.</p> <p>C. Zhao*¹, G. Yang¹, X. Han¹, Y. Gao¹, X. Li^{1,2}, S. Xie^{1,2}, and S. Zhao^{1,2}, ¹<i>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, China;</i> ²<i>The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China.</i></p>	
15:00	140	<p>Dietary vitamin A differentially affects fat desaturation in porcine stearoyl-CoA desaturase genotypes.</p> <p>J. Estany*¹, S. Gol¹, M. Tor¹, L. Bosch², J. Reixach³, and R. Pena¹, ¹<i>Department of Animal Science, University of Lleida Agrotecnio Center, Lleida, Spain;</i> ²<i>Department of Agriculture Engineering and Food Technology, University of Girona, Girona, Spain;</i> ³<i>Selección Batallé, S.A, Riudarenes, Spain.</i></p>	

- 15:15 141 **Effects of diet supplementation with oleic acid or carbohydrates on *Biceps femoris* transcriptome in growing Iberian pigs.**
R. Benítez^{*1}, B. Isabel², A. Fernández¹, Y. Núñez¹, E. De Mercado³, E. Gómez Izquierdo³, J. García-Casco¹, C. López-Bote², and C. Óvilo¹, ¹INIA, Madrid, Madrid, Spain; ²UCM, Madrid, Madrid, Spain; ³Centro Pruebas Procino Itacyl, Hontalbilla, Segovia, Spain.
- 15:30 142 **Porcine bloodomics: Identification of porcine neutrophil-specific genes through gene expression correlations to neutrophil abundance and comparative expression data.**
 G. Vella^{1,2}, M. Schroyen², H. Beiki², C. L. Loving³, and **C. K. Tuggle**^{*2}, ¹College of Veterinary Medicine, Iowa State University, Ames, IA, USA; ²Department of Animal Science, Iowa State University, Ames, IA, USA; ³Food Safety and Enteric Pathogens Research Unit, USDA-ARS-NADC, Ames, IA, USA.
- 15:45 143 **Is there genetic variation in both resistance and tolerance of pigs to porcine reproductive and respiratory syndrome virus?**
 G. Lough¹, A. Hess⁴, H. Rashidi², H. Mulder², J. Dekkers⁴, I. Kyriazakis³, M. Hess⁴, N. Deeb⁵, A. Kause⁶, B. Rowland⁷, J. Lunney⁸, and **A. Doeschl-Wilson**^{*1}, ¹The Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK; ²Animal Breeding and Genomics, Wageningen University and Research, Wageningen, the Netherlands; ³School of Agriculture Food and Rural Development, Newcastle University, Newcastle upon Tyne, UK; ⁴Iowa State University, Ames, IA, USA; ⁵Genus plc, Hendersonville, TN, USA; ⁶Natural Resources Institute Finland, Jokioinen, Finland; ⁷Kansas State University, Manhattan, KS, USA; ⁸USDA, Beltsville, MD, USA.

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 144 **Integrative and differential analysis of transcriptomes and chromatin accessibility regions reveals regulatory mechanisms involved in pig immune and metabolic functions [FAANG pilot project "FR-AgENCODE"].**
 S. Djebali¹, K. Munyard², N. Villa-Vialaneix³, C. Cabau¹, A. Rau⁴, E. Crisci⁴, T. Derrien⁵, C. Klopp³, M. Zytnicki³, S. Lagarrigue^{6,7}, H. Acloque¹, **S. Foissac**^{*1}, and E. Giuffra⁴, ¹GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Castanet-Tolosan, France; ²Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia; ³MIAT, Université de Toulouse, INRA, Castanet-Tolosan, France; ⁴GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France; ⁵UMR6290 IGDR, CNRS, Université Rennes 1, Rennes, France; ⁶UMR PEGASE, INRA, Rennes, France; ⁷UMR PEGASE, Agrocampus Ouest, Rennes, France.
- 16:45 145 **Genome-wide scanning of the *cis*-effects of sequence variations on enhancer activity in the F6 swine heterogeneous stock.**
Z. Zhang^{*}, Y. Zhu, Z. Zhou, W. Li, and L. Huang, State Key Laboratory of Pig Genetic Improvement and Production Technology, Jiangxi Agricultural University, NanChang, JiangXi Province, China.
- 17:00 146 **The effect of histone acetyl-transferase inhibitor (trichostatin A) administration on porcine mesenchymal stem cells transcriptome.**
A. Gurgul^{*}, J. Opiela, K. Pawlina, T. Szmatoła, and M. Bugno-Poniewierska, National Research Institute of Animal Production, Balice, Poland.
- 17:15 147 **Characterization of 3D genomic interactions in fetal pig muscle.**
M. Marti-Marimon^{*1}, H. Acloque¹, M. Zytnicki², D. Robelin¹, S. Djebali¹, N. Villa-Vialaneix², O. Madsen³, Y. Lahbib-Mansais¹, D. Esquerré¹, F. Mompert¹, L. Liaubet¹, M. Groenen³, M. Yerle-Bouissou¹, and S. Foissac¹, ¹GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France; ²MIAT, University of Toulouse, INRA, Castanet Tolosan, France; ³Animal Breeding and Genomics Centre (ABG), Wageningen University, Wageningen, the Netherlands.
- 17:30 148 **Exploiting long read sequencing technologies to establish high quality highly contiguous pig reference genome assemblies.**
 A. Warr¹, R. Hall², K. Kim², E. Tseng², S. Koren³, A. Phillippy³, D. Birkhart⁴, B. Rosen⁴, S. Schroeder⁴, D. Hume¹, R. Talbot⁵, L. Rund⁶, L. Schook⁶, W. Chow⁷, K. Howe⁷, D. J. Nonneman⁸, G. A. Rohrer⁸, N. Putnam⁹, R. E. Green⁹, R. O'Connor¹⁰, D. Griffin¹⁰, B. M. Skinner¹¹, C. A. Sargent¹¹, N. A. Affara¹¹, C. Tyler-Smith⁷, M. Watson¹, T. P. L. Smith⁸, and **A. Archibald**^{*1}, ¹The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK; ²Pacific Biosciences, Menlo Park, CA, USA; ³National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA; ⁴Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA; ⁵Edinburgh Genomics, University of Edinburgh, Edinburgh, UK; ⁶University of Illinois, Urbana, IL, USA; ⁷The Wellcome Trust Sanger Institute, Hinxton UK; ⁸USDA, ARS, USMARC, Clay Center, NE, USA; ⁹Dovetail Genomics LLC, Santa Cruz, CA, USA; ¹⁰University of Kent, Canterbury, Kent, UK; ¹¹University of Cambridge, Cambridge, UK.

Tuesday



17:45 149 **Updated pig genome resources in Ensembl.**
T. Hourlier*¹, L. Eory², K. Billis¹, C. García Girón¹, L. Haggerty¹, O. Izuogu¹, D. N. Murphy¹, R. Nag¹, F. J. Martin¹, A. L. Archibald², B. Aken¹, and P. Flicek¹, ¹*European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, UK*; ²*The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Edinburgh, UK.*

18:00 **Meeting ends.**

Irish Evening at Taylors Three Rock

Meet at registration desk

18:00 – 22:00

Wednesday, July 19

Registration Desk Open	Atrium, O'Brien Science Building	07:45 – 13:00
Poster Setup	Atrium, O'Brien Science Building	08:00 – 09:00
Exhibition Open	Atrium, O'Brien Science Building	08:00 – 13:00
Posters Open	Atrium, O'Brien Science Building	09:00 – 13:00
Pac Bio Vendor Seminar	George Moore Auditorium, O'Brien Science Building	08:00 – 08:45

Pac Bio Vendor Seminar: SMRT Sequencing for Complete Genomes

Long-read SMRT sequencing delivers the most comprehensive views of animal genomes and transcriptomes

Emily Hatas, PacBio

A high-quality genome assembly for water buffalo

John Williams, The University of Adelaide

ORAL SESSIONS

Plenary Session II

Chairs: **Elisabetta Giuffra, INRA, and Christopher Tuggle, Iowa State University**
O'Reilly Hall

09:00	The role of enhancers in mammalian disease and development: Stories from more than thirty mouse knockouts. <i>Diane E. Dickel, Lawrence Berkeley National Laboratory (LBNL).</i>
10:00	How animal genomic research contributes to basic biology. <i>Leif Andersson, Uppsala University and Texas A&M University; guest professor at the Swedish University of Agricultural Sciences.</i>

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30
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11:30	Filling the gap until the FAANG data comes in: Comparative annotation of sheep reveals selection has acted on the proximal regulatory machinery. <i>James Kijas, CSIRO, and Laura Clarke, EMBL-EBI.</i>
13:00	Meeting ends.

TOURS

Meet at registration desk	(Preregistration for all tours is mandatory)	13:00 – 18:00
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Tour 1: The Irish Equine Centre/Weatherbys and the Irish National Stud

Tour 2: Irish Beef Data and Genomics Programme

Tour 3: Book of Kells and St. Patrick's Cathedral

Tour 4: Powerscourt House and Gardens

Thursday, July 20

Registration Desk Open	Atrium, O'Brien Science Building	08:00 – 18:00
Exhibition and Posters Open	Atrium, O'Brien Science Building	08:00 – 18:00

ORAL SESSIONS

Plenary Session III

Chairs: **Ernest Bailey, University of Kentucky,**
and David MacHugh, University College Dublin
O'Reilly Hall

09:00	Will animal genetics innovations be embraced or eschewed? The #Scicomm challenge facing agricultural biotechnology. Alison Van Eenennaam, <i>University of California, Davis.</i>
10:00	Molecular regulation of pregnancy establishment in cattle. Pat Lonergan, <i>University College Dublin (UCD).</i>

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30
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11:30	Is it time to change the paradigm? Mammals are not just genes interacting with their environment. Julian Marchesi, <i>Imperial College London.</i>
12:30	150 Novel, Groundbreaking Research/Methodology Presentation: Sheep parchment as a genetic resource. M. Teasdale* , <i>Trinity College Dublin, Dublin, Ireland.</i>

Lunch	Atrium, O'Brien Science Building	13:00 – 14:00
Neogen Vendor Presentation	George Moore Auditorium, O'Brien Science Building	13:30 – 14:15

Neogen Vendor Presentation: Traditional chicken breeds in the Netherlands
 Dr. Richard Crooijmans

Applied Genetics of Companion Animals

Chair: **Sofia Mikko, Swedish University of Agricultural Sciences**
Lynch Theatre, O'Brien Science Building

14:30	Welcoming Remarks.
14:35	Dog CT Duty Lab Report.
14:50	Dog CT Analysis Lab Report.
15:05	Discussion.

- 15:30 151 **AgriSeq targeted sequencing panel for determination of canine parentage and genetic health.**
M. Karberg^{*1}, A. Burrell¹, P. Siddavatam¹, A. Allred¹, M. de Groot², and W. van Haeringen², ¹*Thermo Fisher Scientific, Austin, TX, USA;* ²*VHL Genetics, Wageningen, the Netherlands.*
****Being presented by Christopher Adams**
- 15:45 152 **Pedigree and genomic-based relationships in a dog population.**
A. Talenti^{*1}, D. L. Dreger², F. Danelli¹, S. Frattini¹, B. Coizet¹, S. P. Marelli¹, G. Pagnacco¹, G. Gandini¹, M. Polli¹, R. Caniglia³, M. Galaverni³, E. A. Ostrander², and P. Crepaldi¹, ¹*Department of Veterinary Medicine, University of Milan, Milan, Italy;* ²*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA;* ³*Laboratorio di Genetica, Istituto Superiore per la Protezione e la Ricerca Ambientale, Ozzano dell'Emilia, Italy.*

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 **Cat CT Duty Lab Report.**
- 16:45 **Cat CT Analysis Lab Report.**
- 17:00 **Discussion.**
- 17:15 **General Discussion on SNP Panels for Domestic Cat and Dog Parentage.**
- 17:30 **Workshop Business Meeting and Elections.**
- 18:00 **Meeting ends.**

Applied Sheep and Goat Genetics

Chair: **Gesine Luehken, University of Giessen**
George Moore Auditorium, O'Brien Science Building

- 14:30 153 **Introgression of wool-shedding genes into the Romane breed sheep.**
L. Drouilhet^{*1}, B. Pena¹, C. Huau¹, D. Marcon², Y. Bourdillon², and D. Allain¹, ¹*GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France;* ²*INRA UE0322, La Sapinière, Bourges, France.*
- 14:45 154 **Community-based sheep breeding programs in Ethiopia resulted in substantial genetic gains.**
A. Haile^{*1}, T. Mirkena³, G. Duguma², S. Gizaw², M. Wurzinger⁴, J. Solkner⁴, O. Mwai², T. Dessie², A. Abebe⁶, M. Mamiru⁸, T. Tadesse⁷, R. N. B. Lobo⁵, and B. Rischkowsky¹, ¹*International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia;* ²*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, and Nairobi, Kenya;* ³*FAO, Addis Ababa, Ethiopia;* ⁴*BOKU University, Vienna, Austria;* ⁵*EMBRAPA-goat and sheep, Sobral, Brazil;* ⁶*Debre Berhan Agricultural Research Center, Debre Berhan, Ethiopia;* ⁷*Bako Agricultural Research Center, Bako, Ethiopia;* ⁸*Bonga Agricultural Research Center, Bonga, Ethiopia.*
- 15:00 155 **Identification of two major genes affecting prolificacy in the French Noire du Velay sheep.**
L. Chantepie^{*}, L. Bodin, F. Woloszyn, J. Sarry, and S. Fabre, *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France.*
- 15:15 156 **Genomic regions associated with entropion in Columbia, Polypay, and Rambouillet breeds of sheep.**
M. R. Mouse^{*1,2} and S. N. White^{1,3}, ¹*Animal Disease Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Pullman, WA, USA;* ²*Paul G. Allen School of Global Animal Health, Washington State University, Pullman, WA, USA;* ³*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.*
- 15:30 157 **Genome-wide scan reveals *NF1* locus is associated with fat tail phenotype rather than high-altitude adaptation in Asian sheep.**
K. Dong^{1,2}, M. Yang¹, N. Gorkhali¹, Y. Ma¹, and **L. Jiang^{*1}**, ¹*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China;* ²*USDA, Agricultural Research Service, Avian Disease and Oncology Laboratory, East Lansing, MI, USA.*

- 15:45 158 **Investigating genetic associations with meiotic recombination in rams.**
K. M. Davenport*, A. M. Rodriguez, R. J. Sawyer, T. M. Badigian, H. K. Jaeger, M. A. Follett, and B. M. Murdoch, *University of Idaho, Moscow, ID, USA.*
- 16:00 **Decisions on sheep and goat comparison tests for 2018-19.**
- 16:05 **Meeting ends.**

Coffee/Tea break

Atrium, O'Brien Science Building

16:05 – 16:30

Comparative and Functional Genomics

Chair: **Fiona McCarthy, The University of Arizona**
Elan Theatre, O'Brien Science Building

- 14:30 **Welcoming Remarks.**
- 14:30 159 **Identification of regulatory elements in livestock species.**
H. Zhou*¹, P. Ross¹, C. Kern¹, P. Saelao¹, Y. Wang¹, M. Halstead¹, K. Chanthavixay¹, I. Korf¹, M. Delany¹, H. Cheng², J. Medrano¹, A. Van Eenennaam¹, C. Tuggle³, and C. Ernst⁴, ¹*University of California, Davis, Davis, CA, USA;* ²*USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA;* ³*Iowa State University, Ames, IA, USA;* ⁴*Michigan State University, East Lansing, MI, USA.*
- 15:00 160 **Transcription factor binding sites enrichment in ruminant and cetartiodactyl specific conserved non-coding elements.**
L. Buggiotti*, M. Farrè, and D. Larkin, *Royal Veterinary College, London, UK.*
- 15:15 161 **Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhancers.**
A. Massa*¹, M. Mouse^{2,1}, B. Murdoch³, and S. White^{2,1}, ¹*Washington State University, Pullman, WA, USA;* ²*United States Department of Agriculture-ADRU, Pullman, WA, USA;* ³*University of Idaho, Moscow, ID, USA.*
- 15:30 163 **The reconstruction and evolutionary history of eutherian chromosomes.**
 J. Kim¹, M. Farre², L. Auvil³, B. Capitanu³, J. Ma⁴, H. A. Lewin⁵, and **D. M. Larkin***¹, ¹*Department of Biomedical Science and Engineering, Konkuk University, Seoul, Korea;* ²*Royal Veterinary College, University of London, London, UK;* ³*Illinois Informatics Institute, University of Illinois at Urbana-Champaign, Urbana, IL, USA;* ⁴*Computational Biology Department, School of Computer Science, Carnegie Mellon University, Pittsburgh, PA, USA;* ⁵*Department of Evolution and Ecology, University of California, Davis, CA, USA.*
- 15:45 164 **iTRAQ-based proteomic analysis reveals key proteins affecting muscle growth and lipid deposition in pig.**
Z. Wang*^{1,2}, P. Shang^{1,2}, Q. Li³, L. Wang¹, H. Zhang¹, and C. Wu¹, ¹*China Agricultural University, Beijing, China;* ²*Tibet Agriculture and Animal Husbandry University, Linzhi, China;* ³*Anhui Academy of Agricultural Sciences, Hefei, China.*

Coffee/Tea break

Atrium, O'Brien Science Building

16:00 – 16:30

- 16:30 165 **Hypothalamus transcriptome during the early rise in LH secretion related to puberty age in bull calves.**
 J. Liron¹, **M. Fernández***², A. Prando³, A. Baldo³, and G. Giovambattista², ¹*Center of Veterinary Research (CIVETAN, CONICET), Faculty of Veterinary Sciences, UNCPBA, Tandil, Buenos Aires, Argentina.;* ²*Institute of Veterinary Genetics (IGEVET, CONICET), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina;* ³*Cátedra de Zootecnia Especial (II Parte), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina.*

- 16:45 166 **Integrative genomics of human and bovine tuberculosis.**
 K. E. Killick^{*1,2}, M. P. Mullen³, T. Hall¹, N. C. Nalpas⁴, I. W. Richardson⁵, D. A. Magee¹, C. N. Correia¹, J. A. Browne¹, D. P. Berry⁶, D. Bradley⁷, V. Naranbhai⁸, A. Hill⁹, E. Gormley⁹, S. V. Gordon^{2,9}, D. E. MacHugh^{1,2}, ¹University College Dublin, UCD College of Health and Agricultural Sciences, University College Dublin, Dublin, Ireland; ²University College Dublin, UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland; ³Athlone Institute of Technology, Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland; ⁴University of Tübingen, Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany; ⁵IdentiGEN Ltd, IdentiGEN Ltd., Blackrock Business Park, Blackrock, Dublin, Ireland; ⁶Teagasc, Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland; ⁷Trinity College, Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin, Ireland; ⁸University of Oxford, Wellcome Trust Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, Oxford, UK; ⁹University College Dublin, UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland.
- 17:00 167 **Circulating microRNAs as potential novel biomarkers to diagnose *Mycobacterium avium* ssp. *paratuberculosis* infection in cattle.**
 K. Zhao¹, S. Hendrick², and L. Guan^{*1}, ¹Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada; ²Coaldale Veterinary Clinic, Lethbridge, Canada.
- 17:15 168 **Generating customized integrated functional annotation datasets with BovineMine.**
 C. Elsik^{*}, D. Unni, A. Tayal, and D. Hagen, University of Missouri, Columbia, Missouri, USA.
- 17:30 169 **The Vertebrate Gene Nomenclature Committee (VGNC).**
 P. Denny^{*}, B. Yates, S. Tweedie, B. Braschi, K. Gray, R. Seal, and E. Bruford, European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Hinxton, Cambridgeshire, UK.
- 17:45 **Workshop Business Meeting.**
- 18:00 **Meeting ends.**

Genetics and Genomics of Aquaculture Species

Chair: **Ross Houston, The Roslin Institute, and Francesca Bertolini,**
Iowa State University
Intel Theatre, O'Brien Science Building

- 14:30 170 **Invited Workshop Speaker: Comparative genomics of disease resistance traits in salmonids.**
 J. M. Yáñez^{*}, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile.
- 15:00 171 **GWAS reveals the architecture of two maturation traits in Tasmanian Atlantic salmon.**
 J. Kijas^{*1}, A. Mohamed¹, S. McWilliam¹, B. Evans², H. King³, P. Kube³, and K. Verbyla⁴, ¹CSIRO, Brisbane, Queensland, Australia; ²SALTAS, Hobart, Tasmania, Australia; ³CSIRO, Hobart, Tasmania, Australia; ⁴Data61, Canberra, ACT, Australia.
- 15:15 172 **Optimum-contribution selection increases genetic gain in Atlantic salmon breeding schemes.**
 B. Hillestad^{*1} and M. Henryon², ¹SalmoBreed AS, Bergen, Norway; ²Seges, Copenhagen, Denmark.
- 15:30 173 **Exploiting linkage disequilibrium information in turbot selection programs.**
 M. Saura^{*1}, A. Fernández¹, J. Fernández¹, M. Toro², P. Martínez³, A. Millán⁴, M. Hermida³, A. Blanco³, S. Cabaleiro⁵, A. Doeschl-Wilson⁶, and B. Villanueva¹, ¹Departamento de Mejora Genética Animal, INIA, Madrid, Spain; ²Departamento de Producción Agraria, ETS Ingenieros Agrónomos, Madrid, Spain; ³Departamento de Xenética, Facultade de Veterinaria, Universidade de Santiago de Compostela, Lugo, Spain; ⁴Geneaqua SL, Lugo, Spain; ⁵CETGA, Cluster de Acuicultura de Galicia, Aguiño-Ribeira, Spain; ⁶Division of Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian, Scotland, UK.
- 174 **Withdrawn by authors**

- 16:30 175 **Transcriptomic profile of *Salmo salar* skin in response to the Chilean sea louse *Caligus rogercresseyi* using *de novo* transcriptome assembly.**
K. Neumann*¹, D. Cichero², and V. Martinez¹, ¹FAVET-INBIOGEN-Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile; ²Blue Genomic SPA, Puerto Varas, Chile.
- 16:45 176 **Mining the European Sea Bass (*Dicentrarchus labrax*) genome for the characterization of tandem repeat variability.**
F. Bertolini*^{1,2}, S. Bovo^{2,3}, M. F. Rothschild¹, and L. Fontanesi², ¹Department of Animal Science, Iowa State University, Ames, IA, USA; ²Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy; ³Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy.
- 17:00 177 **Reconstructing the complex structure of the sex determination locus in Atlantic herring using SMRT sequencing.**
N. Rafati*¹, C.-J. Rubin¹, C. Feng¹, M. Petterson¹, A. B. Martinez², S. Lamichhane¹, I. Bunikis³, and L. Andersson^{1,5}, ¹Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; ²Science for Life Laboratory, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden; ³Science for Life Laboratory, National Genomics Infrastructure, Uppsala University, Uppsala, Sweden; ⁴Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁵Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA.
- 17:15 178 **Rapid cold shock induces only slight shift in gene expression of rainbow trout (*Oncorhynchus mykiss*).**
T. Goldammer*¹, A. Borchel^{1,2}, M. Verleih¹, and A. Rebl¹, ¹Leibniz Institute for Farm Animal Biology, Inst. for Genome Biology, Dummerstorf, Germany; ²University of Bergen, SLCR-Sea Lice Research Centre, Bergen, Norway.
- 17:30 179 **Allele-specific expression analysis related with jaw deformities in Yellowtail kingfish (*Seriola lalandi*) larvae.**
P. Dettleff*¹, A. Patel, and V. Martinez, FAVET-INBIOGEN, Faculty of Veterinary Science, University of Chile, Santiago, Chile.
- 17:45 **Workshop Business Meeting.**
- 18:00 **Meeting ends.**

Livestock Genomics for Developing Countries

Chair: **Ntanganedzeni Mapholi, University of South Africa, South Africa**
Icon Theatre, O'Brien Science Building

- 14:30 180 **Development of genomic tools to select for economic traits in tropical adapted cattle breeds.**
F. F. Cardoso*^{1,2}, G. S. Campos², C. C. Gulas-Gomes¹, B. P. Sollero¹, and A. R. Caetano³, ¹Embrapa Pecuária Sul, Bagé, RS, Brazil; ²Universidade Federal de Pelotas, Pelotas, RS, Brazil; ³Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil.
- 14:55 181 **Genomic selection based on current status in developing countries.**
R. Mrode*¹, J. Ojango¹, O. Mwai¹, and J. M. Mwacharo², ¹Animal Biosciences, International Livestock Research Institute, Nairobi, Kenya; ²Small Ruminant Genetics and Genomics Group, International Centre for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia.
- 15:20 182 **Genetic admixture and identity by descent in Senegalese dairy cattle.**
P. J. N. Ema^{1,3}, A. Missohou¹, K. Marshal², S. F. Tebug², J. Juga⁴, and **M. Tapio***⁵, ¹Interstate School of Veterinary Science and Medicine of Dakar, Dakar, Senegal; ²International Livestock Research Institute, Nairobi, Kenya; ³University of Ngaoundere, Ngaoundere, Cameroon; ⁴University of Helsinki, Helsinki, Finland; ⁵Natural Resources Institute Finland, Jokioinen, Finland.
- 15:35 183 **Towards the unraveling of the genomic basis of milk production traits in African dairy zebu cattle.**
A. Tijjani*^{1,4}, J. Kim³, R. Mrode², B. Salim⁵, N. Oyekanmi⁴, H. Kim³, and O. Hanotte^{1,2}, ¹School of Life Sciences, University of Nottingham, Nottingham, UK; ²International Livestock Research Institute (ILRI), Nairobi, Kenya; ³C&K genomics, Seoul National University Research Park, Seoul, South Korea; ⁴National Biotechnology Development Agency, Lugbe, Abuja, Nigeria; ⁵Department of Parasitology, Faculty of Veterinary Medicine, University of Khartoum, Khartoum, Sudan.

- 15:50 184 **Matching breeds to production clusters using high-density SNP arrays: The case of East Africa.**
F. D. N. Mujibi*¹, E. K. Cheruiyot², T. Dusingizimana³, M. Chagunda⁴, J. Ojango⁵, and R. Mrode^{4,5}, ¹*Nelson Mandela Africa Institution for Science and Technology (NMAIST), Arusha, Tanzania;* ²*University of Nairobi, Nairobi, Kenya;* ³*University of Rwanda, Kigali, Rwanda;* ⁴*Scotland Rural University College, SRUC, Edinburgh, Scotland;* ⁵*International Livestock Research Institute, Nairobi, Kenya.*

Coffee/Tea break

Atrium, O'Brien Science Building

16:05 – 16:30

- 16:30 185 **Finding optimum levels of admixture in crossbred sheep populations in Ethiopia by use of ancestry informative genetic markers and phenotypes.**
T. Getachew^{1,2}, H. J. Huson³, M. Wurzinger¹, J. Burgstaller⁴, S. Gizaw⁵, A. Haile⁶, B. Rischkowsky⁶, G. Brem⁴, S. A. Boison¹, G. Mészáros¹, A. O. Mwai⁷, and **J. Sölkner***¹, ¹*University of Natural Resources and Life Sciences, Vienna, Austria;* ²*Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia;* ³*Cornell University, Ithaca, NY, USA;* ⁴*University of Veterinary Medicine, Vienna, Austria;* ⁵*International Livestock Research Institute, Addis Ababa, Ethiopia;* ⁶*International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia;* ⁷*International Livestock Research Institute, International Livestock Research Institute, Nairobi, Kenya.*
- 16:55 186 **Can genomics be used in the smallholder livestock sector? Case studies from South Africa.**
F. C. Muchadeyi*¹, *Agriculture Research Council, Biotechnology Platform, Pretoria, South Africa.*
- 17:15 187 **Withdrawn**
- 17:30 **Discussion and concluding remarks.**
- 18:00 **Meeting ends.**

Gala Dinner

O'Reilly Hall

19:00 – 00:00

Friday, July 21

Registration Desk Open	Atrium, O'Brien Science Building	08:00 – 11:30
Exhibition and Posters Open	Atrium, O'Brien Science Building	08:00 – 11:30

ORAL SESSIONS

Plenary Session IV

Chairs: **Clare Gill, Texas A&M University, and Sinead Waters, Teagasc O'Reilly Hall**

09:00	GBLUPs Me, GBLUPs Me Not: Marrying molecular biology and statistical genomics. Toni Reverter, <i>SIRO Agriculture and Food</i> .
10:00	Picking the bones out: Ancient animal genomics of the Fertile Crescent. Daniel G. Bradley, <i>Smurfit Institute of Genetics</i> .

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30
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ISAG Business Meeting and Awards	O'Reilly Hall	11:30 – 13:30
Clear Exhibition and Posters	Atrium, O'Brien Science Building	11:30 – 13:00
Registration Breakdown	Atrium, O'Brien Science Building	11:30 – 13:00
Debriefing Meeting of LOC, PCO, FASS, and Executive Committee	Boardroom H1.47, O'Brien Science Building	14:00 – 15:00

POSTER SESSION I: Monday/Tuesday
Atrium, O'Brien Science Building

Animal Epigenetics

- MT1 **DNA methylation profiles in red blood cells of adult hens correlate to their previous rearing conditions.**
F. Pértille*^{1,2}, M. Brantsæter⁴, J. Nordgreen⁴, L. Coutinho¹, A. Janczak⁴, P. Jensen², and C. Guerrero-Bosagna², ¹Linköping University, Linköping, Östergötland, Sweden; ²University of São Paulo, Piracicaba, São Paulo, Brazil; ³Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁴Faculty of Veterinary Medicine, Oslo, Norway.
- MT2 **DNA methylation of bactericidal/permeability-increasing protein (BPI) gene promoter is involved in the regulation of its mRNA expression in pigs.**
H. Wang*, S. Wu, and W. Bao, College of Animal Science and Technology, Yangzhou University, Yangzhou, Jiangsu, China.
- MT3 **Global quantification of DNA hydroxymethylation and DNA methylation in the bovine brain.**
B. Cantrell*¹, H. Lachance¹, R. Funston², R. Weaber³, and S. McKay¹, ¹University of Vermont, Burlington, VT, USA; ²University of Nebraska, North Platte, NE, USA; ³Kansas State University, Manhattan, KS, USA.
- MT4 **Methylation of CpG within IGF2R DMR2 are associated with prenatal nutrition and genetic potential for residual feed intake from birth to slaughter in purebred Angus cattle.**
C. Fitzsimmons*^{1,2}, J. Devos^{1,2}, C. Straathof², F. Paradis^{1,2}, C. Li^{1,2}, H. Block⁴, M. Colazo³, and H. Bruce², ¹Agriculture and Agri-Food Canada, Edmonton, Alberta, Canada; ²University of Alberta, Edmonton, Alberta, Canada; ³Alberta Agriculture and Forestry, Edmonton, Alberta, Canada; ⁴Agriculture and AgriFood Canada, Lacombe, Alberta, Canada.
- MT5 **Methylation assessment of selected bovine genes in relation to aging and inflammation in dairy cattle.**
T. Zabek*¹, E. Semik¹, A. Gurgul¹, T. Szmatoła¹, K. Pawlina¹, and E. Bagnicka², ¹National Research Institute of Animal Production, Balice, Poland; ²Institute of Genetics and Animal Breeding of the Polish Academy of Sciences, Jastrzebiec, Poland.
- MT6 **Analysis of differentially expressed genes and long non-coding RNAs from multiple pig tissues using RRBS and RNA-seq.**
M.-K. Choi, J. Lee, D. Kim, B. Y. Ahn*, and C. Park, Department of Animal Biotechnology, Konkuk University, Seoul, South Korea.
- MT7 **Small non-coding RNA from frozen bull sperm cells: biomarkers of male fertility?**
E. Sellem*¹, S. Marthey², H. Kiefer², C. Le Danvic¹, A. Allais-Bonnet¹, J. Perrier², L. Jouneau², A. Rau², H. Jammes², and L. Schibler¹, ¹ALLICE, Paris, France; ²INRA, Jouy-en-Josas, France.
- MT8 **Maternal nutrition during the first 50 days of gestation alters expression of histone and histone modifying genes in bovine fetal liver.**
M. S. Crouse*¹, J. S. Caton¹, R. A. Cushman³, K. J. McLean², C. R. Dahlen¹, P. P. Borowicz¹, L. P. Reynolds¹, and A. K. Ward¹, ¹Department of Animal Sciences, North Dakota State University, Fargo, ND, USA; ²Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, USA; ³USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA.
- MT9 **Evaluating the role of epigenomic modifications in host-pathogen interaction for bovine alveolar macrophages infected with Mycobacterium bovis.**
A. O'Doherty*¹, K. Rue-Albrecht², J. Browne¹, T. Hall¹, N. Nalpas³, D. Magee¹, S. Gordon^{1,4}, D. Vernimmen⁵, and D. MacHugh^{1,6}, ¹Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland; ²NDM Research Building, University of Oxford, Oxford, UK; ³Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany; ⁴UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland; ⁵The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK; ⁶UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.
- MT10 **Genome-wide analysis of H3K4me3 and H3K27me3 in three tissues in pigs.**
C. Kern*¹, Y. Wang¹, P. Saelao¹, K. Chanthavixay¹, I. Korf¹, C. K. Tuggle², C. Ernst³, P. Ross¹, and H. Zhou¹, ¹University of California-Davis, Davis, CA, USA; ²Iowa State University, Ames, IA, USA; ³Michigan State University, East Lansing, MI, USA.
- MT11 **Update on DNA methylation datasets of FAANG reference samples for the chicken and pig.**
N. Trakooljul*¹, H. Zhou², P. Ross², I. Korf³, M. E. Delany², H. H. Cheng⁴, C. Ernst⁵, C. Kern², F. Hadlich¹, S. Ponsuksili¹, and K. Wimmers¹, ¹Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany; ²Department of Animal Science, University of California, Davis, CA, USA; ³Genome Center, University of California, Davis, CA, USA; ⁴USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA; ⁵Department of Animal Science, Michigan State University, East Lansing, MI, USA.

- MT12 **Transgenerational phenotypic and epigenetic inheritance across three generations in layers induced by Poly(I:C).**
 L. Liu*, D. Wang, Z. Y. Duan, S. Yang, G. Y. Xu, N. Yang, and Y. Yu, *China Agricultural University, Beijing, China.*
- MT13 **Genome-wide identification of imprinted genes and its methylation statuses in various tissues of Hanwoo.**
 K.-T. Lee*, K.-S. Lim, B.-H. Choi, H.-H. Chai, J.-E. Park, E.-W. Park, G.-W. Jang, and D. Lim, *National Institute of Animal Science, RDA, Wanju, Jeonbuk, South Korea.*
- MT14 **Effects of maternal nutrition on the transcriptome and epigenome of the offspring.**
 H. Namous¹, F. Peñagaricano², M. Del Corvo³, E. Capra⁴, A. Stella⁴, J. Williams⁵, P. A. Marsan³, and H. Khatib*¹, ¹*University of Wisconsin, Madison, WI, USA;* ²*University of Florida, Gainesville, FL, USA;* ³*Università Cattolica del S. Cuore, Piacenza, Italy;* ⁴*Istituto di Biologia e Biotecnologia Agraria, Lodi, Italy;* ⁵*University of Adelaide, Roseworthy, Australia.*
- MT15 **The effect of histone acetyl-transferase inhibitor (trichostatin A) administration on porcine mesenchymal stem cells transcriptome.**
 A. Gurgul*, J. Opiela, K. Pawlina, T. Szmatoła, and M. Bugno-Poniewierska, *National Research Institute of Animal Production, Balice, Poland.*
- MT16 **DNA methylation and microRNA modifications in scrapie.**
 J. Toivonen¹, A. Sanz¹, O. López-Pérez^{1,2}, D. Sanz-Rubio¹, M. Salinas-Pena¹, J. Alejo¹, R. Bolea², J. Espinosa³, J. Badiola², P. Zaragoza¹, J. Torres³, and I. Martín-Burriel*^{1,2}, ¹*Laboratorio de Genética Bioquímica, IIS Aragón, IA2, Universidad de Zaragoza, Zaragoza, Spain;* ²*Centro de Investigación en Encefalopatías y Enfermedades Transmisibles Emergentes, IIS Aragón, IA2, Universidad de Zaragoza, Zaragoza, Spain;* ³*Centro de Investigación en Sanidad Animal, CISA-INIA, Valdeolmos, Madrid, Spain.*

Animal Forensic Genetics

- MT17 **Comparison of the effectiveness of 19 STR and 22 STR panels for forensic DNA analysis of canine in Poland.**
 A. Radko*, A. Podbielska, and M. Miszczak, *National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice, Poland.*

Applied Genetics and Genomics in Other Species of Economic Importance

- MT18 **Camel milk protein polymorphisms and their potential use.**
 Y. Öner and Y. N. Berhane*, *Uludag University, Özlüce Mahallesi, Nilüfer/Bursa, Turkey.*
- MT19 **Investigation of the ferret genome to identify evolutionary relevant markers and domestication related genomic features.**
 V. J. Utzeri¹, L. Penso-Dolfin², G. Schiavo¹, A. Ribani¹, G. Etherington², L. Fontanesi*¹, and F. Di Palma², ¹*Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy;* ²*Earlham Institute, Norwich, UK.*
- MT20 **Genetic differentiation of farm and wild populations of the red fox in Poland.**
 M. Zaton-Dobrowolska*¹, A. Mucha¹, D. Morrice², H. Wierzbicki¹, M. Moska¹, and M. Dobrowolski³, ¹*Department of Genetics, Wrocław University of Environmental and Life Sciences, Wrocław, Poland;* ²*The Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK;* ³*Institute of Animal Breeding, Wrocław University of Environmental and Life Sciences, Wrocław, Poland.*
- MT21 **Genetic distances between farm and wild populations of the red fox in Poland.**
 M. Zaton-Dobrowolska*¹, A. Mucha¹, D. Morrice², H. Wierzbicki¹, M. Moska¹, and M. Dobrowolski³, ¹*Department of Genetics, Wrocław University of Environmental and Life Sciences, Wrocław, Poland;* ²*The Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK;* ³*Institute of Animal Breeding, Wrocław University of Environmental and Life Sciences, Wrocław, Poland.*
- MT22 **A de novo hybrid assembly of a dromedary camel.**
 H. Holl*¹, D. Miller², S. Abdalla³, B. Shykind³, J. Malek³, Y. Mohamoud³, A. Ahmed³, K. Pasha⁴, A. Khalili⁴, D. Antczak², and S. Brooks¹, ¹*University of Florida, Gainesville, FL, USA;* ²*Cornell University, Ithaca, NY, USA;* ³*Weill Cornell Medical College in Qatar, Doha, Qatar;* ⁴*Tharab Veterinary Hospital, Doha, Qatar.*

- MT23 **SNP genotyping of reindeer (*Rangifer tarandus*) using BovineHD BeadChips.**
V. Kharzinova*¹, A. Dotsev¹, V. Fedorov², G. Brem^{1,3}, K. Wimmers⁴, H. Reyer⁴, and N. Zinovieva¹, ¹L.K. Ernst Institute of Animal Husbandry, Moscow, Russia; ²Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russia; ³Institute of Animal Breeding and Genetics, VMU, Vienna, Austria; ⁴Institute of Genome Biology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.
- MT24 **The population and landscape genetics of the European badger (*Meles meles*) in Ireland.**
A. Allen*¹, J. Guerrero², A. Byrne^{1,3}, J. Lavery¹, E. Presho¹, G. Kelly¹, E. Courcier⁴, J. O'Keefe⁵, U. Fogarty⁶, D. O'Meara⁷, G. Wilson⁸, D. Ensing¹, C. McCormick¹, R. Biek⁹, R. Skuce^{1,3}, ¹Agri Food and Biosciences Institute, Belfast, Northern Ireland; ²CEFE-CNRS, Centre D'Ecologie Fonctionnelle et Evolutive, Montpellier, France; ³School of Biological Sciences, Queen's University Belfast, Belfast, Northern Ireland; ⁴Department of Agriculture, Environment and Rural Affairs, Belfast, Northern Ireland; ⁵Department of Agriculture Food and the Marine, Dublin, Republic of Ireland; ⁶Irish Equine Centre, Johnstown, Republic of Ireland; ⁷Waterford Institute of Technology, Waterford, Republic of Ireland; ⁸Animal and Plant Health Agency (APHA), Stonehouse, Gloucestershire, England; ⁹University of Glasgow, Glasgow, Scotland.
- MT25 **Genomic selection for performance and reproduction traits in American mink.**
K. Karimi*¹, M. Sargolzaei^{2,3}, and Y. Miar¹, ¹Department of Animal Science and Aquaculture, Dalhousie University, Nova Scotia, Canada; ²Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada; ³Semex Alliance, Ontario, Canada.
- MT26 **Plains bison triallelic SNPs for determining parentage, estimating cattle introgression, and inbreeding.**
T. Kalbfleisch*¹, J. Tait², V. Basnayake², B. Simpson², T. Smith³, and M. Heaton³, ¹University of Louisville, Louisville, KY, USA; ²GeneSeek, Lincoln, NE, USA; ³USMARC, USDA, Clay Center, NE, USA.
- MT27 **Characterisation of a family of alpacas exhibiting disproportionate dwarfism.**
K. A. Munyard* and T. Y. K. Tan, *School of Biomedical Sciences, Curtin Health Innovation Research Institute, Curtin University, Perth, Western Australia, Australia.*
- MT28 **Withdrawn**
- MT29 **Withdrawn**

Avian Genetics and Genomics

- MT30 **Effects of dietary fiber content in interaction with a locus on GGA4 on growth, body composition and feed efficiency in chicken of an advanced intercross population.**
M. K. Nassar*¹, S. Lyu², J. Zentek³, and G. A. Brockmann², ¹Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt; ²Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Humboldt-Universität zu Berlin, Berlin, Germany; ³Department of Veterinary Medicine, Institute of Animal Nutrition, Freie Universität Berlin, Berlin, Germany.
- MT31 **Sire influence on hatchability and heritability estimates of quails in a humid tropical environment.**
U. K. Oke*, O. C. Obi, and U. K. Ibe, *Department of Animal Breeding and Physiology, Michael Okpara University of Agriculture, Umudike, Nigeria, West Africa.*
- MT32 **Mitochondrial DNA polymorphism in Nigeria indigenous turkey population.**
D. M. Ogah*, *Nasarawa State University keffi, Shabu-Lafia campus, Nasarawa State, Nigeria.*
- MT33 **Aflatoxin B₁ induced apoptosis in chicken hepatocytes and rescue effects of selenium.**
M. Jameel*¹, X. Peng², A. A. Kamboh³, and J. Fang¹, ¹Sichuan Agricultural University, Chengdu, Sichuan, China; ²China West Normal University, Nanchong, Sichuan, China; ³Sindh Agriculture University, Tandojam, Sindh, Pakistan.
- MT34 **Scanning signals of artificial selection in the chicken genome.**
Y. Ma*, L. Gu, L. Yang, and S. Li, *Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction, Ministry of Education, and Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture; Huazhong Agricultural University, Wuhan, Hubei, China.*
- MT35 **Forty-two shades of pink: Sex assignment and parentage analysis in a captive colony of Greater flamingos (*Phoenicopterus roseus*).**
C. Biolatti*¹, C. Beltramo¹, A. Dogliero², V. Campia¹, S. Peletto¹, S. Colussi¹, P. Modesto¹, and P. Acutis¹, ¹Regional Center for Exotic Animals, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy; ²Department of Veterinary Science, University of Turin, Grugliasco, Turin, Italy.

