ISAG 2017

36th International Society for Animal Genetics Conference

16th - 21st July 2017

University College Dublin | Ireland

Bioinformatics · Comparative Genomics · Computational Biology
Epigenetics · Functional Genomics · Genome Diversity · Geno
Genome Sequencing · Immunogenetics · Integrative Geno
Microbiomics · Population Genomics · Systems Biolog
Genetic Markers and Selection · Genetics and Dis
Gene Editing · Bioinformatics · Comparative
Computational Biology · Epigenetics · Fu
Genome Diversity · Genome Sequeng
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Genetics and Diseas
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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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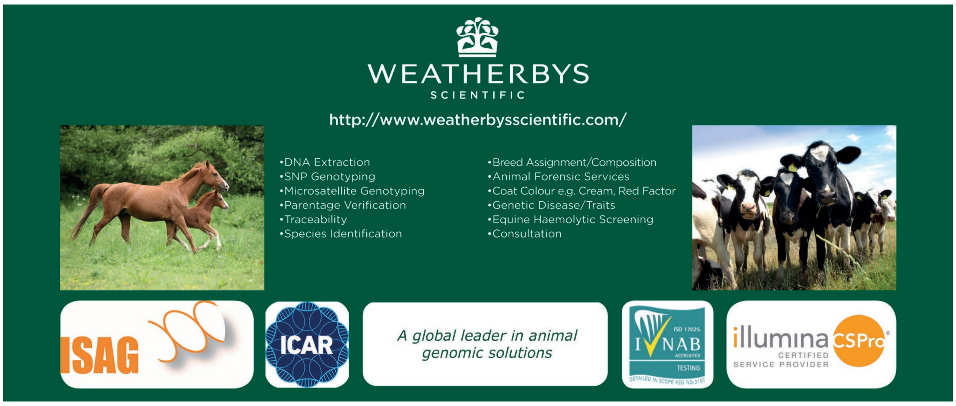

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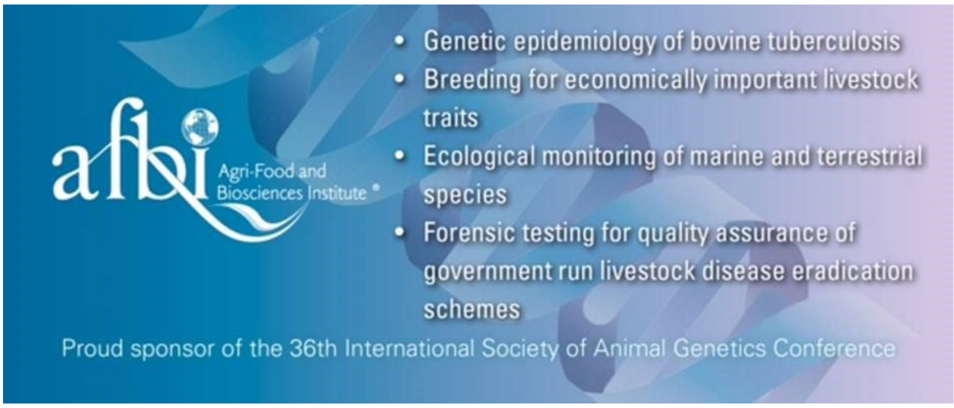

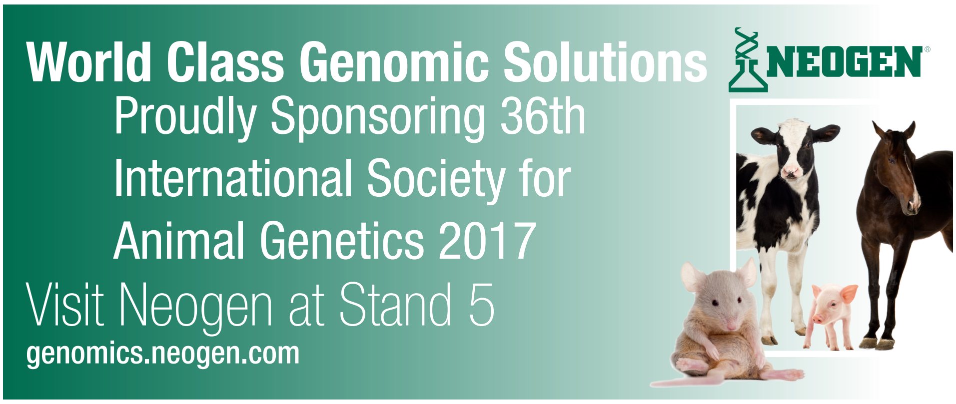

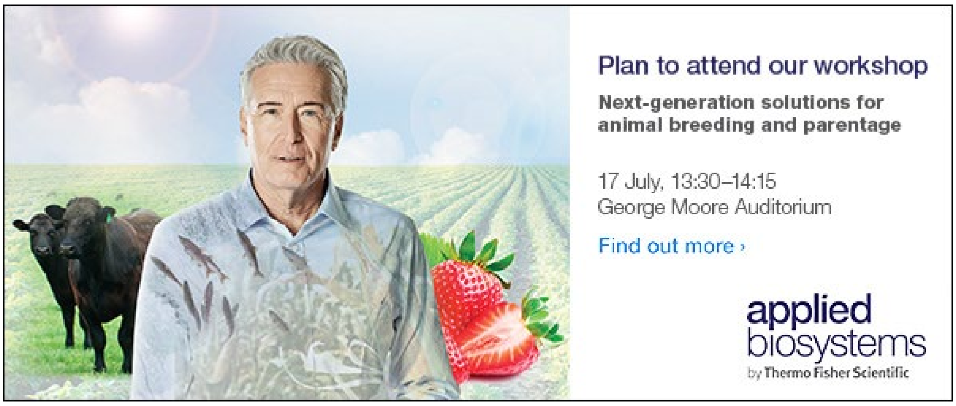

ISAG 2017
36th International Society for
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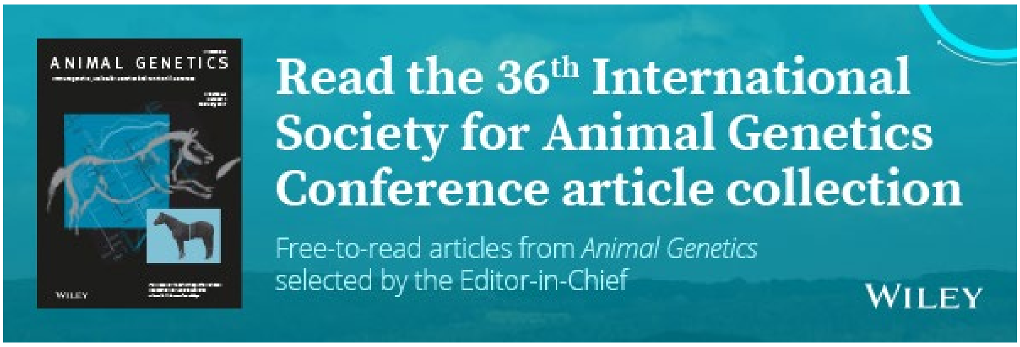
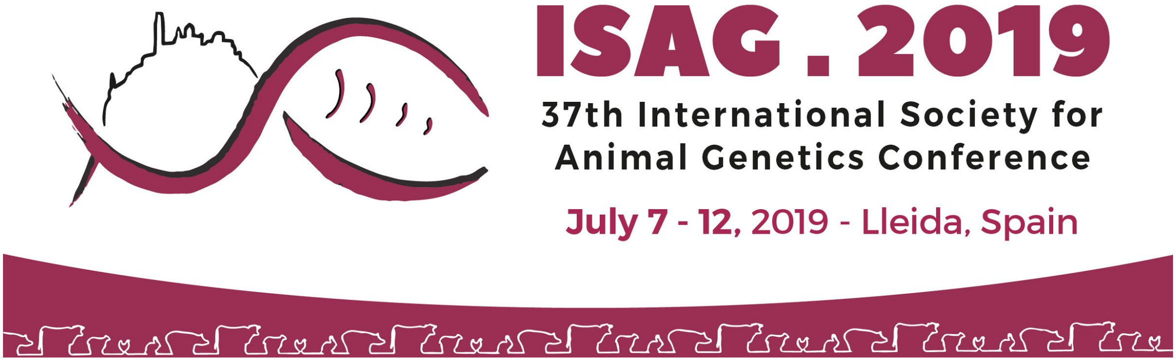
Contents





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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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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

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 ***De novo*** **genome assembly of** ***Agapornis roseicollis*** **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 (*****Meles meles)*** **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 Fonctionelle et Evolutie, Montpelier, 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. Ramírez*[1], A. Cuscó[1], A. Sánchez[2], O. Francino[2], and L. Altet[1], [1]*Vetgenomics, Barcelona, Spain;* [2]*Molecular Genetics Veterinary Service (SVGM), Barcelona, Spain*.

15:45 7 **Application of multiplex microsatellite panel in *Felidae* family.**
A. Podbielska*[1], A. Radko[1], W. Nizanski[2], J. Kochan[3], A. Nowak[3], and M. Bugno-Poniewierska[1], [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, Wroclaw University of Environmental and Life Sciences, Wroclaw, 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. Tait[2], V. Basnayake[2], B. Simpson[2], T. Smith[3], and M. Heaton[3], [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. Jin[1], N.-R. Choi[1], D. Seo[1], P. Manjula[1], H.-Y. Kim[2], S. H. Lee[1], 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. Holl[2], D. Miller[3], S. Abdalla[4], B. Shykind[4], J. Malek[4], Y. Mohamoud[4], K. Pasha[5], A. Khalili[5], D. F. Antczak[3], and S. Brooks[1], [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. Miar[1], [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. Dotsev[1], V. Fedorov[2], G. Brem[1,3], K. Wimmers[4], H. Reyer[4], and N. Zinovieva[1], [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. Wang[1], P. Saelao[1], K. Chanthavixay[1], I. Korf[1], C. K. Tuggle[2], C. Ernst[3], P. Ross[1], and H. Zhou[1], [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. Namous[1], F. Peñagaricano[2], M. Del Corvo[3], E. Capra[4], A. Stella[4], J. Williams[5], P. A. Marsan[3], 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. Foissac[1], **S. Djebali***[1], H. Acloque[1], FR-AgENCODE Consortium[2], M. H. Pinard-Van der Laan[2], S. Lagarrigue[3], and E. Giuffra[2], [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. Djebali[2], T. Derrien[3], C. Cabau[2], C. Klopp[4], D. Esquerré[2,5], K. Munyard[6], G. Tosser-Klopp[2], H. Acloque[2], E. Giuffra[7], S. Foissac[2], and S. Lagarrigue[1], [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. Dry[1], S. Lillico[2], C. B. A. Whitelaw[2], and B. Dalziel[1], [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. Cooksey[1], C. Gresham[2], and B. Nanduri[2], [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. Schwartz[1], D. Bickhart[2], T. Smith[3], and J. Hammond[1], [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. Wang[1], Q. Q. Qiu[1], G. Zhang[3,4], R. Heller[3], H. R. Siegismund[3], 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. Brauning[2], S. Clarke[2], A. McCulloch[2], N. Cockett[3], G. Saunders[4], M. Naval Sanchez[1], H. Daetwyler[5,6], and J. Kijas[1], [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. Damas[1], R. E. O'Connor[2], M. Farre[1], H. Martell[2], E. A. Slack[1], E. Allanson[1], L. Kiazim[2], R. Jennings[2], A. Mandawala[3], S. Joseph[2], K. E. Fowler[3], D. K. Griffin[2], 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. Lillico*[1], C. Proudfoot[1], C. Burkard[1], F. Urnov[2], J. Oatley[3], B. Telugu[4], A. Mileham[5], and B. Whitelaw[1], [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. Song[1], 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*.