- MT36 The widespread introgression in Chinese indigenous chicken breeds from commercial breeds.**
 C. Zhang^{*1,2}, D. Peng², R. Yung², J. Wang², and D. Lin^{1,2}, ¹Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University, Beijing, China; ²State Key Laboratory for Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, China.
- MT37 Genetic association between carcass traits and DNA microsatellite marker genotype in chickens.**
 K. Tatsuda*, Hyogo Prefectural Institute of Agriculture, Forestry and Fisheries, Kasai, Hyogo, Japan.
- MT38 MtDNA D-loop genetic diversity of Middle East and North African indigenous chicken.**
 A. Al-Jumaili^{*1}, S. Al-Bayatti², A. A. Essa², R. Alatiyat³, A. Ahbara¹, J. Mwacharo⁴, O. Hanotte¹, and R. Aljumaah³, ¹University of Nottingham, School of Life Sciences, Nottingham, Nottinghamshire, UK; ²Ministry of Agriculture, Directorate of Animal Resources, Genetic Resources Division, Baghdad, Iraq; ³King Saud University, Animal Science Department, College of Food and Agriculture, Riyadh, Kingdom of Saudi Arabia; ⁴The International Centre for Agricultural Research in Dry Areas (ICARDA), Small Ruminant Genetics and Genomics Group, Addis Ababa, Ethiopia.
- MT39 Diversity analysis of AvBD gene region in Japanese quail.**
 T. Ishige^{*1}, H. Hara², T. Hirano², and K. Hanzawa², ¹Tokyo University of Agriculture, Setagaya, Tokyo, Japan; ²Tokyo University of Agriculture, Atsugi, Tokyo, Japan.
- MT40 Signature of selection in domestic chicken comparison between the White Leghorn, Indonesian and Langshan chicken.**
 T. Goto^{*1,2}, R. A. Lawal¹, D.-D. Wu³, Y.-P. Zhang^{3,4}, P. M. Hocking⁵, D. W. Burt⁵, and O. Hanotte^{1,6}, ¹The University of Nottingham, Nottingham, UK; ²Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan; ³Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China; ⁴Yunnan University, Kunming, China; ⁵The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK; ⁶International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.
- MT41 Identification of candidate genes and variants associated with resistance to Marek's disease virus.**
 J. Smith^{*1}, E. Lipkin², M. Soller², J. Fulton³, and D. Burt¹, ¹The Roslin Institute, Midlothian, Edinburgh, UK; ²The Hebrew University of Jerusalem, Jerusalem, Israel; ³Hy-line International, Dallas Center, IA, USA.
- MT42 Three differential expression clusters showed acclimation mechanism of White Pekin duck under heat stress.**
 J.-M. Kim¹, K.-S. Lim¹, K.-T. Lee¹, Y.-R. Yang², H.-H. Chai¹, J. Hwangbo¹, B.-H. Choi¹, D. Lim¹, Y.-H. Choi², and J.-E. Park^{*1}, ¹National Institute of Animal Science, Rural Development Administration, Wanju-gun, Jeollabuk-do, Republic of Korea; ²Gyeongsang National University, Jinju-si, Gyeongsangnam-do, Republic of Korea.
- MT43 Molecular genetics unveiled unknown family relationships and hybrids in an ex-situ colony of African penguins (*Spheniscus demersus*).**
 P. Modesto^{*1}, C. Biolatti¹, L. Favaro², S. Colussi¹, S. Peletto¹, S. Piga³, M. V. Riina¹, D. Pessani², E. Trincas³, V. Isaja³, and P. L. Acutis¹, ¹Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy; ²Laboratorio di Zoologia e Biologia Marina, Dipartimento Scienze della Vita e Biologia dei Sistemi, Turin, Italy; ³Zoom Torino, Turin, Italy.
- MT44 Genomic variability in Mexican chicken population.**
 M. G. Strillacci^{*1}, E. Gorla¹, M. C. Cozzi¹, S. I. Roman-Ponce², F. J. Ruiz², V. E. Vega-Murillo², F. Bertolini^{3,4}, L. Fontanesi³, S. Cerolini¹, and A. Bagnato¹, ¹Department of Veterinary Medicine, University of Milan, Milano, Italy; ²Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Col. Centro Veracruz, Mexico; ³Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy; ⁴Department of Animal Science, Iowa State University, Ames, IA, USA.
- MT45 Response of the hepatic transcriptomes of domesticated and wild turkey to aflatoxin B₁.**
 K. Reed^{*1}, K. Mendoza¹, J. Abrahamte¹, and R. Coulombe², ¹University of Minnesota, St. Paul, MN, USA; ²Utah State University, Logan, UT, USA.
- MT46 Genetic diversity and LD size between commercial and native chickens in Korea.**
 D. Seo*, D. Lee, N. Choi, S. Jin, P. Sudrajad, S. H. Lee, and J. H. Lee, Division of Animal and Dairy Science, Chungnam National University, Daejeon, South Korea.
- MT47 Mapping QTLs affecting Marek's disease by selective genotyping in F6 of full-sib intercross population.**
 E. Lipkin^{*1}, J. Smith², D. Burt², M. Soller¹, and J. Fulton³, ¹Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel; ²The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK; ³Hy-Line International, Dallas Center, IA, USA.
- MT48 Copy number variation in SOX6 contributes to chicken muscle development.**
 X. Zhang*, Department of Animal Genetics, Breeding and Reproduction, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong, China.

- MT49 **Phenotype and multi-tissue transcriptome response to diet changes in laying hens.**
M. Brenet^{1,2}, A. Rau³, C. Désert^{1,2}, M. Boutin^{1,2}, K. Muret^{1,2}, S. Leroux⁴, D. Esquerre⁵, C. Klopp⁶, D. Gourichon⁷, F. Pitel⁴, T. Zerjal³, and S. Lagarrigue^{*1,2}, ¹INRA, UMR1348, PEGASE, St Gilles, France; ²Agrocampus-Ouest, UMR1348, Rennes, France; ³INRA, AgroParisTech, Université Paris-Saclay, UMR GABI, Jouy-en-Josas, France; ⁴INRA/INPT ENSAT/INPT ENVT, GenPhySE, Castanet Tolosan, France; ⁵INRA, Plateforme GENOTOUL, Castanet-Tolosan, France; ⁶INRA, SIGENAE, Castanet-Tolosan, France; ⁷INRA, PEAT, Nouzilly, France.
- MT50 **Addition to the chicken W-chromosome specific repetitive landscape.**
A. Saifitdinova, S. Galkina*, A. Dyomin, M. Kulak, E. Koshel, and E. Gaginskaya, *Saint-Petersburg State University, Saint-Petersburg, Russia.*
- MT51 **MicroRNAs associated with high rate of egg production in chicken ovaries.**
U. Gaur*, N. Wu, M. Yang, and D. Li, *Sichuan Agricultural University, Chengdu, Sichuan, China.*
- MT52 **Genome wide association study of complex traits in response to Newcastle Disease Virus in chickens.**
K. Rowland^{*1}, H. Zhou², R. Gallardo³, T. Kelly^{2,3}, A. Wolc^{1,4}, and S. J. Lamont¹, ¹Iowa State University, Department of Animal Science, Ames, IA, USA; ²University of California-Davis, Department of Animal Science, Davis, CA, USA; ³University of California-Davis, School of Veterinary Medicine, Davis, CA, USA; ⁴Hy-Line International, Dallas Center, IA, USA.
- MT53 **Goose transcriptome provides insights into novel mechanisms of adipogenesis.**
G. Wang^{*2,1}, Y. Liu¹, L. Jin¹, D. Shang¹, C. Gill², M. Li¹, and J. Wang¹, ¹Sichuan Agricultural University, Chengdu, Sichuan, China; ²Texas A&M University, College Station, TX, USA.
- MT54 **The broiler chicken transcriptome.**
C. Schmidt^{*1} and S. Lamont², ¹University of Delaware, Newark, DE, USA; ²Iowa State University, Ames, IA, USA.
- MT55 **The evolving chicken genome reference.**
W. Warren^{*1}, L. Hillier¹, C. Tomlinson¹, P. Minx¹, M. Kremitski¹, T. Graves¹, S. Sullivan², I. Liachko², M. Delaney³, J. Fulton⁴, M. Abrahamsen⁵, R. Hawken⁵, M. Miller⁶, and H. Cheng⁷, ¹Washington University School of Medicine, St Louis, MO, USA; ²Phase Genomics Inc, Seattle, WA, USA; ³University of California-Davis, Davis, CA, USA; ⁴Hy-Line International, Dallas Center, IA, USA; ⁵Cobb-Vantress Inc, Siloam Springs, AR, USA; ⁶Beckman Research Institute, Duarte, CA, USA; ⁷USDA-ARS, East Lansing, MI, USA.
- MT56 **Liver and whole blood transcriptome response to chronic heat exposure in laying hens.**
F. Jehl¹, A. Rau¹, C. Désert^{2,3}, M. Boutin^{2,3}, K. Muret^{2,3}, S. Leroux⁴, D. Esquerre⁵, C. Klopp⁶, D. Gourichon⁷, F. Pitel⁴, A. Collin⁸, S. Lagarrigue^{2,3}, and T. Zerjal^{*1}, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ²INRA, UMR1348 Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'élevage, Saint-Gilles, France; ³Agrocampus-Ouest, UMR1348, Rennes, France; ⁴UMR INRA/INPT ENSAT/INPT ENVT - GenPhySE, Castanet Tolosan, France; ⁵INRA, Plateforme GENOTOUL, Castanet-Tolosan, France; ⁶INRA, SIGENAE, Castanet-Tolosan, France; ⁷INRA-PEAT, Nouzilly, France; ⁸URA, INRA, Nouzilly, France.
- MT57 **The not-so-missing genes in birds.**
T. Hron*, H. Farkasova, P. Pajer, J. Paces, P. Bartunek, and D. Elleder, *Institute of Molecular Genetics of the AV CR, v.v.i., Vídenská, Prague, Czech Republic.*
- MT58 **Integrating genome and transcriptome profiling for dissection of the mechanism of muscle growth and lipid deposition in ducks.**
L. Wang*, X. Li, J. Ma, Y. Zhang, and H. Zhang, *Lab of Animal Genetic Resource and Molecular Breeding, China Agricultural University, Beijing, P.R. China.*
- MT59 **Genome-wide detection of SNPs and CNVs in chickens associated with beak deformity using chicken high-density 600K SNP arrays.**
H. Bai, Y. Y. Sun, D. L. Li, Y. F. Liu, F. G. Xue, Y. L. Li, S. S. Xu, A. X. Ni, and J. L. Chen*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*
- MT60 **De novo genome assembly of *Agapornis roseicollis* and SNP discovery for parentage verification.**
H. van der Zwan^{*1}, R. van der Sluis¹, and C. Visser², ¹North-West University, Potchefstroom, North-West, South Africa; ²University of Pretoria, Pretoria, Gauteng, South Africa.

- MT61** **Low number of mitochondrial DNA sequences inserted into the turkey (*Meleagris gallopavo*) nuclear genome: Implications for evolutionary inferences.**
G. Schiavo¹, M. G. Strillacci², S. Bovo^{1,3}, A. Ribani¹, S. I. Roman-Ponce⁴, S. Cerolini², F. Bertolini^{1,5}, A. Bagnato², and L. Fontanesi^{*1},
¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy; ²Department of Veterinary Medicine, University of Milan, Milano, Italy; ³Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy; ⁴Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agrícola y Pecuarías (INIFAP), Col. Centro Veracruz, Mexico; ⁵Department of Animal Science, Iowa State University, Ames, IA, USA.
- MT62** **Mapping QTLs affecting Marek's disease by selective DNA pooling in eight lines across 15 generations.**
E. Lipkin^{*1}, J. Smith², D. Burt², M. Soller¹, and J. Fulton³, ¹Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel; ²The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK; ³Hy-Line International, Dallas Center, IA, USA.
- MT63** **An evaluation of the ISAG recommended parentage and identification panel for the domestic pigeon (*Columba livia domestica*).**
M. de Groot^{*}, VHLGenetics, Wageningen, the Netherlands.
- MT64** **Evaluation of semen characteristic of the high and low sperm motility groups in two different strains of chicken.**
M. Farahi, A. A. Masoudi^{*}, and A. Ehsani, Tarbiat Modares University, Tehran, Iran.
- MT65** **Discrimination of native chicken breeds using SNP marker combination.**
S. Jin¹, N.-R. Choi¹, D. Seo¹, P. Manjula¹, H.-Y. Kim², S. H. Lee¹, and J. H. Lee^{*1}, ¹Chungnam National University, Daejeon, Republic of Korea; ²Insilicogen Inc, Yongin, Republic of Korea.
- MT66** **A novel approach for mapping of animal genome assemblies to a chromosomal level applied to avian genomes.**
J. Damas¹, R. E. O'Connor², M. Farre¹, H. Martell², E. A. Slack¹, E. Allanson¹, L. Kiazim², R. Jennings², A. Mandawala³, S. Joseph², K. E. Fowler³, D. K. Griffin², and D. M. Larkin^{*1}, ¹Department of Comparative Biomedical Sciences, Royal Veterinary College, University of London, London, UK; ²School of Biosciences, University of Kent, Canterbury, Kent, UK; ³Canterbury Christchurch University, Canterbury, Kent, UK.
- MT67** **In situ and in silico improvement of the Japanese quail genome assembly.**
S. Galkina^{*1}, M. Kulak¹, A. Saifitdinova¹, A. Komissarov¹, A. Dyomin¹, V. Volodkina¹, J. Damas², M. Farre², D. Griffin³, D. Larkin², and E. Gaginskaya¹, ¹Saint-Petersburg State University, Saint-Petersburg, Russia; ²Royal Veterinary College, University of London, London, UK; ³University of Kent, Kent, UK.
- MT68** **Withdrawn**

Cattle Molecular Markers and Parentage Testing

- MT69** **Identification of distribution single nucleotide polymorphism of Cytochrome b gene in Kebumen Ongole grade cattle and Brahman cattle.**
T. Hartatik^{*}, D. Maharani, J. H. P. Sidadolog, A. Fathoni, and Sumadi, Laboratory of Animal Genetic and Breeding, Department of Animal Breeding and Reproduction, Faculty of Animal Science, Universitas Gadjah Mada, Yogyakarta, Indonesia.
- MT70** **Phylogenetic analysis of three yak breeds or populations based on several molecular markers.**
J. Gao, S. Y. Jin, L. Huang, and Y. C. Zheng^{*}, College of Life Science and Technology, Southwest University for Nationalities, Chengdu, Sichuan, China.
- MT71** **Improving accuracy of genomic prediction for economically important traits in North American Holstein dairy cattle.**
S. Nayeri^{*1}, M. K. Abo-Ismael^{1,2}, M. Sargolzaei^{2,3}, S. P. Miller^{2,4}, F. Schenkel², S. S. Moore^{1,5}, and P. Stothard¹, ¹University of Alberta, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; ²University of Guelph, Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, ON, Canada; ³The Semex Alliance, The Semex Alliance, Guelph, ON, Canada; ⁴Angus Genetics Inc., American Angus Association, St. Joseph, MO, USA; ⁵University of Queensland, Agriculture and Food Innovation, Centre for Animal Science, University of Queensland, St. Lucia, QLD, Australia.

- MT72 **Effect of single nucleotide polymorphisms in the *ABCG2*, *β-LG*, *CSN3*, *FASN*, *IGF1*, *PPARGC1A* and *SCD* genes on milk production traits in dairy cattle.**
M. A. Alim^{*1,2}, D. Sun², Z. Yi², Z. Yuan², Z. Qin², and L. Lin³, ¹Division of Animal Biotechnology, National Institute of Biotechnology, Ganakbari, Asulia, Savar, Dhaka, Bangladesh; ²College of Animal Science and Technology, Key Laboratory of Animal Genetics and Breeding of Ministry of Agriculture, National Engineering Laboratory for Animal Breeding, China Agricultural University, Beijing, China; ³Beijing Dairy Cattle Center, Beijing, China.
- MT73 **Genome-wide association study for displacement of abomasum in dairy cattle.**
H. Huang^{*1}, J. Cao², G. Guo³, X. Li³, Y. Wang¹, Y. Yu¹, S. Zhang¹, Q. Zhang¹, and Y. Zhang¹, ¹Key Laboratory of Animal Genetics and Breeding of Ministry of Agriculture, National Engineering Laboratory of Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China; ²Department of Clinical Veterinary Medicine, College of Veterinary Medicine, China Agricultural University, Beijing, China; ³Beijing Sunlon Livestock Co Ltd, Beijing, China.
- MT74 **Genomic single-step national evaluation of Holstein cattle in the Czech Republic.**
A. Kranjcevicova^{*1}, J. Pribyl¹, J. Splichal², J. Bauer², J. Motycka³, and L. Vostry¹, ¹Institute of Animal Science, Prague, Czech Republic; ²Plemdat (Czech Moravia Breeders Corporation), Hradistko, Czech Republic; ³Holstein Cattle Breeders Association, Hradistko, Czech Republic.
- MT75 **Identification of hypotrachosis in Kazakh Whiteheaded beef cattle breed in Kazakhstan.**
T. Yechshzhanov^{*2}, R. Uskenov¹, Y. Mukhanbetkaliyev¹, S. Zhamaliyeva², and A. Smakova¹, ¹S.Seifullin Kazakh AgroTechnical University, Astana, Kazakhstan; ²L.N.Gumilyov Eurasian National University, Astana, Kazakhstan.
- MT76 **Genomic profiles to assess accuracy of breed composition and hybrid vigor in crossbred beef cattle.**
M. K. Abo-Ismaïl^{*1,2}, J. Crowley^{1,3}, E. C. Akanno¹, G. Manafiazar¹, C. Li^{1,4}, G. Plastow¹, M. D. MacNeil⁶, D. Berry⁷, P. Stothard¹, and J. Basarab^{1,5}, ¹Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; ²Animal and Poultry Production, Damanhour University, Damanhour, Egypt; ³Canadian Beef Breeds Council, Calgary, AB, Canada; ⁴Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada; ⁵Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada; ⁶Delta G, Department of Animal, Wildlife and Grassland Sciences, Bloemfontein, South Africa; ⁷Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Co., Cork, Ireland.
- MT77 **Residual feed intake candidate gene associations.**
N. A. Zulkifli^{*1,2}, W. S. Pitchford², and C. D. K. Bottema², ¹School of Environmental Science and Natural Resources, The National University of Malaysia, Bangi, Selangor, Malaysia; ²School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy, Australia.
- MT78 **Impact of genomic selection for feed efficiency on heifer reproduction and calf performance traits.**
E. Akanno^{*1}, C. Ekin-Dzivenu¹, M. Abo-Ismaïl^{1,2}, M. MacNeil^{3,4}, C. Li^{1,5}, C. Fitzsimmons^{1,5}, J. Basarab^{1,6}, and G. Plastow¹, ¹Livestock Gentec, AFNS, University of Alberta, Edmonton, AB, Canada; ²Department of Animal and Poultry Production, Damanhour University, Damanhour, Egypt; ³Delta G, Miles City, MT, USA; ⁴Department of Animal, Wildlife and Grassland Sciences, University Free State, Bloemfontein, South Africa; ⁵Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada; ⁶Alberta Agriculture and Forestry, Lacombe Research and Development Centre, Lacombe, AB, Canada.
- MT79 **Bilateral iridal hypopigmentation in Holstein Friesian cattle.**
A. K. Hollmann¹, M. Bleyer², A. Tipold³, J. N. Neßler³, W. E. Wemheuer¹, E. Schütz¹, and B. Brenig^{*1}, ¹Institute of Veterinary Medicine, University of Goettingen, Goettingen, Germany; ²Pathology Unit, German Primate Center, Leibniz-Institute for Primate Research, Goettingen, Germany; ³Dept. Small Animal Medicine and Surgery, University of Veterinary Medicine Hannover, Hannover, Germany.
- MT80 **The price of looking for something no one wants to talk about: The search, quantification, and cost of genetic diseases in Ireland.**
J. McClure^{*1}, P. Flynn², S. Waters³, M. Mullen⁴, T. Pabiou¹, R. Schnabel⁵, J. Taylor⁵, F. Kearney¹, R. Weld², and M. McClure¹, ¹The Irish Cattle Breeding Federation, Highfield House, Shinagh, Bandon, Co. Cork Ireland; ²Weatherbys DNA Laboratory, Johnstown, Co. Kildare; ³Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath; ⁴Department of Life and Physical Sciences, Faculty of Health and Science, Athlone Institute of Technology, Athlone, Co. Westmeath, Ireland; ⁵Department of Animals Sciences, University of Missouri, Columbia, MO, USA.
- MT81 **The OpenArray SNP parentage panel in cattle—Preliminary studies.**
A. Piestrzynska-Kajtoch^{*}, D. Rubis, A. Fornal, and A. Radko, National Research Institute of Animal Production, Balice, Poland.

- MT82 **Pedigree, microsatellite and genomic based inbreeding coefficient correlations in a highly fragmented population, the Lidia bovine breed.**
O. Cortés*, S. Dunner, P. Eusebi, and J. Cañón, *Department Animal Production, Veterinary Faculty, University Complutense of Madrid, Madrid, Spain.*
- MT83 **SNP data quality control in a National Beef and Dairy Cattle System and highly accurate SNP-based parentage verification and identification.**
M. McClure*¹, J. McCarthy¹, R. Weld², P. Flynn², M. Kean¹, K. O'Connell¹, and J. Kearney¹, ¹*Irish Cattle Breeding Federation, Bandon, Cork, Ireland;* ²*Weatherbys Ireland, Johnstown, Kildare, Ireland.*
- MT84 **Next-generation targeted sequencing panel for verification of bovine parentage.**
A. Burrell*¹, P. Siddavatam¹, A. Allred¹, C. Willis¹, R. Ferretti², and A. Raeber¹, ¹*Thermo Fisher Scientific;* ²*Neogen GeneSeek Operations.*
- MT85 **High cross-platform genotyping concordance of Axiom high-density microarrays and Eureka low-density targeted NGS assays.**
M. A. Patil* and A. Pirani, *Thermo Fisher Scientific, Santa Clara, CA, USA.*
- MT86 **Effectiveness of SNPs genotyping assay as a tool for genetic traceability of cattle production chain.**
A. Pozzi*¹, C. Previtali¹, R. Capoferri¹, S. Arabi¹, A. Galli², and G. Bongioni¹, ¹*Istituto Sperimentale Italiano L. Spallanzani, Rivolta d'Adda, Cremona, Italy;* ²*Centro di ricerca per le produzioni foraggere e lattiero-casearie CREA, Lodi, Italy.*

Companion Animal Genetics and Genomics

- MT87 **Complete mitogenome sequence of Lagomorphs from Upper Palaeolithic in the Balkan refuge.**
V. Brajkovic*¹, S. Radovic², D. Brajkovic², M. Girardi³, S. Krebs⁵, I. Medugorac⁴, I. Curik¹, P. T. Miracle⁶, C. Vernesi³, and V. Curbic-Curik¹, ¹*Department of Animal Science, Faculty of Agriculture University of Zagreb, Zagreb, Croatia;* ²*Institute for Quaternary Palaeontology and Geology, Croatian Academy of Sciences and Arts, Zagreb, Croatia;* ³*Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all'Adige (TN), Italy;* ⁴*Chair of Animal Genetics and Husbandry, LMU Munich, Munich, Germany;* ⁵*Laboratory for Functional Genome Analysis (LAFUGA), Gene Centre Munich, LMU Munich, Munich, Germany;* ⁶*McDonald Institute for Archaeological Research, University of Cambridge, Cambridge, UK;* ⁷*Private, Zagreb, Croatia.*
- MT88 **Genotype imputation in dogs.**
J. Friedrich*, R. Antolin, S. Hoj-Edwards, J. Hickey, and P. Wiener, *The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush, Midlothian, UK.*
- MT89 **Characterizing the proteic deposits in feline amyloidosis: A proteomic approach using FFPEs.**
F. Genova¹, M. Longeri*¹, L. A. Lyons², F. G. Scalvini¹, G. Tedeschi¹, G. Sironi¹, and S. Nonnis¹, ¹*Dept. of Veterinary Medicine, Università degli Studi di Milano, Milan, Italy;* ²*Dept. of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA.*
- MT90 **Genetic dissection of complex traits in a popular dog breed.**
P. Wiener*¹, J. Ilska², E. Sánchez-Molano¹, M. J. Haskell², Z. Polgar¹, S. E. Lofgren³, D. N. Clements¹, J. A. Woolliams¹, and S. C. Blott⁴, ¹*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush, UK;* ²*Scotland's Rural College, Edinburgh, UK;* ³*Youth Science Institute, Los Gatos, CA, USA;* ⁴*School of Veterinary Medicine and Science, University of Nottingham, Sutton Bonington, UK.*
- MT91 **Identification of the mutation causing progressive retinal atrophy in Old Danish Pointing Dogs.**
P. Karlskov-Mortensen* and M. Fredholm, *Department of Veterinary and Animal Science, Faculty of Health & Medical Sciences, University of Copenhagen, Copenhagen, Denmark.*
- MT92 **The impact of selection on genetics within the Siberian Husky breed.**
K. Ellis* and H. J. Huson, *Cornell University, Ithaca, NY, USA.*
- MT93 **Combined clinical, genetic, and pathophysiological investigations of inherited pulmonary fibrosis in West Highland white terriers.**
E. E. Patterson*¹, K. M. Minor¹, D. A. Feeney¹, and P. B. Bitterman², ¹*University of Minnesota College of Veterinary Medicine, Saint Paul, MN, USA;* ²*University of Minnesota School of Medicine, Minneapolis, MN, USA.*

- MT94 Genetic variants in *ATP1B2* and *KCNJ10* in Belgian Shepherd dogs with ataxia.**
N. Mauri¹, M. Kleiter², M. Leschnik², S. Högl³, E. Dietschi¹, C. Monney⁴, A. Oevermann⁴, D. Henke⁵, M. Wiedmer¹, J. Dietrich¹, F. Steffen⁶, S. Schuller⁷, C. Gurtner⁸, N. Stokar-Regenscheit⁸, D. O'Toole⁹, T. Bilzer¹⁰, C. Herden¹¹, V. Jagannathan¹, and T. Leeb^{*1},
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- MT95 Detection and characterisation of a genetic association with Norwich terrier upper airway syndrome.**
T. Marchant^{*1}, E. Dietschi², R. Harrington¹, M. Drögemüller², U. Rytz³, T. Leeb², and J. Schoenebeck¹, ¹The Royal (Dick) School for Veterinary Studies and Roslin Institute, The University of Edinburgh, Edinburgh, Midlothian, UK; ²The Institute of Genetics, Vetsuisse Faculty, The University of Bern, Bern, Switzerland; ³Department of Clinical Veterinary Medicine, Division of Small Animal Surgery, Vetsuisse Faculty, The University of Bern, Bern, Switzerland.
- MT96 Canine diversity and disease: Genome analysis in Australian dogs.**
S.-A. Mortlock, J. Marin-Cely, R. Booth, P. Soh, M.-S. Khatkar, and P. Williamson*, *The University of Sydney, Sydney, NSW, Australia.*
- MT97 Early events of cat domestication uncovered through ancient mitochondrial DNA analysis.**
E.-M. Geigl^{*1}, C. Ottoni^{1,2}, and T. Grange¹, ¹Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France; ²KU Leuven, University of Leuven, Department of Imaging and Pathology, Center for Archaeological Sciences; University Hospitals Leuven, Laboratory of Forensic Genetics and Molecular Archaeology, Leuven, Belgium.
- MT98 AgriSeq targeted sequencing panel for determination of canine parentage and genetic health.**
M. Karberg^{*1}, A. Burrell¹, P. Siddavatam¹, A. Allred¹, M. de Groot², and W. van Haeringen², ¹Thermo Fisher Scientific, Austin, TX, USA; ²VHL Genetics, Wageningen, Netherlands.
- MT99 An analysis of canine caudal fossa morphology and its genetics.**
R. Harrington*, T. Marchant, D. Argyle, D. Clements, T. Liuti, T. Schwarz, K. Marioni-Henry, and J. Schoenebeck, *Royal (Dick) School of Veterinary Studies and Roslin Institute, The University of Edinburgh, Easter Bush, Midlothian, UK.*
- MT100 Revealing the genetic basis of diabetes mellitus in Burmese cats.**
G. Samaha¹, J. Beatty¹, L. Lyons², C. Wade³, and B. Haase^{*1}, ¹School of Veterinary Science, Faculty of Science, University of Sydney, Sydney, NSW, Australia; ²College of Veterinary Medicine, University of Missouri, Columbia, MO, USA; ³School of Life and Environmental Sciences, Faculty of Science, University of Sydney, Sydney, NSW, Australia.
- MT101 Insights into 115 domestic cat and 17 wild felid genomes.**
L. Lyons*, *University of Missouri, Columbia, MO, USA.*
- MT102 Characterization of Plakophilin-2 expression in canine skin and identification of differential gene expression in non-lesional skin from dogs affected by atopic dermatitis.**
G. Andersson^{*1}, K. Tengvall^{2,3}, B. Ardesjö-Lundgren^{1,2}, S. Kozyrev², M. Kierczak², M. Olsson^{2,3}, F. F. Farias², Å. Hedhammar⁴, K. Bergvall⁴, and K. Lindblad-Toh^{2,5}, ¹Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ²Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, BMC, Uppsala University, Uppsala, Sweden; ³Center for Molecular Medicine, Neuroimmunology Unit, Department of Clinical Neuroscience, and Rheumatology Unit, Department of Medicine, Karolinska University Hospital, Karolinska Institutet, Stockholm, Sweden; ⁴Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁵Broad Institute of MIT and Harvard, Cambridge, MA, USA.
- MT103 Localizing the regions of causative mutations in feline amyloidosis: A next-generation genomic approach.**
F. Genova^{*1}, B. Gandolfi², A. Thomas³, E. Creighton², L. Lyons², and M. Longeri¹, ¹Department of Veterinary Medicine, Università degli Studi di Milano, Milan, Italy; ²Department of Veterinary Medicine and Surgery, College of Veterinary Medicine, University of Missouri, Columbia, MO, USA; ³Antagene, La tour de Salvagny, France.

- MT104 **Phylogenetic analysis of Angora, Van and stray cats of Anatolia.**
 N. Bilgen*, B. C. Kul, M. Akkurt, O. Cildir, O. Ozmen, and O. Ertugrul, *Ankara University Faculty of Veterinary Medicine Department of Genetics, Ankara, Turkey.*
- MT105 **Canine brachycephaly is associated with a retrotransposon-induced missplicing of *SMOC2*.**
 T. Marchant¹, E. Johnson¹, R. Harrington¹, L. McTier¹, C. Johnson¹, A. Gow¹, T. Liuti¹, D. Kuehn², K. Svenson³, M. Bermingham⁴, M. Drögemüller⁵, M. Nussbaumer⁶, M. Davey¹, D. Argyle¹, R. Powell⁷, S. Guilherme⁸, J. Lang⁹, G. Ter Haar¹, T. Leeb⁵, T. Schwarz¹, R. Mellanby¹, D. Clements¹, and J. Schoenebeck^{1*}, ¹Royal (Dick) School of Veterinary Studies and Roslin Institute, The University of Edinburgh, Midlothian, UK; ²Friendship Hospital for Animals, Washington, DC, USA; ³The Jackson Laboratory Bar Harbor, Bar Harbor, ME, USA; ⁴Institute of Genetics and Molecular Medicine, The University of Edinburgh, Edinburgh, UK; ⁵Institute of Genetics, University of Bern, Bern, Switzerland; ⁶Naturhistorisches Museum, Bern, Switzerland; ⁷Powell Torrance Diagnostic Services, Hertfordshire, UK; ⁸Davies Veterinary Specialists, Hertfordshire, UK; ⁹Department of Clinical Veterinary Medicine, University of Bern, Bern, Switzerland; ¹⁰Department of Clinical Sciences and Services, The Royal Veterinary College, Hertfordshire, UK.
- Comparative MHC Genetics: Populations and Polymorphism**
- MT106 **MHC Class III gene *Tenascin-XB (TNXB)* is associated with mature weight in U.S. Rambouillet, Targhee, Polypay, and Suffolk sheep.**
 M. U. Cinar^{*1,2}, M. R. Mousel^{3,4}, M. K. Herndon¹, M. A. Highland^{3,4}, J. B. Taylor⁵, D. P. Knowles^{1,3}, and S. N. White^{1,3}, ¹Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA; ²Erciyes University, Faculty of Agriculture, Department of Animal Science, Kayseri, Turkey; ³Animal Disease Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Pullman, WA, USA; ⁴Paul G. Allen School of Global Animal Health, Washington State University, Pullman, WA, USA; ⁵Range Sheep Production Efficiency Research, Dubois, ID, USA; ⁶Center for Reproductive Biology, Washington State University, Pullman, WA, USA.
- MT107 **Characterization of the diversity of LEI0258 microsatellite locus in Ethiopian indigenous chicken populations.**
 A. Kebede^{*1,2}, O. Hanotte³, T. Dessie³, N. Spark⁴, G. Belay¹, K. Tesfaye¹, J. Jung'a⁵, M. Kyalo⁶, W. Ekaya⁶, and R. Pelle⁶, ¹Addis Ababa University (AAU), Addis Ababa, Ethiopia; ²Amhara Regional Agricultural Research Institute (ARARI), Bahir Dar, Ethiopia; ³International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia; ⁴Center for Tropical Livestock Genetics and Health (CTLGH), Scotland, UK; ⁵University of Nairobi (UoN), Nairobi, Kenya; ⁶Biosciences eastern and central Africa (BecA), Nairobi, Kenya.
- MT108 **Evolution by gene duplication of the horse major histocompatibility complex class II structure.**
 A. Viluma*, S. Mikko, G. Andersson, and T. F. Bergström, *Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences (SLU).*
- MT109 **Major update to the Swine Leukocyte Antigen (SLA) Nomenclature System of the International Society for Animal Genetics (ISAG) and the International Union of Immunological Societies (IUIS).**
 S. Ho^{*1}, J. Lunney², A. Ando³, C. Rogel-Gaillard⁴, J.-H. Lee⁵, L. Schook⁶, and S. Hammer⁷, ¹Gift of Life Michigan, Ann Arbor, MI, USA; ²USDA, Beltsville, MD, USA; ³Tokai University School of Medicine, Isehara, Kanagawa, Japan; ⁴INRA, Jouy-en-Josas, France; ⁵Chungnam National University, Daejeon, Korea; ⁶University of Illinois, Urbana, IL, USA; ⁷University of Veterinary Medicine Vienna, Vienna, Austria.
- MT110 **A rapid, direct-sequencing based MHC genotyping system for populations with insufficient information on allelic variation.**
 J. Buitkamp* and J. Semmer, *Bavarian State Research Center for Agriculture Institute of Animal Breeding, Grub, Bavaria, Germany.*
- MT111 **Molecular characterisation of Ovar-MHC class II region reveals novel alleles in the Djallonke and Sahelian sheep breeds of Ghana.**
 M. Yaro^{*1}, K. Munyard¹, E. Morgan¹, M. Stear², and D. Groth¹, ¹Curtin University, Perth, WA, Australia; ²La Trobe University, Melbourne, VIC, Australia.
- MT112 **Withdrawn**
- MT113 **Large-scale analysis of the specificities of livestock MHC class I and II molecules.**
 D. B. Steen-Jensen¹, T. Østerbye¹, M. Rasmussen¹, M. Nielsen², A. Stryhn¹, and S. Buus^{*1}, ¹Laboratory of Experimental Immunology, University of Copenhagen, Copenhagen, Denmark; ²Center for Biological Sequence Analysis, Technical University of Denmark, Lyngby, Denmark.
- MT114 **Withdrawn**

- MT115 **IPD-MHC 2.0: An improved interspecies database for the study of the major histocompatibility complex.**
 G. Maccari*^{1,2}, J. Robinson^{2,3}, K. Ballingal⁴, L. Guethlein⁵, U. Grimholt⁶, J. Kaufman⁷, C. Ho⁸, N. de Groot⁹, R. Bontrop⁹, P. Flicek¹⁰, J. Hammond¹, and S. Marsh^{2,3}, ¹The Pirbright Institute, Pirbright, Woking, Surrey, UK; ²Anthony Nolan Research Institute, Royal Free Hospital, London, UK; ³UCL Cancer Institute, Royal Free Campus, London, UK; ⁴Moredun Research Institute, Pentlands Science Park, Scotland, UK; ⁵Stanford University, Stanford, CA, USA; ⁶Norwegian Veterinary Institute, Oslo, Norway; ⁷University of Cambridge, Cambridge, UK; ⁸Gift of Life Michigan, Michigan, USA; ⁹Biomedical Primate Research Centre, Rijswijk, Netherlands; ¹⁰European Molecular Biology Laboratory, Wellcome Genome Campus, Hinxton, UK.
- MT116 **Chicken MHC-B diversity detected by a high-density SNP panel.**
 J. E. Fulton*¹, B. Bed Hom², and M. M. Miller³, ¹Hy-Line International, Dallas Center, IA, USA; ²GABI, INRA, AgroParisTech, Jouy-en-Josas, France; ³Department of Molecular and Cellular Biology, Duarte, CA, USA.
- MT117 **Studies of MHC class II content in three common Arabian horse haplotypes.**
 D. Miller*¹, A. Case¹, L. Younger¹, J. Tseng¹, H. Holl², Y. Ali Mohamoud³, A. Ahmed³, J. Malek³, S. Brooks², and D. Antczak¹, ¹Cornell University, Ithaca, NY, USA; ²University of Florida, Gainesville, FL, USA; ³Weill Cornell Medicine, Doha, Qatar.

Domestic Animal Sequencing and Annotation

- MT118 **A population-scale discovery of large deletions in Holstein, Jersey and Nordic Red Cattle genome.**
 M. Mesbah-Uddin*^{1,2}, B. Guldbrandtsen¹, J. Vilkkii³, D. J. De Koning⁴, D. Boichard², M. S. Lund¹, and G. Sahana¹, ¹Department of Molecular Biology and Genetics, Center for Quantitative Genetics and Genomics, Aarhus University, Tjele, Denmark; ²UMR 1313 GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ³Green technology, Natural Resources Institute Finland, Myllytie 1, Jokioinen, Finland; ⁴Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- MT119 **CNVcaller: An ultra-fast population copy number variation detector for animals and plants.**
 X. Wang*, Z. Zheng, Y. Cai, T. Chen, and Y. Jiang, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.
- MT120 **Candidate variants confirmation by GWAS applied to large cow data sets.**
 A. G. Marete*^{1,2}, M. Lund², and D. Boichard¹, ¹INRA, Paris, France; ²Aarhus University, Denmark.
- MT121 **Extensive sequencing of a tropically adapted breed—The Brahman sequencing project.**
 L. Koufariotis¹, B. Hayes¹, M. Kelly², B. Burns³, R. Lyons⁴, and S. Moore*¹, ¹Centre of Animal Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD, Australia; ²Australian Agricultural Company (AACo), Brisbane, QLD, Australia; ³Queensland Department of Agriculture and Fisheries, Rockhampton, QLD, Australia; ⁴School of Veterinary Science, University of Queensland, Gatton, QLD, Australia.
- MT122 **Withdrawn**
- MT123 **Reference sequence of the horse Y chromosome.**
 T. Raudsepp*¹, J. Janecka², B. Davis³, S. Ghosh¹, N. Paria⁴, P. J. Das⁵, M. Nielsen⁶, L. A. A. Orlando⁷, M. Schubert⁷, T. A. E. Stout⁸, and B. P. Chowdhary¹, ¹Texas A&M University, College Station, TX, USA; ²Duquesne University, Pittsburgh, PA, USA; ³National Institutes of Health, Bethesda, MD, USA; ⁴Texas Scottish Rite Hospital for Children, Dallas, TX, USA; ⁵National Research Centre on Yak, Dirang, India; ⁶University of Kentucky, Lexington, KY, USA; ⁷Natural History Museum of Denmark, Copenhagen, Denmark; ⁸Utrecht University, Utrecht, the Netherlands.
- MT124 **SNP discovery in indigenous Afrikaner, Drakensberger and Nguni cattle breeds of South Africa.**
 A. A. Zwane*^{1,2}, A. Choudhury³, M. L. Makgahlela¹, A. Maiwashe^{1,5}, E. Van Marle-Koster², and J. F. Taylor⁴, ¹Department of Animal Breeding and Genetics, ARC-API, Irene, South Africa; ²Department of Animal and Wildlife Sciences, University of Pretoria, Hatfield, Pretoria, South Africa; ³Sydney Brenner Institute of Molecular Bioscience, University of the Witwatersrand, Parktown, Johannesburg, South Africa; ⁴Division of Animal Sciences, University of Missouri, Columbia, MO, USA; ⁵Department of Animal, Wildlife and Grassland Sciences, University of the Free State, Bloemfontein, South Africa.

- MT125 Exploiting long-read sequencing technologies to establish high quality highly contiguous pig reference genome assemblies.**
 A. Warr¹, R. Hall², K. Kim², E. Tseng², S. Koren³, A. Phillippy³, D. Birkhart⁴, B. Rosen⁴, S. Schroeder⁴, D. Hume⁵, R. Talbot⁵, L. Rund⁶, L. Schook⁶, W. Chow⁷, K. Howe⁷, D. J. Nonneman⁸, G. A. Rohrer⁸, N. Putnam⁹, R. E. Green⁹, R. O'Connor¹⁰, D. Griffin¹⁰, B. M. Skinner¹¹, C. A. Sargent¹¹, N. A. Affara¹¹, C. Tyler-Smith⁷, M. Watson¹, T. P. L. Smith⁸, and A. Archibald*¹, ¹The Roslin Institute and R(D) SVS, University of Edinburgh, Easter Bush, Midlothian, UK; ²Pacific Biosciences, Menlo Park, CA, USA; ³National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA; ⁴Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA; ⁵Edinburgh Genomics, University of Edinburgh, Edinburgh, UK; ⁶University of Illinois, Urbana, IL, USA; ⁷The Wellcome Trust Sanger Institute, Hinxton UK; ⁸USDA, ARS, USMARC, Clay Center, NE, USA; ⁹Dovetail Genomics LLC, Santa Cruz, CA, USA; ¹⁰University of Kent, Canterbury, Kent, UK; ¹¹University of Cambridge, Cambridge, UK.
- MT126 Beyond sequencing: Assigning function to novel ncRNAs.**
 F. McCarthy*¹, A. Cooksey¹, C. Gresham², and B. Nanduri², ¹University of Arizona, Tucson, AZ, USA; ²Mississippi State University, Starkville, MS, USA.
- MT127 Profiling the landscape of transcription, chromatin accessibility and chromosome conformation of cattle, pig, chicken and goat genomes [FAANG pilot project "FR-AgENCODE"].**
 S. Foissac¹, S. Djebali*¹, H. Aclouque¹, FR-AgENCODE Consortium², M. H. Pinard Van der Laan², S. Lagarrigue³, and E. Giuffra², ¹GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Toulouse, France; ²GABI, AgroParisTech, INRA, Université Paris Saclay, Paris, France; ³PEGASE, INRA, Agrocampus Ouest, Rennes, France.
- MT128 Integrative and differential analysis of transcriptomes and chromatin accessibility regions reveals regulatory mechanisms involved in pig immune and metabolic functions [FAANG pilot project 'FR-AgENCODE'].**
 S. Djebali¹, K. Munyard², N. Villa-Vialaneix³, C. Cabau¹, A. Rau⁴, E. Crisci⁴, T. Derrien⁵, C. Klopp³, M. Zytnecki³, S. Lagarrigue^{6,7}, H. Aclouque¹, S. Foissac*¹, and E. Giuffra⁴, ¹GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Castanet-Tolosan, France; ²Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia; ³MIAT, Université de Toulouse, INRA, Castanet-Tolosan, France; ⁴GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France; ⁵UMR6290 IGDR, CNRS, Université Rennes 1, Rennes, France; ⁶UMR PEGASE, INRA, Rennes, France; ⁷UMR PEGASE, Agrocampus Ouest, Rennes, France.
- MT129 Pinpointing causal mutations among imputed sequence variant genotypes in three cattle breeds.**
 H. Pausch*^{1,2}, I. MacLeod¹, P. Bowman^{1,3}, R. Emmerling⁴, R. Fries⁵, B. Gredler-Grandl⁶, H. Daetwyler^{1,3}, and M. Goddard^{1,7}, ¹Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, VIC, Australia; ²Animal Genomics, Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland; ³School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia; ⁴Institute of Animal Breeding, Bavarian State Research Centre for Agriculture, Poing-Grub, Germany; ⁵Chair of Animal Breeding, Technische Universität München, Freising, Germany; ⁶Qualitas AG, Zug, Switzerland; ⁷Faculty of Veterinary and Agricultural Science, University of Melbourne, Melbourne, VIC, Australia.

Equine Genetics and Thoroughbred Parentage Testing

- MT130 Characteristics of the two primitive horse breeds (Polish Primitive Horse and Hucul) maternal lines using mtDNA D-loop sequence variation.**
 L. Wodas*¹, J. Cieslak¹, A. Borowska¹, E. G. Cothran², A. M. Khanshour³, and M. Mackowski^{1,4}, ¹Department of Horse Breeding, Poznan University of Life Sciences, Poznan, Poland; ²Department of Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Science, Texas A&M University, College Station, TX, USA; ³Texas Scottish Rite Hospital for Children, Dallas, TX, USA; ⁴Horse Genetic Markers Laboratory, Poznan University of Life Sciences, Poznan, Poland.
- MT131 Investigation of fine-scale recombination rate variability in the horse.**
 S. Beeson*, J. Mickelson, and M. McCue, University of Minnesota College of Veterinary Medicine, Saint Paul, MN, USA.
- MT132 Molecular genetic diversity of donkey (*Equus asinus*) by microsatellite marker and mitochondrial DNA analysis in Korea.**
 S. Yun*¹, C. Park², J. Hwang², S. Kim², and G. Cho², ¹Animal and Plant Quarantine Agency, Pusan, Korea; ²of Veterinary Medicine, Kyungpook National University, Daegu, Korea.
- MT133 Unique gene expression patterns in equine articular chondrocytes.**
 E. N. Adam and J. N. MacLeod*, University of Kentucky, Lexington, KY, USA.
- MT134 Rate of sex reversal cases in horses of Argentina.**
 M. Martinez*, M. Costa, B. Elguero, and C. Ratti, Laboratorio de Genética Aplicada, Sociedad Rural Argentina, Buenos Aires, Argentina.

- MT135 **Characterization of equine STR panel '15 TKY system' by imputation from dense SNP genotypes in a Thoroughbred population.**
M. Kikuchi*, H. Kakoi, T. Tozaki, K. Hirota, and S. Nagata, *Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan.*

Genetics of Immune Response and Disease Resistance

- MT136 **Two novel and differentially expressed SNPs in the promoter of CD4 gene are associated with mastitis resistance in dairy cattle.**
T. Usman*, S. Ayaz, S. Gul, and I. Khattak, *Abdul Wali Khan University Mardan, Khyber Pakhtunkhwa, Pakistan.*
- MT137 **Comparative analyses of PBMC transcriptome profiles between German Landrace and Pietrain pigs following PRRSV vaccination.**
M. A. Islam¹, M. J. Pröll¹, S. Rony¹, C. Große-Brinkhaus¹, M. J. Uddin², D. Tesfaye¹, M. Hölker¹, E. Tholen¹, K. Schellander¹, and C. Neuhoﬀ*¹, ¹*Institute of Animal Science, Animal Breeding and Husbandry group, University of Bonn, Bonn, Germany;* ²*School of Veterinary Science, The University of Queensland, Gatton campus, QLD, Australia.*
- MT138 **Experimentally induced *S. aureus* or *E. coli* mammary gland infection impacts the liver transcriptome in heifers selected for divergent mastitis susceptibility.**
A. Heimes*¹, A. Hehl¹, W. Demasius¹, J. Guenther¹, R. Weikard¹, F. Hadlich¹, H.-M. Seyfert¹, L. Rohmeier², M. Meyerholz^{2,4}, W. Petzl², H. Zerbe², M. Hoedemaker³, H.-J. Schuberth⁴, S. Engelmann⁵, C. Kuehn¹, ¹*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;* ²*Clinic for Ruminants with Ambulance and Herd Health Services, Centre for Clinical Veterinary Medicine, Ludwig-Maximilians-University, Munich, Germany;* ³*Clinic for Cattle, University of Veterinary Medicine Foundation, Hanover, Germany;* ⁴*Immunology Unit, University of Veterinary Medicine Foundation, Hanover, Germany;* ⁵*Institute of Microbiology, Technical University Braunschweig, Braunschweig, Germany.*
- MT139 **Genetic variation and regulation of TLR4 in relation to bovine mastitis.**
F. Korkmaz* and D. Kerr, *University of Vermont, Burlington, VT, USA.*
- MT140 **Pneumonia, *Pithomyces* and Purkinje cells: Genomics and animal health in sheep.**
K. M. McRae*, S. J. Rowe, P. L. Johnson, H. J. Baird, R. Brauning, and S. M. Clarke, *AgResearch, Mosgiel, New Zealand.*
- MT141 **Withdrawn**
- MT142 **MicroRNAs associated with antibody response to bovine leukemia virus in Holstein cattle.**
E. Casas* and T. M. Taxis, *USDA, ARS, National Animal Disease Center, Ames, IA, USA.*
- MT143 **Polyphenols and the regulatory interplay between immunogenomics and the bovine microbiome.**
M. Worku* and S. Adjei-Fremah, *NC A&T State University, Greensboro, NC, USA.*
- MT144 **Declining genetic trend of lameness health in North American Holsteins.**
G. Abdel-Azim* and R. Fourdraine, *CRI International Center for Biotechnology.*
- MT145 **Identification of a genomic region with a major effect on IgM antibodies binding autoantigens in chickens.**
M. Bao*¹, H. Bovenhuis¹, M. G. B. Nieuwland², H. K. Parmentier², and J. J. van der Poel¹, ¹*Wageningen University & Research Animal Breeding and Genomics, Wageningen, Gelderland, the Netherlands;* ²*Adaptation Physiology Group, Wageningen, Gelderland, the Netherlands.*
- MT146 **Transcriptomic analysis reveals the potential of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus to modulate immune system activation related to host-pathogen and damage associated signaling in infected porcine monocytes.**
L. C. Miller*¹, D. S. Fleming¹, X. Li², F. Blecha³, and Y. Sang^{4,3}, ¹*USDA, Agricultural Research Service, National Animal Disease Center, Virus and Prion Research Unit, Ames, IA, USA;* ²*National Research Center for Veterinary Medicine, China, Luo Yang City, China;* ³*Kansas State University, Manhattan, KS, USA;* ⁴*Tennessee State University, Nashville, TN, USA.*
- MT147 **Validation of polymorphisms in the GBP1, Mx1, and CD163 genes on host responses to PRRSV infection in pigs.**
B. Lim*¹, W.-I. Kim², C. K. Park³, S.-W. Kim¹, and K.-S. Kim¹, ¹*Chungbuk National University, Cheongju, Korea;* ²*Chunbuk National University, Iksan, Korea;* ³*Kyungpook National University, Taegu, Korea.*

- MT148 **Single nucleotide polymorphisms in the bovine MHC region of Japanese Black cattle are associated with bovine leukemia virus proviral load.**
 S. Takeshima^{*1}, S. Sasaki², P. Meripet¹, Y. Sugimoto², and Y. Aida¹, ¹*Viral Infectious Diseases Unit, RIKEN, Wako, Saitama, Japan;* ²*Shirakawa Institute of Animal Genetics, Japan Livestock Technology Association, Nishigo, Fukushima, Japan.*
- MT149 ***Staphylococcus aureus* genotype modulates the *in vitro* immune response of bovine mammary epithelial cells.**
 O. M. Keane^{*}, D. Niedziela, and M. Murphy, *Teagasc, Grange, Dunsany, Co. Meath, Ireland.*
- MT150 **Suppression of proviral load by the bovine leukemia virus vaccine targeting susceptible cattle.**
 Y. Aida^{*1,2}, L. Bai^{1,2}, P. He¹, N. Okimoto³, J. Yamagishi³, J. Kohara⁴, and S.-N. Takeshima^{1,2}, ¹*Viral Infectious Diseases Unit, RIKEN, Wako, Saitama, Japan;* ²*Bovine Leukemia Virus Vaccine Laboratory, RIKEN Innovation Center, RIKEN, Wako, Saitama, Japan;* ³*Computational Biology Research, Core, Quantitative Biology Center, RIKEN, Suita, Osaka, Japan;* ⁴*Animal Research Center, Hokkaido Research Organization, Shintoku, Hokkaido, Japan.*
- MT151 **Polymorphism of innate immunity genes in the conserved and selected populations of the Czech Red Pied cattle.**
 K. Novák^{*1}, M. Bjelka², A. Kalashnikov³, T. Valčíková⁴, and V. Mátlová¹, ¹*Institute of Animal Science, Prague-Uhrineves, Czech Republic;* ²*Breeding Cooperative Impuls, Bohdalec, Czech Republic;* ³*L.K. Ernst Research Institute of Animal Husbandry, Dubrovitsy, Russia;* ⁴*Czech University of Life Sciences, Prague-Suchdol, Czech Republic.*
- MT152 **PRNP gene polymorphism in Polish native sheep breeds.**
 A. Piestrzynska-Kajtoch^{*}, G. Smolucha, A. Kawecka, M. Koscielny, and A. Miksza-Cybulska, *National Research Institute of Animal Production, Balice, Poland.*
- MT153 **Expression profiles of immune genes in milk somatic cells and MIR predicted mineral contents in milk as indicators of mastitis.**
 C. Marchitelli^{*1}, F. Signorelli¹, F. Napolitano¹, L. Buttazzoni¹, C. Grelet², A. Vanlierde², F. Dehareng², H. Soyeurt³, M. Crowe⁴, and GpluSE Consortium⁵, ¹*Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA)-Centro di Ricerca per la Produzione delle Carni e il Miglioramento genetico, Monterotondo, Italy;* ²*Centre Wallon De Recherches Agronomiques, Gembloux, Belgium;* ³*University of Liège, Gembloux, Belgium;* ⁴*UCD School of Veterinary Medicine, Dublin, Ireland;* ⁵*GpluSE Consortium, Dublin, Ireland.*
- MT154 **Comparison of the cattle leukocyte receptor complex with related livestock species.**
 J. C. Schwartz^{*1}, D. Heimeier¹, D. M. Bickhart², T. P. L. Smith³, J. F. Medrano⁴, and J. A. Hammond¹, ¹*The Pirbright Institute, Pirbright, Surrey, UK;* ²*USDA-ARS, Madison, WI, USA;* ³*USDA-ARS, Clay Center, NE, USA;* ⁴*University of California, Davis, Davis, CA, USA.*
- MT155 **Genetic variants in the innate immune system associated with *Salmonella* shedding and colonization in Ontario pigs.**
 M. H. Ainslie¹, V. Farzan^{1,2}, M. Jafarikia^{3,4}, and B. N. Lillie^{*1}, ¹*Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada;* ²*Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada;* ³*Canadian Centre for Swine Improvement Inc., Guelph, Ontario, Canada;* ⁴*Department of Animal Biosciences, Ontario Agricultural College, University of Guelph, Guelph, Ontario, Canada.*
- MT156 **Serum IL10 response to *Eimeria* challenge in commercial and backcross chickens.**
 K. Boulton^{*1}, M. Nolan², A. Psifidi¹, Z. Wu¹, K. Harman², R. Hawken³, M. Abrahamsen³, F. Tomley², D. Blake², and D. Hume¹, ¹*Roslin Institute, University of Edinburgh, Easter Bush, Midlothian, UK;* ²*Royal Veterinary College, University of London, Hatfield, UK;* ³*Cobb-Vantress Inc, Siloam Springs, AR, USA.*
- MT157 **Mammary epithelial cells, rather than professional immune cells dictate the pathogen species-specific immune reaction of the udder.**
 J. Hehl^{*1}, M. Koy², A. Berthold¹, H.-J. Schuberth², M. Weinert³, S. Engelmann³, C. Kühn¹, H.-M. Seyfert¹, and J. Günther¹, ¹*Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany;* ²*Immunology Unit, University of Veterinary Medicine Foundation, Hannover, Germany;* ³*Institute of Microbiology, Technical University Braunschweig, Braunschweig, Germany.*
- MT158 **Combining targeted next-generation sequencing and microarray analysis for cis expression quantitative loci analysis of the porcine innate immunome.**
 R. S. Fraser¹, H. N. Snyman^{1,2}, A. Meyer^{1,3}, J. D. Hammermüller¹, and B. N. Lillie^{*1}, ¹*Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada;* ²*Animal Health Centre, BC Ministry of Agriculture, Abbotsford, BC, Canada;* ³*Ontario Institute for Cancer Research, Toronto, Ontario, Canada.*
- MT159 **Haplotype resolution of leukocyte receptor complex in cattle through targeted enrichment and SMRT sequencing.**
 D. Heimeier^{*1}, J. Schwartz¹, D. Bickhart², T. Smith³, and J. Hammond¹, ¹*The Pirbright Institute, Woking, Surrey, UK;* ²*Cell Wall Biology and Utilization Research, USDA-ARS, Madison, WI, USA;* ³*Meat Animal Research Center, USDA-ARS, Clay Center, NE, USA.*

- MT160 **Identification of putative key transcription factors in canine macrophages after infection with *Leishmania infantum* and stimulation with a Toll like receptor-2 agonist.**
L. Solano-Gallego², S. Montserrat², F. Mayer¹, A. Castello¹, L. Alborch², S. Heath³, A. Esteve-Codina³, J. Gomez-Garrido³, R. A. Cigliano⁴, and A. Clop^{*1}, ¹Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Valles, Catalonia, Spain; ²Universitat Autònoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain; ³Centre Nacional d'Anàlisi Genòmica CNAG-CRG, Barcelona, Catalonia, Spain; ⁴Sequentia Biotech, Barcelona, Catalonia, Spain.
- MT161 **Genetic basis for resistance to avian influenza in commercial egg layer chicken lines.**
W. Drobik-Czwarono^{*1}, A. Wolc^{2,3}, J. Fulton³, T. Jankowski⁴, J. Arango³, P. Settar³, N. O'Sullivan³, and J. Dekkers², ¹Department of Animal Genetics and Breeding, Faculty of Animal Science, Warsaw University of Life Sciences, Warsaw, Poland; ²Department of Animal Science, Iowa State University, Ames, IA, USA; ³Hy-Line International, West Des Moines, IA, USA; ⁴NutriBiogen, Poznan, Poland.
- MT162 **The ligands and polymorphic residues of chicken MHC YF class I-like molecules.**
R. M. Goto¹, G. Gugiu¹, B. M. Stadtmueller², P. J. Bjorkman², and M. M. Miller^{*1}, ¹Beckman Research Institute, City of Hope, Duarte, CA, USA; ²California Institute of Technology, Pasadena, CA, USA.
- MT163 **Polymorphism in TLR2 in different dairy cattle breeds suggests immune functional modulation.**
M. Bartens^{*}, K. Tombacz, A. Gibson, and D. Werling, Department of Pathobiology and Population Sciences, Royal Veterinary College, University of London, Hatfield, UK.
- MT164 **Porcine bloodomics: Identification of porcine neutrophil-specific genes through gene expression correlations to neutrophil abundance and comparative expression data.**
G. Vella^{1,2}, M. Schroyen², H. Beiki², C. L. Loving³, and C. K. Tuggle^{*2}, ¹College of Veterinary Medicine, Iowa State University, Ames, IA, USA; ²Department of Animal Science, Iowa State University, Ames, IA, USA; ³Food Safety and Enteric Pathogens Research Unit, USDA-ARS-NADC, Ames, IA, USA.
- MT165 **Analysis of the genomic regions associated to response to coccidiosis caused by *Eimeria maxima* in broiler chickens.**
B. Bed Hom^{*1}, P.-v. d. L. Marie-Hélène¹, R. Hawken², and H. Edin¹, ¹INRA, Jouy-en-Josas, France; ²Cobb-Vantress Inc, Siloam Springs, AR, USA.
- MT166 **Enhanced genetic disease control with selection for low susceptibility and infectivity.**
S. Tsairidou^{*}, O. Anacleto, J. A. Woolliams, and A. Doeschl-Wilson, Roslin Institute, Edinburgh, UK.
- MT167 **Genome-wide CRISPR knockout screening for host factors involved in bovine herpes virus type 1 infection.**
W. Tan^{*1}, I. Dry¹, S. Lilloco², C. B. A. Whitelaw², and B. Dalziel¹, ¹Division of Infection and Immunity, the Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK; ²Division of Developmental Biology, the Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK.
- MT168 **Genetic individual variability of vaccine responses in pigs.**
F. Blanc^{*1}, G. Lemonnier¹, J. Leplat^{1,2}, E. Bouguyon³, Y. Billon⁴, J. Estelle¹, and C. Rogel-Gaillard¹, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ²CEA, DRF/IRCM/SREIT/LREG, Jouy-en-Josas, France; ³VIM-INRA-Université Paris-Saclay, Jouy-en-Josas, France; ⁴GenESI, INRA, Surgères, France.
- MT169 **The association of copy number variations with tick count in South African Nguni cattle.**
L. Pickering^{*1}, K. Dzama¹, F. Muchadeyi², and M. Wang², ¹Animal Science Department, University of Stellenbosch, Stellenbosch, Western Cape, South Africa; ²Agriculture Research Council Biotechnology Platform, Pretoria, Gauteng, South Africa.
- MT170 **Integrated network analysis for mRNAs and miRNAs expressed in PRRSV vaccinated peripheral blood mononuclear cells of pigs.**
M. A. Islam¹, C. Neuhoff^{*1}, S. Rony¹, C. Große-Brinkhaus¹, M. J. Uddin², M. Hölker¹, D. Tesfaye¹, E. Tholen¹, M. J. Pröll¹, and K. Schellander¹, ¹Institute of Animal Science, Animal Breeding and Husbandry Group, University of Bonn, Bonn, Germany; ²School of Veterinary Science, The University of Queensland, Gatton campus, QLD, Australia.
- MT171 **QTLs associated with resistance to MAP infection in Holstein-Friesian cattle.**
S. Mallikarjunappa^{*1,3}, M. Sargolzaei⁴, K. Meade², N. Karrow³, and S. Pant¹, ¹Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW, Australia; ²Teagasc Animal and Bioscience Research Department, Grange, Co. Meath, Ireland; ³Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada; ⁴The Semex Alliance, Guelph, ON, Canada.
- MT172 **Investigating genetic control of resistance to avian pathogenic *Escherichia coli* colonization in chickens.**
M. Monson^{*1}, M. Kaiser¹, A. Wolc^{1,2}, and S. Lamont¹, ¹Iowa State University, Ames, IA, USA; ²Hy-Line International, Dallas Center, IA, USA.

- MT173 **Integrative network genomics of the bovine host response to infection with *Mycobacterium bovis*.**
 T. J. Hall*¹, K. E. Killick^{1,2}, M. P. Mullen³, K. E. McLoughlin¹, N. C. Nalpas⁴, I. W. Richardson⁵, D. A. Magee¹, C. N. Correia¹, J. A. Browne¹, H. M. Vordermeier⁶, B. Villarreal-Ramos⁶, D. P. Berry⁷, E. Gormley⁸, S. V. Gordon^{2,8}, D. E. MacHugh^{1,2}, ¹*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland*; ²*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*; ³*Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland*; ⁴*Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany*; ⁵*IdentiGEN Ltd, Blackrock Business Park, Blackrock, Dublin, Ireland*; ⁶*Animal and Plant Health Agency (APHA), Weybridge, Addlestone, Surrey, UK*; ⁷*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland*; ⁸*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland.*

Genome Edited Animals

- MT174 **The role of leptin in nonalcoholic obesity, diabetes and hepatic fibrosis.**
 T. Tan*^{1,2}, Z. Song¹, Y. Xing^{1,2}, X. Hu^{1,2}, and N. Li^{1,2}, ¹*College of Biological Sciences, China Agricultural University, Beijing, China*; ²*State Key Laboratory for Agro-Biotechnology, Beijing, China.*
- MT175 **Editing the future of the domestic pig.**
 S. Lilloco*¹, C. Proudfoot¹, C. Burkard¹, F. Urnov², J. Oatley³, B. Telugu⁴, A. Mileham⁵, and B. Whitelaw¹, ¹*The Roslin Institute, Roslin, Midlothian, UK*; ²*Sangamo Biosciences, Richmond, CA, USA*; ³*Washington State University, Pullman, WA, USA*; ⁴*University of Maryland, Beltsville, MD, USA*; ⁵*Genus Plc, DeForest, WI, USA.*
- MT176 **Pest-off: Could gene drive help drive out Australia's invasive pest animals?**
 M. Tizard*¹, T. Strive², P. Brown³, S. Henry², A. Sunarto¹, K. McColl¹, C. Cooper¹, D. Moro⁴, M. Byrne⁴, and T. Doran¹, ¹*CSIRO Health & Biosecurity, Australian Animal Health Laboratory, Geelong, Victoria, Australia*; ²*CSIRO Health & Biosecurity, Black Mountain Laboratory, Canberra, ACT, Australia*; ³*CSIRO Agriculture & Food, Black Mountain Laboratory, Canberra, ACT, Australia*; ⁴*Department of Parks and Wildlife, Kensington, Western Australia, Australia.*
- MT177 **Developing and exploiting new technologies to advance understanding of the avian immune system.**
 A. Balic*¹, H. Sang¹, and M. McGrew¹, *The Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK.*

Horse Genetics and Genomics

- MT178 **A genome-wide association study for body weight in Japanese thoroughbred racehorses identified candidate regions near *LCORL*, *ZFAT*, and *MSTN* genes.**
 T. Tozaki*¹, M. Kikuchi¹, H. Kakoi¹, K.-I. Hirota¹, and S.-I. Nagata¹, *Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan.*
- MT179 **Investigation of the association between the *DMRT3* 'Gait keeper' mutation and early career performance in Coldblooded trotters.**
 K. J. Fegraeus*¹, C. Olsson², L. Andersson^{3,4}, C. F. Ihler⁵, E. Strand⁵, G. Lindgren¹, and B. D. Velie¹, ¹*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*; ²*The Swedish Trotting Association, Bromma, Sweden*; ³*Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden*; ⁴*Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA*; ⁵*Department of Companion Animal Clinical Sciences, Faculty of Veterinary Medicine, Norwegian University of Life Sciences, Oslo, Norway.*
- MT180 **Whole-genome sequencing of the Jeju, Jeju crossbred, and Thoroughbred horse breeds.**
 H. Seong¹, N.-Y. Kim², D. C. Kim³, N.-H. Hwang¹, I.-C. Yang¹, A. Jang¹, J.-D. Kim¹, J.-W. Choi*¹, W.-H. Chung⁴, and J.-B. Kim¹, ¹*Kangwon National University, Chuncheon, Republic of Korea*; ²*Subtropical Animal Research Institute, National Institute of Animal Science, RDA, Jeju, Republic of Korea*; ³*Jeju Special Self-Governing Province Livestock Promotion, Jeju, Republic of Korea*; ⁴*Division of Nutrition and Metabolism Research, Research Group of Gut Microbiome, Sungnam, Republic of Korea.*
- MT181 **Changes in the gene expression profile of equine arthritic joint tissues induced by the administration of allogeneic mesenchymal stem cells.**
 L. Barrachina*^{1,2}, A. R. Remacha¹, A. Romero^{1,2}, F. J. Vázquez^{1,2}, A. Vitoria^{1,2}, P. Zaragoza¹, and C. Rodellar¹, ¹*Laboratorio de Genética Bioquímica LAGENBIO (Universidad de Zaragoza), Instituto Agroalimentario de Aragón (Universidad de Zaragoza-CITA); Instituto de Investigación Sanitaria de Aragón (IIS), Zaragoza, Spain*; ²*Servicio de Cirugía y Medicina Equina, Hospital Veterinario, Universidad de Zaragoza, Zaragoza, Spain.*

- MT182 Using IgE levels as phenotypes to identify genomic regions associated with insect bite hypersensitivity.**
C. Lamberigts*¹, L. François², B. Velie³, A. Stinckens⁴, H. Hoskens⁴, S. Blott⁵, S. Tinel², L. Peeters⁶, H. Savelkoul⁷, E. Tijhaar⁷, G. Lindgren³, S. Janssens², B. Ducro⁸, N. Buys², A. Schurink⁸, ¹Research Group Livestock Physiology, Department of Biosystems, KU Leuven, Leuven, Belgium; ²Research Group Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium; ³Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁴Laboratory for Genetic Epidemiology, Department of Human Genetics, KU Leuven, Leuven, Belgium; ⁵School of Veterinary Medicine & Science, University of Nottingham, Leicestershire, UK; ⁶Biomedical Research Institute, Hasselt University, Diepenbeek, Belgium; ⁷Cell Biology and Immunology Group, Wageningen University & Research, Wageningen, the Netherlands; ⁸Animal Breeding and Genomics Centre, Wageningen University & Research, Wageningen, the Netherlands.
- MT183 The curly hair trait in the American Bashkir Curly Horse.**
A. Thomer*¹, K. Jung¹, M. Hewicker-Trautwein², O. Distl¹, and J. Metzger¹, ¹Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover Foundation, Hannover, Niedersachsen, Germany; ²Department of Pathology, University of Veterinary Medicine Hannover Foundation, Hannover, Niedersachsen, Germany.
- MT184 Expression patterns of equine skin tissue neoplasia combined with motility and invasiveness of corresponding primary skin fibroblasts.**
W. WitarSKI*, P. Podstawski, K. Ropka-Molik, K. Kowalska, T. Szmatoła, A. Gurgul, and M. Bugno-Poniewierska, National Research Institute of Animal Production, Krakow, Poland.
- MT185 Circulating miRNAs in serum as noninvasive biomarkers for equine asthma.**
M. Kraft*^{1,2}, A. Pacholewska^{1,2}, V. Gerber¹, and V. Jagannathan², ¹Swiss Institute of Equine Medicine, University of Bern and Agro-scope, Bern, Switzerland; ²Institute of Genetics, University of Bern, Bern, Switzerland.
- MT186 Assembly and analysis of subchondral bone and articular cartilage transcriptomes in neonatal and adult horses.**
A. Kemper*¹, M. McCue², and A. McCoy¹, ¹University of Illinois, Champaign, IL, USA; ²University of Minnesota, St Paul, MN, USA.
- MT187 Design and use of the MNEc670k SNP array for precision SNP imputation to millions of markers in 15 horse breeds.**
R. Schaefer*¹, S. Beeson¹, J. Mickelson², and M. McCue¹, ¹Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA; ²Department of Veterinary and Biomedical Science, University of Minnesota, St Paul, MN, USA.
- MT188 Genome-wide analyses of the Jeju, Thoroughbred, and Jeju crossbred horse populations using the high-density SNP array.**
N. Y. Kim*¹, H. Seong², D. C. Kim⁴, I. C. Cho¹, P. N. Seong¹, J. K. Son¹, S. M. Shin¹, S. H. Park¹, J. H. Woo¹, N. G. Park¹, W.-H. Chung³, and J.-W. Choi², ¹Subtropical Animal Research Institute, National Institute of Animal Science, RDA, Jeju, Jeju, Republic of Korea; ²College of Animal Life Science, Kangwon National University, Chuncheon, Kangwon, Republic of Korea; ³Division of Nutrition and Metabolism Research, Research Group of Gut Microbiome, Korea Food Research Institute, Sungnam, Gyeonggi, Republic of Korea; ⁴Jeju Special Self-Governing Province Livestock Promotion Agency, Jeju, Jeju, Republic of Korea.
- MT189 Genetic characterization of native horses in Myanmar and Laos using haplotypes of mitochondrial DNA and Y-chromosomal markers.**
Y. Okuda*¹, H. Moe², K. Moe², B. Kounnavongsa³, S. Keonouchanh³, B. Bouahom³, T. Shimogiri⁴, H. Mannen⁵, M. Kanemaki⁶, Y. Yamamoto⁷, and T. Kunieda¹, ¹Okayama University, Okayama, Okayama, Japan; ²University of Veterinary Science, Yezin, Nay Pyi Taw, Myanmar; ³National Agriculture and Forestry Research Institute, Xaythany, Vientiane, Lao PDR; ⁴Kagoshima University, Kagoshima, Kagoshima, Japan; ⁵Kobe University, Kobe, Hyogo, Japan; ⁶Institute of Animal Science, Nagoya, Aichi, Japan; ⁷Hiroshima University, Higashi-Hiroshima, Hiroshima, Japan.
- MT190 Genetic characteristics of Kazakhstan native horses.**
H. Ezo*¹, Y. Okuda¹, M. Nishibori², H. Mannen³, Y. Takahashi⁴, K. Nomura⁴, T. Yamagata⁵, Y. Yamamoto², K. Tsunoda⁶, M. Bakhtin⁷, P. Kazymbet⁷, M. Alykhan⁸, M. Suleimenov⁸, O. Safronova⁹, T. Kunieda¹, ¹Okayama University, Okayama, Okayama, Japan; ²Hiroshima University, Higashihiroshima, Hiroshima, Japan; ³Kobe University, Kobe, Hyogo, Japan; ⁴Tokyo University of Agriculture, Setagaya, Tokyo, Japan; ⁵Nagoya University, Nagoya, Aichi, Japan; ⁶Showa University, Shinagawa, Tokyo, Japan; ⁷Astana Medical University, Astana, Akmola, Kazakhstan; ⁸Institute of Zoology, Almaty, Almaty, Kazakhstan; ⁹LLP Kazak tulpar, Kostanay, Kostanay, Kazakhstan.
- MT191 The most over-represented molecular pathways regulated during training in Arabian horse muscle tissue.**
K. Ropka-Molik*¹, M. Stefaniuk-Szmukier², K. Zukowski¹, and K. Piórkowska¹, ¹National Research Institute of Animal Production, Balice, Poland; ²University of Agriculture in Cracow, Cracow, Poland.
- MT192 Genomic and pedigree analysis of population structure of Old Kladruber horse.**
L. Vostry^{1,2}, H. Vostra-Vydrova², J. Bauer³, A. Kranjčevićová*^{1,2}, and J. Příbyl², ¹Czech University of Life Sciences Prague, Prague, Czech Republic; ²Institut of Animal Science, Prague, Czech Republic; ³Czech-Moravian Breeders Corporation, Hradistko, Czech Republic.

- MT193 Population structure and admixture in closely related Czech draft horse populations.**
 H. Vostra-Vydrova², L. Vostry^{1,2}, N. Moravcikova³, B. Hofmanova¹, Z. Vesela², A. Svitakova^{*2}, J. Schmidova², and R. Kasarda³, ¹*Czech University of Life Sciences Prague, Prague, Czech Republic*; ²*Institut of Animal Science, Prague, Czech Republic*; ³*Slovak University of Agriculture in Nitra, Nitra, Slovak Republic*.
- MT194 Analysis of DNA methylation profiles of genes encoding miR-101 and -200a in equine sarcoids.**
 K. Pawlina^{*1}, E. Semik¹, A. Fornal¹, T. Zabek¹, C. Koch², K. Mählmann^{2,3}, M. Witkowski⁴, and M. Bugno-Poniewierska¹, ¹*National Research Institute of Animal Production, Balice, Poland*; ²*University of Bern and Agroscope, Bern, Switzerland*; ³*Free University of Berlin, Berlin, Germany*; ⁴*University of Agriculture, Krakow, Poland*.
- MT195 Analysis of the influence of DNA methylation on altered expression of S100A14 gene in equine sarcoids.**
 E. Semik^{*1}, T. Zabek¹, A. Fornal¹, K. Pawlina¹, J. Klukowska-Rötzler², C. Koch², K. Mählmann^{2,3}, and M. Bugno-Poniewierska¹, ¹*National Research Institute of Animal Production, Balice, Poland*; ²*University of Bern and Agroscope, Bern, Switzerland*; ³*Freie Universität Berlin, Berlin, Germany*.
- MT196 Genetic diversity of Malopolski horse stallions.**
 A. Fornal^{*}, A. Radko, and A. Piestrzynska-Kajtoch, *National Research Institute of Animal Production, Krakow, Poland*.
- MT197 The known variants of the TBX3 gene do not explain the variability of grullo coat color shades in Polish Primitive Horse (Konik).**
 J. Cieslak^{*1}, L. Wodas¹, and M. Mackowski^{1,2}, ¹*Department of Horse Breeding, Poznan University of Life Sciences, Poznan, Poland*; ²*Horse Genetic Markers Laboratory, Poznan University of Life Sciences, Poznan, Poland*.
- MT198 Transcriptome profiling and comparison of whole blood and gluteus medius muscle of Arabian horses during 24 weeks of race training.**
 M. Stefaniuk-Szmukier^{*1}, K. Ropka-Molik², K. Zukowski², K. Piórkowska², and M. Bugno-Poniewierska², ¹*University of Agriculture in Cracow, Cracow, Poland*; ²*National Research Institute of Animal Production, Balice, Poland*.
- MT199 Characterisation of a congenital cardiac defect in an Arabian horse family.**
 N. A. Hamilton^{*1}, C. Halliday², R. Crisman³, C. M. Wade¹, and N. Beijerink², ¹*School of Life and Environmental Sciences, Faculty of Science, University of Sydney, Sydney, NSW, Australia*; ²*Sydney School of Veterinary Science, Faculty of Science, University of Sydney, Sydney, NSW, Australia*; ³*Somersby Animal Hospital, Somersby, NSW, Australia*.
- MT200 Withdrawn**
- MT201 Evidence for introgression of a CXCL16 allele from non-caballine horses to caballine horses.**
 E. Bailey^{*1}, T. Kalbfleisch², J. C. Stevens³, J. Eberth¹, J. S. DePriest², and U. B. R. Balasuriya¹, ¹*University of Kentucky, Lexington, KY, USA*; ²*University of Louisville, Louisville, KY, USA*; ³*Genomics GPS, Guilford, CT, USA*.
- MT202 Genetic diversity and population structure in Chinese Mongolian horses.**
 H. Han^{*1}, K. Bryan¹, W. Shiraigol², M. Dugarjaviin², and E. Hill¹, ¹*UCD School of Agriculture and Food Science, Dublin, Ireland*; ²*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China*.
- MT203 Cuanhama horses from Angola as a possible expression of centuries of slave trade.**
 J. L. Vega-Pla^{*1}, C. Ribeiro², O. Cortes³, F. T. P. S. Sereno⁴, M. R. T. Costa⁵, and L. Telo da Gama⁶, ¹*Laboratorio de Investigacion Aplicada. Servicio de Cria Caballar de las Fuerzas Armadas, Cordoba, Spain*; ²*Instituto Superior Politecnico da Tudavala, Lubango, Angola*; ³*Departamento de Produccion Animal, Universidad Complutense de Madrid, Madrid, Spain*; ⁴*Faculdade de Agronomia e Medicina Veterinaria, Brasilia, Brazil*; ⁵*Empresa Brasileira de Pesquisa Agropecuaria, Amazonia Oriental, Belem, Brazil*; ⁶*Faculdade de Medicina Veterinaria, Universidade de Lisboa, Lisboa, Portugal*.
- MT204 Imputation of microsatellite alleles from dense SNP genotypes of Mangalarga Marchador Horses.**
 K. T. Souza^{*1}, C. T. F. S. Diniz², R. M. G. Lima¹, C. L. P. Meneses¹, and C. B. N. Campos¹, ¹*Linhagen Biotecnologia, Belo Horizonte, MG, Brazil*; ²*Pontificia Universidade Catolica de Minas Gerais, Belo Horizonte, MG, Brazil*.
- MT205 Novel KIT variants underlying dominant white phenotypes in horses.**
 R. Hoban¹, K. Castle², N. Hamilton³, and B. Haase^{*1}, ¹*Sydney School of Veterinary Science, Faculty of Science, University of Sydney, Sydney, NSW, Australia*; ²*Practical Horse Genetics, Redfern, NSW, Australia*; ³*School of Life and Environmental Science, Faculty of Science, University of Sydney, Sydney, NSW, Australia*.
- MT206 A genome-wide association analysis of exercise-induced pulmonary haemorrhage in Thoroughbred racehorses.**
 S. C. Blott^{*} and H. L. Cunningham, *University of Nottingham, School of Veterinary Medicine and Science, Sutton Bonington, Leicestershire, UK*.

- MT207 Signatures of airway hyper-responsiveness in the equine pasture asthma-restricted lung transcriptome.**
S. Mack¹, T. Mansour¹, J. Bowser², A. Eddy², C. Mochal², A. Claude², A. Cooley², M. Johnson², and C. Swiderski*², ¹College of Veterinary Medicine, University of California, Davis, CA, USA; ²College of Veterinary Medicine, Mississippi State University, Mississippi State, MS, USA.
- MT208 Mapping transcriptional regulation at multiple layers using ChRO-seq.**
T. Chu^{1,2}, L. Choate^{1,2}, Z. Wang^{1,2}, E. Rice^{1,2}, and C. Danko*^{1,2}, ¹Baker Institute for Animal Health, Ithaca, NY, USA; ²Cornell University, Ithaca, NY, USA.
- MT209 EquCab3.**
T. Kalbfleisch*¹, M. DePriest¹, L. Orlando², and J. MacLeod³, ¹University of Louisville, Louisville, KY, USA; ²University of Copenhagen, Copenhagen, Denmark; ³University of Kentucky, Lexington, KY, USA.
- MT210 Epigenetic characterization of centromeric chromatin in equids.**
S. G. Nergadze¹, R. Gamba¹, F. M. Piras¹, E. Cappelletti¹, M. Corbo¹, F. Gozzo¹, D. Miller², D. Antczak², E. Raimondi¹, K. Sullivan³, and E. Giulotto*¹, ¹University of Pavia, Department of Biology and Biotechnology, Pavia, Italy; ²Cornell University, College of Veterinary Medicine, Ithaca, NY, USA; ³National University of Ireland, Centre for Chromosome Biology, Galway, Ireland.
- MT211 Zooming in on chronic progressive lymphedema using a high-density array in the Belgian draught horse.**
L. François*¹, A. Schurink², B. Velie³, A. Stinckens¹, S. Blott⁴, B. Ducro², C. Lamberigts⁵, S. Tinel¹, K. De Keyser¹, M. Oosterlinck⁶, G. Lindgren³, S. Janssens¹, and N. Buys¹, ¹Research Group Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium; ²Animal Breeding and Genomics Centre, Wageningen University & Research, Wageningen, the Netherlands; ³Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁴School of Veterinary Medicine & Science, University of Nottingham, Leicestershire, United Kingdom; ⁵Research Group Livestock Physiology, Department of Biosystems, KU Leuven, Leuven, Belgium; ⁶Department of Surgery and Anesthesiology of Domestic Animals, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium.
- MT212 Unraveling gene function using co-expression networks in the domestic horse.**
R. Schaefer*¹, E. Norton¹, J. Mickelson², and M. McCue¹, ¹Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA; ²Department of Veterinary and Biomedical Science, University of Minnesota, St Paul, MN, USA.
- MT213 Progress toward functional annotation of the equine genome.**
J. Petersen*¹, E. Burns², M. Bordbari², E. Scott³, B. Ming-Whitfield², V. Affolter², C. Ramirez Alanis², M. Barro², M. Mack², G. Gianino², F. Gianino², E. Giulotto³, K. Hilburger², T. Kalbfleisch⁴, J. MacLeod⁵, M. Mienaltowski², S. Katzman², T. Leeb⁶, T. Raudsep⁷, P. Saelao², S. Vig², H. Zhou², R. Bellone², and C. Finno², ¹University of Nebraska-Lincoln, Lincoln, NE, USA; ²University of California-Davis, Davis, CA, USA; ³University of Pavia, Pavia, Italy; ⁴University of Louisville, Louisville, KY, USA; ⁵University of Kentucky, Lexington, KY, USA; ⁶University of Bern, Bern, Switzerland; ⁷Texas A&M, College Station, TX, USA.
- MT214 The potential of Y-chromosomal markers for individual lineage tracking in horses.**
S. Felkel¹, D. Rigler¹, C. Vogl¹, M. Neuditschko², S. Rieder², V. Jagannathan³, T. Leeb³, T. Rattei⁴, C. Schlotterer⁵, G. Brem¹, and B. Wallner*¹, ¹Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria; ²Agroscope, Swiss National Stud Farm, Avenches, Switzerland; ³Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland; ⁴Department of Microbiology and Ecosystems Science, Division of Computational Systems Biology, University of Vienna, Vienna, Austria; ⁵Institute of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria.
- MT215 Genetic contributions to measured speed in Thoroughbred racehorses during early training.**
G. Farries*¹, B. A. McGivney, K. F. Gough, L. M. Katz, and E. W. Hill, *University College Dublin, Belfield, Dublin, Ireland.*
- MT216 Genetic diagnosis of sex chromosome aberrations in horses based on analysis of microsatellite and X- and Y-linked markers.**
J. A. Bouzada*¹, J. M. Lozano, M. R. Maya, A. Trigo, I. Bonet, F. Castillo, J. Fernández-León, T. Mayoral, E. Anadón, and L. B. Pitarch, *Laboratorio de Genética y Control, Algete, Madrid, Spain.*
- MT217 Withdrawn**
- MT218 Genetic diversity, evolution and selection in the major histocompatibility complex DRB and DQB genes in the family Equidae.**
M. Klumplerova¹, P. Splichalova¹, J. Oppelt², P. Musilova³, S. Kubickova³, R. Vodicka⁴, J. Vahala⁵, L. Orlando⁶, and P. Horin*¹, ¹Ceitec VFU, University of Veterinary and Pharmaceutical Sciences, Dept. of Animal Genetics, Brno, Czech Republic; ²Ceitec MU, Masaryk University, National Centre for Biomolecular Research, Faculty of Science, Brno, Czech Republic; ³Veterinary Research Institute, Dept. of Reproduction and Genetics, Brno, Czech Republic; ⁴Zoo Prague, Prague, Czech Republic; ⁵Zoo Dvur Kralove nad Labem, Dvur Kralove nad Labem, Czech Republic; ⁶Centre for GeoGenetics Natural History Museum of Denmark University of Copenhagen, Copenhagen, Denmark.