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 Insitute, 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. Klumplerova[1], P. Splichalova[1], J. Oppelt[2], P. Musilova[3], S. Kubickova[3], R. Vodicka[4], J. Vahala[5], L. Orlando[6], and P**. Horin***[1], [1]*Ceitec VFU, University of Veterinary and Pharmaceutical Sciences, Dept. of Animal Genetics*, *Brno, Czech Republic;* [2]*Ceitec MU, Masaryk University, National Centre for Biomolecular Research, Faculty of Science*, *Brno, Czech Republic;* [3]*Veterinary Research Institute, Dept. of Reproduction and Genetics*, *Brno, Czech Republic;* [4]*Zoo Prague*, *Prague, Czech Republic;* [5]*Zoo Dvur Kralove nad Labem*, *Dvur Kralove nad Labem, Czech Republic;* [6]*Centre 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. Felkel[1], D. Rigler[1], C. Vogl[1], M. Neuditschko[2], S. Rieder[2], V. Jagannathan[3], T. Leeb[3], T. Rattei[4], C. Schlötterer[5], G. Brem[1], and **B. Wallner***[1], [1]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna*, *Vienna, Austria;* [2]*Agroscope, Swiss National Stud Farm*, *Avenches, Switzerland;* [3]*Institute of Genetics, Vetsuisse Faculty, University of Bern*, *Bern, Switzerland;* [4]*Department of Microbiology and Ecosystems Science, Division of Computational Systems Biology, University of Vienna*, *Vienna, Austria;* [5]*Institute 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. Schurink[2], B. Velie[3], A. Stinckens[1], S. Blott[4], B. Ducro[2], C. Lamberigts[5], S. Tinel[1], K. De Keyser[1], M. Oosterlinck[6], G. Lindgren[3], S. Janssens[1], and N. Buys[1], [1]*Research Group Livestock Genetics, Department of Biosystems, KU Leuven*, *Leuven, Belgium;* [2]*Animal Breeding and Genomics Centre, Wageningen University & Research*, *Wageningen, the Netherlands;* [3]*Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences*, *Uppsala, Sweden;* [4]*School of Veterinary Medicine & Science, University of Nottingham*, *Leicestershire, United Kingdom;* [5]*Research Group Livestock Physiology, Department of Biosystems, KU Leuven*, *Leuven, Belgium;* [6]*Department 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. Nergadze[1], R. Gamba[1], F. M. Piras[1], E. Cappelletti[1], M. Corbo[1], F. Gozzo[1], D. Miller[2], D. Antczak[2], E. Raimondi[1], K. Sullivan[3], and **E. Giulotto***[1], [1]*University of Pavia, Department of Biology and Biotechnology, Pavia, Italy;* [2]*Cornell University, College of Veterinary Medicine, Ithaca, NY, USA;* [3]*National 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. Norton[1], J. Mickelson[2], and M. McCue[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA;* [2]*Department 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], [1]*Baker Institute for Animal Health, Ithaca, NY, USA;* [2]*Cornell University, Ithaca, NY, USA.*
17:15	39	**EquCab3.** **T. Kalbfleisch***[1], M. DePriest[1], L. Orlando[2], and J. MacLeod[3], [1]*University of Louisville, Louisville, KY, USA;* [2]*University of Copenhagen, Copenhagen, Denmark;* [3]*University 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. MacLeod[2], and T. S. Kalbfleisch[1], [1]*University of Louisville, Louisville, KY, USA;* [2]*University of Kentucky, Lexington, KY, USA.*
17:45	41	**Progress toward functional annotation of the equine genome.** **J. Petersen***[1], E. Burns[2], M. Bordbari[2], E. Scott[2], B. Ming-Whitfield[2], V. Affolter[2], C. Ramirez Alanis[2], M. Barro[2], M. Mack[2], G. Gianino[2], F. Gianino[2], E. Giulotto[3], K. Hilburger[2], T. Kalbfleisch[4], J. MacLeod[5], M. Mienaltowski[2], S. Katzman[2], T. Leeb[6], T. Raudsep[7], P. Saelao[2], S. Vig[2], H. Zhou[2], R. Bellone[2], and C. Finno[2], [1]*University of Nebraska-Lincoln, Lincoln, NE, USA;* [2]*University of California-Davis, Davis, CA, USA;* [3]*University of Pavia, Pavia, Italy;* [4]*University of Louisville, Louisville, KY, USA;* [5]*University of Kentucky, Lexington, KY, USA;* [6]*University of Bern, Bern, Switzerland;* [7]*Texas 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, *Wageningen University & Research*.

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]*Washington University School of Medicine*, *St Louis, MO, USA;* [2]*Phase Genomics Inc, Seattle, WA, USA;* [3]*University of California-Davis, Davis, CA, USA;* [4]*Hy-Line International*, *Dallas Center, IA, USA;* [5]*Cobb-Vantress Inc, Siloam Springs, AR, USA;* [6]*Beckman Research Institute*, *Duarte, CA, USA;* [7]*USDA-ARS*, *East Lansing, MI, USA*.

09:25 43 **Low number of mitochondrial DNA sequences inserted into the turkey (*Meleagris gallopavo*) 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]*Department of Agricultural and Food Sciences, University of Bologna*, *Bologna, Italy;* [2]*Department of Veterinary Medicine, University of Milan, Milano. Italy;* [3]*Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna*, *Bologna, Italy;* [4]*Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agricola y Pecuarias (INIFAP), Col. Centro Veracruz, Mexico;* [5]*Department of Animal Science, Iowa State University*, *Ames, IA, USA*.

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]*Saint-Petersburg State University*, *Saint-Petersburg, Russia;* [2]*Royal Veterinary College, University of London*, *London, UK;* [3]*University of Kent*, *Kent, UK*.

09:55 45 **The broiler chicken transcriptome.**
C. Schmidt*[1] and S. Lamont[2], [1]*University of Delaware*, *Newark, DE, USA*, [2]*Iowa State University*, *Ames, IA, USA*.

10:15 46 **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*.

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, *Tarbiat Modares University, Tehran, Tehran, Iran*.

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]*Sichuan Agricultural University, Chengdu, Sichuan, China;* [2]*Texas A&M University, College Station, TX, USA*.

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, *Lab of Animal Genetic Resource and Molecular Breeding, China Agricultural University, Beijing, China*.

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]*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* [2]*INRA, UMR1348 Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'élevage, Saint-Gilles, France;* [3]*Agrocampus-Ouest, UMR1348, Rennes, France;* [4]*UMR INRA/INPT ENSAT/INPT ENVT-GenPhySE, Castanet Tolosan, France;* [5]*INRA, Plateforme GENOTOUL, Castanet-Tolosan, France;* [6]*INRA, SIGENAE, Castanet-Tolosan, France;* [7]*INRA-PEAT, Nouzilly, France;* [8]*URA, INRA, Nouzilly, France*.

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]*Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel;* [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK;* [3]*Hy-Line International, Dallas Center, IA, USA*.

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]*Iowa State University, Department of Animal Science, Ames, IA, USA;* [2]*University of California-Davis, Department of Animal Science, Davis, CA, USA;* [3]*University of California-Davis, School of Veterinary Medicine, Davis, CA, USA;* [4]*Hy-Line International, Dallas Center, IA, USA*.

12:30 **Concluding Remarks.**
Richard Crooijmans, *Wageningen University & Research*.

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]*The Pirbright Institute, Pirbright, Woking, Surrey, UK;* [2]*Anthony Nolan Research Institute, Royal Free Hospital, London, UK;* [3]*UCL Cancer Institute, Royal Free Campus, London, UK;* [4]*Moredun Research Institute, Pentlands Science Park, Scotland, UK;* [5]*Stanford University, Stanford, CA, USA;* [6]*Norwegian Veterinary Institute, Oslo, Norway;* [7]*University of Cambridge, Cambridge, UK;* [8]*Gift of Life Michigan, Michigan, USA;* [9]*Biomedical Primate Research Centre, Rijswijk, Netherlands;* [10]*European Molecular Biology Laboratory, Wellcome Genome Campus, Hinxton, UK*.

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. Lunney[2], A. Ando[3], C. Rogel-Gaillard[4], J.-H. Lee[5], L. Schook[6], and S. Hammer[7], [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. Case[1], L. Younger[1], J. Tseng[1], H. Holl[2], Y. A. Mohamoud[3], A. Ahmed[3], J. Malek[3], S. Brooks[2], and D. Antczak[1], [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. Munyard[1], E. Morgan[1], M. Stear[2], and D. Groth[1], [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. Goto[1], G. Gugiu[1], B. M. Stadtmueller[2], P. J. Bjorkman[2], 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'Hom[2], and M. M. Miller[3], [1]*Hy-Line International, Dallas Center, IA, USA;* [2]*GABI, INRA, AgroParisTech, 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-Szmukier[2], A. Piestrzynska-Kajtoch[1], A. Fornal[1], and K. Ropka-Molik[1], [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-Czwarno*[1], A. Wolc[2,3], J. Fulton[3], T. Jankowski[4], J. Arango[3], P. Settar[3], N. O'Sullivan[3], and J. Dekkers[2], [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. Islam[1], **C. Neuhoff***[1], S. Rony[1], C. Große-Brinkhaus[1], M. J. Uddin[2], M. Hölker[1], D. Tesfaye[1], E. Tholen[1], M. J. Pröll[1], and K. Schellander[1], [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. Koy[2], A. Berthold[1], H.-J. Schuberth[2], M. Weinert[3], S. Engelmann[3], C. Kühn[1], H.-M. Seyfert[1], and J. Günther[1], [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. Mullen[3], K. E. McLoughlin[1], N. C. Nalpas[4], I. W. Richardson[5], D. A. Magee[1], C. N. Correia[1], J. A. Browne[1], H. M. Vordermeier[6], B. Villarreal-Ramos[6], D. P. Berry[7], E. Gormley[8], 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, United Kingdom.; [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.*

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-Gallego[2], S. Montserrat[2], F. Mayer[1], A. Castello[1], L. Alborch[2], S. Heath[3], A. Esteve-Codina[3], J. Gomez-Garrido[3], R. A. Cigliano[4], and **A. Clop***[1], *[1]Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Valles, Catalonia, Spain; [2]Universitat Autonoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain; [3]Centre Nacional d'Anàlisi Genómica CNAG-CRG, Barcelona, Catalonia, Spain; [4]Sequentia 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 Laan[1], R. Hawken[2], and H. Edin[1], *[1]INRA, Jouy-en-Josas, France; [2]Cobb-Vantress Inc, Siloam Springs, AR, USA.*

10:45 79 **Genetic individual variability of vaccine responses in pigs.**
F. Blanc*[1], G. Lemonnier[1], J. Leplat[1,2], E. Bouguyon[3], Y. Billon[4], J. Estelle[1], and C. Rogel-Gaillard[1], *[1]GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France; [2]CEA, DRF/IRCM/SREIT/LREG, Jouy-en-Josas, France; [3]VIM-INRA-Université Paris-Saclay, Jouy-en-Josas, France; [4]GenESI, 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. Sargolzaei[4], K. Meade[2], N. Karrow[3], and S. Pant[1], *[1]Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW, Australia; [2]Teagasc Animal and Bioscience Research Department, Grange, Co. Meath, Ireland; [3]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada; [4]The 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. Dzama[1], F. Muchadeyi[2], and M. Wang[2], *[1]Animal Science Department, University of Stellenbosch, Stellenbosch, Western Cape, South Africa; [2]Agriculture 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. Kaiser[1], A. Wolc[1,2], and S. Lamont[1], *[1]Iowa State University, Ames, IA, USA; [2]Hy-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 diarrhea virus in F_2 and F_3 Nellore-Angus halfblood steers.**
K. M. S. Davila*[1], A. D. Herring[1], J. E. Sawyer[1], J. F. Ridpath[2,3], and C. A. Gill[1], *[1]Texas A&M University, College Station, TX, USA; [2]National Animal Disease Center, Ames, IA, USA; [3]Ridpath Consulting, Ames, IA, USA.*

12:19 85 **Lightning Talk: 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.*

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. Sodhi[2], P. Jain[1], M. Kumar[2], and M. Mukesh[2], *[1]University Institute of Engineering & Technology, Kurukshetra, Haryana, India; [2]National 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]*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*.
09:30	88	**Withdrawn**
09:45	89	**When *taurus* met *indicus*. Exploring admixture events in ancient cattle.** **M. Verdugo***, *Trinity College Dublin, Dublin, Ireland*.
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]*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*.
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]*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*.
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]*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*.
10:45	93	**Ancient whole mitochondrial genomes and insights into the prehistory of goats.** **K. Daly***, *Smurfit Institute of Genetics, Trinity College, Dublin, Ireland*.
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]*The University of Nottingham, Nottingham, Nottinghamshire, UK;* [2]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*.
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]*Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt-Mariensee, Höltystraße 10, Germany;* [2]*University of Göttingen, Animal Breeding and Genetics Group, Göttingen, Albrecht-Thaer-Weg 3, Germany*.
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]*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, United Kingdom*.
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. Crovetti[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]*INIA, Madrid, Spain;* [2]*UNIBO, Bologna, Italy;* [3]*UNIFI, Firenze, Italy;* [4]*KIS, Ljubljana, Slovenia;* [5]*INRA, Toulouse, France;* [6]*IFIP, Paris, France*.