- MT219 **Whole-genome sequencing reveals two Shetland pony specific variants affecting body size and shape.**
 J. Metzger*, F. Naccache, A. Christmann, and O. Distl, *Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover Foundation, Hannover, Niedersachsen, Germany.*
- MT220 **Preliminary results of genetic monitoring of the occurrence of three genetic diseases (CA, SCID; LFS) in Arabian horses from Poland.**
 M. Bugno-Poniewierska*¹, M. Stefaniuk-Szmukier², A. Piestrzynska-Kajtoch¹, A. Fornal¹, and K. Ropka-Molik¹, ¹*National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Krakow, Poland;* ²*University of Agriculture, Department of Horse Breeding, Kraków, Poland.*
- MT221 **Protein-coding gene and transcript sequences quantify progress toward the new equine reference genome assembly.**
 M. S. DePriest*^{1,2}, J. N. MacLeod², and T. S. Kalbfleisch¹, ¹*University of Louisville, Louisville, KY, USA;* ²*University of Kentucky, Lexington, KY, USA.*

ISAG-FAO Genetic Diversity

- MT222 **Genome-wide assessment of genetic diversity and population structure in Chinese indigenous cattle.**
 W. Zhang*, J. Li, Y. Chen, L. Xu, L. Zhang, X. Gao, and H. Gao, *Institute of Animal Science, Chinese Academy of Agriculture Science, Beijing, China.*
- MT223 **Phylogenetic analysis of Kazakhstani goats using mtDNA HV1 and SRY gene sequences.**
 R. Tabata*¹, S. Sasazaki¹, M. Bakhtin², P. Kazymbet², M. Alyan³, M. Suleimenov³, M. Nishibori⁴, and H. Mannen¹, ¹*Graduate School of Agricultural Science, Kobe University, Kobe-shi, Japan;* ²*Astana Medical University, Radiobiological Research Institute, Astana, Kazakhstan;* ³*Institute of Zoology, Almaty, Japan;* ⁴*Graduate School of Biosphere Science, Hiroshima University, Higashi-Hiroshima, Japan.*
- MT224 **Genetic diversity and admixture of the Mexican Lidia population inferred from medium-density genotypic data.**
 P. G. Eusebi*, O. Cortés, S. Dunner, and J. Cañon, *Universidad Complutense de Madrid, Madrid, Spain.*
- MT225 **Novel Y chromosomal haplotype of domestic sheep (*Ovis aries*) in China.**
 W. Yan* and L. Xu, *Faculty of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*
- MT226 **Analysis on geographical distribution and characteristics of Chinese indigenous chicken breeds.**
 Z. Mengmeng*, X. Ran, and W. Keliang, *China Agricultural University, Haidian District, Beijing, China.*
- MT227 **Genetic structure and relationships among 11 cattle populations using indel markers.**
 H. Yamanaka*¹, S. Sasazaki¹, M. Lwin², H. Moe³, T. Shimogiri³, and H. Mannen¹, ¹*Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Japan;* ²*University of Veterinary Science, Yezin, Myanmar;* ³*Faculty of Agriculture, Kagoshima University, Kagoshima, Japan.*
- MT228 **Genetic analysis of fauna from the Early Neolithic site of Chaves, Huesca, Spain.**
 I. Ureña*^{1,2}, H. Bolívar³, M. A. Galindo-Pellicena², J. L. Arsuaga², C. Ginja¹, and C. Valdiosera^{4,2}, ¹*CIBIO-InBIO—Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, Vairão, Portugal;* ²*Centro Mixto UCM-ISCIH de Evolución y Comportamiento humanos, Madrid, Spain;* ³*Laboratorio de Evolución humana, Departamento de Ciencias Históricas y Geografía, Universidad de Burgos, Burgos, Spain;* ⁴*Department of Archaeology and History, La Trobe University, Melbourne, VIC, Australia.*
- MT229 **Genetic analysis of the Estonian Native horse.**
 C. Castaneda¹, R. Juras*¹, T. Raudsepp¹, I. Randlaht², and E. G. Cothran¹, ¹*Texas A&M University, College Station, TX, USA;* ²*Estonian Native Horse Conservation Society, Estonia.*
- MT230 **Genetic relationships and admixture between European and American local pig breeds.**
 A. M. Martínez*^{1,2} and B. Consortium¹, ¹*University of Cordoba, Cordoba, Spain;* ²*Animal Breeding Consulting S.L, Cordoba, Spain.*
- MT231 **Genetic diversity in a Colombian population of Brahman cattle breeds Mantel and spatial autocorrelation analysis.**
 D. A. Montano*, V. Castaneda, and G. Acuna, *Escuela de Artes, Letras y Ciencias, Bogotá, Colombia.*

- MT232 **Genetic diversity among domestic goats (*Capra hircus*) and wild goats (*Capra aegagrus*) in Turkey.**
 I. S. Yildirim¹, M. Nizamlioglu¹, M. D. Oncu², E. K. Bastanlar², and Z. Bulut^{*1}, ¹*Selcuk University, Faculty of Veterinary Medicine, Departments of Biochemistry, Konya, Turkey;* ²*TUBITAK-MAM, Genetic Engineering and Biotechnology Institute, Gebze, Kocaeli, Turkey.*
- MT233 **Comparative genome-wide characterisation of five rare British Isles cattle breeds.**
 P. Flynn^{*1,2}, J. Carlsson², and D. Berry³, ¹*Weatherbys DNA Laboratory, Johnstown, Naas, Co. Kildare, Ireland;* ²*University College Dublin, School of Biology & Environmental Science, UCD, Belfield, Dublin, Ireland;* ³*Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.*
- MT234 **Genetic continuity of maternal lineages in Iberian cattle populations since Roman times.**
 L. Simões¹, A. E. Pires^{2,3}, C. Detry⁴, I. Ureña², E. Svensson¹, J. Matos⁵, C. Rodriguez-Fernández⁶, A. M. Arruda⁴, I. Fernandes⁷, S. Davis³, A. Götherström⁸, and C. Ginja^{*2}, ¹*Department of Organismal Biology, Uppsala University, Uppsala, Sweden;* ²*CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, Vairão, Portugal;* ³*Laboratório de Arqueociências-InBIO, DGCP, Lisboa, Portugal;* ⁴*UNIARQ, Centro de Arqueologia da Universidade de Lisboa, Faculdade de Letras, Universidade de Lisboa, Lisboa, Portugal;* ⁵*Grupo de Biologia Molecular, Instituto Nacional de Investigação Agrária e Veterinária, Oeiras, Portugal;* ⁶*Departamento de Historia, Facultad de Filosofía y Letras, Universidad de León, León, Spain;* ⁷*Câmara Municipal de Palmela, Palmela, Portugal;* ⁸*Archaeological Research Laboratory, Department of Archaeology and Ancient History, Stockholm University, Stockholm, Sweden.*
- MT235 **An ancient genomic perspective on the horse domestication process.**
 P. Librado¹, A. Fages^{1,2}, C. Gaunitz¹, N. Khan¹, K. Hanghøj^{1,2}, C. Gamba¹, C. Der Sarkissian¹, M. Leonardi¹, M. Schubert¹, and L. Orlando^{*1,2}, ¹*University of Copenhagen, Centre for GeoGenetics, Natural History Museum of Denmark, Copenhagen, Denmark;* ²*Université de Toulouse, University Paul Sabatier (UPS), Laboratoire AMIS, CNRS UMR 5288, Toulouse, France.*
- MT236 **Genome-wide assessment of genetic diversity in the Synbreed Chicken Diversity Panel.**
 S. Weigend^{*1}, A. Weigend¹, D. Malomane², and H. Simianer², ¹*Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt-Mariensee, Höltystraße, Germany;* ²*University of Göttingen, Animal Breeding and Genetics Group, Göttingen, Albrecht-Thaer-Weg 3, Germany.*

Microbiomes

- MT237 **16SrRNA amplicon sequencing of mock microbial populations to investigate DNA extraction methodology, primer selection and PCR cycles.**
 E. McGovern^{*1,2}, M. S. McCabe¹, A. K. Kelly², D. A. Kenny¹, P. Cormican¹, and S. M. Waters¹, ¹*Teagasc, Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Grange, Dunsany, County Meath, Ireland;* ²*University College Dublin, School of Agriculture and Food Science, Belfield, Dublin, Ireland.*
- MT238 **Characterization of the gut microbiome along the digestive tract of Iberian pigs.**
 D. Crespo-Piazuelo^{*1,2}, J. Estellé³, M. Revilla^{1,2}, L. Criado-Mesas^{1,2}, Y. Ramayo-Caldas³, C. Óvilo⁴, A. I. Fernández⁴, M. Ballester⁵, and J. M. Folch^{1,2}, ¹*Plant and Animal Genomics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB Consortium, Bellaterra, Barcelona, Spain;* ²*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain;* ³*Génétique Animale et Biologie Intégrative (GABI), Institut National de la Recherche Agronomique (INRA), AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* ⁴*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain;* ⁵*Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Caldes de Montbui, Barcelona, Spain.*
- MT239 **Host genetics influences gut microbiota composition in pigs.**
 J. Estellé^{*1}, N. Mach^{1,2}, Y. Ramayo-Caldas³, F. Levenez², G. Lemonnier¹, C. Denis¹, M. Berri³, M.-J. Mercat⁴, Y. Billon⁵, J. Doré², C. Larzul^{1,6}, P. Lepage², and C. Rogel-Gaillard¹, ¹*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* ²*MICALIS, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* ³*ISP, INRA, Université de Tours, Nouzilly, France;* ⁴*IFIP-BIO-PORC, Pôle génétique, Le Rheu, France;* ⁵*GENESI, INRA, Surgères, France;* ⁶*GenPhySe, INRA, INP, ENSAT, Université de Toulouse, Castanet-Tolosan, France.*
- MT240 **Advanced bioinformatics and molecular analysis of whole-genome-shotgun metagenomics data from rumen microbiomes reveals remarkable diversity, structure and function.**
 M. Watson^{*1}, R. Stewart¹, A. Warr¹, T. Snelling³, M. Auffret², A. Walker³, R. Wallace³, and R. Roehe², ¹*The Roslin Institute, University of Edinburgh, Easter Bush, Scotland;* ²*SRUC, Easter Bush, Scotland;* ³*The Rowett Institute, University of Aberdeen, Aberdeen, Scotland.*

MT241 **The MetaPig project: Leveraging potentials in pig genomics and metagenomics to boost feed efficiency and gut health in modern pig production.**
 P. Karlskov-Mortensen*¹, A. Ø. Pedersen¹, N. Canibe², P. Kiilerich³, K. Kristiansen³, and M. Fredholm¹, ¹Department of Veterinary and Animal Science, Faculty of Health & Medical Sciences, University of Copenhagen, Frederiksberg, Denmark; ²Department of Animal Science, Aarhus University, Tjele, Denmark; ³Department of Biology, Faculty of Science, University of Copenhagen, Copenhagen, Denmark.

MT242 **Bovine genes regulate the rumen microbial composition.**
 O. Gonzalez-Recio*¹, I. Zubiria², A. García-Rodríguez², A. Hurtado³, and R. Atxaerandio², ¹Departamento de Mejora Genética Animal. Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain; ²Departamento de Producción Animal. NEIKER-Tecnalia. Granja Modelo de Arkaute, Vitoria-Gasteiz, Alava, Spain; ³Departamento de Salud Animal. NEIKER-Tecnalia, Derio, Bilbao, Spain.

Pig Genetics and Genomics

MT243 **Quantitative trait loci (QTL) mapping of growth and conformation traits in F₂ intercross progenies of Nigerian indigenous and Large white pigs.**
 V. M. O. Okoro*, C. L. Okoro, and C. A. Mbajiorgu, University of South Africa, Johannesburg, Gauteng, South Africa.

MT244 **Convergent and divergent genetic changes in Chinese and European pig domestication.**
 J. Wang*, H. Zou, N. Li, X. Hu, Y. Zhao, and Y. Zhao, China Agricultural University, Beijing, China.

MT245 **Identification and prioritization of SNPs potentially involved in transcriptomic and phenotypic differences between pure and crossbred Iberian pigs.**
 M. Ayuso*^{1,2}, J. Garrayo³, A. Fernandez³, Y. Nuñez³, R. Benitez³, C. Garcia-Contreras³, M. Vazquez-Gomez¹, B. Isabel¹, A. Fernandez³, A. Rey¹, A. Golzalez-Bulnes⁴, C. Lopez-Bote¹, and C. Ovilo³, ¹Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense, Madrid, Spain; ²Applied Veterinary Morphology, Department of Veterinary Sciences, University of Antwerp, Wilrijk, Antwerp, Belgium; ³Departamento de Mejora Genética Animal, INIA, Madrid, Spain; ⁴Comparative Physiology Lab SGIT-INIA, Madrid, Spain.

MT246 **Investigating the genomic basis of pigs that have died in transit.**
 F. Bertolini*¹, K. Zurbrigg², T. van Dreumel², T. O'Sullivan², and M. F. Rothschild¹, ¹Department of Animal Science, Iowa State University, Ames, IA, USA; ²University of Guelph, Guelph, Ontario, Canada.

MT247 **GWAS on coat color in wuzhishan pig using the Porcine SNP80 BeadChip.**
 X. Qiao* and F. Meiyang, China Agricultural University, Beijing, Beijing, China.

MT248 **Genetic polymorphism of candidate genes in SSC13q41 region affecting Indian pigs differentially adhesive to diarrhoeagenic *E.coli*.**
 N. R. Sahoo*¹, R. Sinha^{1,2}, C. Rawat¹, W. SS¹, P. Kumar¹, S. Qureshi¹, A. Kumar¹, S. Kumar¹, and B. Bhushan¹, ¹ICAR-Indian Veterinary Research Institute, Izatnagar, UP, India; ²ICAR-National Dairy Research Institute, Karnal, Haryana, India.

MT249 **Genome-wide analysis reveals important contribution of structure variants to environmental adaptations and artificial selections in Chinese pigs.**
 R. Yang*^{1,2}, S. Fang², J. Wang², C. Zhang², R. Zhang², D. Liu⁴, Y. Zhao^{1,2}, X. Hu^{2,3}, and N. Li², ¹Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University, Beijing, China; ²State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, China; ³National Engineering Laboratory for Animal Breeding, China Agricultural University, Beijing, China; ⁴Institute of Animal Industry, Heilongjiang Academy of Agricultural Sciences, Harbin, Heilongjiang, China.

MT250 **Transcriptome analysis reveals long intergenic noncoding RNAs involved in skeletal muscle growth and development in pig.**
 C. Zou*, J. Li, W. Luo, L. Li, A. Hu, Y. Fu, Y. Hou, and C. Li, College of Animal Science, Huazhong Agricultural University, Wuhan, Hubei province, China.

MT251 **pigFit—Genetic analysis of immunological competence, survivability and postnatal growth of piglets.**
 M. J. Pröll*¹, E. Heuß¹, C. Große-Brinkhaus¹, H. Henne², A. K. Appel², K. Schellander¹, and E. Tholen¹, ¹Institute of Animal Science, University of Bonn, Bonn, Germany; ²BHZP GmbH, Dahlenburg-Ellringen, Germany.

- MT252 An integrative gene network analysis of the genetic determination of pig fatty-acid composition based on adipose tissue RNA sequencing.**
M. Revilla^{*1,2}, D. Crespo-Piazuelo^{1,2}, A. Rau³, Y. Ramayo-Caldas³, J. Estellé³, A. Castelló^{1,2}, A. I. Fernández⁴, M. Ballester⁵, and J. M. Folch^{1,2}, ¹Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Barcelona, Spain; ²Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain; ³Génétique Animale et Biologie Intégrative (GABI), Institut National de la Recherche Agronomique (INRA), AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ⁴Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain; ⁵Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain.
- MT253 Identification of key expression regulators of candidate genes for fatty acid composition in pig muscle.**
L. Criado-Mesas^{*1,2}, M. Revilla^{1,2}, D. Crespo-Piazuelo^{1,2}, A. Castelló^{1,2}, A. I. Fernández³, M. Ballester⁴, and J. M. Folch^{1,2}, ¹Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Barcelona, Spain; ²Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain; ³Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain; ⁴Departament de Genètica i Millora Animal, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain.
- MT254 SNP association analyses for meat tenderness and thaw and cooking losses in Iberian pigs.**
M. A. Fernández-Barroso^{*1,2}, E. Alves², L. Silió², C. Rodríguez², F. Sánchez-Esquiliche³, J. M. García-Casco^{1,2}, and M. Muñoz^{1,2}, ¹Centro de I+D en Cerdo Ibérico, INIA, Zafra, Badajoz, Spain; ²Departamento de Mejora Genética Animal, INIA, Madrid, Spain; ³Sánchez-Romero Carvajal, Jabugo, Huelva, Spain.
- MT255 Genome-wide identification and functional analysis of Long Noncoding RNA in the pig multi-tissue transcriptome.**
P. Zhao^{*}, W. Feng, X. Zheng, and J.-F. Liu, China Agricultural University, Beijing, China.
- MT256 Small non-coding RNAs (sncRNA) regulate gene silencing and modify homeostatic status in animals faced with porcine reproductive and respiratory syndrome virus (PRRSV).**
D. S. Fleming^{*1,2} and L. Miller¹, ¹USDA-ARS-NADC, Ames, IA, USA; ²ORISE-ORAU, Oak Ridge, TN, USA.
- MT257 Molecular cloning and characterization of the promoter region of the porcine stearoyl-CoA desaturase gene.**
S. Gol^{*}, M. Tor, J. Estany, and R. Pena, University of Lleida, Lleida, Spain.
- MT258 Expression QTL for longissimus dorsi muscle gene transcripts co-localized with phenotypic QTL for meat quality traits in an F2 Duroc × Pietrain resource population.**
D. Velez-Irizarry^{*1}, S. Casiró¹, Y. B. Rubio², R. Bates¹, N. Raney¹, J. Steibel^{1,3}, and C. Ernst¹, ¹Department of Animal Science, Michigan State University, East Lansing, MI, USA; ²Department of Epidemiology and Biostatistics, Michigan State University, East Lansing, MI, USA; ³Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI, USA.
- MT259 Mitochondrial DNA, Y-chromosome, and MC1R data shed light on ancestry of Nigerian indigenous pigs.**
A. C. Adeola^{*1,2}, O. O. Oluwole³, M. O. Oladele-Bukola³, Olorungbounmi³, B. A. Boladuro³, S. C. Olaogun⁴, L. M. Nneji¹, O. J. Sanke⁵, P. M. Dawuda⁶, O. G. Omitogun⁷, L. Frantz⁸, R. W. Murphy^{1,9}, H.-B. Xie^{1,2}, M.-S. Peng^{1,10}, Y.-P. Zhang^{1,11}, ¹State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China; ²Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, China; ³Institute of Agricultural Research and Training, Obafemi Awolowo University, Ibadan, Nigeria; ⁴Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria; ⁵Taraba State Ministry of Agriculture and Natural Resources, Jalingo, Taraba State, Nigeria; ⁶Department of Veterinary Surgery and Theriogenology, College of Veterinary Medicine, University of Agriculture Makurdi, Makurdi, Benue State, Nigeria; ⁷Department of Animal Sciences, Obafemi Awolowo University, Ile-Ife, Nigeria; ⁸The Palaeogenomics and Bio-Archaeology Research Network, Research Laboratory for Archaeology, University of Oxford, Oxford, UK; ⁹Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, Canada; ¹⁰Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China; ¹¹State Key Laboratory for Conservation and Utilization of Bio-Resources, Yunnan University, Kunming, China.
- MT260 Functional analysis on microRNAs by comparing the expression of milk and exosome in porcine.**
Y. Xie^{1,2}, M. Zhao^{1,3}, Z. Wang^{1,3}, R. Nai^{1,3}, L. Mi^{1,2}, L. Ma^{1,4}, Y. Zhao^{1,4}, J. Li^{1,2}, H. Xiao^{1,3}, and Z. Liu^{*1,2}, ¹Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China; ²The Ministry of Agriculture Key Laboratory of animal genetics and breeding of sheep, Hohhot, Inner Mongolia, China; ³Inner Mongolia Key Laboratory of animal genetics, breeding and reproduction, Hohhot, Inner Mongolia, China; ⁴Inner Mongolia Engineering Center of goat genetics and breeding, Hohhot, Inner Mongolia, China.
- MT261 Identification of a stop mutation in the porcine BMP15 gene causing female infertility.**
G. Flossmann^{*1}, H. Pausch^{1,4}, C. Wurmser¹, G. Dahinten², K.-U. Götz², D. Seichter³, and I. Russ³, ¹Lehrstuhl für Tierzucht, TU München, Freising, Germany; ²Institut für Tierzucht, Bayerische Landesanstalt für Landwirtschaft, Poing, Germany; ³Tierzuchtforschung e.V. München, Poing, Germany; ⁴Animal Genomics, Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland.

- MT262 **Genetic dissection of mechanisms underlying heat adaptation in pigs.**
J. Riquet^{*1}, H. Gilbert¹, K. Fève¹, Y. Labruno¹, R. Rose², Y. Billon³, M. Giorgi², T. Loyau², J. Gourdine², and D. Renaudeau⁴, ¹*INRA-GenPhySE, Castanet-Tolosan, France*; ²*INRA-URZ, Petit-Bourg, France*; ³*INRA-GenESI, Surgères, France*; ⁴*INRA-PEGASE, Saint-Gilles, France*.
- MT263 **Can targeted-enrichment next-generation sequencing be a potential screening tool for searching for molecular markers of growth traits in pigs?**
K. Piórkowska^{*1}, A. Stuczynska², and K. Zukowski¹, ¹*National Research Institute of Animal Production, Cracow, Poland*; ²*University of Agriculture in Cracow, Cracow, Poland*.
- MT264 **Allele Specific Expression and imprinting analysis of selected genes in the brain of pigs.**
M. Oczkowicz^{*}, T. Szmatoła, K. Piórkowska, and K. Ropka-Molik, *National Research Institute of Animal Production*.
- MT265 **Expression QTL regulating mRNA levels in the porcine skeletal muscle and liver mostly act in a tissue-specific manner.**
R. Gonzalez-Prendes¹, R. Quintanilla², A. Zidi¹, Y. R. Caldas², T. F. Cardoso^{1,4}, A. Manunza¹, A. Canovas³, A. Castello¹, and M. Amills^{*1}, ¹*Center for Research in Agricultural Genomics, Bellaterra, Spain*; ²*IRTA, Caldes de Montbui, Spain*; ³*University of Guelph, Guelph, Ontario, Canada*; ⁴*CAPES Foundation, Brasilia, Brazil*.
- MT266 **Development of a simple SLA-1 copy-number variation typing and the comparison of typing accuracy between real-time quantitative PCR and droplet digital PCR.**
J. Lee, M. T. Le, M.-K. Choi, C. Q. Le, H. Lee, and C. Park^{*}, *Department of Animal Biotechnology, Konkuk University, Seoul, South Korea*.
- MT267 **Food intake promotes changes in microRNA muscle expression profile in pigs.**
E. Mármol-Sánchez^{*1}, R. Quintanilla², T. F. Cardoso^{1,3}, J. Tibau⁴, O. González-Rodríguez², R. González-Prendes¹, M. Ballester², and M. Amills¹, ¹*Center for Research in Agricultural Genomics, Bellaterra, Spain*; ²*IRTA, Caldes de Montbui, Spain*; ³*CAPES Foundation, Brasilia, Brazil*; ⁴*IRTA-Monells, Monells, Spain*.
- MT268 **Nutrient supply drives changes in the muscular expression of protein-encoding and non-coding RNA genes.**
T. F. Cardoso^{*1,2}, R. Quintanilla³, J. Tibau⁴, M. Gil⁴, E. Mármol-Sánchez¹, O. González-Rodríguez³, R. González-Prendes¹, and M. Amills¹, ¹*Center for Research in Agricultural Genomics, Bellaterra, Spain*; ²*CAPES Foundation, Brasilia, Brazil*; ³*IRTA, Caldes de Montbui, Spain*; ⁴*IRTA-Monells, Monells, Spain*.
- MT269 **Influence of high fat diet on lipid metabolism in ham muscle of finishing Iberian pigs.**
Y. Nuñez^{*1}, A. Fernández¹, J. Segura², R. Benítez¹, J. Olivas³, J. Viguera⁴, C. López-Bote², L. Calvo³, and C. Óvilo¹, ¹*INIA, Madrid, Spain*; ²*UCM, Madrid, Spain*; ³*Incarlopsa SA, Toledo, Spain*; ⁴*IMASDE, Madrid, Spain*.
- MT270 **RNA-sequencing of liver in pigs divergent for residual feed intake and meat quality.**
J. Horodyska^{*1,2}, R. M. Hamill¹, H. Reyer², N. Trakooljul², P. G. Lawlor³, and K. Wimmers², ¹*Teagasc, Food Research Centre, Ash-town, Dublin, Ireland*; ²*Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*; ³*Teagasc, Pig Production Development Unit, Moorepark Research Centre, Fermoy, Co. Cork, Ireland*.
- MT271 **Transcriptomic analysis of adipose tissue from pigs divergent in residual feed intake and muscle adiposity.**
J. Horodyska^{1,2}, H. Reyer², K. Wimmers², N. Trakooljul², P. G. Lawlor³, and R. M. Hamill^{*1}, ¹*Teagasc, Food Research Centre, Ash-town, Dublin, Ireland*; ²*Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*; ³*Teagasc, Pig Production Development Unit, Moorepark Research Centre, Fermoy, Co. Cork, Ireland*.
- MT272 **Genome wide association studies for haematological traits in Italian Large White pigs.**
S. Bovo^{1,2}, G. Mazzoni^{1,3}, G. Schiavo¹, F. Bertolini^{1,4}, G. Galimberti⁵, A. B. Samorè¹, S. Dall'Olio¹, and L. Fontanesi^{*1}, ¹*Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy*; ²*Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy*; ³*Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, Copenhagen, Denmark*; ⁴*Department of Animal Science, Iowa State University, Ames, IA, USA*; ⁵*Department of Statistical Sciences 'Paolo Fortunati', University of Bologna, Bologna, Italy*.
- MT273 **In silico analysis of non-synonymous SNPs in the selective sweeps of Landrace genome.**
K.-H. Won^{*}, D. Shin, and K.-D. Song, *Department of Animal Biotechnology, Chonbuk National University, Jeonju-si, Jeollabuk-do, Republic of Korea*.
- MT274 **In silico approaches to identify functional impact of non-synonymous SNPs in the Yorkshire selective sweep regions.**
S. Son, D. Shin^{*}, and K.-D. Song, *Department of Animal Biotechnology, Chonbuk National University, Jeonju-si, Jeollabuk-do, Korea*.

- MT275 **Rewiring of porcine mRNA and miRNA networks in response to selection for residual feed intake.**
H. Beiki¹, M. Schroyen^{*1,2}, A. Rakhshandeh³, N. Gabler¹, J. Dekkers¹, and C. Tuggle¹, ¹Department of Animal Science, Iowa State University, Ames, IA, USA; ²Département AgroBioChem, Université de Liège, Gembloux, Belgium; ³Department of Animal and Food Sciences, Texas Tech University, Lubbock, TX, USA.
- MT276 **Analyses of hypothalamic transcriptome to explore porcine growth and fatness regulation in Iberian genetic backgrounds.**
M. Muñoz^{*1,2}, A. Martínez-Montes², Y. Núñez², A. Fernández², J. Folch^{3,4}, and A. Fernández^{2,5}, ¹Centro de I+D en Cerdo Ibérico INIA-Zafra, Zafra, Badajoz, Spain; ²Departamento Mejora Genética (INIA), Madrid, Madrid, Spain; ³CRAG, Plant and Animal Genomics, Bellaterra, Barcelona, Spain; ⁴Universitat Autònoma de Barcelona, Departament de Ciència Animal i dels Aliments, Bellaterra, Barcelona, Spain; ⁵Hospital Universitario Gregorio Marañón, Servicio Cardiología, Madrid, Madrid, Spain.
- MT277 **Effect of SCD and LEPR mutations on blood free fatty acid profiling and milk fat composition.**
R. Pena^{*1}, M. Tor¹, F. Vilaró², R. Ros-Freixedes¹, J. Álvarez-Rodríguez¹, L. Bosch³, J. Reixach⁴, and J. Estany¹, ¹Department of Animal Science, University of Lleida - Agrotecnio Center, Lleida, Spain; ²Scientific- Technical Services, DATCEM, University of Lleida - Agrotecnio Center, Lleida, Spain; ³Departament d'Enginyeria Química, Agrària i Tecnologia Agroalimentària, University of Girona, Girona, Spain; ⁴Selección Batallé S.A, Riudarenes, Spain.
- MT278 **Genetic architecture of a QTL for teat number on porcine chromosome 7.**
M. van Son¹, M. S. Lopes², J. Kongsro¹, L. E. Gangsei³, E. Grindflek¹, E. F. Knol², and B. Harlizius^{*2}, ¹Norsvin SA, Hamar, Norway; ²TopigsNorsvinResearch Center, Beuningen, the Netherlands; ³Animalia, Oslo, Norway.
- MT279 **Genome wide association of changes in feeding behavior due to heat stress in pigs.**
A. J. Cross¹, B. N. Keel², T. M. Brown-Brandl², and G. A. Rohrer^{*2}, ¹South Dakota State University, Brookings, SD, USA; ²US Meat Animal Research Center, USDA Agricultural Research Service, Clay Center, NE, USA.
- MT280 **Identification of SNPs associated with meat pHu in Italian Duroc pigs.**
R. Davoli¹, P. Di Battista², M. Zappaterra¹, and P. Zambonelli^{*1}, ¹Department of Agricultural and-Food Sciences (DISTAL), Bologna University, Bologna, Italy; ²Centro Interdipartimentale di Ricerca Industriale Agroalimentare (CIRI Agroalimentare), Cesena, Italy.
- MT281 **Alentejano pig: A puzzle piece to uncover the genetic basis of lipogenesis.**
A. Amaral^{*1,2}, M. Bressan³, C. Bettencourt³, J. Almeida³, J. Sá², M. Gama-Carvalho², J. Santos-Silva³, A. Belo³, H. Bovenhuis⁴, O. Moreira³, R. Bessa⁵, and L. Gama⁵, ¹Instituto de Medicina Molecular, Lisbon, Portugal; ²BioISI- Biosystems and Integrative Sciences Institute, Lisbon, Portugal; ³Instituto Nacional de Investigação Agrária e Veterinária, Santarém, Portugal; ⁴Animal Breeding and Genomics Centre, Wageningen, Netherlands; ⁵Faculdade de Medicina Veterinária, Lisbon, Portugal.
- MT282 **Heterospermic fertility index applied to frozen and refrigerated swine semen.**
C. Previtali¹, G. Bongioni^{*1}, and A. Galli², ¹Istituto Sperimentale Italiano Lazzaro Spallanzani, Rivolta d'Adda, Cremona, Italy; ²Centro di ricerca per le produzioni foraggere e lattiero-casearie CREA, Lodi, Italy.
- MT283 **The genetics of phosphorus and calcium levels in serum towards improved phosphorus efficiency in pigs.**
H. Reyer^{*1}, M. Oster^{1,2}, F. Just^{1,2}, S. Ponsuksili¹, and K. Wimmers^{1,2}, ¹Institute for Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany; ²Leibniz Science Campus Phosphorus Research, Rostock, Germany.
- MT284 **RNA-Seq analysis of gut-associated lymphoid tissue in pigs revealed few differences in transcription profiles of ileal and jejunal Peyer's patches.**
T. Maroille¹, M. Berri², D. Esquerré³, C. Chevalere⁴, G. Lemonnier¹, J. J. Leplat^{1,4}, S. Vincent-Naulleau^{1,4}, M. J. Mercat⁵, Y. Billon⁶, P. Lepage⁷, C. Rogel-Gaillard¹, and J. Estellé^{*1}, ¹GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; ²ISP, INRA, Université de Tours, Nouzilly, France; ³GenPhySe, INRA, INP, ENSAT, Université de Toulouse, Castanet-Tolosan, France; ⁴CEA, DSV, IRCM, Laboratoire de Radiobiologie et Etude du Génome, Jouy-en-Josas, France; ⁵IFIP-BIOPORC, Pôle génétique, Le Rheu, France; ⁶GENESI, INRA, Surgères, France; ⁷MICALIS, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France.
- MT285 **Assessment of the boar sperm microRNAome by RNA-seq: comparison of two protocols and characterization of the transcriptome profile.**
M. Gòdia^{*1}, A. Castelló¹, M. Montfort², J. Hecht², J.-E. Rodríguez-Gil³, A. Sánchez¹, and À. Clop¹, ¹Center for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Bellaterra, Spain; ²Center for Genomic Regulation (CRG), Barcelona Biomedical Research Park (PRBB), Barcelona, Spain; ³Unit of Animal Reproduction, Department of Animal Medicine and Surgery, Universitat Autònoma de Barcelona, Bellaterra, Spain.

- MT286 Expression of identical genetic mutations across Oncopig cell types results in distinct expression profiles recapitulating transcriptional hallmarks of human tumors.**
K. M. Schachtschneider*¹, R. M. Schwind¹, K. A. Darfour-Oduro², Y. Liu^{2,3}, S. Mäkeläinen^{4,5}, A. K. De², L. A. Rund², O. Madsen⁴, M. A. M. Groenen⁴, R. C. Gaba¹, and L. B. Schook^{1,2}, ¹Department of Radiology, University of Illinois at Chicago, Chicago, IL, USA; ²Department of Animal Sciences, University of Illinois, Champaign-Urbana, IL, USA; ³Department of Animal Genetics and Breeding, Sichuan Agricultural University, Chengdu, China; ⁴Wageningen University & Research, Animal Breeding and Genomics, Wageningen, The Netherlands; ⁵Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.
- MT287 Updated pig genome resources in Ensembl.**
T. Hourlier*¹, L. Eory², K. Billis¹, C. García Girón¹, L. Haggerty¹, O. Izuogu¹, D. N. Murphy¹, R. Nag¹, F. J. Martin¹, A. L. Archibald², B. Aken¹, and P. Flicek¹, ¹European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridgeshire, UK; ²The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Edinburgh, UK.
- MT288 Genome-scale sgRNA library construction and use for CRISPR/Cas9 based genetic screens in the pig.**
C. Zhao*¹, G. Yang¹, X. Han¹, Y. Gao¹, X. Li^{1,2}, S. Xie^{1,2}, and S. Zhao^{1,2}, ¹Key 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, China; ²The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China.
- MT289 Characterization of 3D genomic interactions in fetal pig muscle.**
M. Marti-Marimon*¹, H. Acloque¹, M. Zytnicki², D. Robelin¹, S. Djebali¹, N. Villa-Vialaneix², O. Madsen³, Y. Lahbib-Mansais¹, D. Esquerre¹, F. Mompert¹, L. Liaubet¹, M. Groenen³, M. Yerle-Bouissou¹, and S. Foissac¹, ¹GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France; ²MIAT, University of Toulouse, INRA, Castanet Tolosan, France; ³Animal Breeding and Genomics Centre (ABG), Wageningen University, Wageningen, Netherlands.
- MT290 Genome-wide scanning of the cis-effects of sequence variations on enhancer activity in the F6 swine heterogeneous stock.**
Z. Zhang*, Y. Zhu, Z. Zhou, W. Li, and L. Huang, State Key Laboratory of Pig Genetic Improvement and Production Technology, Jiangxi Agricultural University, NanChang, JiangXi Province, China.
- MT291 A metagenomics study on a non-metagenomics experiment: Mining next-generation sequencing datasets from porcine DNA identified unexpected viral sequences.**
S. Bovo^{1,2}, G. Mazzoni^{1,3}, A. Ribani¹, V. J. Utzeri¹, F. Bertolini^{1,4}, G. Schiavo¹, and L. Fontanesi*¹, ¹Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy; ²Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy; ³Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, Copenhagen, Denmark; ⁴Department of Animal Science, Iowa State University, Ames, IA, USA.
- MT292 Dietary vitamin A differentially affects fat desaturation in porcine stearoyl-CoA desaturase genotypes.**
J. Estany*¹, S. Gol¹, M. Tor¹, L. Bosch², J. Reixach³, and R. Pena¹, ¹Departament of Animal Science, University of Lleida, Agrotecnio Center, Lleida, Spain; ²Departament of Agriculture Engineering and Food Technology, University of Girona, Girona, Spain; ³Selección Batallé, S.A, Riudarenes, Spain.
- MT293 Withdrawn**
- MT294 Distribution of polymorphisms in major and candidate genes for productive and domestication-related traits in European local pig breeds.**
A. Fernández¹, M. Muñoz¹, F. García¹, Y. Núñez¹, C. Geraci², A. Crovetto³, J. García-Casco¹, E. Alves¹, M. Skrlep⁴, J. Riquet⁵, M. Mercat⁶, R. Bozzi³, M. Candek-Potokar⁴, L. Fontanesi², C. Óvilo*¹, ¹INIA, Madrid, Spain; ²UNIBO, Bologna, Italy; ³UNIFI, Firenze, Italy; ⁴KIS, Ljubljana, Slovenia; ⁵INRA, Toulouse, France; ⁶IFIP, Paris, France.

Ruminant Genetics and Genomics

- MT295 Genetic correlations of female fertility and calf survival with VIA carcass traits in UK beef cattle.**
A. Moran*, M. Coffey, and K. Moore, SRUC, Edinburgh, Scotland, UK.
- MT296 A comparative study on reproductive performance of zebu and taurus genotypes.**
M. Khan* and M. Siddiki, Department of Dairy Science, Bangladesh Agricultural University, Mymensingh, Bangladesh.

- MT297 **Co-expression network analysis identifies genes associated with meat tenderness.**
W. Diniz^{*1}, A. Cesar², L. Geistlinger³, P. Tizioto², P. Oliveira³, J. Afonso¹, M. Rocha¹, A. Lima¹, C. Buss¹, L. Coutinho², and L. Regitano³, ¹Departament of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil; ²Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil; ³Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil.
- MT298 **Comparative genome-wide methylation analysis of longissimus dorsi muscles between Japanese Wagyu and Chinese Red Steppes cattle.**
X. Fang¹, Z. Zhao¹, G. Li², X. Yu³, Z. Wei², H. Yu¹, and R. Yang^{*1}, ¹College of Animal Science, Jilin University, Changchun, Jilin Province, China; ²The Key Laboratory of National Education Ministry for Mammalian Reproductive Biology and Biotechnology, Inner Mongolia University, Hohhot, Inner Mongolia Autonomous Region, China; ³Department of Biological Sciences, Clemson University, Clemson, SC, USA.
- MT299 **Scanning of selection signature provides a glimpse into important economic traits in goats (*Capra hircus*).**
D. Guan^{*}, N. Luo, X. Tan, Z. Zhao, Y. Huang, R. Na, J. Zhang, and Y. Zhao, College of Animal Science and Technology, Southwest University, Chongqing, China.
- MT300 **Transcriptome analyses reveal reduced hepatic lipid synthesis and accumulation in more efficient beef cattle.**
R. Mukibi^{*1}, M. Vinsky², C. Fitzsimmons^{1,2}, S. M. Waters³, P. Stothard¹, and C. Li^{1,2}, ¹Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada; ²Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, Alberta, Canada; ³Animal and Bioscience Research Department, Teagasc, Grange, Dunsany, County Meath, Ireland.
- MT301 **Assessment of the pedigree quality on genetic evaluation in Tunisian Holstein cows.**
Y. Ressaissi^{*}, INAT, Tunis, Mahrajène, Tunisia.
- MT302 **Gene networks contributing to skeletal muscle compensatory growth in cattle.**
K. Keogh^{*}, D. A. Kenny, and S. M. Waters, Animal and Bioscience Research Department, Teagasc, Grange, Dunsany Co. Meath, Ireland.
- MT303 **Genome analysis of Sudanese goat breeds identifies regions associated with growth.**
S. A. Rahmatalla^{*1,2}, D. Arends¹, M. Reissmann¹, A. S. Ahmed¹, K. Wimmers³, H. Reyer³, and G. A. Brockmann¹, ¹Albrecht Daniel Thaer-Institut für Agrar- und Gartenbauwissenschaften, Humboldt-Universität zu Berlin, Berlin, Germany; ²Department of Dairy Production, Faculty of Animal Production, University of Khartoum, Khartoum North, Sudan; ³Leibniz-Institut für Nutztierbiologie (FBN), Institut für Genombiologie, Dummerstorf, Germany.
- MT304 **Effects of DNA markers associated with carcass traits and fatty acid composition on fertility traits in Japanese Black cows.**
M. Tsuchimura^{*1}, K. Fukazawa¹, F. Kawaguchi¹, T. Matsuhashi², S. Maruyama³, K. Oyama⁴, S. Sasazaki¹, and H. Mannen¹, ¹Graduate School of Agricultural Science, Kobe University, Kobe, Japan; ²Institute of Advanced Technology Kindai University, Wakayama, Japan; ³Gifu Prefectural Livestock Research Institute, Takayama, Japan; ⁴Food Resources Education & Research Center, Kobe University, Kasai, Japan.
- MT305 **Association of VNN1 gene polymorphism with fatty acid composition in Japanese Black cattle.**
H. Kigoshi^{*1}, Y. Matsumoto¹, F. Kawaguchi¹, Y. Uemoto², E. Kobayashi³, M. Fukushima⁴, E. Iwamoto⁵, E. Yoshida⁵, T. Akiyama⁴, N. Kohama⁴, K. Oyama⁶, T. Honda⁶, H. Mannen¹, and S. Sasazaki¹, ¹Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Japan; ²National Livestock Breeding Center, Fukushima, Japan; ³Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan; ⁴Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, Asago, Japan; ⁵Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, Kasai, Japan; ⁶Food Resources Education & Research Center, Kobe University, Kasai, Japan.
- MT306 **Population genetic structure, inbreeding levels and runs of homozygosity in Swakara pelt producing sheep: Implications on sub-vital performance.**
F. Muchadeyi¹, M. Malesa^{1,2}, P. Soma^{*3}, and E. Dzomba², ¹Agricultural Research Council, Biotechnology Platform, Onderstepoort, South Africa; ²Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa; ³Agricultural Research Council, Animal Production Institute, Irene, South Africa.
- MT307 **Metabolomics and transcriptomics profiling of mammary gland in cows fed different forage source diets.**
H. Sun^{*1,2}, O. Wang², D. Wang¹, H. Liu¹, J. Liu¹, and L. L. Guan², ¹Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, China; ²Department of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.

- MT308** **Genome-wide association study revealed a candidate region for beef marbling on BTA7 in Japanese Black cattle.**
 S. Sasazaki^{*1}, T. Nakajima¹, Y. Uemoto², M. Fukushima³, E. Yoshida⁴, E. Iwamoto⁴, T. Akiyama³, N. Kohama³, E. Kobayashi⁵, K. Oyama⁶, and H. Mannen¹, ¹Graduate School of Agricultural Science, Kobe University, and Kobe, Hyogo, Japan; ²National Livestock Breeding Center, and Nishigo, Fukushima, Japan; ³Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, and Asago, Hyogo, Japan; ⁴Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, and Kasai, Hyogo, Japan; ⁵Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, and Tsukuba, Ibaraki, Japan; ⁶Food Resources Education & Research Center, Kobe University, and Kasai, Hyogo, Japan.
- MT309** **PLAG1 polymorphism (ss319607405) is associated with oleic acid percentage in Japanese Black cattle.**
 F. Kawaguchi^{*1}, H. Kigoshi¹, A. Nakajima¹, Y. Matsumoto¹, Y. Uemoto², M. Fukushima³, E. Yoshida³, E. Iwamoto³, T. Akiyama³, N. Kohama³, E. Kobayashi⁴, T. Honda⁵, K. Oyama⁵, H. Mannen¹, S. Sasazaki¹, ¹Graduate School of Agricultural Science, Kobe University, and Kobe, Japan; ²National Livestock Breeding Center, and Fukushima, Japan; ³Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, and Asago, Japan; ⁴Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, and Tsukuba, Japan; ⁵Food Resources Education & Research Center, Kobe University, and Kasai, Japan.
- MT310** **Tapping the evolutionary potentials by sourcing novel livestock traits from the wild: Insights from the Giraffe genome.**
 E. Ishengoma^{*1,2} and M. Agaba¹, ¹Nelson Mandela African Institution of Science and Technology, and Arusha, Tanzania; ²Mkwawa University College of Education, and Iringa, Tanzania.
- MT311** **Understanding the genetic diversity and demographic dynamics of indigenous goats in Cameroon through maternal DNA and SNP Chip array.**
 G. M. Tarekgn^{*1,2}, F. Meutchieye³, J. Mwacharo⁴, A. Djikeng², M. Raphael⁵, B. Liu⁶, W. Zhang⁷, O. A. Mwai⁵, T. Dessie⁸, C. Mutai², S. Osama⁹, P. Wouobeng³, K. S. Jaures³, and J. Birungi², ¹Department of Animal Production and Technology, Biotechnology Research Institute, Bahir Dar University, Bahir Dar, Ethiopia; ²Biosciences eastern and central Africa-International Livestock Research Institute (BeCA-ILRI) Hub, Nairobi, Kenya; ³Faculty of Agronomy and Agriculture, University of Dschang, Dschang, Cameroon; ⁴Small Ruminant Genetics and Genomics Group, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia; ⁵International Livestock Research Institute (ILRI), Nairobi, Kenya; ⁶Nei Mongol BioNew Technology Co. Ltd, Hohhot, China; ⁷College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China; ⁸International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia; ⁹The University of Queensland, Queensland, Australia.
- MT312** **Genetic characterization of the Hungarian water buffalo population using microsatellite DNA markers.**
 C. Józsa^{*}, B. Bán, and I. Péntek, National Food Chain Safety Office, Animal Breeding Directorate, Laboratory of Genetics, Budapest, Hungary.
- MT313** **Signature selection analysis reveals candidate adaptive genes in Iraqi cattle breeds.**
 A. Alshawi^{*1,2}, S. Albayati³, A. Essa³, and O. Hanotte¹, ¹School of Life Sciences, The University of Nottingham, Nottingham, UK; ²College of Veterinary Medicine, University of Baghdad, Baghdad, Iraq; ³Animal Genetics Resources Department, Ministry of Iraqi Agriculture, Baghdad, Iraq.
- MT314** **Congenital mandibular prognathia in Droughtmaster cattle.**
 S. A. Woolley^{*1}, E. R. Tsimnadis¹, M. S. Khatkar¹, C. E. Willet², B. A. O'Rourke³, and I. Tammen¹, ¹Sydney School of Veterinary Science, The University of Sydney, Camden, NSW, Australia; ²Sydney Informatics Hub, Core Research Facilities, The University of Sydney, Sydney, NSW, Australia; ³The Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, NSW, Australia.
- MT315** **Towards accurate transcriptional analysis of important bovine natural killer receptors.**
 R. Borne^{*}, P. Ribeca, and J. A. Hammond, The Pirbright Institute, Pirbright, Surrey, UK.
- MT316** **Rambouillet sheep genome and FAANG RNA resources.**
 Y. Liu¹, R. A. Harris¹, X. Qin¹, S. Richards¹, J. Rogers¹, Y. Han¹, Q. Meng¹, T. P. Smith², B. P. Dalrymple³, S. N. White⁴, B. Murdoch⁵, J. Kijas⁶, N. E. Cockett⁷, D. M. Muzny¹, K. C. Worley^{*1}, ¹Baylor College of Medicine, Houston, TX, USA; ²USDA Agricultural Research Service, U.S. Meat Animal Research Center, Clay Center, NE, USA; ³University of Western Australia, Institute of Agriculture, Perth, Western Australia, Australia; ⁴Washington State University, Veterinary Microbiology and Pathology, Pullman, WA, USA; ⁵University of Idaho, Animal and Veterinary Science, Moscow, ID, USA; ⁶CSIRO, St. Lucia, Australia; ⁷Utah State University, Logan, UT, USA.
- MT317** **Influence of a 1-Mb region of BTA 5 on beef cow stayability in *Bos indicus* × *Bos taurus* crossbred cows.**
 B. N. Engle^{*}, A. D. Herring, J. E. Sawyer, D. G. Riley, J. O. Sanders, and C. A. Gill, Texas A&M University, College Station, TX, USA.
- MT318** **Differences in meiotic chromosome pairing characteristics in spermatocytes of hybrid beefalo.**
 A. Rodriguez^{*}, K. Davenport, H. Jaeger, M. Follett, B. Badigian, R. Sawyer, and B. Murdoch, University of Idaho, Moscow, ID, USA.

- MT319 **Mapping of calf death in Japanese Black cattle.**
T. Hirano^{*1}, S. Nishimura², H. Hara¹, Y. Sugimoto², and K. Hanzawa¹, ¹Tokyo University of Agriculture, Funako, Atsugi, Kanagawa, Japan; ²Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Nishi-shirakawa, Fukushima, Japan.
- MT320 **Melatonin target secondary hair follicle by ROR α receptor gene in cashmere goat.**
Y. Zhao^{1,3}, Z. Liu^{*1,2}, J. Wu^{1,3}, Y. Wang^{1,3}, R. Wang^{1,4}, Y. Zhang^{1,3}, R. Su^{1,3}, J. Li^{1,2}, and H. Xiao^{1,4}, ¹Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China; ²The Ministry of Agriculture Key Laboratory of Animal Genetics and Breeding of Sheep, Hohhot, Inner Mongolia, China; ³Inner Mongolia Key Laboratory of Animal Genetics, Breeding and Reproduction, Hohhot, Inner Mongolia, China; ⁴Inner Mongolia Engineering Center of Goat Genetics and Breeding, Hohhot, Inner Mongolia, China.
- MT321 **Expression quantitative trait loci mapping in dairy cattle.**
A. Chamberlain^{*1}, C. Vander Jagt¹, M. Goddard^{1,2}, C. Reich¹, C. Prowse-Wilkins¹, B. Mason¹, H. Daetwyler^{1,3}, and B. Hayes^{1,4}, ¹Agriculture Victoria, Centre for AgriBiosciences, Bundoora, VIC, Australia; ²Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville, VIC, Australia; ³School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia; ⁴Centre for Animal Science, The University of Queensland, St Lucia, QLD, Australia.
- MT322 **Concordance analysis for fine-mapping QTL in tropical beef cattle.**
L. R. Porto-Neto^{*1}, S. M. McWilliam¹, S. Harburg², S. A. Lehnert¹, and A. Reverter¹, ¹CSIRO Agriculture & Food, Brisbane, QLD, Australia; ²North Australian Pastoral Company, Brisbane, QLD, Australia.
- MT323 **A missense mutation of ADAMTS3 causes pulmonary hypoplasia and anasarca (PHA) syndrome in Cika cattle.**
N. Wiedemar¹, T. Svara², V. Cociancich³, K. Sest⁴, M. Gombac², T. Paller², J. Staric⁴, V. Jagannathan¹, and C. Drögemüller^{*1}, ¹Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland; ²Institute of Pathology, Wild Animals, Fish and Bees, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia; ³National Veterinary Institute, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia; ⁴Clinic for Reproduction and Large Animals, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia.
- MT324 **The sheep gene expression atlas project.**
E. L. Clark^{*}, S. J. Bush, M. E. McCulloch, L. Farquhar, C. B. Whitelaw, M. Watson, K. M. Summers, A. L. Archibald, and D. A. Hume, The Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK.
- MT325 **A joint analysis of bovine tuberculosis resistance in dairy cattle.**
S. Wilkinson^{*1}, S. Bishop¹, A. Allen², S. McBride², R. Skuce^{2,3}, D. Bradley⁴, D. Berry⁵, M. Coffey⁶, G. Banos^{6,1}, M. Mrode⁶, J. Woolliams¹, and E. Glass¹, ¹The Roslin Institute and R(D)SVS, The University of Edinburgh, Easter Bush, UK; ²Agri-Food and Biosciences Institute Stormont, Stoney Road, Belfast, UK; ³Queen's University Belfast, Medical Biology Centre, Belfast, UK; ⁴Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin, Ireland; ⁵Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Co. Cork, Ireland; ⁶Scotland's Rural College, The Roslin Institute Building, Easter Bush, UK.
- MT326 **Runs of homozygosity are unevenly located across the genome in highly inbred cattle.**
D. Goszczynski¹, A. Molina², G. Giovambattista^{*1}, H. Morales Durand¹, and S. Demyda-Peyras¹, ¹Instituto de Genética Veterinaria 'Ing. Fernando N. Dulout' CCT La Plata, CONICET, Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina; ²Departamento de Genética, Universidad de Córdoba, Córdoba, Spain.
- MT327 **Liver transcriptome profiling of beef steers divergent in feed intake or growth rate phenotype.**
R. Mukiibi¹, M. Vinsky², C. Fitzsimmons^{1,2}, S. M. Waters³, P. Stothard¹, and C. Li^{*1,2}, ¹Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada; ²Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, Alberta, Canada; ³Animal and Bioscience Research Department, Teagasc, Grange, Dunsany, County Meath, Ireland.
- MT328 **Detection of *de novo* mutations causing osteogenesis imperfecta and bulldog calf syndrome and assessment of mosaicism in the sires.**
C. Wurmser^{*1}, H. Pausch^{1,2}, S. Ammermüller¹, A. Heldmann¹, and R. Fries¹, ¹Chair of Animal Breeding, TUM, Freising, Germany; ²Animal Genomics, Institute of Agricultural Sciences, ETH, Zurich, Switzerland.
- MT329 **New output formats for Axiom genotyping arrays.**
J. Foster^{*}, A. Davassi, A. Pirani, S. Kaushikkar, B. Wong, M. Patil, and L. Jevons, Thermo Fisher Scientific, Santa Clara, CA, USA.
- MT330 **Genetic diversity and population structure amongst commercial and native cattle breeds using a whole-genome SNP panel.**
I. Jasielczuk^{*}, A. Gurgul, T. Szmatoła, A. Radko, T. Zabek, and M. Bugno-Poniewierska, National Research Institute of Animal Production, Balice, Poland.
- MT331 **Polymorphism of *FGF2* gene and its effect on reproduction traits in Czech Holstein cattle.**
A. Svitakova^{*}, M. Brzakova, L. Vostry, and Z. Vesela, Institute of Animal Science, Prague, Czech Republic.

- MT332 **mRNA-microRNA interaction network revealed that WNT signal pathway is a key to start the hair follicle in Cashmere goat.**
 Z. Liu^{1,2}, M. Zhao^{1,3}, R. Nai^{1,4}, R. Wang^{1,4}, Y. Zhang^{1,3}, R. Su^{1,3}, Z. Wang^{1,4}, Y. Zhao^{1,3}, J. Li^{1,2}, and Y. Xie^{1,3}, ¹Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China; ²The Ministry of Agriculture Key Laboratory of animal genetics and breeding of sheep, Hohhot, Inner Mongolia, China; ³Inner Mongolia Key Laboratory of animal genetics, breeding and reproduction, Hohhot, Inner Mongolia, China; ⁴Inner Mongolia Engineering Center of goat genetics and breeding, Hohhot, Inner Mongolia, China.
- MT333 **Identification of long noncoding RNAs by whole transcriptome analysis in the jejunum of pre-weaned calves.**
 R. Weikard^{*1}, F. Hadlich¹, H. M. Hammon¹, D. Frieten², C. Gerbert³, C. Koch³, G. Dusel², and C. Kühn^{1,4}, ¹Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany; ²University of Applied Sciences, Bingen, Germany; ³Educational and Research Centre for Animal Husbandry, Hofgut Neumühle, Münchweiler, Germany; ⁴University Rostock, Faculty of Agricultural and Environmental Sciences, Rostock, Germany.
- MT334 **Effect of plane of nutrition on the transcriptomic profile of subcutaneous adipose tissue in Holstein-Friesian bull calves.**
 A. M. English^{*1,2}, S. Fair², P. Cormican¹, C. Byrne^{1,3}, S. M. Waters¹, and D. A. Kenny^{1,3}, ¹Animal and Bioscience Research Department, Teagasc, Grange, Dunsany, Co. Meath, Ireland; ²Laboratory of Animal Reproduction, Department of Biological Sciences, School of Natural Sciences, Faculty of Science and Engineering, University of Limerick, Limerick, Ireland; ³School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland.
- MT335 **A copy number variant (CNV) scan in the autochthonous Italian Valdostana Red Pied cattle and comparison with specialized dairy populations.**
 M. G. Strillacci¹, E. Gorla¹, M. C. Cozzi¹, M. Vevey², F. Bertolini^{3,4}, L. Fontanesi³, and A. Bagnato^{*1}, ¹Department of Veterinary Medicine, University of Milan, Milano, Italy; ²Associazione Nazionale Allevatori Bovini Razza Valdostana, Gressan, Italy; ³Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy; ⁴Department of Animal Science, Iowa State University, Ames, IA, USA.
- MT336 **Congenital cataract formation in Holstein Friesian cattle is associated with a nonsense mutation in bovine CPAMD8 gene.**
 A. K. Hollmann^{*1}, I. Dammann², W. M. Wemheuer³, W. E. Wemheuer¹, A. Chilla¹, A. Tipold⁴, W. J. Schulz-Schaeffer³, J. Beck⁵, E. Schütz^{1,5}, and B. Brenig¹, ¹Institute of Veterinary Medicine, University of Goettingen, Goettingen, Germany; ²Prion and Dementia Research Unit, Department of Neuropathology, University Medical Center Goettingen, University of Goettingen, Goettingen, Germany; ³Institute of Neuropathology, University of the Saarland, Germany; ⁴Dept. Small Animal Medicine and Surgery, University of Veterinary Medicine Hannover, Hannover, Germany; ⁵Chronix Biomedical, Goettingen, Germany.
- MT337 **Allele-specific gene expression in liver of Nelore cattle extremes for feed efficiency.**
 M. Rocha^{*1}, M. de Souza¹, A. Zerlotini-Neto², P. Tizioto³, P. de Oliveira⁴, A. de Lima¹, J. Afonso¹, L. Coutinho³, L. Regitano⁴, and S. Niciura⁴, ¹Departament of Genetics and Evolution, Federal University of São Carlos/UFSCar, São Carlos, São Paulo, Brazil; ²Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil; ³Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil; ⁴Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil.
- MT338 **Accuracy of genomic prediction of economically important traits in Brangus cattle using original and imputed low-density SNP genotypes.**
 F. B. Lopes^{1,2}, X. Wu^{*2}, H. Li^{1,2}, J. Xu^{2,3}, T. Perkins⁴, J. Genho⁵, R. Ferretti², M. Wells², R. J. Tait², S. Bauck², and G. J. M. Rosa¹, ¹University of Wisconsin, Madison, WI, USA; ²GeneSeek (An Neogen company), Lincoln, NE, USA; ³University of Nebraska, Lincoln, NE, USA; ⁴International Brangus Breeders Association, San Antonio, TX, USA; ⁵Livestock Genetic Services LLC, Woodville, VA, USA.
- MT339 **Gene mapping and genomic prediction of sire conception rate in US dairy cattle.**
 F. Peñagaricano^{*1}, Y. Han¹, P. Nicolini^{1,2}, G. Morota³, and R. Abdollahi-Arpanahi^{1,4}, ¹University of Florida, Gainesville, FL, USA; ²Universidad de la República, Tacurembó, Uruguay; ³University of Nebraska-Lincoln, Lincoln NE, USA; ⁴University of Tehran, Tehran, Iran.
- MT340 **The Ovine Functional Annotation Project.**
 B. Murdoch^{*1}, S. White^{2,3}, M. Mousel², A. Massa³, K. Worley⁴, A. Archibald⁵, E. Clark⁵, B. Dalrymple⁶, J. Kijas⁷, S. Clarke⁸, R. Brauning⁸, T. Smith⁹, T. Hadfield¹⁰, and N. Cockett¹⁰, ¹University of Idaho, Moscow, ID, USA; ²USDA, ARS, Animal Disease Research Unit, Pullman, WA, USA; ³Washington State University, Pullman, WA, USA; ⁴Baylor College of Medicine, Houston, TX, USA; ⁵The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, Scotland; ⁶University of Western Australia, St Lucia, Queensland, Australia; ⁷CSIRO Agriculture, St Lucia, Queensland, Australia; ⁸AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand; ⁹USDA, ARS U.S. Meat Animal Research Center, Clay Center, NE, USA; ¹⁰Utah State University, Logan, UT, USA.
- MT341 **Effects of SRLV infection on the expression of acute phase protein and cathelicidin genes in goat blood leukocytes and milk somatic cells.**
 D. Reczynska^{*1}, J. Jarczak¹, M. Czopowicz², D. Sloniewska¹, K. Horbanczuk¹, W. Jarmuz¹, J. Kaba², L. Zwierzchowski¹, and E. Bagnicka¹, ¹Institute of Genetics and Animal Breeding PAS in Jastrzebiec, Magdalenka, Poland; ²Warsaw University of Life Sciences-SGGW, Warsaw, Poland.

- MT342 **Sex chromosome-linked cancer/testis antigens (CTAs) and male fertility in cattle.**
W. Liu*, *The Pennsylvania State University, University Park, PA, USA.*
- MT343 **Effects of stage of lactation on the expression of acute phase protein and cathelicidin genes in goat blood leukocytes and milk somatic cells.**
D. Reczynska*¹, J. Jarczak¹, M. Czopowicz², D. Sloniewska¹, M. Mickiewicz², K. Horbanczuk¹, W. Jarmuz¹, J. Kaba², L. Zwierzchowski¹, and E. Bagnicka¹, ¹*Institute of Genetics and Animal Breeding Polish Academy of Sciences in Jastrzebiec, Magdalenka, Poland;* ²*Warsaw University of Life Sciences-SGGW, Warsaw, Poland.*
- MT344 **The level of expression of immune system and milk protein genes in bovine mammary epithelial tissue infected with coagulase-positive and coagulase-negative staphylococci.**
E. Kawecka*^{1,2}, M. Zalewska¹, D. Reczynska¹, E. Kosciuczuk¹, D. Sloniewska¹, S. Marczak¹, W. Jarmuz¹, and E. Bagnicka¹, ¹*Institute of Genetics and Animal Breeding PAS in Jastrzebiec, Magdalenka Poland;* ²*Warsaw University of Life Sciences -SGGW, Warsaw, Poland.*
- MT345 **Characterization of copy number variation in European cattle.**
M. Upadhyay*^{1,2}, H. Megens¹, V. Silva^{1,2}, V. Marleen¹, M. Groenen¹, and R. Crooijmans¹, ¹*Wageningen University and Research, Wageningen, the Netherlands;* ²*Swedish Institute of Agricultural Sciences, Uppsala, Sweden.*
- MT346 **Somatic structural and numerical aberrations in bovine leukemia virus induced tumors.**
K. Durkin*¹, M. Artesi¹, V. Hahaut¹, N. Rosewick^{1,2}, P. Griebel³, N. Arsic³, A. Burny², M. Georges¹, and A. Van den Broeke^{1,2}, ¹*Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Belgium;* ²*Laboratory of Experimental Hematology, Institut Jules Bordet, Université Libre de Bruxelles, Brussels, Belgium;* ³*VIDO, University of Saskatchewan, Saskatoon, Canada.*
- MT347 **Genetic profiles, history and signatures of selection of the Russian native cattle breeds.**
N. S. Yudin¹, A. Yurchenko¹, R. Aitnazarov¹, P. Plysnina¹, and D. Larkin*^{1,2}, ¹*The Federal Research Center Institute of Cytology and Genetics, The Siberian Branch of The Russian Academy of Sciences, Novosibirsk, Russia;* ²*Department of Comparative Biomedical Sciences, Royal Veterinary College, University of London, London, UK.*
- MT348 **Cis-perturbation of cancer drivers by the HTLV-1/BLV Proviruses is a major early determinant of leukemogenesis in humans, cattle, and sheep.**
M. Artesi*¹, N. Rosewick^{1,2}, K. Durkin¹, A. Marçais³, V. Hahaut¹, P. Griebel⁴, N. Arsic⁴, A. Burny², C. Charlier¹, O. Hermine³, M. Georges¹, and A. Van den Broeke^{1,2}, ¹*Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Belgium;* ²*Laboratory of Experimental Hematology, Institut Jules Bordet, ULB, Brussels, Belgium;* ³*Service d'hématologie, Hôpital Universitaire Necker, Paris, France;* ⁴*VIDO/Intervac, USASK, Saskatoon, Canada.*
- MT349 **Withdrawn**
- MT350 **Effect of supplementation with n-3 PUFA and modulation of post-insemination plane of nutrition on bovine uterine endometrial gene expression.**
C. Surlis*¹, S. Waters¹, J. Evans¹, P. Cormican¹, D. Doyle¹, and D. Kenny^{1,2}, ¹*Teagasc, Animal and Bioscience department, Dunsany, Co. Meath, Ireland;* ²*UCD, School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland.*
- MT351 **Expression of key genes of the lipogenesis pathway in adipose tissue of beef cattle phenotypically divergent for RFI.**
C. Mckenna*^{1,2}, S. Waters¹, K. Keogh¹, R. Porter², and D. Kenny¹, ¹*Teagasc Animal and Grassland Innovation and Research Centre, Dunsany, Co. Meath, Ireland;* ²*School of Biochemistry, Trinity College Dublin, Dublin, Ireland.*
- MT352 **Differential expression of microRNA in the peripartum of Holstein Friesian cattle.**
C. Cambuli¹, R. Puglisi¹, F. Fusi², L. Bertocchi², A. Galli³, G. Bongioni*¹, and M. Montedoro¹, ¹*Istituto Sperimentale Italiano Lazzaro Spallanzani, Rivolta d'Adda, CR, Italy;* ²*Italian National Reference Centre for Animal Welfare, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna Bruno Ubertyni, Brescia, Italy;* ³*Centro di ricerca per le produzioni foraggere e lattiero-casearie CREA, Lodi, Italy.*
- MT353 **Identification of genes associated with copper-deficient fatty acid increase in Nelore cattle.**
J. Afonso¹, P. Tizioto², P. Oliveira³, W. Diniz*¹, A. Lima¹, M. Souza¹, M. Rocha¹, J. Silva¹, C. Buss¹, C. Gromboni⁴, G. Mourão², A. Nogueira³, L. Coutinho², and L. Regitano³, ¹*Department of Genetics and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil;* ²*Department of Animal Science, University of São Paulo, Piracicaba, São Paulo, Brazil;* ³*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil;* ⁴*Bahia Federal Institute of Education, Science and Technology, Valença, Bahia, Brazil.*

- MT354 **Identification of pleiotropic loci for daily weight gain and intramuscular fat in cattle using bivariate genome-wide association analysis.**
C. Buss¹, W. Diniz¹, B. Andrade³, M. Rocha¹, A. Lima¹, L. Geistlinger³, J. Afonso¹, R. Tullio³, P. Tizioto², J. Petrini², L. Coutinho², J. Wolf⁴, G. Mourão², and L. Regitano^{*3}, ¹Department of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil; ²Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil; ³Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil; ⁴Department of Biology & Biochemistry, University of Bath, Milner Centre for Evolution Bath, Bath, Somerset, UK.
- MT355 **Complete mitogenome analysis supports multiple origin domestication hypothesis for European cattle.**
V. Cubric-Curik^{*1}, D. Novosel¹, V. Brajkovic¹, S. Krebs², J. Sölkner³, D. Salamon¹, S. Ristov⁴, S. Triviziaki⁵, I. Bizelis⁶, M. Ferenčaković¹, S. Rothhammer⁷, E. Kunz⁷, M. Simčić⁸, P. Dovč⁸, G. Bunevski⁹, H. Bytyqi¹⁰, B. Marković¹¹, M. Brka¹², K. Kume¹³, S. Stojanović¹⁴, V. Nikolov¹⁵, N. Zinovieva¹⁶, M. Cacic¹⁷, I. Curik¹, and I. Medugorac⁷, ¹Faculty of Agriculture, University of Zagreb, Zagreb, Croatia; ²Laboratory for Functional Genome Analysis, Gene Center, Ludwig Maximilians University Munich, Germany; ³Division of Livestock Sciences, University of Natural Sciences and Life Sciences, Vienna, Austria; ⁴Ruder Boškovic Institute, Zagreb, Croatia; ⁵Institute of Animal Genetic Improvement, Thessaloniki, Greece; ⁶Department of Animal Breeding and Husbandry, Faculty of Animal Science and Aquaculture Agricultural University of Athens, Athens, Greece; ⁷Chair of Animal Genetics and Husbandry, LMU Munich, Munich, Germany; ⁸Department of Animal Science, Biotechnical Faculty, University of Ljubljana, Domžale, Slovenia; ⁹Faculty of Agricultural Sciences and Food, University Ss. Cyril and Methodius, Skopje, Macedonia; ¹⁰Department of Animal Science, Faculty of Agriculture and Veterinary, University of Prishtina, Prishtina, Kosovo; ¹¹Department of Livestock Science, Biotechnical Faculty, University of Montenegro, Podgorica, Montenegro; ¹²Institute of Animal Sciences, Faculty of Agriculture, University of Sarajevo, Sarajevo, Bosnia and Herzegovina; ¹³ALBAGENE Association, Tirana, Albania; ¹⁴Ministry of Agriculture and Environmental Protection, Beograd, Serbia; ¹⁵Executive Agency for selection and reproduction in Animal Breeding, Sofia, Bulgaria; ¹⁶Center of Biotechnology and Molecular Diagnostics of the L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation; ¹⁷Croatian Livestock Agency, Zagreb, Croatia.
- MT356 **Genome-wide association analysis for β -hydroxybutyrate concentration in milk using mid-infrared spectroscopy and whole-genome sequence genotypes in North American Holstein dairy cattle.**
S. Nayeri^{*1}, F. Schenkel¹, V. Kroezen¹, A. Fleming¹, M. Sargolzaei^{1,2}, C. Baes¹, J. Squires¹, and F. Miglior^{1,3}, ¹Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, Ontario, Canada; ²The Semex Alliance, Guelph, Ontario, Canada; ³Canadian Dairy Network, Guelph, Ontario, Canada.
- MT357 **Association of candidate SNPs with feed efficiency in Israeli-Holstein lactating cows.**
M. Cohen-Zinder^{*1}, J. Miron², Y. Ben-Meir², E. Lipkin³, and A. Shabtay¹, ¹Dept. of Ruminant Science, Agricultural Research Organization, Neve-Ya'ar Research Center, Ramat Yishay, Israel; ²Dept. of Ruminant Science, Institute of Animal Science, Agricultural Research Organization, Beit Dagan, Israel; ³Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel.
- MT358 **Production of goat milk lacking an allergenic protein (α s1-casein) is possible due to a micro-chromosomal deletion comprising the entire *CSN1S1* gene.**
V. Bâlteanu^{*}, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Cluj, Romania.
- MT359 **When *taurus* met *indicus*. Exploring admixture events in ancient cattle.**
M. Verdugo^{*}, Trinity College Dublin, Dublin, Ireland.
- MT360 **Origin and evolutionary history of the European bison unraveled through ancient DNA.**
T. Grange^{*}, D. Massilani, S. Guimaraes, and E.-M. Giegl, Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France.
- MT361 **Whole-genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry.**
G. Spangler^{*1}, B. Rosen¹, O. Hanotte², T. Sonstegard³, and C. Van Tassell¹, ¹USDA/ARS/AGIL, Beltsville, MD, USA; ²U of Nottingham/School of Life Sciences, Nottingham, UK; ³Acceligen of Recombinetics, St Paul, MN, USA.
- MT362 **A worldwide investigation of the effects of climate selection on goat genomes.**
F. Bertolini^{*1}, E. Rochat², S. Joost², B. Servin³, P. Crepaldi⁴, A. Stella⁵, and M. F. Rothschild¹, ¹Department of Animal Science, Iowa State University, Ames, IA, USA; ²LASIG, EPFL, Lausanne, Switzerland; ³INRA, Castanet-Tolosan, France; ⁴DIMEVET, University of Milan, Milan, Italy; ⁵PTP, Lodi, Italy.
- MT363 **Signals of adaptive introgression between European taurine and indicine cattle revealed by local ancestry inference.**
M. Barbato^{*1}, M. Del Corvo¹, T. Sonstegard², and P. Ajmone-Marsan¹, ¹Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy; ²Recombinetics Inc., St. Paul, Minnesota, USA.

- MT364 **The ruminant biology and evolution revealed by a flock of ruminant *de novo* genomes.**
W. Wang¹, Q. Q. Qiu¹, G. Zhang^{3,4}, R. Heller³, H. R. Siegismund³, and Y. Jiang^{*2}, ¹Northwestern Polytechnical University, Xi'an, Shaanxi, China; ²Northwest A&F University, Yangling, Shaanxi, China; ³University of Copenhagen, Copenhagen, Denmark; ⁴Beijing Genomics Institute at Shenzhen, Shenzheng, Guangdong, China.
- MT365 **Genotyping by sequencing for genomic selection in dairy goats (*Capra hircus*).**
S. Clarke^{*1}, K. Dodds¹, R. Brauning¹, T. Van Stijn¹, R. Anderson¹, M. Wheeler², B. Foote³, A. Cameron⁴, and J. McEwan¹, ¹AgResearch, Mosgiel, Dunedin, New Zealand; ²AgResearch, Ruakura, Hamilton, New Zealand; ³Foote Dairy, Hikurangi, Northland, New Zealand; ⁴Meredith Dairy, Meredith, Victoria, Australia.
- MT366 **Cattle on the Western Atlantic edge of Europe: A time series of ancient cattle genomes through Ireland and Britain.**
V. Mullin^{*}, Trinity College Dublin, Dublin, Ireland.
- MT367 **Genome-wide association study for monocyte count at day 7 post-challenge with bovine viral diarrhoea virus in F₂ and F₃ Nellore-Angus halfblood steers.**
K. M. Sarlo Davila^{*1}, A. D. Herring¹, J. E. Sawyer¹, J. F. Ridpath^{2,3}, and C. A. Gill¹, ¹Texas A&M University, College Station, TX, USA; ²National Animal Disease Center, Ames, IA, USA; ³Ridpath Consulting, Ames, IA, USA.
- MT368 **Evidence from the bovine of major differences between individuals in the rate of *de novo* single nucleotide mutation and transposon mobilization in the germ-line.**
C. Harland^{1,2}, K. Durkin¹, M. Artesi¹, L. Karim^{1,3}, N. Cambisano^{1,3}, M. Deckers^{1,3}, N. Tamma^{1,3}, E. Mullaart⁴, W. Coppieiers^{1,3}, M. Georges¹, and C. Charlier^{*1}, ¹Unit of Animal Genomics, GIGA-R, University of Liège, Liège, Belgium; ²Livestock Improvement Corporation, Research & Development, Hamilton, New Zealand; ³GIGA-Genomics Platform, University of Liège, Liège, Belgium; ⁴CRV, Research & Development, Arnhem, Netherlands.
- MT369 **Identification of polymorphisms modifying gene expression regulation in cattle.**
G. Guillocheau^{*} and D. Rocha, GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France.
- MT370 **GWAS for response to vaccination in Angus calves.**
L. Kramer^{*1}, M. Mayes¹, J. Williams¹, E. Fritz-Waters¹, E. Downey², R. Tait³, A. Woolums⁴, C. Chase⁵, J. Ridpath⁶, and J. Reecy¹, ¹Iowa State University, Ames, IA, USA; ²Elanco Animal Health, Larchwood, IA, USA; ³Neogen GeneSeek Operations, Lincoln, NE, USA; ⁴Mississippi State University, Mississippi State, MS, USA; ⁵South Dakota State University, Brookings, SD, USA; ⁶Ridpath Consulting, Gilbert, IA, USA.
- MT371 **Sheep parchment as a genetic resource.**
M. Teasdale^{*}, Trinity College Dublin, Dublin, Ireland.
- MT372 **SheepGenomesDB: Towards 1000 Genomes.**
S. McWilliam^{*1}, R. Brauning², S. Clarke², A. McCulloch², N. Cockett³, G. Saunders⁴, M. N. Sanchez¹, H. Daetwyler^{5,6}, and J. Kijas¹, ¹CSIRO, St Lucia, QLD, Australia; ²AgResearch Ltd, Invermay Mosgiel, New Zealand; ³Utah State University, Logan, UT, USA; ⁴EMBL-EBI, Cambridge, UK; ⁵Department of Economic Development, Jobs, Transport and Resources, Bundoora, VIC, Australia; ⁶La Trobe University, Bundoora, VIC, Australia.
- MT373 **The water buffalo gene expression atlas.**
R. Young^{*1}, L. Lefevre¹, S. Bush¹, J. Williams², S. Gokhale³, S. Kumar⁴, A. Archibald¹, and D. Hume¹, ¹The Roslin Institute and Royal (Dick) School of Veterinary Studies (RDSVS), Easter Bush, Midlothian, UK; ²School of Animal and Veterinary Sciences, The University of Adelaide, Adelaide, South Australia, Australia; ³BAIF Development Research Foundation, Central Research Station, Pune, Maharashtra, India; ⁴Centre for Cellular and Molecular Biology, Hyderabad, Telangana, India.
- MT374 **Ancient whole mitochondrial genomes and insights into the prehistory of goats.**
K. Daly^{*}, Smurfit Institute of Genetics, Trinity College, Dublin, Ireland.

POSTER SESSION II: Wednesday/Thursday

Atrium, O'Brien Science Building

Applied Genetics of Companion Animals

- WT1 **Genetic trend of the junctional epidermolysis bullosa (JEB) in the German Shorthaired Pointer in Italy.**
S. Frattini*¹, S. P. Marelli¹, A. Picchi¹, F. Danelli¹, J. Riva², E. Moretti², A. Talenti¹, G. Gandini¹, G. Pagnacco¹, M. Polli¹, and P. Crepal-di¹, ¹Department of Veterinary Medicine, University of Milan, Milan, Lombardy, Italy; ²Vetogene - Spin Off University of Milan, Milan, Lombardy, Italy.
- WT2 **Spread of concepts of animal genetics for buyers of purebred dogs in Brazil: A contribution to the improvement of cynophilia.**
F. Stortti, M. Soares, J. M. S. Nunes, J. Neves, and F. M. de Andrade*, Centro Universitário Ritter dos Reis, Uniritter, Porto Alegre, RS, Brazil.
- WT3 **Genetic variation at the K locus and resultant phenotypes.**
R. Grahn*, J. Grahn, and M. Torres Penedo, University of California, Veterinary Genetics Laboratory, Davis, CA, USA.
- WT4 **Application of multiplex microsatellite panel in Felidae family.**
A. Podbielska*¹, A. Radko¹, W. Nizanski², J. Kochan³, A. Nowak³, and M. Bugno-Poniewierska¹, ¹National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice, Cracow, Poland; ²Wroclaw University of Environmental and Life Sciences, Faculty of Veterinary Medicine, Department of Reproduction and Clinic of Farm Animals, Wroclaw, Poland; ³University of Agriculture in Krakow, Institute of Veterinary Science, Faculty of Animal Sciences, Cracow, Poland.
- WT5 **Pedigree and genomic-based relationships in a dog population.**
A. Talenti*¹, D. L. Dreger², F. Danelli¹, S. Frattini¹, B. Coizet¹, S. P. Marelli¹, G. Pagnacco¹, G. Gandini¹, M. Polli¹, R. Caniglia³, M. Galaverni³, E. A. Ostrander², and P. Crepal-di¹, ¹Department of Veterinary Medicine, University of Milan, Milan, Italy; ²National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA; ³Laboratorio di Genetica, Istituto Superiore per la Protezione e la Ricerca Ambientale, Ozzano dell'Emilia, Italy.
- WT6 **Can-ID: The genetic Identification system for Canine samples based on SNPs.**
O. Ramírez*¹, A. Cuscó¹, A. Sánchez², O. Francino², and L. Altet¹, ¹Vetgenomics, Barcelona, Spain; ²Molecular Genetics Veterinary Service (SVGMM), Barcelona, Spain.

Applied Sheep and Goat Genetics

- WT7 **Analysing the genetic diversification among the sheep breeds of Balochistan by utilizing the mitochondrial cytochrome *b* gene.**
A. Hameed*¹, M. Mohsin², A. N. Khosa¹, N. Bangulzai¹, and I. B. Marghazani¹, ¹Lasbela University of Agriculture, Water and Marine sciences, UThal, Balochistan, Pakistan; ²Livestock and Dairy Development Department, Quetta, Balochistan, Pakistan.
- WT8 **Genomic architecture of Punjab Urial.**
T. Hussain*, F. Marikar, M. Babar, M. Musthafa, and K. Periasamy, Virtual University of Pakistan, Lahore, Pakistan.
- WT9 **Construction and functional analysis of expression vector for Tibetan sheep *Fzd4* gene.**
B. B. Qu, L. Huang, Y. Wang, X. D. Zi, Y. Q. Lin, and Y. C. Zheng*, College of Life Science and Technology, Southwest University for Nationalities, Chengdu, Sichuan, China.
- WT10 **ASIP and MC1R: Dominant black and recessive black alleles segregate in native Swedish sheep populations.**
C. Rochus*^{1,2}, K. Westberg-Sunesson¹, E. Jonas¹, S. Mikko¹, and A. Johansson¹, ¹Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine and Animal Science, Swedish University of Agricultural Sciences, Uppsala, Sweden; ²UFR Génétique, Élevage et Reproduction, Sciences de la Vie et Santé, AgroParisTech, Université Paris Saclay and GenPhySE, Animal Genetics Division, INRA, Paris and Castanet-Tolosan, France.