12:30 188 **Genetic diversity among domestic goats (*Capra hircus*) and wild goats (*Capra aegagrus*) in Turkey.**
I. S. Yildirim[1], M. Nizamlioglu[1], M. D. Oncu[2], E. K. Bastanlar[2], 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. Durkin[1], M. Artesi[1], L. Karim[1,3], N. Cambisano[1,3], M. Deckers[1,3], N. Tamma[1,3], E. Mullaart[4], W. Coppieters[1,3], M. Georges[1], 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. MacLeod[1], P. Bowman[1,3], R. Emmerling[4], R. Fries[5], B. Gredler-Grandl[6], H. Daetwyler[1,3], and M. Goddard[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. Dodds[1], R. Brauning[1], T. Van Stijn[1], R. Anderson[1], M. Wheeler[2], B. Foote[3], A. Cameron[4], and J. McEwan[1], [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. Mayes[1], J. Williams[1], E. Fritz-Waters[1], E. Downey[2], R. Tait Jr.[3], A. Woolums[4], C. Chase[5], J. Ridpath[6], and J. Reecy[1], [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. Lefevre[1], S. Bush[1], J. Williams[2], S. Gokhale[3], S. Kumar[4], A. Archibald[1], and D. Hume[1], [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, *Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France*.

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]*Istituto di Zootecnica, Universitá Cattolica del Sacro Cuore, Piacenza, Italy;* [2]*Recombinetics Inc., St. Paul, MN, USA*.

12:00 107 **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*.

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]*USDA/ARS/AGIL, Beltsville, MD, USA;* [2]*U of Nottingham/School of Life Sciences, Nottingham, UK;* [3]*Acceligen of Recombinetics, St Paul, MN*.

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]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*LASIG, EPFL, Lausanne, Switzerland;* [3]*INRA, Castanet-Tolosan, France;* [4]*DIMEVET, University of Milan, Milan, Italy;* [5]*PTP, Lodi, Italy*.

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
Andrew Cromie , The Irish Cattle Breeding Federation

SNP parentage and identification: Making the transition from microsatellites
Paul Flynn, Research and Development, Weatherbys DNA Laboratory

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

14:30		**Invited Workshop Speaker: Dynamics of 4D Nucleome during differentiation of mouse hematopoietic stem cells.** **Keji Zhao***, *National Heart, Lung, and Blood Institute*.
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]*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*.
15:35	111	**Evaluating the role of epigenomic modifications in host-pathogen interaction for bovine alveolar macrophages infected with *Mycobacterium bovis*.** **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]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland;* [2]*NDM Research Building, University of Oxford, Oxford, UK;* [3]*Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany;* [4]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland;* [5]*The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK;* [6]*UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland*.

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]*Department of Animal Sciences, North Dakota State University, Fargo, ND, USA;* [2]*Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, USA;* [3]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA*.
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, *China Agricultural University, Beijing, China*.
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]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;* [2]*Department of Animal Science, University of California, Davis, CA, USA;* [3]*Genome Center, University of California, Davis, CA, USA;* [4]*USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA;* [5]*Department of Animal Science, Michigan State University, East Lansing, MI, USA*.
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, *National Institute of Animal Science, RDA, Wanju, Jeonbuk, South Korea*.
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]*Thermo Fisher Scientific;* [2]*Neogen GeneSeek Operations*.

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]*Irish Cattle Breeding Federation, Bandon, Cork, Ireland;* [2]*Weatherbys Ireland, Johnstown, Kildare, Ireland*.

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, *Thermo Fisher Scientific, Santa Clara, CA, USA*.

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. Mauri[1], M. Kleiter[2], M. Leschnik[2], S. Högler[3], E. Dietschi[1], C. Monney[4], A. Oevermann[4], D. Henke[5], M. Wiedmer[1], J. Dietrich[1], F. Steffen[6], S. Schuller[7], C. Gurtner[8], N. Stokar-Regenscheit[8], D. O'Toole[9], T. Bilzer[10], C. Herden[11], V. Jagannathan[1], 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-University, 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. Marchant[1], E. Johnson[1], R. Harrington[1], L. McTier[1], C. Johnson[1], A. Gow[1], T. Liuti[1], D. Kuehn[2], K. Svenson[3], M. Bermingham[4], M. Drögemüller[5], M. Nussbaumer[6], M. Davey[1], D. Argyle[1], R. Powell[7], S. Guilherme[8], J. Lang[9], G. Ter Haar[1], T. Leeb[5], T. Schwarz[1], R. Mellanby[1], D. Clements[1], 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. Samaha[1], J. Beatty[1], L. Lyons[2], C. Wade[3], 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. Gandolfi[2], A. Thomas[3], E. Creighton[2], L. Lyons[2], and M. Longeri[1], [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. Kozyrev[2], M. Kierczak[2], M. Olsson[2,3], F. F. Farias[2], Å. Hedhammar[4], K. Bergvall[4], and K. Lindblad-Toh[2,5], [1]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [2]*Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, BMC, Uppsala University, Uppsala, Sweden;* [3]*Center for Molecular Medicine, Department of Medicine, Karolinska University Hospital, Karolinska Institutet, Stockholm, Sweden;* [4]*Department of Clinical Sciences, Swedish University of Agricultural Sciences, Sweden;* [5]*Broad 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. Dietschi[2], R. Harrington[1], M. Drögemüller[2], U. Rytz[3], T. Leeb[2], and J. Schoenebeck[1], [1]*The Royal (Dick) School for Veterinary Studies and Roslin Institute, The University of Edinburgh, Edinburgh, Midlothian, UK;* [2]*The Institute of Genetics, Vetsuisse Faculty, The University of Bern, Bern, Switzerland;* [3]*Department 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. Stewart[1], A. Warr[1], T. Snelling[3], M. Auffret[2], A. Walker[3], R. Wallace[3], and R. Roehe[2], [1]*The Roslin Institute, University of Edinburgh, Easter Bush, Scotland;* [2]*SRUC, Easter Bush, Scotland;* [3]*The Rowett Institute, University of Aberdeen, Aberdeen, Scotland*.

14:55 131 **Bovine genes regulate the rumen microbial composition.**
O. Gonzalez-Recio*[1], I. Zubiria[2], A. García-Rodriguez[2], A. Hurtado[3], and R. Atxaerandio[2], [1]*Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain;* [2]*Departamento de Producción Animal. NEIKER-Tecnalia, Granja Modelo de Arkaute, Vitoria-Gasteiz, Alava, Spain;* [3]*Departmento 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. McCabe[1], A. K. Kelly[2], D. A. Kenny[1], P. Cormican[1], and S. M. Waters[1], [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*.

15:35 134 **Host genetics influences gut microbiota composition in pigs.**
J. Estellé*[1], N. Mach[1,2], Y. Ramayo-Caldas[1], F. Levenez[2], G. Lemonnier[1], C. Denis[1], M. Berri[3], M.-J. Mercat[4], Y. Billon[5], J. Doré[2], C. Larzul[1,6], P. Lepage[2], and C. Rogel-Gaillard[1], [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-BIOPORC, Pôle génétique, Le Rheu, France;* [5]*GENESI, INRA, Surgères, France;* [6]*GenPhySe, INRA, INP, ENSAT, Université de Toulouse, Castanet-Tolosan, France*.

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

16:30 135 **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. Pedersen[1], N. Canibe[2], P. Kiilerich[3], K. Kristiansen[3], and M. Fredholm[1], [1]*Department of Veterinary and Animal Science, Faculty of Health & Medical Sciences, University of Copenhagen, Frederiksberg, Denmark;* [2]*Department of Animal Science, Aarhus University, Tjele, Denmark;* [3]*Department of Biology, Faculty of Science, University of Copenhagen, Copenhagen, Denmark.*

16:50 136 **Characterization of the gut microbiome along the digestive tract of Iberian pigs.**
D. Crespo-Piazuelo*[1,2], J. Estellé[3], M. Revilla[1,2], L. Criado-Mesas[1,2], Y. Ramayo-Caldas[3], C. Óvilo[4], A. I. Fernández[4], M. Ballester[5], 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.*

17:10 137 **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. Ribani[1], V. J. Utzeri[1], F. Bertolini[1,4], G. Schiavo[1], 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.*

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 **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. Schwind[1], K. A. Darfour-Oduro[2], Y. Liu[2,3], S. Mäkeläinen[4,5], A. K. De[2], L. A. Rund[2], O. Madsen[4], M. A. M. Groenen[4], R. C. Gaba[1], and L. B. Schook[1,2], [1]*Department of Radiology, University of Illinois at Chicago, Chicago, IL, USA;* [2]*Department of Animal Sciences, University of Illinois, Champaign-Urbana, IL, USA;* [3]*Department of Animal Genetics and Breeding, Sichuan Agricultural University, Chengdu, China;* [4]*Wageningen University & Research, Animal Breeding and Genomics, Wageningen, The Netherlands;* [5]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.*

14:45 139 **Genome-scale sgRNA library construction and use for CRISPR/Cas9-based genetic screens in the pig.**
C. Zhao*[1], G. Yang[1], X. Han[1], Y. Gao[1], X. Li[1,2], S. Xie[1,2], and S. Zhao[1,2], [1]*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;* [2]*The Cooperative Innovation Center for Sustainable Pig Production, Huazhong Agricultural University, Wuhan, China.*

15:00 140 **Dietary vitamin A differentially affects fat desaturation in porcine stearoyl-CoA desaturase genotypes.**
J. Estany*[1], S. Gol[1], M. Tor[1], L. Bosch[2], J. Reixach[3], and R. Pena[1], [1]*Department of Animal Science, University of Lleida Agrotecnio Center, Lleida, Spain;* [2]*Department of Agriculture Engineering and Food Technology. University of Girona, Girona, Spain;* [3]*Selección Batallé, S.A, Riudarenes, Spain.*

15:15 141 **Effects of diet supplementation with oleic acid or carbohydrates on *Biceps femoris* transcriptome in growing Iberian pigs.**

R. Benítez*[1], B. Isabel[2], A. Fernández[1], Y. Núñez[1], E. De Mercado[3], E. Gómez Izquierdo[3], J. García-Casco[1], C. López-Bote[2], and C. Óvilo[1], [1]*INIA, Madrid, Madrid, Spain*; [2]*UCM, Madrid, Madrid, Spain*; [3]*Centro 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. Schroyen[2], H. Beiki[2], C. L. Loving[3], and **C. K. Tuggle***[2], [1]*College of Veterinary Medicine, Iowa State University, Ames, IA, USA;* [2]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [3]*Food 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. Lough[1], A. Hess[4], H. Rashidi[2], H. Mulder[2], J. Dekkers[4], I. Kyriazakis[3], M. Hess[4], N. Deeb[5], A. Kause[6], B. Rowland[7], J. Lunney[8], and **A. Doeschl-Wilson***[1], [1]*The Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, UK;* [2]*Animal Breeding and Genomics, Wageningen University and Research, Wageningen, the Netherlands;* [3]*School of Agriculture Food and Rural Development, Newcastle University, Newcastle upon Tyne, UK;* [4]*Iowa State University, Ames, IA, USA;* [5]*Genus plc, Hendersonville, TN, USA;* [6]*Natural Resources Institute Finland, Jokioinen, Finland;* [7]*Kansas State University, Manhattan, KS, USA;* [8]*USDA, 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. Djebali[1], K. Munyard[2], N. Villa-Vialaneix[3], C. Cabau[1], A. Rau[4], E. Crisci[4], T. Derrien[5], C. Klopp[3], M. Zytnicki[3], S. Lagarrigue[6,7], H. Acloque[1], **S. Foissac***[1], and E. Giuffra[4], [1]*GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Castanet-Tolosan, France;* [2]*Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia;* [3]*MIAT, Université de Toulouse, INRA, Castanet-Tolosan, France;* [4]*GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France;* [5]*UMR6290 IGDR, CNRS, Université Rennes 1, Rennes, France;* [6]*UMR PEGASE, INRA, Rennes, France;* [7]*UMR 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. Szmatola, 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. Acloque[1], M. Zytnicki[2], D. Robelin[1], S. Djebali[1], N. Villa-Vialaneix[2], O. Madsen[3], Y. Lahbib-Mansais[1], D. Esquerré[1], F. Mompart[1], L. Liaubet[1], M. Groenen[3], M. Yerle-Bouissou[1], and S. Foissac[1], [1]*GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France;* [2]*MIAT, University of Toulouse, INRA, Castanet Tolosan, France;* [3]*Animal 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. Warr[1], R. Hall[2], K. Kim[2], E. Tseng[2], S. Koren[3], A. Phillippy[3], D. Birkhart[4], B. Rosen[4], S. Schroeder[4], D. Hume[1], R. Talbot[5], L. Rund[6], L. Schook[6], W. Chow[7], K. Howe[7], D. J. Nonneman[8], G. A. Rohrer[8], N. Putnam[9], R. E. Green[9], R. O'Connor[10], D. Griffin[10], B. M. Skinner[11], C. A. Sargent[11], N. A. Affara[11], C. Tyler-Smith[7], M. Watson[1], T. P. L. Smith[8], and **A. Archibald***[1], [1]*The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK;* [2]*Pacific Biosciences, Menlo Park, CA, USA;* [3]*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA;* [4]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA;* [5]*Edinburgh Genomics, University of Edinburgh, Edinburgh, UK;* [6]*University of Illinois, Urbana, IL, USA;* [7]*The Wellcome Trust Sanger Institute, Hinxton UK;* [8]*USDA, ARS, USMARC, Clay Center, NE, USA;* [9]*Dovetail Genomics LLC, Santa Cruz, CA, USA;* [10]*University of Kent, Canterbury, Kent, UK;* [11]*University of Cambridge, Cambridge, UK.*