- WT11 **Tracing the effect of *FecB* gene on transcriptome profile in ovine oocyte and cumulus cells using single-cell RNA-Seq.**
X.-F. Guo^{*1,2}, X.-Y. Wang¹, R. Di¹, Q.-Y. Liu¹, W.-P. Hu¹, X.-Y. He¹, X.-H. Cao¹, and M.-X. Chu¹, ¹*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*; ²*College of Animal Science and Technology, China Agricultural University, Beijing, China.*
- WT12 **Withdrawn**
- WT13 **Preliminary differential transcriptomic analysis of abomasal mucosa from resistant and susceptible sheep to gastrointestinal nematodes (GINs) after an experimental infection with *T. circumcincta*.**
P. K. Chitneedi^{*1}, J. J. Arranz¹, A. Suarez-Vega¹, M. Martínez-Valladares^{2,3}, and B. Gutiérrez-Gil¹, ¹*Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, Spain*; ²*Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, León, Spain*; ³*Instituto de Ganadería de Montaña, CSIC-ULE, León, Spain.*
- WT14 **Underdominant KCC3b R31I association with blood sodium concentration in domestic sheep suggests role in dimerization.**
S. N. White^{*1,2}, R. D. Oliveira², M. R. Mousel^{1,4}, M. V. Gonzalez^{2,5}, M. A. Highland¹, J. B. Taylor⁶, and D. P. Knowles^{1,2}, ¹*USDA-ARS Animal Disease Research, Pullman, WA, USA*; ²*Dept. Veterinary Microbiology & Pathology, Washington State University, Pullman, WA, USA*; ³*Center for Reproductive Biology, Washington State University, Pullman, WA, USA*; ⁴*School for Global Animal Health, Washington State University, Pullman, WA, USA*; ⁵*Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA*; ⁶*USDA-ARS Range Sheep Production Efficiency Research, Dubois, ID, USA.*
- WT15 **Non-linked SNPs in promoter and exon 2 of *MTNR1A* gene are associated to reproductive seasonality in Rasa Aragonesa sheep breed.**
J. H. Calvo^{*1,3}, M. Serrano², A. Martínez-Royo¹, B. Lahoz¹, P. Sarto¹, A. Ibañez-Deler¹, J. Folch¹, and J. L. Alabart¹, ¹*Centro de Investigación y Tecnología agroalimentaria de Aragón (CITA)-IA2, Zaragoza, Spain*; ²*Instituto Nacional de Investigaciones agrarias (INIA), Madrid, Spain*; ³*ARAID, Zaragoza, Spain.*
- WT16 **Association analysis between *ABCG2* gene and milk production in dairy sheep breeds kept in the Czech Republic: Preliminary results.**
J. Rychtarova^{*}, A. Svitakova, and Z. Sztankoova, *Institute of Animal Science, Prague, Czech Republic.*
- WT17 **Are *TMEM154* and *CCR5* variants promising markers for selection against maedi-visna susceptibility in German sheep flocks?**
V. Molaei, M. Eltanany, and G. Lühken^{*}, *Department of Animal Breeding and Genetics, Justus-Liebig University, Giessen, Germany.*
- WT18 **Allelic and genotypic frequencies of *PRNP* gene polymorphisms in some Italian goat populations.**
C. Sebastiani¹, M. Torricelli¹, M. Ciullo¹, G. Vaccari², E. Lasagna³, F. Sarti³, S. Ceccobelli³, N. D'Avino¹, M. Panicià¹, and M. Biagetti^{*1}, ¹*Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Perugia, Italy*; ²*Istituto Superiore di Sanità - Dipartimento di Sanità Pubblica Veterinaria e Sicurezza Alimentare, Roma, Italy*; ³*Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Università degli Studi di Perugia, Perugia, Italy.*
- WT19 **Accelerating genetic improvement in sheep by increased pedigree accuracy.**
H. Koshinsky, A. Pirani, M. Patil^{*}, V. Missirian, V. Joshi, and J. Curry, *Thermo Fisher Scientific, Santa Clara, CA, USA.*
- WT20 **Molecular study of the melanocortin 1 receptor gene in association with coat color variation of Iranian native sheep.**
M. A. Eshghabadi¹, A. A. Masoudi^{*1}, H. Emrani², and S. Amirina², ¹*Tarbiat Modares University, Tehran, Tehran, Iran*; ²*Animal Science Research Institute, Tehran, Tehran, Iran.*
- WT21 **Detecting selection footprints from production system-driven genomic divergence of South African sheep breeds.**
E. Dzomba^{*1}, M. Snyman², M. Chimonyo¹, and F. Muchadeyi³, ¹*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa*; ²*Grootfontein Agriculture Development Institute, Middelburg, Eastern Cape, South Africa*; ³*Agriculture Research Council-Biotechnology Platform, Onderstepoort, Gauteng, South Africa.*
- WT22 **Effect *ACACA*, *FASN* on fat acid and somatic cells in sheep—Preliminary results.**
Z. Sztankoova^{*1}, M. Borkova², A. Svitakova¹, J. Kyselova¹, and T. Kott¹, ¹*Institute of Animal Science, Prague, Czech Republic*; ²*Institute of Dairy Research, Prague, Czech Republic.*
- WT23 **Genetic investigation of sheep and goat families demonstrating the entropion eye condition.**
T. Hadfield^{*} and N. Cockett, *Utah State University, Logan, UT, USA.*
- WT24 **DNA polymorphism of melanocortin 4 receptor gene in Bligon goat.**
L. Latifah¹, D. A. Priyadi¹, K. Kustantinah², and T. Hartatik^{*1}, ¹*Departement of Breeding and Reproduction, Faculty of Animal Science, University of Gadjah Mada, Yogyakarta, Indonesia*; ²*Department of Animal Nutrition and Feed Science, Faculty of Animal Science, University of Gadjah Mada, Yogyakarta, Indonesia.*

- WT25 Using genomic estimated breeding values to detect (cryptic) microevolution in body weight of a wild mammal.**
 B. Ashraf*¹, J. Slate¹, J. Pemberton², C. Berenos², J. Pilkington², and S. Johnson², ¹*Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK;* ²*IEB, University of Edinburgh, Edinburgh, UK.*
- WT26 Detection of selection signals between Merino and Churra sheep breeds.**
 B. Gutierrez-Gil*¹, P. K. Chitneedi¹, A. Suarez-Vega¹, P. Wiener², C. Esteban-Blanco¹, and J. J. Arranz¹, ¹*Department of Animal Production, Faculty of Veterinary Sciences, University of León, León, Spain;* ²*Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush Campus, Midlothian, UK.*
- WT27 Introgression of wool-shedding genes into the Romane breed sheep.**
 L. Drouilhet*¹, B. Pena¹, C. Huau¹, D. Marcon², Y. Bourdillon², and D. Allain¹, ¹*GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France;* ²*INRA UE0322, La Sapinière, Bourges, France.*
- WT28 Investigating genetic associations with meiotic recombination in rams.**
 K. M. Davenport*, A. M. Rodriguez, R. J. Sawyer, T. M. Badigian, H. K. Jaeger, M. A. Follett, and B. M. Murdoch, *University of Idaho, Moscow, ID, USA.*
- WT29 Genomic regions associated with entropion in Columbia, Polypay, and Rambouillet breeds of sheep.**
 M. R. Mousel*^{1,2} and S. N. White^{1,3}, ¹*Animal Disease Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Pullman, WA, USA;* ²*Paul G. Allen School of Global Animal Health, Washington State University, Pullman, WA, USA;* ³*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.*
- WT30 Community-based sheep breeding programs in Ethiopia resulted in substantial genetic gains.**
 A. Haile*¹, T. Mirkena³, G. Duguma², S. Gizaw², M. Wurzingner⁴, J. Solkner⁴, O. Mwai², T. Dessie², A. Abebe⁶, M. Mamiru⁸, T. Tadesse⁷, R. N. B. Lobo⁵, and B. Rischkowsky¹, ¹*International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia;* ²*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, and Nairobi, Kenya;* ³*FAO, Addis Ababa, Ethiopia;* ⁴*BOKU University, Vienna, Austria;* ⁵*EMBRAPA-goat and sheep, Sobral, Brazil;* ⁶*Debre Berhan Agricultural Research Center, Debre Berhan, Ethiopia;* ⁷*Bako Agricultural Research Center, Bako, Ethiopia;* ⁸*Bonga Agricultural Research Center, Bonga, Ethiopia.*
- WT31 Identification of two major genes affecting prolificacy in the French Noire du Velay sheep.**
 L. Chantepie*, L. Bodin, F. Woloszyn, J. Sarry, and S. Fabre, *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France.*
- WT32 Genome-wide scan reveals *NF1* locus is associated with fat tail phenotype rather than high-altitude adaptation in Asian sheep.**
 K. Dong^{1,2}, M. Yang¹, N. Gorkhali¹, Y. Ma¹, and L. Jiang*¹, ¹*Institute of Animal Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China;* ²*USDA, Agricultural Research Service, Avian Disease and Oncology Laboratory, East Lansing, MI, USA.*
- WT33 Diversity of sheep breeds in Russia based on SNP analysis.**
 T. Deniskova*¹, A. Dotsev¹, M. Selionova², K. Wimmers³, H. Reyer³, V. Kharzinova¹, E. Gladyr¹, G. Brem^{1,4}, and N. Zinovieva¹, ¹*L.K. Ernst Institute of Animal Husbandry, Podolsk, Moscow region, Russia;* ²*All-Russian Research Institute of Sheep and Goat, Stavropol, Stavropol region, Russia;* ³*Institute of Genome Biology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany;* ⁴*Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

Comparative and Functional Genomics

- WT34 Maternal nutrient restriction in early gestation upregulates myogenic genes in cattle fetal muscle tissue.**
 A. K. Ward*¹, M. S. Crouse¹, R. A. Cushman², K. J. McLean³, C. R. Dahlen¹, P. P. Borowicz¹, L. P. Reynolds¹, and J. S. Caton¹, ¹*North Dakota State University, Fargo, ND, USA;* ²*USDA-ARS-MARC U.S. Meat Animal Research Center, Clay Center, NE, USA;* ³*University of Kentucky, Lexington, KY, USA.*
- WT35 Altered gene expression of the appetite regulation pathway in low-birth-weight piglets.**
 M. Vázquez-Gómez*¹, C. García-Contreras², R. Benítez², Y. Nuñez², A. Fernández², A. González-Bulnes², B. Isabel¹, and C. Óvilo², ¹*UCM, Madrid, Spain;* ²*INIA, Madrid, Spain.*

- WT36 **Machine learning based model selection strategy for powerful and efficient genomic prediction.**
L. Yin^{1,2}, X. Zhou^{3,4}, Y. Ma^{1,2}, M. Zhu^{1,2}, X. Li^{1,2}, X. Liu^{*1,2}, and S. Zhao^{1,2}, ¹Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction, Ministry of Education; Key Laboratory of Swine Genetics and Breeding, Ministry of Agriculture; Huazhong Agricultural University, Wuhan, Hubei, China; ²The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China; ³Department of Biostatistics, University of Michigan, Ann Arbor, MI, USA; ⁴Center for Statistical Genetics, University of Michigan, Ann Arbor, MI, USA.
- WT37 **Characterization of perirenal fat transcriptome from suckling lambs.**
A. Suárez-Vega^{*1}, J. Arranz¹, J. Mateo², and B. Gutiérrez-Gil¹, ¹Department of Animal Production, Faculty of Veterinary Sciences, University of León, León, Castilla y León, Spain; ²Department of Food Science and Technology, Faculty of Veterinary Sciences, University of León, León, Castilla y León, Spain.
- WT38 **Whole blood RNA-Seq profiling of early lactation dairy cows of diverse fertility clusters.**
M. Salavati^{*1} and G+E Genotype Plus Environment Consortium², ¹Royal Veterinary College, London, UK; ²Names and addresses are listed on the Gpluse website: <http://www.gpluse.eu/index.php/project/partners/>.
- WT39 **Comparative genomic identification and functional characterisation of β -defensin genes in the *Ovis aries* genome.**
T. J. Hall^{*1,2}, C. McQuillan¹, E. Finlay¹, C. O'Farrelly³, S. Fair⁴, and K. G. Meade¹, ¹Animal & Bioscience Research Department, Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co Meath, Ireland; ²Vet sciences centre, School of agriculture, UCD, Dublin, Ireland; ³Comparative Immunology Group, School of Biochemistry and Immunology, Trinity Biomedical Sciences Institute, Trinity College Dublin, Dublin, Ireland; ⁴Laboratory of Animal Reproduction, School of Natural Sciences, Faculty of Science and Engineering, University of Limerick, Limerick, Ireland.
- WT40 **Modulating the genetic expression of canine mesenchymal stem cells (MSCs) on two types of scaffolds: Contact lenses and equine amniotic membrane.**
A. R. Remacha^{*1}, A. L. Ortilles², A. de Torre², M. E. Lebrero², P. Zaragoza¹, and C. Rodellar¹, ¹LAGENBIO, Departamento de Anatomía, Embriología y Genética Animal, Facultad de Veterinaria, Universidad de Zaragoza, Zaragoza, Spain; ²Departamento de Patología Animal, Área de Medicina y Cirugía Animal, Facultad de Veterinaria, Universidad de Zaragoza, Zaragoza, Spain.
- WT41 **A simple, cheap and universal nucleic acid integrity assay based on the ubiquitin C gene (UBC).**
M. Van Poucke^{*} and L. Peelman, Ghent University, Merelbeke, Belgium.
- WT42 **Effect of fetal genotype and weight on muscle transcriptome in Iberian pigs.**
C. García-Contreras¹, O. Madsen², M. Vázquez-Gómez³, S. Astiz¹, R. Benítez¹, Y. Núñez¹, A. Rey³, B. Isabel³, M. Groenen², A. González-Bulnes¹, and C. Óvilo^{*1}, ¹INIA, Madrid, Spain; ²WUR, Wageningen, Netherlands; ³UCM, Madrid, Spain.
- WT43 **RT-qPCR to analyze the expression of oligosaccharides metabolism genes (*ST3GALT1*, *ST6GALT1*, *LALBA* and *B4GALT1*) during goat lactation.**
A. Crisà^{*}, C. Marchitelli, and B. Moioli, Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA), Animal Production Research Centre, Monterotondo (RM), Italy.
- WT44 **Building the sequence map of the Caprini pan-genome and their ancestor genome.**
Y. Jiang^{*}, R. Li, S. Gao, Y. Zhao, and W. Fu, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.
- WT45 **Late fetal blood transcriptomic approach to get insight into biology related to birth survival.**
L. Liaubet^{*1}, V. Voillet¹, Y. Lippi², N. Iannuccelli¹, C. Lascor¹, Y. Billon³, M. San Cristobal¹, and L. Canario¹, ¹GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France; ²Toxalim (Research Centre in Food Toxicology), Université de Toulouse, INRA, ENVT, INP-Purpan, UPS, Toulouse, France; ³INRA UE1372 GenESI, Surgères, France.
- WT46 **Association of desmosomal gene polymorphisms and arrhythmogenic right ventricular cardiomyopathy in *Pan troglodytes* (chimpanzees): A genetic investigation.**
J. Gorzynski^{*1,2}, E. Flach³, E. Ashley¹, R. Shave⁴, and A. Boswood², ¹Stanford University, Stanford, CA, USA; ²Royal Veterinary College, London, UK; ³Zoological Society London, London, UK; ⁴Cardiff Metropolitan University, Cardiff, UK.
- WT47 **RNA transcript biomarker development for bovine tuberculosis using the NanoString nCounter Analysis System.**
S. L. Faherty-O'Donnell^{*1}, K. E. McLoughlin¹, C. N. Correia¹, N. C. Nalpas², D. A. Magee¹, J. A. Browne¹, K. Rue-Albrecht³, H. M. Vordermeier⁴, B. Villarreal-Ramos⁴, E. Gormley⁵, S. V. Gordon^{5,6}, and D. E. MacHugh^{1,6}, ¹Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland; ²Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany; ³NDM Research Building, University of Oxford, Oxford, UK; ⁴Animal and Plant Health Agency (APHA), Weybridge, Addlestone, Surrey, United Kingdom; ⁵UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland; ⁶UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.

- WT48 Selective genotyping for genome-enabled prediction in mice.**
R. P. Savegnago^{*1}, S. B. Ramos², A. P. Sbardela¹, G. B. Nascimento¹, L. A. Freitas¹, P. A. Bernardes¹, and D. P. Munari¹, ¹*Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil;* ²*Universidade de Franca, Franca, São Paulo, Brazil.*
- WT49 Cross-Species Genomics Explorer for disease mutation identification through cross-species analysis.**
S. Wong^{*}, S. Häkkinen, M. Kuisma, H. Edgren, and K. Ojala, *Medisapiens Ltd, Helsinki, Finland.*
- WT50 Introduction to a new online database of animal rDNA loci.**
J. Sochorová^{*1}, S. Garcia², F. Gálvez³, R. Symonová⁴, and A. Kovarik¹, ¹*Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic;* ²*Institut Botànic de Barcelona (IBB-CSIC-ICUB), Barcelona, Catalonia, Spain;* ³*Bioscripts - Centro de Investigación y Desarrollo de Recursos Científicos, Sevilla, Andalusia, Spain;* ⁴*Research Institute for Limnology, Mondsee, University of Innsbruck, Mondsee, Austria.*
- WT51 Transcriptomic analysis of the immune response to vaccination and vaccine components by high-throughput RNA sequencing (RNA-Seq) in sheep.**
E. Varela-Martínez¹, N. Abendaño¹, J. Asín², M. Sistiaga-Poveda¹, R. Reina³, D. de Andrés³, L. Luján², and B. M. Jugo^{*1}, ¹*Faculty of Science and Technology, University of the Basque Country (UPV/EHU), Leioa, Spain;* ²*Veterinary Faculty, University of Zaragoza, Zaragoza, Spain;* ³*Institute of Agrobiotechnology (CSIC-UPNa), Pamplona, Spain.*
- WT52 Globin mRNA depletion is an unnecessary step in RNA-seq transcriptomics studies of peripheral blood from cattle.**
C. N. Correia^{*1}, K. E. McLoughlin¹, N. C. Nalpas², D. A. Magee¹, J. A. Browne¹, K. Rue-Albrecht³, H. M. Vordermeier⁴, B. Villarreal-Ramos⁴, S. V. Gordon^{5,6}, and D. E. MacHugh^{1,6}, ¹*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland;* ²*Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany;* ³*NDM Research Building, University of Oxford, Oxford, UK;* ⁴*Animal and Plant Health Agency (APHA), Weybridge, Addlestone, Surrey, United Kingdom;* ⁵*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland;* ⁶*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.*
- WT53 Effects of diet supplementation with oleic acid or carbohydrates on *Biceps femoris* transcriptome in growing Iberian pigs.**
R. Benítez^{*1}, B. Isabel², A. Fernández¹, Y. Núñez¹, E. De Mercado³, E. Gómez Izquierdo³, J. García-Casco¹, C. López-Bote², and C. Óvilo¹, ¹*INIA, Madrid, Madrid, Spain;* ²*UCM, Madrid, Madrid, Spain;* ³*Centro Pruebas Procino Itacyl, Hontalbilla, Segovia, Spain.*
- WT54 Transcription factor binding sites enrichment in ruminant and cetartiodactyl specific conserved non-coding elements.**
L. Buggiotti^{*}, M. Farrè, and D. Larkin, *Royal Veterinary College, London, UK.*
- WT55 Integrative genomics of human and bovine tuberculosis.**
K. E. Killick^{*1,2}, M. P. Mullen³, T. Hall¹, N. C. Nalpas⁴, I. W. Richardson⁵, D. A. Magee¹, C. N. Correia¹, J. A. Browne¹, D. P. Berry⁶, D. Bradley⁷, V. Naranbhai⁸, A. Hill⁸, E. Gormley⁹, S. V. Gordon^{2,9}, D. E. MacHugh^{1,2}, ¹*University College Dublin, UCD College of Health and Agricultural Sciences, University College Dublin, Dublin, Ireland;* ²*University College Dublin, UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland;* ³*Athlone Institute of Technology, Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, Ireland;* ⁴*University of Tübingen, Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany;* ⁵*IdentiGEN Ltd, IdentiGEN Ltd., Blackrock Business Park, Blackrock, Dublin, Ireland;* ⁶*Teagasc, Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, Ireland;* ⁷*Trinity College, Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin, Ireland;* ⁸*University of Oxford, Wellcome Trust Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, Oxford, UK;* ⁹*University College Dublin, UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland.*
- WT56 Hypothalamus transcriptome during the early rise in LH secretion related to puberty age in bull calves.**
J. Liron¹, M. Fernández^{*2}, A. Prando³, A. Baldo³, and G. Giovambattista², ¹*Center of Veterinary Research (CIVETAN, CONICET), Faculty of Veterinary Sciences, UNCPBA, Tandil, Buenos Aires, Argentina.;* ²*Institute of Veterinary Genetics (IGEVET, CONICET), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina;* ³*Cátedra de Zootecnia Especial (II Parte)), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina.*
- WT57 Generating customized integrated functional annotation datasets with BovineMine.**
C. Elsik^{*}, D. Unni, A. Tayal, and D. Hagen, *University of Missouri, Columbia, MO, USA.*
- WT58 Identification of regulatory elements in livestock species.**
H. Zhou^{*1}, P. Ross¹, C. Kern¹, P. Saelao¹, Y. Wang¹, M. Halstead¹, K. Chanthavixay¹, I. Korfi¹, M. Delany¹, H. Cheng², J. Medrano¹, A. Van Eenennaam¹, C. Tuggle³, and C. Ernst⁴, ¹*University of California, Davis, Davis, CA, USA;* ²*USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA;* ³*Iowa State University, Ames, IA, USA;* ⁴*Michigan State University, East Lansing, MI, USA.*

- WT59 **The Vertebrate Gene Nomenclature Committee (VGNC).**
P. Denny*, B. Yates, S. Tweedie, B. Braschi, K. Gray, R. Seal, and E. Bruford, *European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Hinxton, Cambridgeshire, UK.*
- WT60 **Circulating microRNAs as potential novel biomarkers to diagnose *Mycobacterium avium* ssp. *paratuberculosis* infection in cattle.**
K. Zhao¹, S. Hendrick², and L. Guan*¹, ¹Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada; ²Coaldale Veterinary Clinic, Lethbridge, Canada.
- WT61 **The reconstruction and evolutionary history of eutherian chromosomes.**
J. Kim¹, M. Farre², L. Auvil³, B. Capitanu³, J. Ma⁴, H. A. Lewin⁵, and D. M. Larkin*¹, ¹Department of Biomedical Science and Engineering, Konkuk University, Seoul, Korea; ²Royal Veterinary College, University of London, London, UK; ³Illinois Informatics Institute, University of Illinois at Urbana-Champaign, Urbana, IL, USA; ⁴Computational Biology Department, School of Computer Science, Carnegie Mellon University, Pittsburgh, PA, USA; ⁵Department of Evolution and Ecology, University of California, Davis, CA, USA.
- WT62 **iTRAQ-based proteomic analysis reveals key proteins affecting muscle growth and lipid deposition in pig.**
Z. Wang*¹, P. Shang^{1,2}, Q. Li³, L. Wang¹, H. Zhang¹, and C. Wu¹, ¹China Agricultural University, Beijing, China; ²Tibet Agriculture and Animal Husbandry University, Linzhi, China; ³Anhui Academy of Agricultural Sciences, Hefei, China.
- WT63 **Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhancers.**
A. Massa*¹, M. Mouse^{2,1}, B. Murdoch³, and S. White^{2,1}, ¹Washington State University, Pullman, WA, USA; ²United States Department of Agriculture-ADRU, Pullman, WA, USA; ³University of Idaho, Moscow, ID, USA.

Gene Function

- WT64 **Genome-wide survey by ChIP-seq explores the regulatory mechanism of c-Myc in chicken skeletal muscle differentiation.**
W. Luo* and X. Zhang, *Department of Animal Genetics, Breeding and Reproduction, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong Province, China.*
- WT65 **Insights into the dynamic proteomic changes of bovine mammary gland between peak and late lactation stages with tandem mass tags assay.**
X. Zheng*¹, C. Ning¹, Y. Yu¹, L. Jiang¹, Y. Dong², P. Zhao¹, H. Wang³, and J. Liu¹, ¹China Agricultural University, Beijing, China; ²Haian County Agricultural Commission, Nantong, Jiangsu, China; ³Yang Zhou University, Yangzhou, Jiangsu, China.
- WT66 **The Functional Annotation of Animal Genomes (FAANG) Project: Metadata, data sharing, and the FAANG data portal.**
L. Clarke*¹, P. Harrison¹, L. Eory², R. Kuo², G. Cochrane¹, A. Archibald², D. Zerbino¹, and P. Flicek¹, ¹European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK; ²The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK.
- WT67 **Identification and characterization of miRNAs for milk protein in Chinese Holstein cows.**
W. Cai*¹, C. Li, C. Zhou, H. Yin, S. Liu, and S. Zhang, *College of Animal Science and Technology, China Agricultural University, Beijing, China.*
- WT68 **Degree of coat color reddening in F₂ Nellore-Angus cattle demonstrates multilocus influences.**
K. Scienski*¹, T. Womack, and C. A. Gill, *Texas A&M University, Texas A&M AgriLife Research, College Station, TX, USA.*
- WT69 **Long-non coding RNAs repertoires in liver and two T lymphocyte cell types in four livestock species [FAANG pilot project "FR-AgENCODER"].**
K. Muret*¹, S. Djebali², T. Derrien³, C. Cabau², C. Klopp⁴, D. Esquerré^{2,5}, K. Munyard⁶, G. Tosser-Klopp², H. Acloque², E. Giuffra⁷, S. Foissac², and S. Lagarrigue¹, ¹UMR PEGASE INRA, Agrocampus Ouest UMR PEGASE, Rennes, France; ²UMR GenPhySE, INRA, INPT, ENVT, Université de Toulouse, Castanet-Tolosan, France; ³IGDR, CNRS-University Rennes 1, Rennes, France; ⁴SIGENAE, INRA, Castanet-Tolosan, France; ⁵Plateforme GENOTOUL, INRA, Castanet-Tolosan, France; ⁶School of Biomedical Sciences, Curtin Health Innovation Research Institute, Western Australian Biomedical Research Institute, Curtin University, Perth, Western Australia, Australia; ⁷UMR GABI, INRA, AgroParisTech, Université Paris Saclay, Jouy-en-Josas, France.
- WT70 **Combining transcriptome and epigenetic analysis of H3K36me3 and H3K4me3 marks to explore mechanisms of liver-specific gene expression in pigs.**
J. Huang, M. Schroyen, N. Gabler, J. Dekkers, and C. Tuggle*, *Department of Animal Science, Iowa State University, Ames, IA, USA.*

Genetics and Genomics of Aquaculture Species

- WT71 **The distribution of repetitive DNAs between regular and supernumerary chromosomes in the cavefish genome.**
 S. F. Ahmad^{*1}, M. Jehangir¹, A. Cardoso¹, G. T. Valente², and C. Martins¹, ¹Department of Morphology, Institute of Biosciences, UNESP, São Paulo State University, Botucatu, SP, Brazil; ²Bioprocess and Biotechnology Department, Agronomical Science Faculty, UNESP, São Paulo State University, Botucatu, SP, Brazil.
- WT72 **Mate selection accounting for genetic variability of progeny in coho salmon.**
 G. Yoshida^{*1,2}, J. Yáñez², S. Queiroz¹, J. Lhorente³, and R. Caralheiro¹, ¹School of Agricultural and Veterinarian Sciences, São Paulo State University (Unesp), Jaboticabal, São Paulo, Brazil; ²Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile; ³Aquainnovo S.A, Puerto Montt, Chile.
- WT73 **Predictive sexing of African catfish based on body and morphometric measurements using statistical discriminant methods.**
 O. T. Abanikandda¹, L. A. Awosanya¹, A. O. Giwa¹, O. N. Ottun², K. Z. Awusinu¹, and F. H. Abanikandda^{*2}, ¹Lagos State University, Ojo, Lagos, Nigeria; ²University of Lagos, Akoka, Lagos, Nigeria.
- WT74 **Genome sequencing of Tasmanian Atlantic salmon used to characterize multiple sex determination loci.**
 S. McWilliam^{*1}, M. N. Sanchez¹, B. Evans², H. King³, P. Kube³, K. Verbyla⁴, M. Menzies¹, and J. Kijas¹, ¹CSIRO, St Lucia, QLD, Australia; ²SALTAS, Hobart, TAS, Australia; ³CSIRO, Hobart, TAS, Australia; ⁴Data61, Canberra, ACT, Australia.
- WT75 **Prediction of the genetic sex in *Seriola lalandi lalandi* using whole-genome sequencing.**
 V. Martinez^{*1}, P. Dettleff¹, S. Escobar¹, and P. Zamorano², ¹FAVET-INBIOGEN, Faculty of Veterinary Science, University of Chile, Santiago, Chile; ²University of Antofagasta, Antofagasta, Chile.
- WT76 **Evaluation of microsatellite markers for the study of genetic contribution of broodstock in communal spawnings of Yellowtail kingfish (*Seriola lalandi*).**
 P. Dettleff^{*} and V. Martinez, FAVET-INBIOGEN, Faculty of Veterinary Science, University of Chile, Santiago, Chile.
- WT77 **Allele-specific expression analysis related with jaw deformities in Yellowtail kingfish (*Seriola lalandi*) larvae.**
 P. Dettleff^{*}, A. Patel, and V. Martinez, FAVET-INBIOGEN, Faculty of Veterinary Science, University of Chile, Santiago, Chile.
- WT78 **Exploiting linkage disequilibrium information in turbot selection programs.**
 M. Saura^{*1}, A. Fernández¹, J. Fernández¹, M. Toro², P. Martínez³, A. Millán⁴, M. Hermida³, A. Blanco³, S. Cabaleiro⁵, A. Doeschl-Wilson⁶, and B. Villanueva¹, ¹Departamento de Mejora Genética Animal, INIA, Madrid, Spain; ²Departamento de Producción Agraria, ETS Ingenieros Agrónomos, Madrid, Spain; ³Departamento de Xenética, Facultad de Veterinaria, Universidade de Santiago de Compostela, Lugo, Spain; ⁴Geneaqua SL, Lugo, Spain; ⁵CETGA, Cluster de Acuicultura de Galicia, Aguiño-Ribeira, Spain; ⁶Division of Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian, UK.
- WT79 **Optimum-contribution selection increases genetic gain in Atlantic salmon breeding schemes.**
 B. Hillestad^{*1} and M. Henryon², ¹SalmoBreed AS, Bergen, Norway; ²Seges, Copenhagen, Denmark.
- WT80 **Comparative genomics of disease resistance traits in salmonids.**
 J. M. Yáñez^{*}, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile.
- WT81 **Transcriptomic profile of *Salmo salar* skin in response to the Chilean sea louse *Caligus rogercresseyi* using *de novo* transcriptome assembly.**
 K. Neumann^{*1}, D. Cichero², and V. Martinez¹, ¹FAVET-INBIOGEN-Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile; ²Blue Genomic SPA, Puerto Varas, Chile.
- WT82 **Rapid cold shock induces only slight shift in gene expression of rainbow trout (*Oncorhynchus mykiss*).**
 T. Goldammer^{*1}, A. Borchel^{1,2}, M. Verleih¹, and A. Rebl¹, ¹Leibniz Institute for Farm Animal Biology, Inst. f. Genome Biology, Dummerstorf, Germany; ²University of Bergen, SLCR-Sea Lice Research Centre, Bergen, Norway.
- WT83 **Mining the European Sea Bass (*Dicentrarchus labrax*) genome for the characterization of tandem repeat variability.**
 F. Bertolini^{*1,2}, S. Bovo^{2,3}, M. F. Rothschild¹, and L. Fontanesi², ¹Department of Animal Science, Iowa State University, Ames, IA, USA; ²Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy; ³Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy.
- WT84 **Withdrawn**
- WT85 **GWAS reveals the architecture of two maturation traits in Tasmanian Atlantic salmon.**
 J. Kijas^{*1}, A. Mohamed¹, S. McWilliam¹, B. Evans², H. King³, P. Kube³, and K. Verbyla⁴, ¹CSIRO, Brisbane, Queensland, Australia; ²SALTAS, Hobart, Tasmania, Australia; ³CSIRO, Hobart, Tasmania, Australia; ⁴Data61, Canberra, ACT, Australia.

- WT86 **Reconstructing the complex structure of the sex determination locus in Atlantic herring using SMRT sequencing.**
N. Rafati*¹, C.-J. Rubin¹, C. Feng¹, M. Petterson¹, A. Bario Martinez², S. Lamichhane¹, I. Bunikis³, and L. Andersson^{1,5}, ¹Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; ²Science for Life Laboratory, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden; ³Science for Life Laboratory, National Genomics Infrastructure, Uppsala University, Uppsala, Sweden; ⁴Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁵Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA.

Livestock Genomics for Developing Countries

- WT87 **Genomic diversity and population structure analysis reveal few genetic differences among Ethiopian indigenous sheep populations.**
A. Ahbara*^{1,2}, J. Mwacharo³, H. Bahbahani⁴, S. Mastrangelo⁵, F. Pilla⁶, E. Ciani⁷, and O. Hanotte¹, ¹School of Life Sciences, University of Nottingham, Nottingham, Nottinghamshire, UK; ²Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya; ³Small Ruminant Genetics and Genomics Group, International Center for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia; ⁴Department of Biological Sciences, Faculty of Science, Kuwait University, Safat, Kuwait; ⁵Dipartimento di Scienze Agrarie e Forestali, University of Palermo, Palermo, Italy; ⁶Dipartimento Agricoltura, Ambiente e Alimenti, Università degli Studi del Molise, Campobasso, Italy; ⁷Dipartimento di Bioscienze, Biotecnologie e Biofarmaceutica, Università degli Studi di Bari 'Aldo Moro', Bari, Italy.
- WT88 **Genetic admixture in indigenous Ugandan goat breeds using genome-wide SNP data.**
R. B. Onzima*^{1,3}, M. R. Upadhyay¹, R. Mukibi², E. Kanis¹, and R. Crooijmans¹, ¹Wageningen University and Research Animal Breeding and Genomics, Wageningen, the Netherlands; ²Department of Agriculture, Food and Nutritional Sciences (AFNS), Faculty of Agriculture, Life and Environmental Sciences University of Alberta, Alberta, Canada; ³National Agricultural Research Organization (NARO), Entebbe, Uganda.
- WT89 **Genome-wide association study of growth traits in Nelore cattle.**
R. B. Costa*¹, A. P. N. Terakado², G. M. F. Camargo¹, R. Carvalheiro², and L. G. Albuquerque², ¹Federal University of Bahia, Salvador, BA, Brazil; ²Sao Paulo State University, Jaboticabal, SP, Brazil.
- WT90 **Linkage disequilibrium, linkage phase and effective population size estimates in four Philippine riverine buffalo populations.**
J. R. V. Herrera*^{1,3}, E. B. Flores², C. Gondro³, and J. H. van der Werf³, ¹Philippine Carabao Center-University of the Philippines College, Laguna Philippines; ²Philippine Carabao Center National Headquarters, Muñoz, Nueva Ecija, Philippines; ³School of Environmental and Rural Science, University of New England, Armidale, NSW, Australia.
- WT91 **Genomic diversity and autozygosity within the SA Drakensberger beef cattle breed.**
S. F. Lashmar^{1,2}, C. Visser*¹, and F. C. Muchadeyi², ¹University of Pretoria, Pretoria, Gauteng, South Africa; ²Biotechnology Platform (Agricultural Research Council), Pretoria, Gauteng, South Africa.
- WT92 **Genome-wide SNP diversity of the South African domestic and wild pig populations.**
N. Hlongwane*^{1,2}, E. Dzomba², K. Mdladla^{1,2}, P. Soma³, and F. Muchadeyi¹, ¹Agricultural Research Council, Biotechnology Platform, Onderstepoort, South Africa; ²Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa; ³Agricultural Research Council, Animal Production Institute, Irene, South Africa.
- WT93 **Genetic characterization of Argentine and Bolivian creole cattle using HD SNPs microarray.**
M. Fernandez¹, M. Ortega Masague², J. Orellana³, F. Valdez⁴, S. Peña⁵, A. Rogberg Muñoz^{1,6}, L. Gutierrez², M. Baudoin⁵, D. M. Posik¹, E. E. Villegas Castagnasso¹, I. P. Manrique Osinaga³, F. D. Holgado², J. P. Lirón⁷, D. E. Goszczynski¹, P. P. García¹, C. Bomblat⁵, E. Salas⁴, J. A. Pereira Rico³, and G. Giovambattista¹, ¹Instituto de Genética Veterinaria (IGEVET), CCT La Plata CONICET - Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina; ²Instituto de Investigación Animal del Chaco Semiárido (IIACS – INTA Leales), Leales, Tucumán, Argentina; ³Facultad de Ciencias Veterinarias, Universidad Autónoma Gabriel René Moreno, Santa Cruz de la Sierra, Santa Cruz, Bolivia; ⁴Centro de Investigación Agrícola Tropical (CIAT), Santa Cruz de la Sierra, Santa Cruz, Bolivia; ⁵CEASIP, Fundación Simón I Patiño, Santa Cruz de la Sierra, Santa Cruz, Bolivia; ⁶Departamento de Producción, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina; ⁷INPA–Unidad Ejecutora UBA CONICET de Investigaciones en Producción Animal, CABA, Argentina; ⁷Center of Veterinary Research (CIVETAN, CONICET) Faculty of Veterinary Sciences, UNCPBA, Tandil, Buenos Aires, Argentina.
- WT94 **Genomic population structure and relationship between the South African Nguni Sheep.**
K. S. Nxumalo*^{1,2}, J. P. Grobler¹, K. Ehlers¹, K. Ncube³, F. C. Muchadeyi³, and N. O. Mapholi², ¹University of Free State, Department of Genetics, Bloemfontein, Free State, South Africa; ²Agricultural Research Council-Animal Production Institute, Irene-Pretoria, Gauteng, South Africa; ³Agricultural Research Council-Biotechnology Platform, Onderstepoort-Pretoria, South Africa.

- WT95 **Genome-wide analysis for signature of selection in domestic chicken and red jungle fowl.**
 R. A. Lawal*¹ and O. Hanotte^{1,2}, ¹The University of Nottingham, Nottingham, Nottinghamshire, UK; ²International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.
- WT96 **Genetic admixture and identity by descent in Senegalese dairy cattle.**
 P. J. N. Ema^{1,3}, A. Missohou¹, K. Marshal², S. F. Tebug², J. Juga⁴, and M. Tapio*⁵, ¹Interstate School of Veterinary Science and Medicine of Dakar, Dakar, Senegal; ²International Livestock Research Institute, Nairobi, Kenya; ³University of Ngaoundere, Ngaoundere, Cameroon; ⁴University of Helsinki, Helsinki, Finland; ⁵Natural Resources Institute Finland, Jokioinen, Finland.
- WT97 **Can genomics be used in the smallholder livestock sector? Case studies from South Africa.**
 F. C. Muchadeyi*, Agriculture Research Council – Biotechnology Platform, Pretoria, South Africa.
- WT98 **Towards the unraveling of the genomic basis of milk production traits in African dairy zebu cattle.**
 A. Tijjani*^{1,4}, J. Kim³, R. Mrode², B. Salim⁵, N. Oyekanmi⁴, H. Kim³, and O. Hanotte^{1,2}, ¹School of life Sciences, University of Nottingham, Nottingham, United Kingdom; ²International Livestock Research institute (ILRI), Nairobi, Kenya; ³C&K genomics, Seoul National University Research Park, Seoul, South Korea; ⁴National Biotechnology Development Agency, Lugbe, Abuja, Nigeria; ⁵Department of Parasitology, Faculty of Veterinary Medicine, University of Khartoum, Khartoum, Sudan.
- WT99 **Development of genomic tools to select for economic traits in tropical adapted cattle breeds.**
 F. F. Cardoso*^{1,2}, G. S. Campos², C. C. Gulias-Gomes¹, B. P. Sollero¹, and A. R. Caetano³, ¹Embrapa Pecuária Sul, Bagé, RS, Brazil; ²Universidade Federal de Pelotas, Pelotas, RS, Brazil; ³Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil.
- WT100 **Finding optimum levels of admixture in crossbred sheep populations in Ethiopia by use of ancestry informative genetic markers and phenotypes.**
 T. Getachew^{1,2}, H. J. Huson³, M. Wurzinger¹, J. Burgstaller⁴, S. Gizaw⁵, A. Haile⁶, B. Rischkowsky⁶, G. Brem⁴, S. A. Boison¹, G. Mészáros¹, A. O. Mwai⁷, and J. Sölkner*¹, ¹University of Natural Resources and Life Sciences, Vienna, Austria; ²Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia; ³Cornell University, Ithaca, NY, USA; ⁴University of Veterinary Medicine, Vienna, Austria; ⁵International Livestock Research Institute, Addis Ababa, Ethiopia; ⁶International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia; ⁷International Livestock Research Institute, International Livestock Research Institute, Nairobi, Kenya.
- WT101 **Matching breeds to production clusters using high-density SNP arrays: The case of East Africa.**
 F. D. N. Mujibi*¹, E. K. Cheruiyot², T. Dusingizimana³, M. Chagunda⁴, J. Ojango⁵, and R. Mrode^{4,5}, ¹Nelson Mandela Africa Institution for Science and Technology (NMAIST), Arusha, Tanzania; ²University of Nairobi, Nairobi, Kenya; ³University of Rwanda, Kigali, Rwanda; ⁴Scotland Rural University College, SRUC, Edinburgh, UK; ⁵International Livestock Research Institute, Nairobi, Kenya.
- WT102 **Genomic selection based on current status in developing countries.**
 R. Mrode*¹, J. Ojango¹, O. Mwai¹, and J. M. Mwacharo², ¹Animal Biosciences, International Livestock Research Institute, Nairobi, Kenya; ²Small Ruminant Genetics and Genomics Group, International Centre for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia.
- WT103 **Withdrawn**
- WT104 **Selection of SNP markers for a dromedary camel genotyping array.**
 M. Al Abri*¹, H. M. Holl², D. Miller³, S. Abdalla⁴, B. Shykind⁴, J. Malek⁴, Y. Mohamoud⁴, K. Pasha⁵, A. Khalili⁵, D. F. Antczak³, and S. Brooks¹, ¹Sultan Qaboos University, Department of Animal and Veterinary Sciences, Muscat, Sultanate of Oman; ²University of Florida, Department of Animal Sciences, Gainesville, Florida, USA; ³Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA; ⁴Weill Cornell Medical College in Qatar, Cornell University, Doha, Qatar; ⁵Tharb Veterinary Hospital, Doha, Qatar.
- WT105 **Delineating Indian native cattle specific allelic variants and haplotypes in lactoferrin gene: A potential candidate for disease resistance.**
 A. Sharma*^{1,2}, M. Sodhi², P. Jain¹, M. Kumar², and M. Mukesh², ¹University Institute of Engineering & Technology, Kurukshetra, Haryana, India; ²National Bureau of Animal Genetics Resources, Karnal, Haryana, India.

Author Index

Numbers following names refer to abstract numbers. A number alone indicates an oral presentation; an MT preceding the number indicates a Monday/Tuesday poster (Poster Session I) and a WT indicates a Wednesday/Thursday poster (Poster Session II) poster. Orals are listed first, followed by posters in session and numeric 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.

A

Abanikannda, F. H., WT73
 Abanikannda, O. T., WT73
 Abdalla, S., 11, MT22, WT104
 Abdel-Azim, G., MT144
 Abdollahi-Arpanahi, R., MT339
 Abebe, A., 154, WT30
 Abendaño, N., WT51
 Abo-Ismael, M., MT78
 Abo-Ismael, M. K., MT71, MT76
 Abrahamsen, M., 42, MT55, MT156
 Abrahante, J., MT45
 Acloque, H., 19, 20, 144, 147, MT127,
 MT128, MT289, WT69
 Acuna, G., MT231
 Acutis, P., MT35
 Acutis, P. L., MT43
 Adam, E. N., MT133
 Adeola, A. C., MT259
 Adjei-Fremah, S., MT143
 Affolter, V., 41, MT213
 Afonso, J., MT297, MT337, MT353, MT354
 Agaba, M., MT310
 Ahbara, A., MT38, WT87
 Ahmad, S. F., WT71
 Ahmed, A., 58, MT22, MT117
 Ahmed, A. S., MT303
 Ahn, B. Y., MT6
 Aida, Y., MT148, MT150
 Ainslie, M. H., MT155
 Aitnazarov, R., MT347
 Ajmone-Marsan, P., 106, MT363
 Akanno, E., MT78
 Akanno, E. C., MT76
 Aken, B., 149, MT287
 Akiyama, T., MT305, MT308, MT309
 Akkurt, M., 120, MT104
 Al Abri, M., 11, WT104
 Alabart, J. L., WT15
 Alatiyat, R., MT38
 Albayati, S., MT313
 Al-Bayatti, S., MT38
 Alborch, L., 77, MT160
 Albuquerque, L. G., WT89

Alejo, J., 110, MT16
 Alim, M. A., MT72
 Aljumaah, R., MT38
 Al-Jumaili, A., MT38
 Allain, D., 153, WT27
 Allais-Bonnet, A., MT7
 Allanson, E., 26, MT66
 Allen, A., 4, MT24, MT325
 Allred, A., 116, 151, MT84, MT98
 Almeida, J., MT281
 Alshawi, A., MT313
 Altet, L., 6, WT6
 Álvarez-Rodríguez, J., MT277
 Alves, E., 98, MT254, MT294
 Alyan, M., MT223
 Alykhan, M., MT190
 Amaral, A., MT281
 Amills, M., MT265, MT267, MT268
 Amirina, S., WT20
 Ammermüller, S., MT328
 Anacleto, O., 71, MT166
 Anadón, E., 67, MT216
 Anderson, R., 101, MT365
 Andersson, G., 65, 126, MT102, MT108
 Andersson, L., 177, MT179, WT86
 Ando, A., 57, MT109
 Andrade, B., MT354
 Antczak, D., 36, 58, MT22, MT117, MT210
 Antczak, D. F., 11, WT104
 Antolin, R., MT88
 Appel, A. K., MT251
 Arabi, S., 3, MT86
 Arango, J., 73, MT161
 Archibald, A., 104, 148, MT125, MT340,
 MT373, WT66
 Archibald, A. L., 149, MT287, MT324
 Ardesjö-Lundgren, B., 126, MT102
 Arends, D., MT303
 Argyle, D., 121, 127, MT99, MT105
 Arranz, J., WT37
 Arranz, J. J., 97, WT13, WT26
 Arruda, A. M., 90, MT234
 Arsic, N., MT346, MT348
 Arsuaga, J. L., MT228
 Artesi, M., 99, MT346, MT348, MT368

Ashley, E., WT46
 Ashraf, B., WT25
 Asín, J., WT51
 Astiz, S., WT42
 Atxaerandio, R., 131, MT242
 Auffret, M., 130, MT240
 Auvil, L., 163, WT61
 Awosanya, L. A., WT73
 Awusinu, K. Z., WT73
 Ayaz, S., MT136
 Ayuso, M., MT245

B

Babar, M., WT8
 Badigian, B., MT318
 Badigian, T. M., 158, WT28
 Badiola, J., 110, MT16
 Baes, C., MT356
 Bagnato, A., 43, MT44, MT61, MT335
 Bagnicka, E., MT5, MT341, MT343, MT344
 Bahbahani, H., WT87
 Bai, H., 50, MT59
 Bai, L., MT150
 Bailey, E., MT201
 Baird, H. J., MT140
 Bakhtin, M., MT190, MT223
 Balasuriya, U. B. R., MT201
 Baldo, A., 165, WT56
 Balic, A., 30, MT177
 Ballester, M., 136, MT238, MT252, MT253,
 MT267
 Ballingal, K., 56, MT115
 Bâlteanu, V., MT358
 Bán, B., MT312
 Bangulzai, N., WT7
 Banos, G., MT325
 Bao, M., MT145
 Bao, W., MT2
 Barbato, M., 106, MT363
 Barrachina, L., MT181
 Barro, M., 41, MT213
 Bartens, M., 85, MT163
 Bartunek, P., 46, MT57
 Basarab, J., MT76, MT78

- Basnayake, V., 8, MT26
 Bastanlar, E. K., 188, MT232
 Bates, R., MT258
 Bauck, S., MT338
 Baudoin, M., WT93
 Bauer, J., MT74, MT192
 Beatty, J., 122, MT100
 Beck, J., MT336
 Bed'Hom, B., 66, 78
 Beeson, S., MT131, MT187
 Beijerinck, N., MT199
 Beiki, H., 142, MT164, MT275
 Belay, G., MT107
 Belo, A., MT281
 Beltramo, C., MT35
 Benitez, R., MT245
 Benítez, R., 141, MT269, WT35, WT42, WT53
 Ben-Meir, Y., MT357
 Berenos, C., WT25
 Bergström, T. F., 65, MT108
 Bergvall, K., 126, MT102
 Berhane, Y. N., MT18
 Bermingham, M., 121, MT105
 Bernardes, P. A., WT48
 Berri, M., 134, MT239, MT284
 Berry, D. P., 76, 91, 166, MT76, MT173,
 MT233, MT325, WT55
 Berthold, A., 75, MT157
 Bertocchi, L., MT352
 Bertolini, F., 43, 109, 137, 176, MT44, MT61,
 MT246, MT272, MT291, MT335, MT362,
 WT83
 Bessa, R., MT281
 Bettencourt, C., MT281
 Bhushan, B., MT248
 Biagetti, M., WT18
 Bickhart, D., 23, MT154, MT159
 Biek, R., 4, MT24
 Bilgen, N., 120, MT104
 Billis, K., 149, MT287
 Billon, Y., 79, 134, MT168, MT239, MT262,
 MT284, WT45
 Biolatti, C., MT35, MT43
 Birkhart, D., 148, MT125
 Birungi, J., MT311
 Bishop, S., MT325
 Bitterman, P. B., MT93
 Bizelis, I., MT355
 Bjelka, M., MT151
 Bjorkman, P. J., 64, MT162
 Blake, D., MT156
 Blanc, F., 79, MT168
 Blanco, A., 173, WT78
 Blecha, F., MT146
 Bleyer, M., MT79
 Block, H., MT4
 Blott, S., 33, MT182, MT211
 Blott, S. C., MT90, MT206
 Bodin, L., 155, WT31
 Boichard, D., MT118, MT120
 Boison, S. A., 185, WT100
 Boladuro, B. A., MT259
 Bolea, R., 110, MT16
 Bolívar, H., MT228
 Bonet, I., 67, MT216
 Bongioni, G., 3, MT86, MT282, MT352
 Bontrop, R., 56, MT115
 Booth, R., 129, MT96
 Borchel, A., 178, WT82
 Bordbari, M., 41, MT213
 Borkova, M., WT22
 Borne, R., MT315
 Borowicz, P. P., 112, MT8, WT34
 Borowska, A., MT130
 Bosch, L., 140, MT277, MT292
 Boswood, A., WT46
 Bottema, C. D. K., MT77
 Bouahom, B., MT189
 Bouguyon, E., 79, MT168
 Boulton, K., MT156
 Bourdillon, Y., 153, WT27
 Boutin, M., 53, MT49, MT56
 Bouzada, J. A., 67, MT216
 Bovenhuis, H., MT145, MT281
 Bovo, S., 43, 137, 176, MT61, MT272, MT291,
 WT83
 Bowman, P., 100, MT129
 Bowser, J., MT207
 Bozzi, R., 98, MT294
 Bradley, D., 166, MT325, WT55
 Brajkovic, D., MT87
 Brajkovic, V., MT87, MT355
 Brantsæter, M., MT1
 Braschi, B., 169, WT59
 Brauning, R., 25, 101, MT140, MT340,
 MT365, MT372
 Brem, G., 15, 32, 92, 185, MT23, MT214,
 WT33, WT100
 Brenet, M., MT49
 Brenig, B., MT79, MT336
 Bressan, M., MT281
 Brockmann, G. A., MT30, MT303
 Brooks, S., 11, 58, MT22, MT117, WT104
 Brown, P., 27, MT176
 Brown-Brandl, T. M., MT279
 Browne, J., 111, MT9
 Browne, J. A., 76, 166, MT173, WT47, WT52,
 WT55
 Bruce, H., MT4
 Bruford, E., 169, WT59
 Bryan, K., MT202
 Brzakova, M., MT331
 Buggiotti, L., 160, WT54
 Bugno-Poniewierska, M., 7, 70, 146, MT15,
 MT184, MT194, MT195, MT198, MT220,
 MT330, WT4
 Buitkamp, J., 59, MT110
 Bulut, Z., 188, MT232
 Bunevski, G., MT355
 Bunikis, I., 177, WT86
 Burgstaller, J., 185, WT100
 Burkard, C., 28, MT175
 Burns, B., MT121
 Burns, E., 41, MT213
 Burny, A., MT346, MT348
 Burrell, A., 116, 151, MT84, MT98
 Burt, D., 54, MT41, MT47, MT62
 Burt, D. W., MT40
 Bush, S., 104, MT373
 Bush, S. J., MT324
 Buss, C., MT297, MT353, MT354
 Buttazzoni, L., MT153
 Buus, S., 63, MT113
 Buys, N., 33, MT182, MT211
 Byrne, A., 4, MT24
 Byrne, C., MT334
 Byrne, M., 27, MT176
- C**
- Cabaleiro, S., 173, WT78
 Cabau, C., 20, 144, MT128, WT69
 Caetano, A. R., 180, WT99
 Cai, W., WT67
 Cai, Y., MT119
 Caldas, Y. R., MT265
 Calvo, J. H., WT15
 Calvo, L., MT269
 Camargo, G. M. F., WT89
 Cambisano, N., 99, MT368
 Cambuli, C., MT352
 Cameron, A., 101, MT365
 Campia, V., MT35
 Campos, C. B. N., MT204
 Campos, G. S., 180, WT99
 Canario, L., WT45
 Candek-Potokar, M., 98, MT294
 Canibe, N., 135, MT241
 Caniglia, R., 152, WT5
 Cañon, J., MT224
 Cañón, J., MT82
 Canovas, A., MT265
 Cantrell, B., MT3
 Cao, J., MT73
 Cao, X.-H., WT11
 Capitanu, B., 163, WT61
 Capoferri, R., 3, MT86
 Cappelletti, E., 36, MT210
 Capra, E., 18, MT14
 Caralheiro, R., WT72

- Cardoso, A., WT71
 Cardoso, F. F., 180, WT99
 Cardoso, T. F., MT265, MT267, MT268
 Carlsson, J., 91, MT233
 Carvalheiro, R., WT89
 Casas, E., MT142
 Case, A., 58, MT117
 Casiró, S., MT258
 Castaneda, C., MT229
 Castaneda, V., MT231
 Castello, A., 77, MT160, MT265
 Castelló, A., MT252, MT253, MT285
 Castillo, F., 67, MT216
 Castle, K., MT205
 Caton, J. S., 112, MT8, WT34
 Ceccobelli, S., WT18
 Cerolini, S., 43, MT44, MT61
 Cesar, A., MT297
 Chagunda, M., 184, WT101
 Chai, H.-H., 115, MT13, MT42
 Chamberlain, A., MT321
 Chantepie, L., 155, WT31
 Chanthavixay, K., 17, 159, MT10, WT58
 Charlier, C., 99, MT348, MT368
 Chase, C., 103, MT370
 Chen, J. L., 50, MT59
 Chen, T., MT119
 Chen, Y., MT222
 Cheng, H., 42, 159, MT55, WT58
 Cheng, H. H., 114, MT11
 Cheruiyot, E. K., 184, WT101
 Chevaleyre, C., MT284
 Chilla, A., MT336
 Chimonyo, M., WT21
 Chitneedi, P. K., 97, WT13, WT26
 Cho, G., MT132
 Cho, I. C., MT188
 Choate, L., 38, MT208
 Choi, B.-H., 115, MT13, MT42
 Choi, J.-W., MT180, MT188
 Choi, M.-K., MT6, MT266
 Choi, N., MT46
 Choi, N.-R., 9, MT65
 Choi, Y.-H., MT42
 Choudhury, A., MT124
 Chow, W., 148, MT125
 Chowdhary, B. P., MT123
 Christmann, A., 35, MT219
 Chu, M.-X., WT11
 Chu, T., 38, MT208
 Chung, W.-H., MT180, MT188
 Ciani, E., WT87
 Cichero, D., 175, WT81
 Cieslak, J., MT130, MT197
 Cigliano, R. A., 77, MT160
 Cildir, O., 120, MT104
 Cinar, M. U., MT106
 Ciullo, M., WT18
 Clark, E., MT340
 Clark, E. L., MT324
 Clarke, L., WT66
 Clarke, S., 25, 101, MT340, MT365, MT372
 Clarke, S. M., MT140
 Claude, A., MT207
 Clements, D., 127, MT99
 Clements, D. N., MT90
 Clop, A., 77, MT160
 Clop, A., MT285
 Cochran, G., WT66
 Cociancich, V., MT323
 Cockett, N., 25, MT340, MT372, WT23
 Cockett, N. E., MT316
 Coffey, M., MT295, MT325
 Cohen-Zinder, M., MT357
 Coizet, B., 152, WT5
 Colazo, M., MT4
 Collin, A., 53, MT56
 Colussi, S., MT35, MT43
 Consortium, B., MT230
 Cooksey, A., 22, MT126
 Cooley, A., MT207
 Cooper, C., 27, MT176
 Coppieters, W., 99, MT368
 Corbo, M., 36, MT210
 Cormican, P., 132, MT237, MT334, MT350
 Correia, C. N., 76, 166, MT173, WT47, WT52, WT55
 Cortes, O., MT203
 Cortés, O., MT82, MT224
 Costa, M., 68, MT134
 Costa, M. R. T., MT203
 Costa, R. B., WT89
 Cothran, E. G., MT130, MT229
 Coulombe, R., MT45
 Courcier, E., 4, MT24
 Coutinho, L., MT1, MT297, MT337, MT353, MT354
 Cozzi, M. C., MT44, MT335
 Creighton, E., 123, MT103
 Crepaldi, P., 109, 152, MT362, WT1, WT5
 Crespo-Piazuelo, D., 136, MT238, MT252, MT253
 Criado-Mesas, L., 136, MT238, MT253
 Crisà, A., WT43
 Crisci, E., 144, MT128
 Crisman, R., MT199
 Crooijmans, R., MT345, WT88
 Cross, A. J., MT279
 Crouse, M. S., 112, MT8, WT34
 Crovetto, A., 98, MT294
 Crowe, M., MT153
 Crowley, J., MT76
 Cubric-Curik, V., MT87, MT355
 Cunningham, H. L., MT206
 Curik, I., MT87
 Curry, J., WT19
 Cuscó, A., 6, WT6
 Cushman, R. A., 112, MT8, WT34
 Czopowicz, M., MT341, MT343
D
 Daetwyler, H., 25, 100, MT129, MT321, MT372
 Dahinten, G., MT261
 Dahlen, C. R., 112, MT8, WT34
 Dall'Olio, S., MT272
 Dalrymple, B., MT340
 Dalrymple, B. P., MT316
 Daly, K., 93, MT374
 Dalziel, B., 21, MT167
 Damas, J., 26, 44, MT66, MT67
 Dammann, I., MT336
 Danelli, F., 152, WT1, WT5
 Danko, C., 38, MT208
 Darfour-Oduro, K. A., 138, MT286
 Das, P. J., MT123
 Davassi, A., MT329
 Davenport, K., MT318
 Davenport, K. M., 158, WT28
 Davey, M., 121, MT105
 Davila, K. M. S., 84
 Davila, K. M. Sarlo, MT367
 D'Avino, N., WT18
 Davis, B., MT123
 Davis, S., 90, MT234
 Davoli, R., MT280
 Dawuda, P. M., MT259
 De, A. K., 138, MT286
 de Andrade, F. M., WT2
 de Andrés, D., WT51
 de Groot, M., 10, 151, MT63, MT98
 de Groot, N., 56, MT115
 De Keyser, K., 33, MT211
 De Koning, D. J., MT118
 de Lima, A., MT337
 De Mercado, E., 141, WT53
 de Oliveira, P., MT337
 de Souza, M., MT337
 de Torre, A., WT40
 Deckers, M., 99, MT368
 Deeb, N., 143
 Dehareng, F., MT153
 Dekkers, J., 16, 73, 143, MT161, MT275, WT70
 Del Corvo, M., 18, 106, MT14, MT363
 Delaney, M., 42, MT55
 Delany, M., 159, WT58
 Delany, M. E., 114, MT11
 Demasius, W., MT138
 Demyda-Peyras, S., MT326

Denis, C., 134, MT239
 Deniskova, T., 92, WT33
 Denny, P., 169, WT59
 DePriest, J. S., MT201
 DePriest, M., 39, MT209
 DePriest, M. S., 40, MT221
 Der Sarkissian, C., 87, MT235
 Derrien, T., 20, 144, MT128, WT69
 Désert, C., 53, MT49, MT56
 Dessie, T., 154, MT107, MT311, WT30
 Detry, C., 90, MT234
 Dettleff, P., 179, WT75, WT76, WT77
 Devos, J., MT4
 Di, R., WT11
 Di Battista, P., MT280
 Di Palma, F., MT19
 Dietrich, J., 119, MT94
 Dietschi, E., 119, 128, MT94, MT95
 Diniz, C. T. F. S., MT204
 Diniz, W., MT297, MT353, MT354
 Distl, O., 35, MT183, MT219
 Djebali, S., 19, 20, 144, 147, MT127, MT128, MT289, WT69
 Djikeng, A., MT311
 Dobrowolski, M., MT20, MT21
 Dodds, K., 101, MT365
 Doeschl-Wilson, A., 71, 143, 173, MT166, WT78
 Dogliero, A., MT35
 Dong, K., 157, WT32
 Dong, Y., WT65
 Doran, T., 27, MT176
 Doré, J., 134, MT239
 Dotsev, A., 15, 92, MT23, WT33
 Dov, P., MT355
 Downey, E., 103, MT370
 Doyle, D., MT350
 Dreger, D. L., 152, WT5
 Drobik-Czwaro, W., 73, MT161
 Drögemüller, C., MT323
 Drögemüller, M., 121, 128, MT95, MT105
 Drouilhet, L., 153, WT27
 Dry, I., 21, MT167
 Duan, Z. Y., 113, MT12
 Ducro, B., 33, MT182, MT211
 Dugarjaviin, M., MT202
 Duguma, G., 154, WT30
 Dunner, S., MT82, MT224
 Durand, H. Morales, MT326
 Durkin, K., 99, MT346, MT348, MT368
 Dusel, G., MT333
 Dusingizimana, T., 184, WT101
 Dyomin, A., 44, MT50, MT67
 Dzama, K., 81, MT169
 Dzomba, E., MT306, WT21, WT92

E

Eberth, J., MT201
 Eddy, A., MT207
 Edgren, H., WT49
 Edin, H., 78, MT165
 Ehlers, K., WT94
 Ehsani, A., 49, MT64
 Ekaya, W., MT107
 Ekine-Dzivenu, C., MT78
 Elguero, B., 68, MT134
 Elleder, D., 46, MT57
 Ellis, K., MT92
 Elsik, C., 168, WT57
 Eltanany, M., WT17
 Ema, P. J. N., 182, WT96
 Emmerling, R., 100, MT129
 Emrani, H., WT20
 Engelmann, S., 75, MT138, MT157
 Engle, B. N., MT317
 English, A. M., MT334
 Ensing, D., 4, MT24
 Eory, L., 149, MT287, WT66
 Ernst, C., 17, 114, 159, MT10, MT11, MT258, WT58
 Ertugrul, O., 120, MT104
 Escobar, S., WT75
 Eshghabadi, M. A., WT20
 Espinosa, J., 110, MT16
 Esquerre, D., MT49
 Esquerré, D., 20, 53, 147, MT56, MT284, MT289, WT69
 Essa, A., MT313
 Essa, A. A., MT38
 Estany, J., 140, MT257, MT277, MT292
 Esteban-Blanco, C., 97, WT26
 Estelle, J., 79, MT168
 Estellé, J., 134, 136, MT238, MT239, MT252, MT284
 Esteve-Codina, A., 77, MT160
 Etherington, G., MT19
 Eusebi, P., MT82
 Eusebi, P. G., MT224
 Evans, B., 171, WT74, WT85
 Evans, J., MT350
 Ezoe, H., MT190

F

Fabre, S., 155, WT31
 Fages, A., 87, MT235
 Faherty-O'Donnell, S. L., WT47
 Fair, S., MT334, WT39
 Fang, J., MT33
 Fang, S., MT249
 Fang, X., MT298
 Farahi, M., 49, MT64

Farias, F. F., 126, MT102
 Farkasova, H., 46, MT57
 Farquhar, L., MT324
 Farre, M., 26, 44, 163, MT66, MT67, WT61
 Farrè, M., 160, WT54
 Farries, G., 34, MT215
 Farzan, V., MT155
 Fathoni, A., MT69
 Favaro, L., MT43
 Fedorov, V., 15, MT23
 Feeney, D. A., MT93
 Fegraeus, K. J., MT179
 Felkel, S., 32, MT214
 Feng, C., 177, WT86
 Feng, W., MT255
 Feren akovi, M., MT355
 Fernandes, I., 90, MT234
 Fernandez, A., MT245
 Fernandez, M., WT93
 Fernández, A., 98, 141, 173, MT269, MT276, MT294, WT35, WT53, WT78
 Fernández, A. I., 136, MT238, MT252, MT253
 Fernández, J., 173, WT78
 Fernández, M., 165, WT56
 Fernández-Barroso, M. A., MT254
 Fernández-León, J., 67, MT216
 Ferretti, R., 116, MT84, MT338
 Fève, K., MT262
 Finlay, E., WT39
 Fitzsimmons, C., MT4, MT78, MT300, MT327
 Flach, E., WT46
 Fleming, A., MT356
 Fleming, D. S., MT146, MT256
 Flicek, P., 56, 149, MT115, MT287, WT66
 Flores, E. B., WT90
 Flossmann, G., MT261
 Flynn, P., 91, 117, MT80, MT83, MT233
 Fogarty, U., 4, MT24
 Foissac, S., 19, 20, 144, 147, MT127, MT128, MT289, WT69
 Folch, J., MT276, WT15
 Folch, J. M., 136, MT238, MT252, MT253
 Follett, M., MT318
 Follett, M. A., 158, WT28
 Fontanesi, L., 43, 98, 137, 176, MT19, MT44, MT61, MT272, MT291, MT294, MT335, WT83
 Foote, B., 101, MT365
 Fornal, A., 70, MT81, MT194, MT195, MT196, MT220
 Foster, J., MT329
 Fourdraine, R., MT144
 Fowler, K. E., 26, MT66
 FR-AgENCODE Consortium, 19, MT127
 Francino, O., 6, WT6

François, L., 33, MT182, MT211
 Frantz, L., MT259
 Fraser, R. S., MT158
 Frattini, S., 152, WT1, WT5
 Fredholm, M., 135, MT91, MT241
 Freitas, L. A., WT48
 Friedrich, J., MT88
 Fries, R., 100, MT129, MT328
 Frieten, D., MT333
 Fritz-Waters, E., 103, MT370
 Fu, W., WT44
 Fu, Y., MT250
 Fukazawa, K., MT304
 Fukushima, M., MT305, MT308, MT309
 Fulton, J., 42, 54, 73, MT41, MT47, MT55,
 MT62, MT161
 Fulton, J. E., 66, MT116
 Funston, R., MT3
 Fusi, F., MT352

G

G+E Genotype Plus Environment
 Consortium, WT38

GplusE Consortium, MT153
 Gaba, R. C., 138, MT286
 Gabler, N., 16, MT275, WT70
 Gaginskaya, E., 44, MT50, MT67
 Galaverni, M., 152, WT5
 Galimberti, G., MT272
 Galindo-Pellicena, M. A., MT228
 Galkina, S., 44, MT50, MT67
 Gallardo, R., 55, MT52
 Galli, A., 3, MT86, MT282, MT352
 Gálvez, F., WT50
 Gama, L., MT281
 Gama-Carvalho, M., MT281
 Gamba, C., 87, MT235
 Gamba, R., 36, MT210
 Gandini, G., 152, WT1, WT5
 Gandolfi, B., 123, MT103
 Gangsei, L. E., MT278
 Gao, H., MT222
 Gao, J., MT70
 Gao, S., WT44
 Gao, X., MT222
 Gao, Y., 139, MT288
 Garcia, S., WT50
 García, F., 98, MT294
 García, P. P., WT93
 García Girón, C., 149
 García-Casco, J., 98, 141, MT294, WT53
 García-Casco, J. M., MT254
 Garcia-Contreras, C., MT245
 García-Contreras, C., WT35, WT42
 García-Rodríguez, A., 131, MT242
 Garrayo, J., MT245
 Gaunitz, C., 87, MT235
 Gaur, U., MT51
 Geigl, E.-M., 125, MT97
 Geistlinger, L., MT297, MT354
 Genho, J., MT338
 Genova, F., 123, MT89, MT103
 Georges, M., 99, MT346, MT348, MT368
 Geraci, C., 98, MT294
 Gerber, V., MT185
 Gerbert, C., MT333
 Getachew, T., 185, WT100
 Ghosh, S., MT123
 Gianino, F., 41, MT213
 Gianino, G., 41, MT213
 Gibson, A., 85, MT163
 Giegl, E.-M., 105, MT360
 Gil, M., MT268
 Gilbert, H., MT262
 Gill, C., 51, MT53
 Gill, C. A., 84, MT317, MT367, WT68
 Ginja, C., 90, MT228, MT234
 Giorgi, M., MT262
 Giovambattista, G., 165, MT326, WT56
 Girardi, M., MT87
 Girón, C. García, MT287
 Giuffra, E., 19, 20, 144, MT127, MT128,
 WT69
 Giulotto, E., 36, 41, MT210, MT213
 Giwa, A. O., WT73
 Gizaw, S., 154, 185, WT30, WT100
 Gladyr, E., 92, WT33
 Glass, E., MT325
 Goddard, M., 100, MT129, MT321
 Gòdia, M., MT285
 Gokhale, S., 104, MT373
 Gol, S., 140, MT257, MT292
 Goldammer, T., 178, WT82
 Golzalez-Bulnes, A., MT245
 Gombac, M., MT323
 Gómez Izquierdo, E., 141
 Gomez-Garrido, J., 77, MT160
 Gondro, C., WT90
 Gonzalez, M. V., WT14
 González-Bulnes, A., WT42
 González-Bulnes, A., WT35
 Gonzalez-Prendes, R., MT265
 González-Prendes, R., MT267, MT268
 Gonzalez-Recio, O., 131, MT242
 González-Rodríguez, O., MT267, MT268
 Gordon, S., 111, MT9
 Gordon, S. V., 76, 166, MT173, WT47, WT52,
 WT55
 Gorkhali, N., 157, WT32
 Gorla, E., MT44, MT335
 Gormley, E., 76, 166, MT173, WT47, WT55
 Gorzynski, J., WT46
 Goszczynski, D., MT326

Goszczynski, D. E., WT93
 Götherström, A., 90, MT234
 Goto, R. M., 64, MT162
 Goto, T., MT40
 Götz, K.-U., MT261
 Gough, K. F., 34, MT215
 Gourdine, J., MT262
 Gourichon, D., 53, MT49, MT56
 Gow, A., 121, MT105
 Gozzo, F., 36, MT210
 Grahn, J., WT3
 Grahn, R., WT3
 Grange, T., 105, 125, MT97, MT360
 Graves, T., 42, MT55
 Gray, K., 169, WT59
 Gredler-Grandl, B., 100, MT129
 Grelet, C., MT153
 Gresham, C., 22, MT126
 Griebel, P., MT346, MT348
 Griffin, D., 44, MT67
 Griffin, D. K., 26, MT66
 Grimholt, U., 56, MT115
 Grindflek, E., MT278
 Grobler, J. P., WT94
 Groenen, M., 147, MT289, MT345, WT42
 Groenen, M. A. M., 138, MT286
 Gromboni, C., MT353
 Große-Brinkhaus, C., 74, MT137, MT170,
 MT251
 Groth, D., 60, MT111
 Gu, L., MT34
 Guan, D., MT299
 Guan, L., 167, WT60
 Guan, L. L., MT307
 Guenther, J., MT138
 Guerrero, J., 4, MT24
 Guerrero-Bosagna, C., MT1
 Guethlein, L., 56, MT115
 Gugiu, G., 64, MT162
 Guillocheau, G., 102, MT369
 Guimaraes, S., 105, MT360
 Gul, S., MT136
 Guldbbrandtsen, B., MT118
 Gulas-Gomes, C. C., 180, WT99
 Günther, J., 75, MT157
 Guo, G., MT73
 Guo, X.-F., WT11
 Gurgul, A., 146, MT5, MT15, MT184, MT330
 Gurtner, C., 119, MT94
 Gutierrez, L., WT93
 Gutierrez-Gil, B., 97, WT13, WT26, WT37

H

Haase, B., 122, MT100, MT205
 Hadfield, T., MT340, WT23
 Hadlich, F., 114, MT11, MT138, MT333

- Hagen, D., 168, WT57
 Haggerty, L., 149, MT287
 Hahaut, V., MT346, MT348
 Haile, A., 154, 185, WT30, WT100
 Häkkinen, S., WT49
 Hall, R., 148, MT125
 Hall, T., 111, 166, MT9, WT55
 Hall, T. J., 76, MT173, WT39
 Halliday, C., MT199
 Halstead, M., 159, WT58
 Hameed, A., WT7
 Hamill, R. M., MT270, MT271
 Hamilton, N., MT205
 Hamilton, N. A., MT199
 Hammer, S., 57, MT109
 Hammermüller, J. D., MT158
 Hammon, H. M., MT333
 Hammond, J., 23, 56, MT115, MT159
 Hammond, J. A., MT154, MT315
 Han, H., MT202
 Han, X., 139, MT288
 Han, Y., MT316, MT339
 Hanghøj, K., 87, MT235
 Hanotte, O., 94, 108, 183, MT38, MT40,
 MT107, MT313, MT361, WT87, WT95,
 WT98
 Hanzawa, K., MT39, MT319
 Hara, H., MT39, MT319
 Harburg, S., MT322
 Harland, C., 99, MT368
 Harlizius, B., MT278
 Harman, K., MT156
 Harrington, R., 121, 127, 128, MT95, MT99,
 MT105
 Harris, R. A., MT316
 Harrison, P., WT66
 Hartatik, T., MT69, WT24
 Haskell, M. J., MT90
 Hawken, R., 42, 78, MT55, MT156, MT165
 Hayes, B., MT121, MT321
 He, P., MT150
 He, X.-Y., WT11
 Heath, S., 77, MT160
 Heaton, M., 8, MT26
 Hecht, J., MT285
 Hedhammar, Å., 126, MT102
 Hehl, A., MT138
 Hehl, J., 75, MT157
 Heimeier, D., 23, MT154, MT159
 Heimes, A., MT138
 Heldmann, A., MT328
 Heller, R., 24, MT364
 Hendrick, S., 167, WT60
 Henke, D., 119, MT94
 Henne, H., MT251
 Henry, S., 27, MT176
 Henryon, M., 172, WT79
 Hermida, M., 173, WT78
 Hermine, O., MT348
 Herndon, M. K., MT106
 Herrera, J. R. V., WT90
 Herring, A. D., 84, MT317, MT367
 Hess, A., 143
 Hess, M., 143
 Heuß, E., MT251
 Hewicker-Trautwein, M., MT183
 Hickey, J., MT88
 Highland, M. A., MT106, WT14
 Hilburger, K., 41, MT213
 Hill, A., 166, WT55
 Hill, E., MT202
 Hill, E. W., 34, MT215
 Hillestad, B., 172, WT79
 Hillier, L., 42, MT55
 Hirano, T., MT39, MT319
 Hirota, K., 69, MT135
 Hirota, K.-I., MT178
 Hlongwane, N., WT92
 Ho, C., 56, MT115
 Ho, S., 57, MT109
 Hoban, R., MT205
 Hocking, P. M., MT40
 Hoedemaker, M., MT138
 Hofmanova, B., MT193
 Högl, S., 119, MT94
 Hoj-Edwards, S., MT88
 Holgado, F. D., WT93
 Hölker, M., 74, MT137, MT170
 Holl, H., 58, MT22, MT117
 Holl, H. M., 11, WT104
 Hollmann, A. K., MT79, MT336
 Hom, B. Bed, MT116, MT165
 Honda, T., MT305, MT309
 Horbanczuk, K., MT341, MT343
 Horin, P., 31, MT218
 Horodyska, J., MT270, MT271
 Hoskens, H., MT182
 Hou, Y., MT250
 Hourlier, T., 149, MT287
 Hron, T., 46, MT57
 Hu, A., MT250
 Hu, W.-P., WT11
 Hu, X., 29, MT174, MT244, MT249
 Huang, H., MT73
 Huang, J., 16, WT70
 Huang, L., 145, MT70, MT290, WT9
 Huang, Y., MT299
 Huau, C., 153, WT27
 Hume, D., 104, 148, MT125, MT156, MT373
 Hume, D. A., MT324
 Hurtado, A., 131, MT242
 Huson, H. J., 185, MT92, WT100
 Hussain, T., WT8
 Hwang, J., MT132
 Hwang, N.-H., MT180
 Hwangbo, J., MT42
- I**
- Iannuccelli, N., WT45
 Ibañez-Deler, A., WT15
 Ibe, U. K., MT31
 Ihler, C. F., MT179
 Ilska, J., MT90
 Isabel, B., 141, MT245, WT35, WT42, WT53
 Isaja, V., MT43
 Ishengoma, E., MT310
 Ishige, T., MT39
 Islam, M. A., 74, MT137, MT170
 Iwamoto, E., MT305, MT308, MT309
 Izquierdo, E. Gómez, WT53
 Izuogu, O., 149, MT287
- J**
- Jaeger, H., MT318
 Jaeger, H. K., 158, WT28
 Jafarikia, M., MT155
 Jagannathan, V., 32, MT185, MT214, MT323
 Jain, P., 86, WT105
 Jameel, M., MT33
 Jammes, H., MT7
 Janczak, A., MT1
 Janecka, J., MT123
 Jang, A., MT180
 Jang, G.-W., 115, MT13
 Jankowski, T., 73, MT161
 Janssens, S., 33, MT182, MT211
 Jarczak, J., MT341, MT343
 Jarmuz, W., MT341, MT343, MT344
 Jasielczuk, I., MT330
 Jaures, K. S., MT311
 Jehangir, M., WT71
 Jehl, F., 53, MT56
 Jennings, R., 26, MT66
 Jensen, P., MT1
 Jevons, L., MT329
 Jiang, L., 157, WT32, WT65
 Jiang, Y., 24, MT119, MT364, WT44
 Jin, L., 51, MT53
 Jin, S., 9, MT46, MT65
 Jin, S. Y., MT70
 Johansson, A., WT10
 Johnson, C., 121, MT105
 Johnson, E., 121, MT105
 Johnson, M., MT207
 Johnson, P. L., MT140
 Johnson, S., WT25
 Jonas, E., WT10
 Joost, S., 109, MT362
 Joseph, S., 26, MT66

Joshi, V., WT19
 Jouneau, L., MT7
 Józsa, C., MT312
 Juga, J., 182, WT96
 Jugo, B. M., WT51
 Jung, K., MT183
 Jung'a, J., MT107
 Juras, R., MT229
 Just, F., MT283

K

Kaba, J., MT341, MT343
 Kaiser, M., 82, MT172
 Kakoi, H., 69, MT135, MT178
 Kalashnikov, A., MT151
 Kalbfleisch, T., 8, 39, 41, MT26, MT201,
 MT209, MT213
 Kalbfleisch, T. S., 40, MT221
 Kamboh, A. A., MT33
 Kanemaki, M., MT189
 Kanis, E., WT88
 Karberg, M., 151, MT98
 Karim, L., 99, MT368
 Karimi, K., 14, MT25
 Karlskov-Mortensen, P., 135, MT91, MT241
 Karrow, N., 80, MT171
 Kasarda, R., MT193
 Katz, L. M., 34, MT215
 Kaufman, J., 56, MT115
 Kause, A., 143
 Kaushikkar, S., MT329
 Kawaguchi, F., MT304, MT305, MT309
 Kawecka, A., MT152
 Kawecka, E., MT344
 Kazymbet, P., MT190, MT223
 Kean, M., 117, MT83
 Keane, O. M., MT149
 Kearney, F., MT80
 Kearney, J., 117, MT83
 Kebede, A., MT107
 Keel, B. N., MT279
 Keliang, W., MT226
 Kelly, A. K., 132, MT237
 Kelly, G., 4, MT24
 Kelly, M., MT121
 Kelly, T., 55, MT52
 Kemper, A., MT186
 Kenny, D., MT350, MT351
 Kenny, D. A., 132, MT237, MT302, MT334
 Keogh, K., MT302, MT351
 Keonouchanh, S., MT189
 Kern, C., 17, 114, 159, MT10, MT11, WT58
 Kerr, D., MT139
 Khalili, A., 11, MT22, WT104
 Khan, M., MT296
 Khan, N., 87, MT235

Khanshour, A. M., MT130
 Kharzinova, V., 15, 92, MT23, WT33
 Khatib, H., 18, MT14
 Khatkar, M. S., MT314
 Khatkar, M.-S., 129, MT96
 Khattak, I., MT136
 Khosa, A. N., WT7
 Kiazim, L., 26, MT66
 Kiefer, H., MT7
 Kierczak, M., 126, MT102
 Kigoshi, H., MT305, MT309
 Kiellerich, P., 135, MT241
 Kijas, J., 25, 171, MT316, MT340, MT372,
 WT74, WT85
 Kikuchi, M., 69, MT135, MT178
 Killick, K. E., 76, 166, MT173, WT55
 Kim, D., MT6
 Kim, D. C., MT180, MT188
 Kim, H., 183, WT98
 Kim, H.-Y., 9, MT65
 Kim, J., 163, 183, WT61, WT98
 Kim, J.-B., MT180
 Kim, J.-D., MT180
 Kim, J.-M., MT42
 Kim, K., 148, MT125,
 Kim, K.-S., MT147
 Kim, N. Y., MT188
 Kim, N.-Y., MT180
 Kim, S., MT132
 Kim, S.-W., MT147
 Kim, W.-I., MT147
 King, H., 171, WT74, WT85
 Kleiter, M., 119, MT94
 Klopp, C., 20, 53, 144, MT49, MT56, MT128,
 WT69
 Klukowska-Rötzler, J., MT195
 Klumplerova, M., 31, MT218
 Knol, E. F., MT278
 Knowles, D. P., MT106, WT14
 Kobayashi, E., MT305, MT308, MT309
 Koch, C., MT194, MT195, MT333
 Kochan, J., 7, WT4
 Kohama, N., MT305, MT308, MT309
 Kohara, J., MT150
 Komissarov, A., 44, MT67
 Kongsro, J., MT278
 Koren, S., 148, MT125
 Korf, I., 17, 114, 159, MT10, MT11, WT58
 Korkmaz, F., MT139
 Koscielny, M., MT152
 Kosciuczuk, E., MT344
 Koshel, E., MT50
 Koshinsky, H., WT19
 Kott, T., WT22
 Koufariotis, L., MT121
 Kounnavongsa, B., MT189
 Kovarik, A., WT50

Kowalska, K., MT184
 Koy, M., 75, MT157
 Kozyrev, S., 126, MT102
 Kraft, M., MT185
 Kramer, L., 103, MT370
 Kranjcevicova, A., MT74
 Kranjcevicová, A., MT192
 Krebs, S., MT87, MT355
 Kremitski, M., 42, MT55
 Kristiansen, K., 135, MT241
 Kroezen, V., MT356
 Kube, P., 171, WT74, WT85
 Kubickova, S., 31, MT218
 Kuehn, C., MT138
 Kuehn, D., 121, MT105
 Kühn, C., 75, MT157, MT333
 Kuisma, M., WT49
 Kul, B. C., 120, MT104
 Kulak, M., 44, MT50, MT67
 Kumar, A., MT248
 Kumar, M., 86, WT105
 Kumar, P., MT248
 Kumar, S., 104, MT248, MT373
 Kunieda, T., MT189, MT190
 Kunz, E., MT355
 Kuo, R., WT66
 Kustantinah, K., WT24
 Kyalo, M., MT107
 Kyriazakis, I., 143
 Kyselova, J., WT22

L

Labrune, Y., MT262
 Lachance, H., MT3
 Lagarrigue, S., 19, 20, 53, 144, MT49, MT56,
 MT127, MT128, WT69
 Lahbib-Mansais, Y., 147, MT289
 Lahoz, B., WT15
 Lamberigts, C., 33, MT182, MT211
 Lamichhaney, S., 177, WT86
 Lamont, S., 45, 82, MT54, MT172
 Lamont, S. J., 55, MT52
 Larkin, D., 44, 160, MT67, MT347, WT54
 Larkin, D. M., 26, 163, MT66, WT61
 Larzul, C., 134, MT239
 Lasagna, E., WT18
 Lascor, C., WT45
 Lashmar, S. F., WT91
 Latifah, L., WT24
 Lavery, J., 4, MT24
 Lawal, R. A., 94, MT40, WT95
 Lawlor, P. G., MT270, MT271
 Le, C. Q., MT266
 Le, M. T., MT266
 Le Danvic, C., MT7
 Lebrero, M. E., WT40