17:45	149	**Updated pig genome resources in Ensembl.** **T. Hourlier***[1], L. Eory[2], K. Billis[1], C. García Girón[1], L. Haggerty[1], O. Izuogu[1], D. N. Murphy[1], R. Nag[1], F. J. Martin[1], A. L. Archibald[2], B. Aken[1], and P. Flicek[1], [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 Chrstopher 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.**
Diane E. Dickel, *Lawrence Berkeley National Laboratory (LBNL)*.

10:00 **How animal genomic research contributes to basic biology.**
Leif Andersson, *Uppsala University and Texas A&M University; guest professor at the Swedish University of Agricultural Sciences*.

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30

11:30 **Filling the gap until the FAANG data comes in: Comparative annotation of sheep reveals selection has acted on the proximal regulatory machinery.**
James Kijas, *CSIRO*, and Laura Clarke, *EMBL-EBI*.

13:00 **Meeting ends.**

TOURS

Meet at registration desk	(Preregistration for all tours is mandatory)	13:00 – 18:00

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, *University of California, Davis*.

10:00 **Molecular regulation of pregnancy establishment in cattle.**
Pat Lonergan, *University College Dublin (UCD)*.

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30

11:30 **Is it time to change the paradigm? Mammals are not just genes interacting with their environment.**
Julian Marchesi, *Imperial College London*.

12:30 150 **Novel, Groundbreaking Research/Methodology Presentation: Sheep parchment as a genetic resource.**
M. Teasdale*, *Trinity College Dublin, Dublin, Ireland*.

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. Burrell[1], P. Siddavatam[1], A. Allred[1], M. de Groot[2], and W. van Haeringen[2], [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. Dreger[2], F. Danelli[1], S. Frattini[1], B. Coizet[1], S. P. Marelli[1], G. Pagnacco[1], G. Gandini[1], M. Polli[1], R. Caniglia[3], M. Galaverni[3], E. A. Ostrander[2], and P. Crepaldi[1], [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. Pena[1], C. Huau[1], D. Marcon[2], Y. Bourdillon[2], and D. Allain[1], [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. Mirkena[3], G. Duguma[2], S. Gizaw[2], M. Wurzinger[4], J. Solkner[4], O. Mwai[2], T. Dessie[2], A. Abebe[6], M. Mamiru[8], T. Tadesse[7], R. N. B. Lobo[5], and B. Rischkowsky[1], [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. 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*.

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. Yang[1], N. Gorkhali[1], Y. Ma[1], 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. Ross[1], C. Kern[1], P. Saelao[1], Y. Wang[1], M. Halstead[1], K. Chanthavixay[1], I. Korf[1], M. Delany[1], H. Cheng[2], J. Medrano[1], A. Van Eenennaam[1], C. Tuggle[3], and C. Ernst[4], [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 enrichement 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. Mousel[2,1], B. Murdoch[3], 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. Kim[1], M. Farre[2], L. Auvil[3], B. Capitanu[3], J. Ma[4], H. A. Lewin[5], 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], P. Shang[1,2], Q. Li[3], L. Wang[1], H. Zhang[1], and C. Wu[1], [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. Liron[1], **M. Fernández***[2], A. Prando[3], A. Baldo[3], and G. Giovambattista[2], [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. Mullen[3], T. Hall[1], N. C. Nalpas[4], I. W. Richardson[5], D. A. Magee[1], C. N. Correia[1], J. A. Browne[1], D. P. Berry[6], D. Bradley[7], V. Naranbhai[8], A. Hill[8], E. Gormley[9], 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*.

17:00 167 **Circulating microRNAs as potential novel biomarkers to diagnose *Mycobacterium avium* ssp. *paratuberculosis* infection in cattle.**
K. Zhao[1], S. Hendrick[2], and **L. Guan***[1], [1]*Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada;* [2]*Coaldale 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. Mohamed[1], S. McWilliam[1], B. Evans[2], H. King[3], P. Kube[3], and K. Verbyla[4], [1]*CSIRO, Brisbane, Queensland, Australia;* [2]*SALTAS, Hobart, Tasmania, Australia;* [3]*CSIRO, Hobart, Tasmania, Australia;* [4]*Data61, Canberra, ACT, Australia*.

15:15 172 **Optimum-contribution selection increases genetic gain in Atlantic salmon breeding schemes.**
B. Hillestad*[1] and M. Henryon[2], [1]*SalmoBreed AS, Bergen, Norway;* [2]*Seges, Copenhagen, Denmark*.

15:30 173 **Exploiting linkage disequilibrium information in turbot selection programs.**
M. Saura*[1], A. Fernández[1], J. Fernández[1], M. Toro[2], P. Martínez[3], A. Millán[4], M. Hermida[3], A. Blanco[3], S. Cabaleiro[5], A. Doeschl-Wilson[6], and B. Villanueva[1], [1]*Departamento de Mejora Genética Animal, INIA, Madrid, Spain;* [2]*Departamento de Producción Agraria, ETS Ingenieros Agrónomos, Madrid, Spain;* [3]*Departamento de Xenética, Facultade de Veterinaria, Universidade de Santiago de Compostela, Lugo, Spain;* [4]*Geneaqua SL, Lugo, Spain;* [5]*CETGA, Cluster de Acuicultura de Galicia, Aguiño-Ribeira, Spain;* [6]*Division of Genetics and Genomics, The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian, Scotland, UK*.

174 **Withdrawn by authors**

Coffee/Tea break Atrium, O'Brien Science Building 15:45 – 16:30

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. Cichero[2], and V. Martinez[1], [1]*FAVET-INBIOGEN-Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile;* [2]*Blue 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. Rothschild[1], and L. Fontanesi[2], [1]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy;* [3]*Biocomputing 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. Rubin[1], C. Feng[1], M. Petterson[1], A. B. Martinez[2], S. Lamichhaney[1], I. Bunikis[3], and L. Andersson[1,5], [1]*Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden;* [2]*Science for Life Laboratory, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden;* [3]*Science for Life Laboratory, National Genomics Infrastructure, Uppsala University, Uppsala, Sweden;* [4]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [5]*Department 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. Verleih[1], and A. Rebl[1], [1]*Leibniz Institute for Farm Animal Biology, Inst. for Genome Biology, Dummerstorf, Germany;* [2]*University 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*, 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. Campos[2], C. C. Gulias-Gomes[1], B. P. Sollero[1], and A. R. Caetano[3], [1]*Embrapa Pecuária Sul, Bagé, RS, Brazil;* [2]*Universidade Federal de Pelotas, Pelotas, RS, Brazil;* [3]*Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil*.

14:55 181 **Genomic selection based on current status in developing countries.**
R. Mrode*[1], J. Ojango[1], O. Mwai[1], and J. M. Mwacharo[2], [1]*Animal Biosciences, International Livestock Research Institute, Nairobi, Kenya;* [2]*Small 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. Missohou[1], K. Marshal[2], S. F. Tebug[2], J. Juga[4], and **M. Tapio***[5], [1]*Interstate School of Veterinary Science and Medicine of Dakar, Dakar, Senegal;* [2]*International Livestock Research Institute, Nairobi, Kenya;* [3]*University of Ngaoundere, Ngaoundere, Cameroon;* [4]*University of Helsinki, Helsinki, Finland;* [5]*Natural 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. Kim[3], R. Mrode[2], B. Salim[5], N. Oyekanmi[4], H. Kim[3], and O. Hanotte[1,2], [1]*School of life Sciences, University of Nottingham, Nottingham, UK;* [2]*International Livestock Research institute (ILRI), Nairobi, Kenya;* [3]*C&K genomics, Seoul National University Research Park, Seoul, South Korea;* [4]*National Biotechnology Development Agency, Lugbe, Abuja, Nigeria;* [5]*Department 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. Cheruiyot[2], T. Dusingizimana[3], M. Chagunda[4], J. Ojango[5], 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. Huson[3], M. Wurzinger[1], J. Burgstaller[4], S. Gizaw[5], A. Haile[6], B. Rischkowsky[6], G. Brem[4], S. A. Boison[1], G. Mészáros[1], A. O. Mwai[7], 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*, *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, *SIRO Agriculture and Food*.

10:00 **Picking the bones out: Ancient animal genomics of the Fertile Crescent.**
Daniel G. Bradley, *Smurfit Institute of Genetics*.

Coffee/Tea break	Atrium, O'Brien Science Building	11:00 – 11:30

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. Brantsæter[4], J. Nordgreen[4], L. Coutinho[1], A. Janczak[4], P. Jensen[2], and C. Guerrero-Bosagna[2], [1]*Linköping University, Linköping, Östergötland, Sweden;* [2]*University of São Paulo, Piracicaba, São Paulo, Brazil;* [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden;* [4]*Faculty 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. Lachance[1], R. Funston[2], R. Weaber[3], and S. McKay[1], [1]*University of Vermont, Burlington, VT, USA;* [2]*University of Nebraska, North Platte, NE, USA;* [3]*Kansas 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. Straathof[2], F. Paradis[1,2], C. Li[1,2], H. Block[4], M. Colazo[3], and H. Bruce[2], [1]*Agriculture and Agri-Food Canada, Edmonton, Alberta, Canada;* [2]*University of Alberta, Edmonton, Alberta, Canada;* [3]*Alberta Agicutlure and Forestry, Edmonton, Alberta, Canada;* [4]*Agriculture 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. Semik[1], A. Gurgul[1], T. Szmatola[1], K. Pawlina[1], and E. Bagnicka[2], [1]*National Research Institute of Animal Production, Balice, Poland;* [2]*Institute 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. Marthey[2], H. Kiefer[2], C. Le Danvic[1], A. Allais-Bonnet[1], J. Perrier[2], L. Jouneau[2], A. Rau[2], H. Jammes[2], and L. Schibler[1], [1]*ALLICE, Paris, France;* [2]*INRA, 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. 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]*Department of Animal Sciences, North Dakota State University, Fargo, ND, USA;* [2]*Department of Animal and Food Sciences, University of Kentucky, Lexington, KY, USA;* [3]*USDA, 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-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]*Animal Genomics Laboratory, UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, Ireland;* [2]*NDM Research Building, University of Oxford, Oxford, UK;* [3]*Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, Tübingen, Germany;* [4]*UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland;* [5]*The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, UK;* [6]*UCD 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. Wang[1], P. Saelao[1], K. Chanthavixay[1], I. Korf[1], C. K. Tuggle[2], C. Ernst[3], P. Ross[1], and H. Zhou[1], [1]*University of California-Davis, Davis, CA, USA;* [2]*Iowa State University, Ames, IA, USA;* [3]*Michigan 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. 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]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;* [2]*Department of Animal Science, University of California, Davis, CA, USA;* [3]*Genome Center, University of California, Davis, CA, USA;* [4]*USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA;* [5]*Department 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. Namous[1], F. Peñagaricano[2], M. Del Corvo[3], E. Capra[4], A. Stella[4], J. Williams[5], P. A. Marsan[3], 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. Szmatola, and M. Bugno-Poniewierska, *National Research Institute of Animal Production*, *Balice, Poland*.

MT16 **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]*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. Utzeri[1], L. Penso-Dolfin[2], G. Schiavo[1], A. Ribani[1], G. Etherington[2], L. Fontanesi*[1], and F. Di Palma[2], [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. Mucha[1], D. Morrice[2], H. Wierzbicki[1], M. Moska[1], and M. Dobrowolski[3], [1]*Department of Genetics, Wroclaw University of Environmental and Life Sciences*, *Wroclaw, Poland;* [2]*The Roslin Institute, University of Edinburgh*, *Edinburgh, Scotland, UK;* [3]*Institute of Animal Breeding, Wroclaw University of Environmental and Life Sciences*, *Wroclaw, Poland*.

MT21 **Genetic distances between farm and wild populations of the red fox in Poland.**
M. Zaton-Dobrowolska*[1], A. Mucha[1], D. Morrice[2], H. Wierzbicki[1], M. Moska[1], and M. Dobrowolski[3], [1]*Department of Genetics, Wroclaw University of Environmental and Life Sciences*, *Wroclaw, Poland;* [2]*The Roslin Institute, University of Edinburgh*, *Edinburgh, Scotland, UK;* [3]*Institute of Animal Breeding, Wroclaw University of Environmental and Life Sciences*, *Wroclaw, Poland*.

MT22 **A *de novo* hybrid assembly of a dromedary camel.**
H. Holl*[1], D. Miller[2], S. Abdalla[3], B. Shykind[3], J. Malek[3], Y. Mohamoud[3], A. Ahmed[3], K. Pasha[4], A. Khalili[4], D. Antczak[2], and S. Brooks[1], [1]*University of Florida*, *Gainesville, FL, USA;* [2]*Cornell University*, *Ithaca, NY, USA;* [3]*Weill Cornell Medical College in Qatar*, *Doha, Qatar;* [4]*Tharb Veterinary Hospital*, *Doha, Qatar*.

MT23 **SNP genotyping of reindeer (*Rangifer tarandus)* using BovineHD BeadChips.**
V. Kharzinova*[1], A. Dotsev[1], V. Fedorov[2], G. Brem[1,3], K. Wimmers[4], H. Reyer[4], and N. Zinovieva[1], [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*.

MT24 **The population and landscape genetics of the European badger (*Meles meles)* 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 Fonctionelle et Evolutie, Montpelier, 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, Republic of Ireland;* [6]*Irish Equine Centre, Johnstown, Republic of Ireland;* [7]*Waterford Institute of Technology, Waterford, Republic of Ireland;* [8]*Animal and Plant Health Agency (APHA), Stonehouse, Gloucestershire, England;* [9]*University of Glasgow, Glasgow, Scotland*.

MT25 **Genomic selection for performance and reproduction traits in American mink.**
K. Karimi*[1], M. Sargolzaei[2,3], and Y. Miar[1], [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, Ontario, Canada*.

MT26 **Plains bison triallelic SNPs for determining parentage, estimating cattle introgression, and inbreeding.**
T. Kalbfleisch*[1], J. Tait[2], V. Basnayake[2], B. Simpson[2], T. Smith[3], and M. Heaton[3], [1]*University of Louisville, Louisville, KY, USA;* [2]*GeneSeek, Lincoln, NE, USA;* [3]*USMARC, 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. Lyu[2], J. Zentek[3], and G. A. Brockmann[2], [1]*Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt;* [2]*Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences, Humboldt-Universität zu Berlin, Berlin, Germany;* [3]*Department 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 B_1 induced apoptosis in chicken hepatocytes and rescue effects of selenium.**
M. Jameel*[1], X. Peng[2], A. A. Kamboh[3], and J. Fang[1], [1]*Sichuan Agricultural University, Chengdu, Sichuan, China;* [2]*ChinaWest Normal University, Nanchong, Sichuan, China;* [3]*Sindh 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. Beltramo[1], A. Dogliero[2], V. Campia[1], S. Peletto[1], S. Colussi[1], P. Modesto[1], and P. Acutis[1], [1]*Regional Center for Exotic Animals, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Turin, Italy;* [2]*Department 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. Peng[2], R. Yung[2], J. Wang[2], and D. Lin[1,2], [1]*Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University*, *Beijing, China;* [2]*State 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 Fishieries*, *Kasai, Hyogo, Japan*.

MT38 **MtDNA D-loop genetic diversity of Middle East and North African indigenous chicken.**
A. Al-Jumaili*[1], S. Al-Bayatti[2], A. A. Essa[2], R. Alatiyat[3], A. Ahbara[1], J. Mwacharo[4], O. Hanotte[1], and R. Aljumaah[3], [1]*University of Nottingham, School of Life Sciences*, *Nottingham, Nottinghamshire, UK;* [2]*Ministry of Agriculture, Directorate of Animal Resources, Genetic Resources Division*, *Baghdad, Iraq;* [3]*King Saud University,Animal Science Department, College of Food and Agriculture*, *Riyadh, Kingdom of Saudi Arabia;* [4]*The 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. Hara[2], T. Hirano[2], and K. Hanzawa[2], [1]*Tokyo University of Agriculture*, *Setagaya, Tokyo, Japan;* [2]*Tokyo 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. Lawal[1], D.-D. Wu[3], Y.-P. Zhang[3,4], P. M. Hocking[5], D. W. Burt[5], and O. Hanotte[1,6], [1]*The University of Nottingham*, *Nottingham, UK;* [2]*Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro, Japan;* [3]*Kunming Institute of Zoology, Chinese Academy of Sciences*, *Kunming, China;* [4]*Yunnan University*, *Kunming, China;* [5]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh*, *Edinburgh, UK;* [6]*International 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. Lipkin[2], M. Soller[2], J. Fulton[3], and D. Burt[1], [1]*The Roslin Institute*, *Midlothian, Edinburgh, UK;* [2]*The Hebrew University of Jerusalem*, *Jerusalem, Israel;* [3]*Hy-line International*, *Dallas Center, IA, USA*.

MT42 **Three differential expression clusters showed acclimation mechanism of White Pekin duck under heat stress.**
J.-M. Kim[1], K.-S. Lim[1], K.-T. Lee[1], Y.-R. Yang[2], H.-H. Chai[1], J. Hwangbo[1], B.-H. Choi[1], D. Lim[1], Y.-H. Choi[2], and J.-E. Park*[1], [1]*National Institute of Animal Science, Rural Development Administration*, *Wanju-gun, Jeollabuk-do, Republic of Korea;* [2]*Gyeongsang 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. Biolatti[1], L. Favaro[2], S. Colussi[1], S. Peletto[1], S. Piga[3], M. V. Riina[1], D. Pessani[2], E. Trincas[3], V. Isaja[3], and P. L. Acutis[1], [1]*Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta*, *Turin, Italy;* [2]*Laboratorio di Zoologia e Biologia Marina, Dipartimento Scienze della Vita e Biologia dei Sistemi*, *Turin, Italy;* [3]*Zoom Torino*, *Turin, Italy*.

MT44 **Genomic variability in Mexican chicken population.**
M. G. Strillacci*[1], E. Gorla[1], M. C. Cozzi[1], S. I. Roman-Ponce[2], F. J. Ruiz[2], V. E. Vega-Murillo[2], F. Bertolini[3,4], L. Fontanesi[3], S. Cerolini[1], and A. Bagnato[1], [1]*Department of Veterinary Medicine, University of Milan*, *Milano, Italy;* [2]*Centro Nacional de Investigación en Fisiología y Mejoramiento Animal*, *Col. Centro Veracruz, Mexico;* [3]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna*, *Bologna, Italy;* [4]*Department of Animal Science, Iowa State University*, *Ames, IA, USA*.

MT45 **Response of the hepatic transcriptomes of domesticated and wild turkey to aflatoxin B_1.**
K. Reed*[1], K. Mendoza[1], J. Abrahante[1], and R. Coulombe[2], [1]*University of Minnesota*, *St. Paul, MN, USA;* [2]*Utah 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. Smith[2], D. Burt[2], M. Soller[1], and J. Fulton[3], [1]*Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem*, *Jerusalem, Israel;* [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh*, *Easter Bush, Midlothian, UK;* [3]*Hy-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. Rau[3], C. Désert[1,2], M. Boutin[1,2], K. Muret[1,2], S. Leroux[4], D. Esquerre[5], C. Klopp[6], D. Gourichon[7], F. Pitel[4], T. Zerjal[3], and S. Lagarrigue*[1,2], [1]*INRA, UMR1348, PEGASE, St Gilles, France;* [2]*Agrocampus-Ouest, UMR1348, Rennes, France;* [3]*INRA, AgroParisTech, Université Paris-Saclay, UMR GABI, Jouy-en-Josas, France;* [4]*INRA/INPT ENSAT/INPT ENVT, GenPhySE, Castanet Tolosan, France;* [5]*INRA, Plateforme GENOTOUL, Castanet-Tolosan, France;* [6]*INRA, SIGENAE, Castanet-Tolosan, France;* [7]*INRA, 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. Zhou[2], R. Gallardo[3], T. Kelly[2,3], A. Wolc[1,4], and S. J. Lamont[1], [1]*Iowa State University, Department of Animal Science, Ames, IA, USA;* [2]*University of California-Davis, Department of Animal Science, Davis, CA, USA;* [3]*University of California-Davis, School of Veterinary Medicine, Davis, CA, USA;* [4]*Hy-Line International, Dallas Center, IA, USA*.

MT53 **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]*Sichuan Agricultural University, Chengdu, Sichuan, China;* [2]*Texas A&M University, College Station, TX, USA*.

MT54 **The broiler chicken transcriptome.**
C. Schmidt*[1] and S. Lamont[2], [1]*University of Delaware, Newark, DE, USA;* [2]*Iowa State University, Ames, IA, USA*.

MT55 **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]*Washington University School of Medicine, St Louis, MO, USA;* [2]*Phase Genomics Inc, Seattle, WA, USA;* [3]*University of California-Davis, Davis, CA, USA;* [4]*Hy-Line International, Dallas Center, IA, USA;* [5]*Cobb-Vantress Inc, Siloam Springs, AR, USA;* [6]*Beckman Research Institute, Duarte, CA, USA;* [7]*USDA-ARS, East Lansing, MI, USA*.

MT56 **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]*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* [2]*INRA, UMR1348 Physiologie, Environnement et Génétique pour l'Animal et les Systèmes d'élevage, Saint-Gilles, France;* [3]*Agrocampus-Ouest, UMR1348, Rennes, France;* [4]*UMR INRA/INPT ENSAT/INPT ENVT - GenPhySE, Castanet Tolosan, France;* [5]*INRA, Plateforme GENOTOUL, Castanet-Tolosan, France;* [6]*INRA, SIGENAE, Castanet-Tolosan, France;* [7]*INRA-PEAT, Nouzilly, France;* [8]*URA, 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 Sluis[1], and C. Visser[2], [1]*North-West University, Potchefstroom, North-West, South Africa;* [2]*University 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. 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]*Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy;* [2]*Department of Veterinary Medicine, University of Milan, Milano, Italy;* [3]*Biocomputing Group, Department of Biological, Geological, and Environmental Sciences, University of Bologna, Bologna, Italy;* [4]*Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agricola y Pecuarias (INIFAP), Col. Centro Veracruz, Mexico;* [5]*Department 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. Smith[2], D. Burt[2], M. Soller[1], and J. Fulton[3], [1]*Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel;* [2]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Easter Bush, Midlothian, UK;* [3]*Hy-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. Jin[1], N.-R. Choi[1], D. Seo[1], P. Manjula[1], H.-Y. Kim[2], S. H. Lee[1], and J. H. Lee*[1], [1]*Chungnam National University, Daejeon, Republic of Korea;* [2]*Insilicogen Inc, Yongin, Republic of Korea*.

MT66 **A novel approach for mapping of animal genome assemblies to a chromosomal level applied to avian genomes.**
J. Damas[1], R. E. O'Connor[2], M. Farre[1], H. Martell[2], E. A. Slack[1], E. Allanson[1], L. Kiazim[2], R. Jennings[2], A. Mandawala[3], S. Joseph[2], K. E. Fowler[3], D. K. Griffin[2], 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, Kent, UK;* [3]*Canterbury Christchurch University, Canterbury, Kent, UK*.