- Lee, D., MT46
 Lee, H., MT266
 Lee, J., MT6, MT266
 Lee, J. H., 9, MT46, MT65
 Lee, J.-H., 57, MT109
 Lee, K.-T., 115, MT13, MT42
 Lee, S. H., 9, MT46, MT65
 Leeb, T., 32, 128, MT95, MT214
 Lefevre, L., 104, MT373
 Lehnert, S. A., MT322
 Lemonnier, G., 79, 134, MT168, MT239, MT284
 Leonardi, M., 87, MT235
 Lepage, P., 134, MT239, MT284
 Leplat, J., 79, MT168
 Leplat, J. J., MT284
 Leroux, S., 53, MT49, MT56
 Leschnik, M., 119, MT94
 Levenez, F., 134, MT239
 Lewin, H. A., 163, WT61
 Lhorente, J., WT72
 Li, C., MT4, MT76, MT78, MT250, MT300, MT327, WT67
 Li, D., MT51
 Li, D. L., 50, MT59
 Li, G., MT298
 Li, H., MT338
 Li, J., MT222, MT250, MT260, MT320, MT332
 Li, L., MT250
 Li, M., 51, MT53
 Li, N., 29, MT174, MT244, MT249
 Li, Q., 164, WT62
 Li, R., WT44
 Li, S., MT34
 Li, W., 145, MT290
 Li, X., 52, 139, MT58, MT73, MT146, MT288, WT36
 Li, Y. L., 50, MT59
 Liachko, I., 42, MT55
 Liaubet, L., 147, MT289, WT45
 Librado, P., 87, MT235
 Lilloco, S., 21, 28, MT167, MT175
 Lillie, B. N., MT155, MT158
 Lim, B., MT147
 Lim, D., 115, MT13, MT42
 Lim, K.-S., 115, MT13, MT42
 Lima, A., MT297, MT353, MT354
 Lima, R. M. G., MT204
 Lin, D., MT36
 Lin, L., MT72
 Lin, Y. Q., WT9
 Lindblad-Toh, K., 126, MT102
 Lindgren, G., 33, MT179, MT182, MT211
 Lipkin, E., 54, MT41, MT47, MT62, MT357
 Lippi, Y., WT45
 Liron, J., 165, WT56
 Lirón, J. P., WT93
 Liu, B., MT311
 Liu, D., MT249
 Liu, H., MT307
 Liu, J., MT307, WT65
 Liu, J.-F., MT255
 Liu, L., 113, MT12
 Liu, Q.-Y., WT11
 Liu, S., WT67
 Liu, W., MT342
 Liu, X., WT36
 Liu, Y., 51, 138, MT53, MT286, MT316
 Liu, Y. F., 50, MT59
 Liu, Z., MT260, MT320, MT332
 Liuti, T., 121, 127, MT99, MT105
 Lobo, R. N. B., 154, WT30
 Lofgren, S. E., MT90
 Longeri, M., 123, MT89, MT103
 Lopes, F. B., MT338
 Lopes, M. S., MT278
 López-Bote, C., 141, MT245, MT269, WT53
 López-Pérez, O., 110, MT16
 Lough, G., 143
 Loving, C. L., 142, MT164
 Loyau, T., MT262
 Lozano, J. M., 67, MT216
 Lühken, G., WT17
 Luján, L., WT51
 Lund, M., MT120
 Lund, M. S., MT118
 Lunney, J., 57, 143, MT109
 Luo, N., MT299
 Luo, W., MT250, WT64
 Lwin, M., MT227
 Lyons, L., 122, 123, 124, MT100, MT101, MT103
 Lyons, L. A., MT89
 Lyons, R., MT121
 Lyu, S., MT30
- M**
- Ma, J., 52, 163, MT58, WT61
 Ma, L., MT260
 Ma, Y., 157, MT34, WT32, WT36
 Maccari, G., 56, MT115
 Mach, N., 134, MT239
 MacHugh, D., 111, MT9
 MacHugh, D. E., 76, 166, MT173, WT47, WT52, WT55
 Mack, M., 41, MT213
 Mack, S., MT207
 Mackowski, M., MT130, MT197
 MacLeod, I., 100, MT129
 MacLeod, J., 39, 41, MT209, MT213
 MacLeod, J. N., 40, MT133, MT221
 MacNeil, M., MT78
 MacNeil, M. D., MT76
 Madsen, O., 138, 147, MT286, MT289, WT42
 Magee, D., 111, MT9
 Magee, D. A., 76, 166, MT173, WT47, WT52, WT55
 Maharani, D., MT69
 Mählmann, K., MT194, MT195
 Maiwashe, A., MT124
 Mäkeläinen, S., 138, MT286
 Makgahlela, M. L., MT124
 Malek, J., 11, 58, MT22, MT117, WT104
 Malesa, M., MT306
 Mallikarjunappa, S., 80, MT171
 Malomane, D., 95, MT236
 Mamiru, M., 154, WT30
 Manafiazar, G., MT76
 Mandawala, A., 26, MT66
 Manjula, P., 9, MT65
 Mannen, H., MT189, MT190, MT223, MT304, MT305, MT308, MT309
 Mannen, H., MT227
 Manrique Osinaga, I. P., WT93
 Mansour, T., MT207
 Manunza, A., MT265
 Mapholi, N. O., WT94
 Marçais, A., MT348
 Marchant, T., 121, 127, 128, MT95, MT99, MT105
 Marchitelli, C., MT153, WT43
 Marcon, D., 153, WT27
 Marczak, S., MT344
 Marelli, S. P., 152, WT1, WT5
 Marete, A. G., MT120
 Marghazani, I. B., WT7
 Marie-Hélène, P.-v. d. L., MT165
 Marikar, F., WT8
 Marin-Cely, J., 129, MT96
 Marioni-Henry, K., 127, MT99
 Marleen, V., MT345
 Mármol-Sánchez, E., MT267, MT268
 Maroilley, T., MT284
 Marsan, P. A., 18, MT14
 Marsh, S., 56, MT115
 Marshal, K., 182, WT96
 Martell, H., 26, MT66
 Marthey, S., MT7
 Marti-Marimon, M., 147, MT289
 Martin, F. J., 149, MT287
 Martín-Burriel, I., 110, MT16
 Martinez, A. B., 177
 Martinez, A. Barrio, WT86
 Martinez, A. M., MT230
 Martinez, M., 68, MT134
 Martinez, V., 175, 179, WT75, WT76, WT77, WT81
 Martínez, P., 173, WT78
 Martínez-Montes, A., MT276

- Martinez-Royo, A., WT15
 Martínez-Valladares, M., WT13
 Martins, C., WT71
 Maruyama, S., MT304
 Mason, B., MT321
 Masoudi, A. A., 49, MT64, WT20
 Massa, A., 161, MT340, WT63
 Massilani, D., 105, MT360
 Mastrangelo, S., WT87
 Mateo, J., WT37
 Mátlová, V., MT151
 Matos, J., 90, MT234
 Matsushashi, T., MT304
 Matsumoto, Y., MT305, MT309
 Mauri, N., 119, MT94
 Maya, M. R., 67, MT216
 Mayer, F., 77, MT160
 Mayes, M., 103, MT370
 Mayoral, T., 67, MT216
 Mazzoni, G., 137, MT272, MT291
 Mbajjorgu, C. A., MT243
 McBride, S., MT325
 McCabe, M. S., 132, MT237
 McCarthy, F., 22, MT126
 McCarthy, J., 117, MT83
 McClure, J., MT80
 McClure, M., 117, MT80, MT83
 McColl, K., 27, MT176
 McCormick, C., 4, MT24
 McCoy, A., MT186
 McCue, M., 37, MT131, MT186, MT187,
 MT212
 McCulloch, A., 25, MT372
 McCulloch, M. E., MT324
 McEwan, J., 101, MT365
 McGivney, B. A., 34, MT215
 McGovern, E., 132, MT237
 McGrew, M., 30, MT177
 McKay, S., MT3
 Mckenna, C., MT351
 McLean, K. J., 112, MT8, WT34
 McLoughlin, K. E., 76, MT173, WT47, WT52
 McQuillan, C., WT39
 McRae, K. M., MT140
 McTier, L., 121, MT105
 McWilliam, S., 25, 171, MT372, WT74, WT85
 McWilliam, S. M., MT322
 Mdladla, K., WT92
 Meade, K., 80, MT171
 Meade, K. G., WT39
 Medrano, J., 159, WT58
 Medrano, J. F., MT154
 Medugorac, I., MT87
 Megens, H., MT345
 Meiyang, F., MT247
 Mendoza, K., MT45
 Meneses, C. L. P., MT204
 Meng, Q., MT316
 Mengmeng, Z., MT226
 Menzies, M., WT74
 Mercat, M., 98, MT294
 Mercat, M. J., MT284
 Mercat, M.-J., 134, MT239
 Meripet, P., MT148
 Mesbah-Uddin, M., MT118
 Mészáros, G., 185, WT100
 Metzger, J., 35, MT183, MT219
 Meutchieye, F., MT311
 Meyer, A., MT158
 Meyerholz, M., MT138
 Mi, L., MT260
 Mir, Y., 14, MT25
 Mickelson, J., 37, MT131, MT187, MT212
 Mickiewicz, M., MT343
 Miglior, F., MT356
 Mikko, S., 65, MT108, WT10
 Miksza-Cybulska, A., MT152
 Mileham, A., 28, MT175
 Millán, A., 173, WT78
 Miller, D., 11, 36, 58, MT22, MT117, MT210,
 WT104
 Miller, L., MT256
 Miller, L. C., MT146
 Miller, M., 42, MT55
 Miller, M. M., 64, 66, MT116, MT162
 Miller, S. P., MT71
 Ming-Whitfield, B., 41, MT213
 Minor, K. M., MT93
 Minx, P., 42, MT55
 Miracle, P. T., MT87
 Mirkena, T., 154, WT30
 Miron, J., MT357
 Missirian, V., WT19
 Missohou, A., 182, WT96
 Miszczak, M., 5, MT17
 Mochal, C., MT207
 Modesto, P., MT35, MT43
 Moe, H., MT189, MT227
 Moe, K., MT189
 Mohamed, A., 171, WT85
 Mohamoud, Y., 11, MT22, WT104
 Mohamoud, Y. A., 58
 Mohamoud, Y. Ali, MT117
 Mohsin, M., WT7
 Moiola, B., WT43
 Molae, V., WT17
 Molina, A., MT326
 Mompert, F., 147, MT289
 Monney, C., 119, MT94
 Monson, M., 82, MT172
 Montano, D. A., MT231
 Montedoro, M., MT352
 Montfort, M., MT285
 Montserrat, S., 77, MT160
 Moore, K., MT295
 Moore, S., MT121
 Moore, S. S., MT71
 Moran, A., MT295
 Moravcikova, N., MT193
 Moreira, O., MT281
 Moretti, E., WT1
 Morgan, E., 60, MT111
 Moro, D., 27, MT176
 Morota, G., MT339
 Morrice, D., MT20, MT21
 Mortlock, S.-A., 129, MT96
 Moska, M., MT20, MT21
 Motycka, J., MT74
 Mourão, G., MT353, MT354
 Mousel, M., 161, MT340, WT63
 Mousel, M. R., 156, MT106, WT14, WT29
 Mrode, M., MT325
 Mrode, R., 181, 183, 184, WT98, WT101,
 WT102
 Mucha, A., MT20, MT21
 Muchadeyi, F., 81, MT169, MT306, WT21,
 WT92
 Muchadeyi, F. C., 186, WT91, WT94, WT97
 Mujibi, F. D. N., 184, WT101
 Mukesh, M., 86, WT105
 Mukhanbetkaliyev, Y., MT75
 Mukiibi, R., MT300, MT327, WT88
 Mulder, H., 143
 Mullaart, E., 99, MT368
 Mullen, M., MT80
 Mullen, M. P., 76, 166, MT173, WT55
 Mullin, V., 107, MT366
 Munari, D. P., WT48
 Muñoz, M., 98, MT254, MT276, MT294
 Munyard, K., 20, 60, 144, MT111, MT128,
 WT69
 Munyard, K. A., 12, MT27
 Murdoch, B., 161, MT316, MT318, MT340,
 WT63
 Murdoch, B. M., 158, WT28
 Muret, K., 20, 53, MT49, MT56, WT69
 Murphy, D. N., 149, MT287
 Murphy, M., MT149
 Murphy, R. W., MT259
 Musilova, P., 31, MT218
 Musthafa, M., WT8
 Mutai, C., MT311
 Muzny, D. M., MT316
 Mwacharo, J., MT38, MT311, WT87
 Mwacharo, J. M., 181, WT102
 Mwai, A. O., 185, WT100
 Mwai, O., 154, 181, WT30, WT102
 Mwai, O. A., MT311

N

Na, R., MT299
 Naccache, F., 35, MT219
 Nag, R., 149, MT287
 Nagata, S., 69, MT135
 Nagata, S.-I., MT178
 Nai, R., MT260, MT332
 Nakajima, A., MT309
 Nakajima, T., MT308
 Nalpas, N., 111, MT9
 Nalpas, N. C., 76, 166, MT173, WT47, WT52, WT55
 Namous, H., 18, MT14
 Nanduri, B., 22, MT126
 Napolitano, F., MT153
 Naranbhai, V., 166, WT55
 Nascimento, G. B., WT48
 Nassar, M. K., MT30
 Naval Sanchez, M., 25
 Nayeri, S., MT71, MT356
 Ncube, K., WT94
 Nergadze, S. G., 36, MT210
 Neßler, J. N., MT79
 Neuditschko, M., 32, MT214
 Neuhoff, C., 74, MT137, MT170
 Neumann, K., 175, WT81
 Neves, J., WT2
 Ni, A. X., 50, MT59
 Niciura, S., MT337
 Nicolini, P., MT339
 Niedziela, D., MT149
 Nielsen, M., 63, MT113, MT123
 Nieuwland, M. G. B., MT145
 Ning, C., WT65
 Nishibori, M., MT190, MT223
 Nishimura, S., MT319
 Nizamlioglu, M., 188, MT232
 Nizanski, W., 7, WT4
 Nneji, L. M., MT259
 Nogueira, A., MT353
 Nolan, M., MT156
 Nomura, K., MT190
 Nonnis, S., MT89
 Nordgreen, J., MT1
 Norton, E., 37, MT212
 Novák, K., MT151
 Novosel, D., MT355
 Nowak, A., 7, WT4
 Nunes, J. M. S., WT2
 Nuñez, Y., MT245, MT269, WT35
 Núñez, Y., 98, 141, MT276, MT294, WT42, WT53
 Nussbaumer, M., 121, MT105
 Nxumalo, K. S., WT94

O

Oatley, J., 28, MT175
 Obi, O. C., MT31
 O'Connell, K., 117, MT83
 O'Connor, R. E., 26, MT66
 Oczkiewicz, M., MT264
 O'Doherty, A., 111, MT9
 Oevermann, A., 119, MT94
 O'Farrelly, C., WT39
 Ogah, D. M., MT32
 Ojala, K., WT49
 Ojango, J., 181, 184, WT101, WT102
 Oke, U. K., MT31
 O'Keefe, J., 4, MT24
 Okimoto, N., MT150
 Okoro, C. L., MT243
 Okoro, V. M. O., MT243
 Okuda, Y., MT189, MT190
 Oladele-Bukola, M. O., MT259
 Olaogun, S. C., MT259
 Olivas, J., MT269
 Oliveira, P., MT297, MT353
 Oliveira, R. D., WT14
 Olorungbounmi, , MT259
 Olsson, C., MT179
 Olsson, M., 126, MT102
 Oluwole, O. O., MT259
 O'Meara, D., 4, MT24
 Omitogun, O. G., MT259
 Oncu, M. D., 188, MT232
 Öner, Y., MT18
 Onzima, R. B., WT88
 Oosterlinck, M., 33, MT211
 Opiela, J., 146, MT15
 Oppelt, J., 31, MT218
 Orellana, J., WT93
 Orlando, L., 31, 39, 87, MT209, MT218, MT235
 Orlando, L. A. A., MT123
 O'Rourke, B. A., MT314
 Ortega Masague, M., WT93
 Ortillés, A. L., WT40
 Osama, S., MT311
 Oster, M., MT283
 Østerbye, T., 63, MT113
 Ostrander, E. A., 152, WT5
 O'Sullivan, N., 73, MT161
 O'Sullivan, T., MT246
 O'Toole, D., 119, MT94
 Ottoni, C., 125, MT97
 Ottun, O. N., WT73
 Ovilo, C., MT245
 Óvilo, C., 98, 136, 141, MT238, MT269, MT294, WT35, WT42, WT53
 Oyama, K., MT304, MT305, MT308, MT309
 Oyekanmi, N., 183, WT98
 Ozmen, O., 120, MT104

P

Pabiou, T., MT80
 Paces, J., 46, MT57
 Pacholewska, A., MT185
 Pagnacco, G., 152, WT1, WT5
 Pajer, P., 46, MT57
 Paller, T., MT323
 Paniccià, M., WT18
 Pant, S., 80, MT171
 Paradis, F., MT4
 Paria, N., MT123
 Park, C., MT6, MT132, MT266
 Park, C. K., MT147
 Park, E.-W., 115, MT13
 Park, J.-E., 115, MT13, MT42
 Park, N. G., MT188
 Park, S. H., MT188
 Parmentier, H. K., MT145
 Pasha, K., 11, MT22, WT104
 Patel, A., 179, WT77
 Patil, M., MT329, WT19
 Patil, M. A., 118, MT85
 Patterson, E. E., MT93
 Pausch, H., 100, MT129, MT261, MT328
 Pawlina, K., 146, MT5, MT15, MT194, MT195
 Pedersen, A. Ø., 135, MT241
 Peelman, L., WT41
 Peeters, L., MT182
 Peletto, S., MT35, MT43
 Pelle, R., MT107
 Pemberton, J., WT25
 Pena, B., 153, WT27
 Pena, R., 140, MT257, MT277, MT292
 Peña, S., WT93
 Peñagaricano, F., 18, MT14, MT339
 Penedo, M. Torres, WT3
 Peng, D., MT36
 Peng, M.-S., MT259
 Peng, X., MT33
 Penso-Dolfin, L., MT19
 Péntek, I., MT312
 Periasamy, K., WT8
 Perkins, T., MT338
 Perrier, J., MT7
 Pértille, F., MT1
 Pessani, D., MT43
 Petersen, J., 41, MT213
 Petrini, J., MT354
 Petterson, M., 177, WT86
 Petzl, W., MT138
 Phillippy, A., 148, MT125
 Picchi, A., WT1
 Pickering, L., 81, MT169
 Piestrzynska-Kajtoch, A., 70, MT81, MT152, MT196, MT220
 Piga, S., MT43
 Pilkington, J., WT25

- Pilla, F., WT87
 Pinard-Van der Laan, M. H., 19, 78
 Piórkowska, K., MT191, MT198, MT263,
 MT264
 Pirani, A., 118, MT85, MT329, WT19
 Piras, F. M., 36, MT210
 Pires, A. E., 90, MT234
 Pitarch, L. B., 67, MT216
 Pitchford, W. S., MT77
 Pitel, F., 53, MT49, MT56
 Plastow, G., MT76, MT78
 Plysnina, P., MT347
 Podbielska, A., 5, 7, MT17, WT4
 Podstawski, P., MT184
 Polgar, Z., MT90
 Polli, M., 152, WT1, WT5
 Ponsuksili, S., 114, MT11, MT283
 Porter, R., MT351
 Porto-Neto, L. R., MT322
 Posik, D. M., WT93
 Powell, R., 121, MT105
 Pozzi, A., 3, MT86
 Prando, A., 165, WT56
 Presho, E., 4, MT24
 Previtali, C., 3, MT86, MT282
 Pribyl, J., MT74, MT192
 Priyadi, D. A., WT24
 Pröll, M. J., 74, MT137, MT170, MT251
 Proudfoot, C., 28, MT175
 Prowse-Wilkins, C., MT321
 Psifidi, A., MT156
 Puglisi, R., MT352
- Q**
- Qiao, X., MT247
 Qin, X., MT316
 Qin, Z., MT72
 Qiu, Q. Q., 24, MT364
 Qu, B. B., WT9
 Queiroz, S., WT72
 Quintanilla, R., MT265, MT267, MT268
 Qureshi, S., MT248
- R**
- Radko, A., 5, 7, MT17, MT81, MT196, MT330,
 WT4
 Radovic, S., MT87
 Raeber, A., 116, MT84
 Rafati, N., 177, WT86
 Rahmatalla, S. A., MT303
 Raimondi, E., 36, MT210
 Rakhshandeh, A., MT275
 Ramayo-Caldas, Y., 134, 136, MT238,
 MT239, MT252
 Ramírez, O., 6, WT6
 Ramirez Alanis, C., 41, MT213
- Ramos, S. B., WT48
 Ran, X., MT226
 Randalht, I., MT229
 Raney, N., MT258
 Raphael, M., MT311
 Rashidi, H., 143
 Rasmussen, M., 63, MT113
 Rattei, T., 32, MT214
 Ratti, C., 68, MT134
 Rau, A., 53, 144, MT7, MT49, MT56, MT128,
 MT252
 Raudsepp, T., MT123, MT229
 Rawat, C., MT248
 Rebl, A., 178, WT82
 Reczynska, D., MT341, MT343, MT344
 Reecy, J., 103, MT370
 Reed, K., MT45
 Regitano, L., MT297, MT337, MT353, MT354
 Reich, C., MT321
 Reina, R., WT51
 Reissmann, M., MT303
 Reixach, J., 140, MT277, MT292
 Remacha, A. R., MT181, WT40
 Renaudeau, D., MT262
 Ressaissi, Y., MT301
 Reverter, A., MT322
 Revilla, M., 136, MT238, MT252, MT253
 Rey, A., MT245, WT42
 Reyer, H., 15, 92, MT23, MT270, MT271,
 MT283, MT303, WT33
 Reynolds, L. P., 112, MT8, WT34
 Ribani, A., 43, 137, MT19, MT61, MT291
 Ribeca, P., MT315
 Ribeiro, C., MT203
 Rice, E., 38, MT208
 Richards, S., MT316
 Richardson, I. W., 76, 166, MT173, WT55
 Ridpath, J., 103, MT370
 Ridpath, J. F., 84, MT367
 Rieder, S., 32, MT214
 Rigler, D., 32, MT214
 Riina, M. V., MT43
 Riley, D. G., MT317
 Riquet, J., 98, MT262, MT294
 Rischkowsky, B., 154, 185, WT30, WT100
 Ristov, S., MT355
 Riva, J., WT1
 Robelin, D., 147, MT289
 Robinson, J., 56, MT115
 Rocha, D., 102, MT369
 Rocha, M., MT297, MT337, MT353, MT354
 Rochat, E., 109, MT362
 Rochus, C., WT10
 Rodellar, C., MT181, WT40
 Rodriguez, A., MT318
 Rodriguez, A. M., 158, WT28
 Rodriguez, C., MT254
 Rodriguez-Fernández, C., 90, MT234
- Rodríguez-Gil, J.-E., MT285
 Roehe, R., 130, MT240
 Rogberg Muñoz, A., WT93
 Rogel-Gaillard, C., 57, 79, 134, MT109,
 MT168, MT239, MT284
 Rogers, J., MT316
 Rohmeier, L., MT138
 Rohrer, G. A., MT279
 Roman-Ponce, S. I., 43, MT44, MT61
 Romero, A., MT181
 Rony, S., 74, MT137, MT170
 Ropka-Molik, K., 70, MT184, MT191, MT198,
 MT220, MT264
 Rosa, G. J. M., MT338
 Rose, R., MT262
 Rosen, B., 108, 148, MT125, MT361
 Rosewick, N., MT346, MT348
 Ros-Freixedes, R., MT277
 Ross, P., 17, 114, 159, MT10, MT11, WT58
 Rothhammer, S., MT355
 Rothschild, M. F., 109, 176, MT246, MT362,
 WT83
 Rowe, S. J., MT140
 Rowland, B., 143
 Rowland, K., 55, MT52
 Rubin, C.-J., 177, WT86
 Rubio, Y. B., MT258
 Rubis, D., MT81
 Rue-Albrecht, K., 111, MT9, WT47, WT52
 Ruiz, F. J., MT44
 Rund, L., 148, MT125
 Rund, L. A., 138, MT286
 Russ, I., MT261
 Rychtarova, J., WT16
 Rytz, U., 128, MT95
- S**
- Sá, J., MT281
 Saelao, P., 17, 159, MT10, WT58
 Safronova, O., MT190
 Sahana, G., MT118
 Sahoo, N. R., MT248
 Saiftdinova, A., 44, MT50, MT67
 Salamon, D., MT355
 Salavati, M., WT38
 Salim, B., 183, WT98
 Salinas-Pena, M., 110, MT16
 Samaha, G., 122, MT100
 Samorè, A. B., MT272
 San Cristobal, M., WT45
 Sanchez, M. N., MT372, WT74
 Sánchez, A., 6, MT285, WT6
 Sánchez-Esquiliche, F., MT254
 Sánchez-Molano, E., MT90
 Sanders, J. O., MT317
 Sang, H., 30, MT177
 Sang, Y., MT146

- Sanke, O. J., MT259
 Santos-Silva, J., MT281
 Sanz, A., 110, MT16
 Sanz-Rubio, D., 110, MT16
 Sargolzaei, M., 14, 80, MT25, MT71, MT171, MT356
 Sarry, J., 155, WT31
 Sarti, F., WT18
 Sarto, P., WT15
 Sasaki, S., MT148
 Sasazaki, S., MT223, MT227, MT304, MT305, MT308, MT309
 Saunders, G., 25, MT372
 Saura, M., 173, WT78
 Savegnago, R. P., WT48
 Savelkoul, H., MT182
 Sawyer, J. E., 84, MT317, MT367
 Sawyer, R., MT318
 Sawyer, R. J., 158, WT28
 Sbardela, A. P., WT48
 Scalvini, F. G., MT89
 Schachtschneider, K. M., 138, MT286
 Schaefer, R., 37, MT187, MT212
 Schellander, K., 74, MT137, MT170, MT251
 Schenkel, F., MT71, MT356
 Schiavo, G., 43, 137, MT19, MT61, MT272, MT291
 Schibler, L., MT7
 Schlötterer, C., 32, MT214
 Schmidova, J., MT193
 Schmidt, C., 45, MT54
 Schnabel, R., MT80
 Schoenebeck, J., 127, 128, MT95, MT99
 Schook, L., 57, 148, MT109, MT125
 Schook, L. B., 138, MT286
 Schroeder, S., 148, MT125
 Schroyen, M., 16, 142, MT164, MT275, WT70
 Schubert, M., 87, MT123, MT235
 Schubert, H.-J., 75, MT138, MT157
 Schuller, S., 119, MT94
 Schulz-Schaeffer, W. J., MT336
 Schurink, A., 33, MT182, MT211
 Schütz, E., MT79, MT336
 Schwartz, J., 23, MT159
 Schwartz, J. C., MT154
 Schwarz, T., 127, MT99
 Schwind, R. M., 138, MT286
 Scienski, K., WT68
 Scott, E., 41, MT213
 Seal, R., 169, WT59
 Sebastiani, C., WT18
 Segura, J., MT269
 Seichter, D., MT261
 Selionova, M., 92, WT33
 Sellem, E., MT7
 Semik, E., MT5, MT194, MT195
 Semmer, J., 59, MT110
 Seo, D., 9, MT46, MT65
 Seong, H., MT180, MT188
 Seong, P. N., MT188
 Sereno, F. T. P. S., MT203
 Serrano, M., WT15
 Servin, B., 109, MT362
 Sest, K., MT323
 Settar, P., 73, MT161
 Seyfert, H.-M., 75, MT138, MT157
 Shabtay, A., MT357
 Shang, D., 51, MT53
 Shang, P., 164, WT62
 Sharma, A., 86, WT105
 Shave, R., WT46
 Shimogiri, T., MT189, MT227
 Shin, D., MT273, MT274
 Shin, S. M., MT188
 Shiraigol, W., MT202
 Shykind, B., 11, MT22, WT104
 Sidadolog, J. H. P., MT69
 Siddavatam, P., 116, 151, MT84, MT98
 Siddiki, M., MT296
 Siegismund, H. R., 24, MT364
 Signorelli, F., MT153
 Silió, L., MT254
 Silva, J., MT353
 Silva, V., MT345
 Simcic, M., MT355
 Simianer, H., 95, MT236
 Simões, L., 90, MT234
 Simpson, B., 8, MT26
 Sinha, R., MT248
 Sironi, G., MT89
 Sistiaga-Poveda, M., WT51
 Skrlep, M., 98, MT294
 Skuce, R., 4, MT24, MT325
 Slack, E. A., 26, MT66
 Slate, J., WT25
 Sloniewska, D., MT341, MT343, MT344
 Smakova, A., MT75
 Smith, J., 54, MT41, MT47, MT62
 Smith, T., 8, 23, MT26, MT159, MT340
 Smith, T. P., MT316
 Smith, T. P. L., MT154
 Smolucha, G., MT152
 Snelling, T., 130, MT240
 Snyman, H. N., MT158
 Snyman, M., WT21
 Soares, M., WT2
 Sochorová, J., WT50
 Sodhi, M., 86, WT105
 Soh, P., 129, MT96
 Solano-Gallego, L., 77, MT160
 Solkner, J., 154, WT30
 Sölkner, J., 185, MT355, WT100
 Soller, M., 54, MT41, MT47, MT62
 Sollero, B. P., 180, WT99
 Soma, P., MT306, WT92
 Son, J. K., MT188
 Son, S., MT274
 Song, K.-D., MT273, MT274
 Song, Z., 29, MT174
 Sonstegard, T., 106, 108, MT361, MT363
 Souza, K. T., MT204
 Souza, M., MT353
 Soyeurt, H., MT153
 Spangler, G., 108, MT361
 Spark, N., MT107
 Splichal, J., MT74
 Splichalova, P., 31, MT218
 Squires, J., MT356
 SS, W., MT248
 Stadtmueller, B. M., 64, MT162
 Staric, J., MT323
 Stear, M., 60, MT111
 Steen-Jensen, D. B., 63, MT113
 Stefaniuk-Szmukier, M., 70, MT191, MT198, MT220
 Steffen, F., 119, MT94
 Steibel, J., MT258
 Stella, A., 18, 109, MT14, MT362
 Stevens, J. C., MT201
 Stewart, R., 130, MT240
 Stinckens, A., 33, MT182, MT211
 Stokar-Regenscheit, N., 119, MT94
 Stortti, F., WT2
 Stothard, P., MT71, MT76, MT300, MT327
 Stout, T. A. E., MT123
 Straathof, C., MT4
 Strand, E., MT179
 Strillacci, M. G., 43, MT44, MT61, MT335
 Strive, T., 27, MT176
 Stryhn, A., 63, MT113
 Stuczynska, A., MT263
 Su, R., MT320, MT332
 Suarez-Vega, A., 97, WT13, WT26
 Suárez-Vega, A., WT37
 Sudrajad, P., MT46
 Sugimoto, Y., MT148, MT319
 Suleimenov, M., MT190, MT223
 Sullivan, K., 36, MT210
 Sullivan, S., 42, MT55
 Sumadi, , MT69
 Summers, K. M., MT324
 Sun, D., MT72
 Sun, H., MT307
 Sun, Y. Y., 50, MT59
 Sunarto, A., 27, MT176
 Surlis, C., MT350
 Svára, T., MT323
 Svensson, K., 121, MT105
 Svensson, E., 90, MT234

Svitakova, A., MT193, MT331, WT16, WT22
 Swiderski, C., MT207
 Symonová, R., WT50
 Szmatoła, T., 146, MT5, MT15, MT184,
 MT264, MT330
 Sztankooova, Z., WT16, WT22

T

Tabata, R., MT223
 Tadesse, T., 154, WT30
 Tait, J., 8, MT26
 Tait, R., MT370
 Tait, R. J., MT338
 Tait Jr., R., 103
 Takahashi, Y., MT190
 Takeshima, S., MT148
 Takeshima, S.-N., MT150
 Talbot, R., 148, MT125
 Talenti, A., 152, WT1, WT5
 Tamma, N., 99, MT368
 Tammen, I., MT314
 Tan, T., 29, MT174
 Tan, T. Y. K., 12, MT27
 Tan, W., 21, MT167
 Tan, X., MT299
 Tapio, M., 182, WT96
 Tarekegn, G. M., MT311
 Tatsuda, K., MT37
 Taxis, T. M., MT142
 Tayal, A., 168, WT57
 Taylor, J., MT80
 Taylor, J. B., MT106, WT14
 Taylor, J. F., MT124
 Teasdale, M., 150, MT371
 Tebug, S. F., 182, WT96
 Tedeschi, G., MT89
 Telo da Gama, L., MT203
 Telugu, B., 28, MT175
 Tengvall, K., 126, MT102
 Terakado, A. P. N., WT89
 Tesfaye, D., 74, MT137, MT170
 Tesfaye, K., MT107
 Tholen, E., 74, MT137, MT170, MT251
 Thomas, A., 123, MT103
 Thomer, A., MT183
 Tibau, J., MT267, MT268
 Tijhaar, E., MT182
 Tijjani, A., 183, WT98
 Tinel, S., 33, MT182, MT211
 Tipold, A., MT79, MT336
 Tizard, M., 27, MT176
 Tizioto, P., MT297, MT337, MT353, MT354
 Toivonen, J., 110, MT16
 Tombacz, K., 85, MT163
 Tomley, F., MT156
 Tomlinson, C., 42, MT55

Tor, M., 140, MT257, MT277, MT292
 Toro, M., 173, WT78
 Torres, J., 110, MT16
 Torricelli, M., WT18
 Tosser-Klopp, G., 20, WT69
 Tozaki, T., 69, MT135, MT178
 Trakooljul, N., 114, MT11, MT270, MT271
 Trigo, A., 67, MT216
 Trincas, E., MT43
 Triviziaki, S., MT355
 Tsairidou, S., 71, MT166
 Tseng, E., 148, MT125
 Tseng, J., 58, MT117
 Tsimnadis, E. R., MT314
 Tsuchimura, M., MT304
 Tsunoda, K., MT190
 Tuggle, C., 16, 159, MT275, WT58, WT70
 Tuggle, C. K., 17, 142, MT10, MT164
 Tullio, R., MT354
 Tweedie, S., 169, WT59

U

Uddin, M. J., 74, MT137, MT170
 Uemoto, Y., MT305, MT308, MT309
 Unni, D., 168, WT57
 Upadhyay, M., MT345
 Upadhyay, M. R., WT88
 Ureña, I., 90, MT228, MT234
 Urnov, F., 28, MT175
 Uskenov, R., MT75
 Usman, T., MT136
 Utzeri, V. J., 137, MT19, MT291

V

Vaccari, G., WT18
 Vahala, J., 31, MT218
 Valčíková, T., MT151
 Valdez, F., WT93
 Valdiosera, C., MT228
 Valente, G. T., WT71
 Van den Broeke, A., MT346, MT348
 Van der Laan, M. H. Pinard, MT127
 van der Poel, J. J., MT145
 van der Sluis, R., 1, MT60
 van der Werf, J. H., WT90
 van der Zwan, H., 1, MT60
 van Dreumel, T., MT246
 Van Eenennaam, A., 159, WT58
 van Haeringen, W., 151, MT98
 Van Marle-Koster, E., MT124
 Van Poucke, M., WT41
 van Son, M., MT278
 Van Stijn, T., 101, MT365
 Van Tassell, C., 108, MT361
 Vander Jagt, C., MT321

Vanlierde, A., MT153
 Varela-Martínez, E., WT51
 Vázquez, F. J., MT181
 Vazquez-Gomez, M., MT245
 Vázquez-Gómez, M., WT35, WT42
 Vega-Murillo, V. E., MT44
 Vega-Pla, J. L., MT203
 Velez-Irizarry, D., MT258
 Velie, B., 33, MT182, MT211
 Velie, B. D., MT179
 Vella, G., 142, MT164
 Verbyla, K., 171, WT74, WT85
 Verdugo, M., 89, MT359
 Verleih, M., 178, WT82
 Vernesi, C., MT87
 Vernimmen, D., 111, MT9
 Vesela, Z., MT193, MT331
 Vevey, M., MT335
 Viguera, J., MT269
 Vilaró, F., MT277
 Vilkki, J., MT118
 Villanueva, B., 173, WT78
 Villarreal-Ramos, B., 76, MT173, WT47,
 WT52
 Villa-Vialaneix, N., 144, 147, MT128, MT289
 Villegas Castagnasso, E. E., WT93
 Viluma, A., 65, MT108
 Vincent-Naulleau, S., MT284
 Vinsky, M., MT300, MT327
 Visser, C., 1, MT60, WT91
 Vitoria, A., MT181
 Vodicka, R., 31, MT218
 Vogl, C., 32, MT214
 Voillet, V., WT45
 Volodkina, V., 44, MT67
 Vordermeier, H. M., 76, MT173, WT47, WT52
 Vostra-Vydrova, H., MT192, MT193
 Vostry, L., MT74, MT192, MT193, MT331

W

Wade, C., 122, MT100
 Wade, C. M., MT199
 Walker, A., 130, MT240
 Wallace, R., 130, MT240
 Wallner, B., 32, MT214
 Wang, D., 113, MT12, MT307
 Wang, G., 51, MT53
 Wang, H., MT2, WT65
 Wang, J., 51, MT36, MT53, MT244, MT249
 Wang, L., 52, 164, MT58, WT62
 Wang, M., 81, MT169
 Wang, O., MT307
 Wang, R., MT320, MT332
 Wang, W., 24, MT364
 Wang, X., MT119
 Wang, X.-Y., WT11

Wang, Y., 17, 159, MT10, MT73, MT320, WT9, WT58
 Wang, Z., 38, 164, MT208, MT260, MT332, WT62
 Ward, A. K., 112, MT8, WT34
 Warr, A., 130, 148, MT125, MT240
 Warren, W., 42, MT55
 Waters, S., MT80, MT350, MT351
 Waters, S. M., 132, MT237, MT300, MT302, MT327, MT334
 Watson, M., 130, MT240, MT324
 Weaber, R., MT3
 Wei, Z., MT298
 Weigend, A., 95, MT236
 Weigend, S., 95, MT236
 Weikard, R., MT138, MT333
 Weinert, M., 75, MT157
 Weld, R., 117, MT80, MT83
 Wells, M., MT338
 Wemheuer, W. E., MT79, MT336
 Wemheuer, W. M., MT336
 Werling, D., 85, MT163
 Westberg-Sunesson, K., WT10
 Wheeler, M., 101, MT365
 White, S., 161, MT340, WT63
 White, S. N., 156, MT106, MT316, WT14, WT29
 Whitelaw, B., 28, MT175
 Whitelaw, C. B., MT324
 Whitelaw, C. B. A., 21, MT167
 Wiedemar, N., MT323
 Wiedmer, M., 119, MT94
 Wiener, P., 97, MT88, MT90, WT26
 Wierzbicki, H., MT20, MT21
 Wilkinson, S., MT325
 Willet, C. E., MT314
 Williams, J., 18, 103, 104, MT14, MT370, MT373
 Williamson, P., 129, MT96
 Willis, C., 116, MT84
 Wilson, G., 4, MT24
 Wimmers, K., 15, 92, 114, MT11, MT23, MT270, MT271, MT283, MT303, WT33
 Witarski, W., MT184
 Witkowski, M., MT194
 Wodas, L., MT130, MT197
 Wolc, A., 55, 73, 82, MT52, MT161, MT172
 Wolf, J., MT354
 Woloszyn, F., 155, WT31
 Womack, T., WT68
 Won, K.-H., MT273
 Wong, B., MT329
 Wong, S., WT49
 Woo, J. H., MT188
 Woolley, S. A., MT314
 Woolliams, J., MT325
 Woolliams, J. A., 71, MT90, MT166

Woolums, A., 103, MT370
 Worku, M., MT143
 Worley, K., MT340
 Worley, K. C., MT316
 Wouobeng, P., MT311
 Wu, C., 164, WT62
 Wu, D.-D., MT40
 Wu, J., MT320
 Wu, N., MT51
 Wu, S., MT2
 Wu, X., MT338
 Wu, Z., MT156
 Wurmser, C., MT261, MT328
 Wurzinger, M., 154, 185, WT30, WT100

X

Xiao, H., MT260, MT320
 Xie, H.-B., MT259
 Xie, S., 139, MT288
 Xie, Y., MT260, MT332
 Xing, Y., 29, MT174
 Xu, G. Y., 113, MT12
 Xu, J., MT338
 Xu, L., MT222, MT225
 Xu, S. S., 50, MT59
 Xue, F. G., 50, MT59

Y

Yamagata, T., MT190
 Yamagishi, J., MT150
 Yamamoto, Y., MT189, MT190
 Yamanaka, H., MT227
 Yan, W., MT225
 Yáñez, J., WT72
 Yáñez, J. M., 170, WT80
 Yang, G., 139, MT288
 Yang, I.-C., MT180
 Yang, L., MT34
 Yang, M., 157, MT51, WT32
 Yang, N., 113, MT12
 Yang, R., MT249, MT298
 Yang, S., 113, MT12
 Yang, Y.-R., MT42
 Yaro, M., 60, MT111
 Yates, B., 169, WT59
 Yechshzhanov, T., MT75
 Yerle-Bouissou, M., 147, MT289
 Yi, Z., MT72
 Yildirim, I. S., 188, MT232
 Yin, H., WT67
 Yin, L., WT36
 Yoshida, E., MT305, MT308, MT309
 Yoshida, G., WT72
 Young, R., 104, MT373
 Younger, L., 58, MT117

Yu, H., MT298
 Yu, X., MT298
 Yu, Y., 113, MT12, MT73, WT65
 Yuan, Z., MT72
 Yudin, N. S., MT347
 Yun, S., MT132
 Yung, R., MT36
 Yurchenko, A., MT347

Z

Zabek, T., MT5, MT194, MT195, MT330
 Zalewska, M., MT344
 Zambonelli, P., MT280
 Zamorano, P., WT75
 Zappaterra, M., MT280
 Zaragoza, P., 110, MT16, MT181, WT40
 Zaton-Dobrowolska, M., MT20, MT21
 Zentek, J., MT30
 Zerbe, H., MT138
 Zerbino, D., WT66
 Zerjal, T., 53, MT49, MT56
 Zerlotini-Neto, A., MT337
 Zhamaliyeva, S., MT75
 Zhang, C., MT36, MT249
 Zhang, G., 24, MT364
 Zhang, H., 52, 164, MT58, WT62
 Zhang, J., MT299
 Zhang, L., MT222
 Zhang, Q., MT73
 Zhang, R., MT249
 Zhang, S., MT73, WT67
 Zhang, W., MT222, MT311
 Zhang, X., MT48, WT64
 Zhang, Y., 52, MT58, MT73, MT320, MT332
 Zhang, Y.-P., MT40, MT259
 Zhang, Z., 145, MT290
 Zhao, C., 139, MT288
 Zhao, K., 167, WT60
 Zhao, M., MT260, MT332
 Zhao, P., MT255, WT65
 Zhao, S., 139, MT288, WT36
 Zhao, Y., MT244, MT249, MT260, MT299, MT320, MT332, WT44
 Zhao, Z., MT298, MT299
 Zheng, X., MT255, WT65
 Zheng, Y. C., MT70, WT9
 Zheng, Z., MT119
 Zhou, C., WT67
 Zhou, H., 17, 55, 114, 159, MT10, MT11, MT52, WT58
 Zhou, X., WT36
 Zhou, Z., 145, MT290
 Zhu, M., WT36
 Zhu, Y., 145, MT290
 Zi, X. D., WT9
 Zidi, A., MT265

Zinovieva, N., 15, 92, MT23, WT33
Zou, C., MT250
Zou, H., MT244
Zubiria, I., 131, MT242

Zukowski, K., MT191, MT198, MT263
Zulkifli, N. A., MT77
Zurbrigg, K., MT246
Zwane, A. A., MT124

Zwierzchowski, L., MT341, MT343
Zytnicki, M., 144, 147, MT128, MT289

NOTES