MT67 ***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]*Saint-Petersburg State University, Saint-Petersburg, Russia;* [2]*Royal Veterinary College, University of London, London, UK;* [3]*University 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-Ismail[1,2], M. Sargolzaei[2,3], S. P. Miller[2,4], F. Schenkel[2], S. S. Moore[1,5], and P. Stothard[1], [1]*University of Alberta, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada;* [2]*University of Guelph, Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, ON, Canada;* [3]*The Semex Alliance, The Semex Alliance, Guelph, ON, Canada;* [4]*Angus Genetics Inc., American Angus Association, St. Joseph, MO, USA;* [5]*University 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. Sun[2], Z. Yi[2], Z. Yuan[2], Z. Qin[2], and L. Lin[3], [1]*Division of Animal Biotechnology, National Institute of Biotechnology, Ganakbari, Asulia, Savar, Dhaka, Bangladesh;* [2]*College 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;* [3]*Beijing Dairy Cattle Center, Beijing, China.*

MT73 **Genome-wide association study for displacement of abomasum in dairy cattle.**
H. Huang*[1], J. Cao[2], G. Guo[3], X. Li[3], Y. Wang[1], Y. Yu[1], S. Zhang[1], Q. Zhang[1], and Y. Zhang[1], [1]*Key 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;* [2]*Department of Clinical Veterinary Medicine, College of Veterinary Medicine, China Agricultural University, Beijing, China;* [3]*Beijing Sunlon Livestock Co Ltd, Beijing, China.*

MT74 **Genomic single-step national evaluation of Holstein cattle in the Czech Republic.**
A. Kranjcevicova*[1], J. Pribyl[1], J. Splichal[2], J. Bauer[2], J. Motycka[3], and L. Vostry[1], [1]*Institute of Animal Science, Prague, Czech Republic;* [2]*Plemdat (Czech Moravia Breeders Corporation), Hradistko, Czech Republic;* [3]*Holstein Cattle Breeders Association, Hradistko, Czech Republic.*

MT75 **Identification of hypotrichosis in Kazakh Whiteheaded beef cattle breed in Kazakhstan.**
T. Yechshzhanov*[2], R. Uskenov[1], Y. Mukhanbetkaliyev[1], S. Zhamaliyeva[2], and A. Smakova[1], [1]*S.Seifullin Kazakh AgroTechnical University, Astana, Kazakhstan;* [2]*L.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-Ismail*[1,2], J. Crowley[1,3], E. C. Akanno[1], G. Manafiazar[1], C. Li[1,4], G. Plastow[1], M. D. MacNeil[6], D. Berry[7], P. Stothard[1], and J. Basarab[1,5], [1]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada;* [2]*Animal and Poultry Production, Damanhour University, Damanhour, Egypt;* [3]*Canadian Beef Breeds Council, Calgary, AB, Canada;* [4]*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada;* [5]*Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada;* [6]*Delta G, Department of Animal, Wildlife and Grassland Sciences, Bloemfontein, South Africa;* [7]*Animal 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. Pitchford[2], and C. D. K. Bottema[2], [1]*School of Environmental Science and Natural Resources, The National University of Malaysia, Bangi, Selangor, Malaysia;* [2]*School 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. Ekine-Dzivenu[1], M. Abo-Ismail[1,2], M. MacNeil[3,4], C. Li[1,5], C. Fitzsimmons[1,5], J. Basarab[1,6], and G. Plastow[1], [1]*Livestock Gentec, AFNS, University of Alberta, Edmonton, AB, Canada;* [2]*Department of Animal and Poultry Production, Damanhour University, Damanhour, Egypt;* [3]*Delta G, Miles City, MT, USA;* [4]*Department of Animal, Wildlife and Grassland Sciences, University Free State, Bloemfontein, South Africa;* [5]*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, AB, Canada;* [6]*Alberta Agriculture and Forestry, Lacombe Research and Development Centre, Lacombe, AB, Canada.*

MT79 **Bilateral iridal hypopigmentation in Holstein Friesian cattle.**
A. K. Hollmann[1], M. Bleyer[2], A. Tipold[3], J. N. Neßler[3], W. E. Wemheuer[1], E. Schütz[1], and B. Brenig*[1], [1]*Institute of Veterinary Medicine, University of Goettingen, Goettingen, Germany;* [2]*Pathology Unit, German Primate Center, Leibniz-Institute for Primate Research, Goettingen, Germany;* [3]*Dept. 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. Flynn[2], S. Waters[3], M. Mullen[4], T. Pabiou[1], R. Schnabel[5], J. Taylor[5], F. Kearney[1], R. Weld[2], and M. McClure[1], [1]*The Irish Cattle Breeding Federation, Highfield House, Shinagh, Bandon, Co. Cork Ireland;* [2]*Weatherbys DNA Laboratory, Johnstown, Co. Kildare;* [3]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath;* [4]*Department of Life and Physical Sciences, Faculty of Health and Science, Athlone Institute of Technology, Athlone, Co. Westmeath, Ireland;* [5]*Department 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. McCarthy[1], R. Weld[2], P. Flynn[2], M. Kean[1], K. O'Connell[1], and J. Kearney[1], [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. Siddavatam[1], A. Allred[1], C. Willis[1], R. Ferretti[2], and A. Raeber[1], [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. 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*.

Companion Animal Genetics and Genomics

MT87 **Complete mitogenome sequence of Lagomorphs from Upper Palaeolithic in the Balkan refuge.**
V. Brajkovic*[1], S. Radovic[2], D. Brajkovic[7], M. Girardi[3], S. Krebs[5], I. Medugorac[4], I. Curik[1], P. T. Miracle[6], C. Vernesi[3], and V. Cubric-Curik[1], [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. Genova[1], M. Longeri*[1], L. A. Lyons[2], F. G. Scalvini[1], G. Tedeschi[1], G. Sironi[1], and S. Nonnis[1], [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. Ilska[2], E. Sánchez-Molano[1], M. J. Haskell[2], Z. Polgar[1], S. E. Lofgren[3], D. N. Clements[1], J. A. Woolliams[1], and S. C. Blott[4], [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. Minor[1], D. A. Feeney[1], and P. B. Bitterman[2], [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. Mauri[1], M. Kleiter[2], M. Leschnik[2], S. Högler[3], E. Dietschi[1], C. Monney[4], A. Oevermann[4], D. Henke[5], M. Wiedmer[1], J. Dietrich[1], F. Steffen[6], S. Schuller[7], C. Gurtner[8], N. Stokar-Regenscheit[8], D. O'Toole[9], T. Bilzer[10], C. Herden[11], V. Jagannathan[1], 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-University, Gießen, Germany.*

MT95 **Detection and characterisation of a genetic association with Norwich terrier upper airway syndrome.**

T. Marchant*[1], E. Dietschi[2], R. Harrington[1], M. Drögemüller[2], U. Rytz[3], T. Leeb[2], and J. Schoenebeck[1], [1]*The Royal (Dick) School for Veterinary Studies and Roslin Institute, The University of Edinburgh, Edinburgh, Midlothian, UK;* [2]*The Institute of Genetics, Vetsuisse Faculty, The University of Bern, Bern, Switzerland;* [3]*Department 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. Grange[1], [1]*Institut Jacques Monod, CNRS, University Paris Diderot, Paris, France;* [2]*KU 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. Burrell[1], P. Siddavatam[1], A. Allred[1], M. de Groot[2], and W. van Haeringen[2], [1]*Thermo Fisher Scientific, Austin, TX, USA;* [2]*VHL 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. Samaha[1], J. Beatty[1], L. Lyons[2], C. Wade[3], 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.*

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. Kozyrev[2], M. Kierczak[2], M. Olsson[2,3], F. F. Farias[2], Å. Hedhammar[4], K. Bergvall[4], and K. Lindblad-Toh[2,5], [1]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [2]*Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, BMC, Uppsala University, Uppsala, Sweden;* [3]*Center for Molecular Medicine, Neuroimmunology Unit, Department of Clinical Neuroscience, and Reumatology Unit, Department of Medicine, Karolinska University Hospital, Karolinska Institutet, Stockholm, Sweden;* [4]*Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [5]*Broad 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. Gandolfi[2], A. Thomas[3], E. Creighton[2], L. Lyons[2], and M. Longeri[1], [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.*

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. Marchant[1], E. Johnson1, R. Harrington[1], L. McTier[1], C. Johnson[1], A. Gow[1], T. Liuti[1], D. Kuehn[2], K. Svenson[3], M. Bermingham[4], M. Drögemüller[5], M. Nussbaumer[6], M. Davey[1], D. Argyle[1], R. Powell[7], S. Guilherme[8], J. Lang[9], G. Ter Haar[1], T. Leeb[5], T. Schwarz[1], R. Mellanby[1], D. Clements[1], 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.*

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. Herndon[1], M. A. Highland[3,4], J. B. Taylor[5], D. P. Knowles[1,3], and S. N. White[1,3], [1]*Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA;* [2]*Erciyes University, Faculty of Agriculture, Department of Animal Science, Kayseri, Turkey;* [3]*Animal Disease Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Pullman, WA, USA;* [4]*Paul G. Allen School of Global Animal Health, Washington State University, Pullman, WA, USA;* [5]*Range Sheep Production Efficiency Research, Dubois, ID, USA;* [6]*Center 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. Hanotte[3], T. Dessie[3], N. Spark[4], G. Belay[1], K. Tesfaye[1], J. Jung'a[5], M. Kyalo[6], W. Ekaya[6], and R. Pelle[6], [1]*Addis Ababa University (AAU), Addis Ababa, Ethiopia;* [2]*Amhara Regional Agricultural Research Institute (ARARI), Bahir Dar, Ethiopia;* [3]*International Livestock Research institute (ILRI), Addis Ababa, Ethiopia;* [4]*Center for Tropical Livestock Genetics and Health (CTLGH), Scotland, UK;* [5]*University of Nairobi (UoN), Nairobi, Kenya;* [6]*Biosciences 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. Lunney[2], A. Ando[3], C. Rogel-Gaillard[4], J.-H. Lee[5], L. Schook[6], and S. Hammer[7], [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*.

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. Munyard[1], E. Morgan[1], M. Stear[2], and D. Groth[1], [1]*Curtin University, Perth, WA, Australia;* [2]*La 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-Jensen[1], T. Østerbye[1], M. Rasmussen[1], M. Nielsen[2], A. Stryhn[1], and S. Buus*[1], [1]*Laboratory of Experimental Immunology, University of Copenhagen, Copenhagen, Denmark;* [2]*Center 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. 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]*The Pirbright Institute, Pirbright, Woking, Surrey, UK;* [2]*Anthony Nolan Research Institute, Royal Free Hospital, London, UK;* [3]*UCL Cancer Institute, Royal Free Campus, London, UK;* [4]*Moredun Research Institute, Pentlands Science Park, Scotland, UK;* [5]*Stanford University, Stanford, CA, USA;* [6]*Norwegian Veterinary Institute, Oslo, Norway;* [7]*University of Cambridge, Cambridge, UK;* [8]*Gift of Life Michigan, Michigan, USA;* [9]*Biomedical Primate Research Centre, Rijswijk, Netherlands;* [10]*European 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 Hom[2], and M. M. Miller[3], [1]*Hy-Line International, Dallas Center, IA, USA;* [2]*GABI, INRA, AgroParisTech, Jouy-en-Josas, France;* [3]*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. Case[1], L. Younger[1], J. Tseng[1], H. Holl[2], Y. Ali Mohamoud[3], A. Ahmed[3], J. Malek[3], S. Brooks[2], and D. Antczak[1], [1]*Cornell University, Ithaca, NY, USA;* [2]*University of Florida, Gainesville, FL, USA;* [3]*Weill 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. Guldbrandtsen[1], J. Vilkki[3], D. J. De Koning[4], D. Boichard[2], M. S. Lund[1], and G. Sahana[1], [1]*Department of Molecular Biology and Genetics, Center for Quantitative Genetics and Genomics, Aarhus University, Tjele, Denmark;* [2]*UMR 1313 GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* [3]*Green technology, Natural Resources Institute Finland, Myllytie 1, Jokioinen, Finland;* [4]*Department 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. Lund[2], and D. Boichard[1], [1]*INRA, Paris, France;* [2]*Aarhus University, Denmark.*

MT121 **Extensive sequencing of a tropically adapted breed—The Brahman sequencing project.**
L. Koufariotis[1], B. Hayes[1], M. Kelly[2], B. Burns[3], R. Lyons[4], and S. Moore*[1], [1]*Centre of Animal Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD, Australia;* [2]*Australian Agricultural Company (AACo), Brisbane, QLD, Australia;* [3]*Queensland Department of Agriculture and Fisheries, Rockhampton, QLD, Australia;* [4]*4School of Veterinary Science, University of Queensland, Gatton, QLD, Australia.*

MT122 **Withdrawn**

MT123 **Reference sequence of the horse Y chromosome.**
T. Raudsepp*[1], J. Janecka[2], B. Davis[3], S. Ghosh[1], N. Paria[4], P. J. Das[5], M. Nielsen[6], L. A. A. Orlando[7], M. Schubert[7], T. A. E. Stout[8], and B. P. Chowdhary[1], [1]*Texas A&M University, College Station, TX,USA;* [2]*Duquesne University, Pittsburgh, PA, USA;* [3]*National Institutes of Health, Bethesda, MD, USA;* [4]*Texas Scottish Rite Hospital for Children, Dallas, TX, USA;* [5]*National Research Centre on Yak, Dirang, India;* [6]*University of Kentucky, Lexington, KY, USA;* [7]*Natural History Museum of Denmark, Copenhagen, Denmark;* [8]*Utrecht University, Utrecht, the Netherlands.*

MT124 **SNP discovery in indigenous Afrikaner, Drakensberger and Nguni cattle breeds of South Africa.**
A. A. Zwane*[1,2], A. Choudhury[3], M. L. Makgahlela[1], A. Maiwashe[1,5], E. Van Marle-Koster[2], and J. F. Taylor[4], [1]*Department of Animal Breeding and Genetics, ARC-API, Irene, South Africa;* [2]*Department of Animal and Wildlife Sciences, University of Pretoria, Hatfield, Pretoria, South Africa;* [3]*Sydney Brenner Institute of Molecular Bioscience, University of the Witwatersrand, Parktown, Johannesburg, South Africa;* [4]*Division of Animal Sciences, University of Missouri, Columbia, MO, USA;* [5]*Department 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. Warr[1], R. Hall[2], K. Kim[2], E. Tseng[2], S. Koren[3], A. Phillippy[3], D. Birkhart[4], B. Rosen[4], S. Schroeder[4], D. Hume[1], R. Talbot[5], L. Rund[6], L. Schook[6], W. Chow[7], K. Howe[7], D. J. Nonneman[8], G. A. Rohrer[8], N. Putnam[9], R. E. Green[9], R. O'Connor[10], D. Griffin[10], B. M. Skinner[11], C. A. Sargent[11], N. A. Affara[11], C. Tyler-Smith[7], M. Watson[1], T. P. L. Smith[8], and A. Archibald*[1], [1]*The Roslin Institute and R(D)SVS, University of Edinburgh, Easter Bush, Midlothian, UK;* [2]*Pacific Biosciences, Menlo Park, CA, USA;* [3]*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA;* [4]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA;* [5]*Edinburgh Genomics, University of Edinburgh, Edinburgh, UK;* [6]*University of Illinois, Urbana, IL, USA;* [7]*The Wellcome Trust Sanger Institute, Hinxton UK;* [8]*USDA, ARS, USMARC, Clay Center, NE, USA;* [9]*Dovetail Genomics LLC, Santa Cruz, CA, USA;* [10]*University of Kent, Canterbury, Kent, UK;* [11]*University of Cambridge, Cambridge, UK.*

MT126 **Beyond sequencing: Assigning function to novel ncRNAs.**
F. McCarthy*[1], A. Cooksey[1], C. Gresham[2], and B. Nanduri[2], [1]*University of Arizona, Tucson, AZ, USA;* [2]*Mississippi 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. Foissac[1], S. Djebali*[1], H. Acloque[1], FR-AgENCODE Consortium[2], M. H. Pinard Van der Laan[2], S. Lagarrigue[3], and E. Giuffra[2], [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.*

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. Djebali[1], K. Munyard[2], N. Villa-Vialaneix[3], C. Cabau[1], A. Rau[4], E. Crisci[4], T. Derrien[5], C. Klopp[3], M. Zytnicki[3], S. Lagarrigue[6,7], H. Acloque[1], S. Foissac*[1], and E. Giuffra[4], [1]*GenPhySE, INPT, ENVT, INRA, Université de Toulouse, Castanet-Tolosan, France;* [2]*Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia;* [3]*MIAT, Université de Toulouse, INRA, Castanet-Tolosan, France;* [4]*GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France;* [5]*UMR6290 IGDR, CNRS, Université Rennes 1, Rennes, France;* [6]*UMR PEGASE, INRA, Rennes, France;* [7]*UMR PEGASE, Agrocampus Ouest, Rennes, France.*

MT129 **Pinpointing causal mutations among imputed sequence variant genotypes in three cattle breeds.**
H. Pausch*[1,2], I. MacLeod[1], P. Bowman[1,3], R. Emmerling[4], R. Fries[5], B. Gredler-Grandl[6], H. Daetwyler[1,3], and M. Goddard[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.*

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. Cieslak[1], A. Borowska[1], E. G. Cothran[2], A. M. Khanshour[3], and M. Mackowski[1,4], [1]*Department of Horse Breeding, Poznan University of Life Sciences, Poznan, Poland;* [2]*Department of Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Science, Texas A&M University, College Station, TX, USA;* [3]*Texas Scottish Rite Hospital for Children, Dallas, TX, USA;* [4]*Horse 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. Park[2], J. Hwang[2], S. Kim[2], and G. Cho[2], [1]*Animal and Plant Quarantine Agency, Pusan, Korea;* [2]*of 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. Islam[1], M. J. Pröll[1], S. Rony[1], C. Große-Brinkhaus[1], M. J. Uddin[2], D. Tesfaye[1], M. Hölker[1], E. Tholen[1], K. Schellander[1], 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. Hehl[1], W. Demasius[1], J. Guenther[1], R. Weikard[1], F. Hadlich[1], H.-M. Seyfert[1], L. Rohmeier[2], M. Meyerholz[2,4], W. Petzl[2], H. Zerbe[2], M. Hoedemaker[3], H.-J. Schuberth[4], S. Engelmann[5], C. Kuehn[1], [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. Bovenhuis[1], M. G. B. Nieuwland[2], H. K. Parmentier[2], and J. J. van der Poel[1], [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. Fleming[1], X. Li[2], F. Blecha[3], 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. Kim[2], C. K. Park[3], S.-W. Kim[1], and K.-S. Kim[1], [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. Sasaki[2], P. Meripet[1], Y. Sugimoto[2], and Y. Aida[1], [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. He[1], N. Okimoto[3], J. Yamagishi[3], J. Kohara[4], 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. Bjelka[2], A. Kalashnikov[3], T. Valcíková[4], and V. Mátlová[1], [1]*Institute of Animal Science, Prague-Uhríneves, 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. Signorelli[1], F. Napolitano[1], L. Buttazzoni[1], C. Grelet[2], A. Vanlierde[2], F. Dehareng[2], H. Soyeurt[3], M. Crowe[4], and GplusE Consortium[5], [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. Heimeier[1], D. M. Bickhart[2], T. P. L. Smith[3], J. F. Medrano[4], and J. A. Hammond[1], [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. Ainslie[1], 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. Nolan[2], A. Psifidi[1], Z. Wu[1], K. Harman[2], R. Hawken[3], M. Abrahamsen[3], F. Tomley[2], D. Blake[2], and D. Hume[1], [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. Koy[2], A. Berthold[1], H.-J. Schuberth[2], M. Weinert[3], S. Engelmann[3], C. Kühn[1], H.-M. Seyfert[1], and J. Günther[1], [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. Fraser[1], H. N. Snyman[1,2], A. Meyer[1,3], J. D. Hammermüller[1], 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. Schwartz[1], D. Bickhart[2], T. Smith[3], and J. Hammond[1], [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-Gallego[2], S. Montserrat[2], F. Mayer[1], A. Castello[1], L. Alborch[2], S. Heath[3], A. Esteve-Codina[3], J. Gomez-Garrido[3], R. A. Cigliano[4], and A. Clop*[1], [1]*Centre for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Cerdanyola del Valles, Catalonia, Spain;* [2]*Universitat Autonoma de Barcelona, Cerdanyola del Valles, Catalonia, Spain;* [3]*Centre Nacional d'Anàlisi Genómica CNAG-CRG, Barcelona, Catalonia, Spain;* [4]*Sequentia Biotech, Barcelona, Catalonia, Spain.*

MT161 **Genetic basis for resistance to avian influenza in commercial egg layer chicken lines.**
W. Drobik-Czwarno*[1], A. Wolc[2,3], J. Fulton[3], T. Jankowski[4], J. Arango[3], P. Settar[3], N. O'Sullivan[3], and J. Dekkers[2], [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.*

MT162 **The ligands and polymorphic residues of chicken MHC YF class I-like molecules.**
R. M. Goto[1], G. Gugiu[1], B. M. Stadtmueller[2], P. J. Bjorkman[2], and M. M. Miller*[1], [1]*Beckman Research Institute, City of Hope, Duarte, CA, USA;* [2]*California 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. Schroyen[2], H. Beiki[2], C. L. Loving[3], and C. K. Tuggle*[2], [1]*College of Veterinary Medicine, Iowa State University, Ames, IA, USA;* [2]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [3]*Food 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-Hélène[1], R. Hawken[2], and H. Edin[1], [1]*INRA, Jouy-en-Josas, France;* [2]*Cobb-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. Dry[1], S. Lillico[2], C. B. A. Whitelaw[2], and B. Dalziel[1], [1]*Division of Infection and Immunity, the Roslin Institute, University of Edinburgh, Edinburgh, Scotland, UK;* [2]*Division 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. Lemonnier[1], J. Leplat[1,2], E. Bouguyon[3], Y. Billon[4], J. Estelle[1], and C. Rogel-Gaillard[1], [1]*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* [2]*CEA, DRF/IRCM/SREIT/LREG, Jouy-en-Josas, France;* [3]*VIM-INRA-Université Paris-Saclay, Jouy-en-Josas, France;* [4]*GenESI, INRA, Surgères, France.*

MT169 **The association of copy number variations with tick count in South African Nguni cattle.**
L. Pickering*[1], K. Dzama[1], F. Muchadeyi[2], and M. Wang[2], [1]*Animal Science Department, University of Stellenbosch, Stellenbosch, Western Cape, South Africa;* [2]*Agriculture 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. Islam[1], C. Neuhoff*[1], S. Rony[1], C. Große-Brinkhaus[1], M. J. Uddin[2], M. Hölker[1], D. Tesfaye[1], E. Tholen[1], M. J. Pröll[1], and K. Schellander[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.*

MT171 **QTLs associated with resistance to MAP infection in Holstein-Friesian cattle.**
S. Mallikarjunappa*[1,3], M. Sargolzaei[4], K. Meade[2], N. Karrow[3], and S. Pant[1], [1]*Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW, Australia;* [2]*Teagasc Animal and Bioscience Research Department, Grange, Co. Meath, Ireland;* [3]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada;* [4]*The Semex Alliance, Guelph, ON, Canada.*

MT172 **Investigating genetic control of resistance to avian pathogenic *Escherichia coli* colonization in chickens.**
M. Monson*[1], M. Kaiser[1], A. Wolc[1,2], and S. Lamont[1], [1]*Iowa State University, Ames, IA, USA;* [2]*Hy-Line International, Dallas Center, IA, USA.*

MT173 **Integrative network genomics of the bovine host response to infection with M*ycobacterium bovis*.**
T. J. Hall*[1], K. E. Killick[1,2], M. P. Mullen[3], K. E. McLoughlin[1], N. C. Nalpas[4], I. W. Richardson[5], D. A. Magee[1], C. N. Correia[1], J. A. Browne[1], H. M. Vordermeier[6], B. Villarreal-Ramos[6], D. P. Berry[7], E. Gormley[8], 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. Song[1], 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. Lillico*[1], C. Proudfoot[1], C. Burkard[1], F. Urnov[2], J. Oatley[3], B. Telugu[4], A. Mileham[5], and B. Whitelaw[1], [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. Strive[2], P. Brown[3], S. Henry[2], A. Sunarto[1], K. McColl[1], C. Cooper[1], D. Moro[4], M. Byrne[4], and T. Doran[1], [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*, H. Sang, and M. McGrew, *The Roslin Insitute, 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*, M. Kikuchi, H. Kakoi, K.-I. Hirota, and S.-I. Nagata, *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. Olsson[2], L. Andersson[3,4], C. F. Ihler[5], E. Strand[5], G. Lindgren[1], and B. D. Velie[1], [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. Seong[1], N.-Y. Kim[2], D. C. Kim[3], N.-H. Hwang[1], I.-C. Yang[1], A. Jang[1], J.-D. Kim[1], J.-W. Choi*[1], W.-H. Chung[4], and J.-B. Kim[1], [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. Remacha[1], A. Romero[1,2], F. J. Vázquez[1,2], A. Vitoria[1,2], P. Zaragoza[1], and C. Rodellar[1], [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. François[2], B. Velie[3], A. Stinckens[2], H. Hoskens[4], S. Blott[5], S. Tinel[2], L. Peeters[6], H. Savelkoul[7], E. Tijhaar[7], G. Lindgren[3], S. Janssens[2], B. Ducro[8], N. Buys[2], A. Schurink[8], [1]*Research Group Livestock Physiology, Department of Biosystems, KU Leuven, Leuven, Belgium;* [2]*Research Group Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium;* [3]*Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [4]*Laboratory for Genetic Epidemiology, Department of Human Genetics, KU Leuven, Leuven, Belgium;* [5]*School of Veterinary Medicine & Science, University of Nottingham, Leicestershire, UK;* [6]*Biomedical Research Institute, Hasselt University, Diepenbeek, Belgium;* [7]*Cell Biology and Immunology Group, Wageningen University & Research, Wageningen, the Netherlands;* [8]*Animal 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. Jung[1], M. Hewicker-Trautwein[2], O. Distl[1], and J. Metzger[1], [1]*Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover Foundation, Hannover, Niedersachsen, Germany;* [2]*Department 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. Szmatola, 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. Gerber[1], and V. Jagannathan[2], [1]*Swiss Institute of Equine Medicine, University of Bern and Agroscope, Bern, Switzerland;* [2]*Institute 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. McCue[2], and A. McCoy[1], [1]*University of Illinois, Champaign, IL, USA;* [2]*University 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. Beeson[1], J. Mickelson[2], and M. McCue[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA;* [2]*Department 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. Seong[2], D. C. Kim[4], I. C. Cho[1], P. N. Seong[1], J. K. Son[1], S. M. Shin[1], S. H. Park[1], J. H. Woo[1], N. G. Park[1], W.-H. Chung[3], and J.-W. Choi[2], [1]*Subtropical Animal Research Institute, National Institute of Animal Science, RDA, Jeju, Jeju, Republic of Korea;* [2]*College of Animal Life Science, Kangwon National University, Chuncheon, Kangwon, Republic of Korea;* [3]*Division of Nutrition and Metabolism Research, Research Group of Gut Microbiome, Korea Food Research Institute, Sungnam, Gyeonggi, Republic of Korea;* [4]*Jeju 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. Moe[2], K. Moe[2], B. Kounnavongsa[3], S. Keonouchanh[3], B. Bouahom[3], T. Shimogiri[4], H. Mannen[5], M. Kanemaki[6], Y. Yamamoto[7], and T. Kunieda[1], [1]*Okayama Univercity, Okayama, Okayama, Japan;* [2]*University of Veterinary Science, Yezin, Nay Pyi Taw, Myanmar;* [3]*National Agriculture and Forestry Research Institute, Xaythany, Vientiane, Lao PDR;* [4]*Kagoshima University, Kagoshima, Kagoshima, Japan;* [5]*Kobe University, Kobe, Hyogo, Japan;* [6]*Institute of Animal Science, Nagoya, Aichi, Japan;* [7]*Hiroshima University, Higashi-Hiroshima, Hiroshima, Japan*.

MT190 **Genetic characteristics of Kazakhstan native horses.**
H. Ezoe*[1], Y. Okuda[1], M. Nishibori[2], H. Mannen[3], Y. Takahashi[4], K. Nomura[4], T. Yamagata[5], Y. Yamamoto[2], K. Tsunoda[6], M. Bakhtin[7], P. Kazymbet[7], M. Alykhan[8], M. Suleimenov[8], O. Safronova[9], T. Kunieda[1], [1]*Okayama University, Okayama, Okayama, Japan;* [2]*Hiroshima University, Higashihiroshima, Hiroshima, Japan;* [3]*Kobe University, Kobe, Hyogo, Japan;* [4]*Tokyo University of Agriculture, Setagaya, Tokyo, Japan;* [5]*Nagoya University, Nagoya, Aichi, Japan;* [6]*Showa University, Shinagawa, Tokyo, Japan;* [7]*Astana Medical University, Astana, Akmola, Kazakhstan;* [8]*Institute of Zoology, Almaty, Almaty, Kazakhstan;* [9]*LLP 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-Szmukier[2], K. Zukowski[1], and K. Piórkowska[1], [1]*National Research Institute of Animal Production, Balice, Poland;* [2]*University of Agriculture in Cracow, Cracow, Poland*.

MT192 **Genomic and pedigree analysis of population structure of Old Kladruber horse.**
L. Vostry[1,2], H. Vostra-Vydrova[2], J. Bauer[3], A. Kranjcevicová*[1,2], and J. Pribyl[2], [1]*Czech University of Life Sciences Prague, Prague, Czech Republic;* [2]*Institut of Animal Science, Prague, Czech Republic;* [3]*Czech-Moravian Breeders Corporation, Hradistko, Czech Republic*.

MT193 **Population structure and admixture in closely related Czech draft horse populations.**
H. Vostra-Vydrova[2], L. Vostry[1,2], N. Moravcikova[3], B. Hofmanova[1], Z. Vesela[2], A. Svitakova*[2], J. Schmidova[2], and R. Kasarda[3], [1]*Czech University of Life Sciences Prague, Prague, Czech Republic;* [2]*Institut of Animal Science, Prague, Czech Republic;* [3]*3Slovak 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. Semik[1], A. Fornal[1], T. Zabek[1], C. Koch[2], K. Mählmann[2,3], M. Witkowski[4], and M. Bugno-Poniewierska[1], [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. Zabek[1], A. Fornal[1], K. Pawlina[1], J. Klukowska-Rötzler[2], C. Koch[2], K. Mählmann[2,3], and M. Bugno-Poniewierska[1], [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. Wodas[1], 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-Molik[2], K. Zukowski[2], K. Piórkowska[2], and M. Bugno-Poniewierska[2], [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. Halliday[2], R. Crisman[3], C. M. Wade[1], and N. Beijerink[2], [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. Kalbfleisch[2], J. C. Stevens[3], J. Eberth[1], J. S. DePriest[2], and U. B. R. Balasuriya[1], [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. Bryan[1], W. Shiraigol[2], M. Dugarjaviin[2], and E. Hill[1], [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. Ribeiro[2], O. Cortes[3], F. T. P. S. Sereno[4], M. R. T. Costa[5], and L. Telo da Gama[6], [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. Diniz[2], R. M. G. Lima[1], C. L. P. Meneses[1], and C. B. N. Campos[1], [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. Hoban[1], K. Castle[2], N. Hamilton[3], and B. Haase*[1], [1]*Sydney Schoold 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. Mack[1], T. Mansour[1], J. Bowser[2], A. Eddy[2], C. Mochal[2], A. Claude[2], A. Cooley[2], M. Johnson[2], and C. Swiderski*[2], [1]*College of Veterinary Medicine, University of California, Davis, CA, USA;* [2]*College 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], [1]*Baker Institute for Animal Health, Ithaca, NY, USA;* [2]*Cornell University, Ithaca, NY, USA*.

MT209 **EquCab3.**
T. Kalbfleisch*[1], M. DePriest[1], L. Orlando[2], and J. MacLeod[3], [1]*University of Louisville, Louisville, KY, USA;* [2]*University of Copenhagen, Copenhagen, Denmark;* [3]*University of Kentucky, Lexington, KY, USA*.

MT210 **Epigenetic characterization of centromeric chromatin in equids.**
S. G. Nergadze[1], R. Gamba[1], F. M. Piras[1], E. Cappelletti[1], M. Corbo[1], F. Gozzo[1], D. Miller[2], D. Antczak[2], E. Raimondi[1], K. Sullivan[3], and E. Giulotto*[1], [1]*University of Pavia, Department of Biology and Biotechnology, Pavia, Italy;* [2]*Cornell University, College of Veterinary Medicine, Ithaca, NY, USA;* [3]*National 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. Schurink[2], B. Velie[3], A. Stinckens[1], S. Blott[4], B. Ducro[2], C. Lamberigts[5], S. Tinel[1], K. De Keyser[1], M. Oosterlinck[6], G. Lindgren[3], S. Janssens[1], and N. Buys[1], [1]*Research Group Livestock Genetics, Department of Biosystems, KU Leuven, Leuven, Belgium;* [2]*Animal Breeding and Genomics Centre, Wageningen University & Research, Wageningen, the Netherlands;* [3]*Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [4]*School of Veterinary Medicine & Science, University of Nottingham, Leicestershire, United Kingdom;* [5]*Research Group Livestock Physiology, Department of Biosystems, KU Leuven, Leuven, Belgium;* [6]*Department 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. Norton[1], J. Mickelson[2], and M. McCue[1], [1]*Department of Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA;* [2]*Department 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. Burns[2], M. Bordbari[2], E. Scott[2], B. Ming-Whitfield[2], V. Affolter[2], C. Ramirez Alanis[2], M. Barro[2], M. Mack[2], G. Gianino[2], F. Gianino[2], E. Giulotto[3], K. Hilburger[2], T. Kalbfleisch[4], J. MacLeod[5], M. Mienaltowski[2], S. Katzman[2], T. Leeb[6], T. Raudsep[7], P. Saelao[2], S. Vig[2], H. Zhou[2], R. Bellone[2], and C. Finno[2], [1]*University of Nebraska-Lincoln, Lincoln, NE, USA;* [2]*University of California-Davis, Davis, CA, USA;* [3]*University of Pavia, Pavia, Italy;* [4]*University of Louisville, Louisville, KY, USA; 5University of Kentucky, Lexington, KY, USA;* [6]*University of Bern, Bern, Switzerland;* [7]*Texas A&M, College Station, TX, USA.*

MT214 **The potential of Y-chromosomal markers for individual lineage tracking in horses.**
S. Felkel[1], D. Rigler[1], C. Vogl[1], M. Neuditschko[2], S. Rieder[2], V. Jagannathan[3], T. Leeb[3], T. Rattei[4], C. Schlötterer[5], G. Brem[1], and B. Wallner*[1], [1]*Institute of Animal Breeding and Genetics, University of Veterinary Medicine Vienna, Vienna, Austria;* [2]*Agroscope, Swiss National Stud Farm, Avenches, Switzerland;* [3]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland;* [4]*Department of Microbiology and Ecosystems Science, Division of Computational Systems Biology, University of Vienna, Vienna, Austria;* [5]*Institute of Population Genetics, University of Veterinary Medicine Vienna, Vienna, Austria*.

MT215 **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, *Universitty 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*, 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. Klumplerova[1], P. Splichalova[1], J. Oppelt[2], P. Musilova[3], S. Kubickova[3], R. Vodicka[4], J. Vahala[5], L. Orlando[6], and P. Horin*[1], [1]*Ceitec VFU, University of Veterinary and Pharmaceutical Sciences, Dept. of Animal Genetics, Brno, Czech Republic;* [2]*Ceitec MU, Masaryk University, National Centre for Biomolecular Research, Faculty of Science, Brno, Czech Republic;* [3]*Veterinary Research Institute, Dept. of Reproduction and Genetics, Brno, Czech Republic;* [4]*Zoo Prague, Prague, Czech Republic;* [5]*Zoo Dvur Kralove nad Labem, Dvur Kralove nad Labem, Czech Republic;* [6]*Centre 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-Szmukier[2], A. Piestrzynska-Kajtoch[1], A. Fornal[1], and K. Ropka-Molik[1], [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. MacLeod[2], and T. S. Kalbfleisch[1], [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. Sasazaki[1], M. Bakhtin[2], P. Kazymbet[2], M. Alyan[3], M. Suleimenov[3], M. Nishibori[4], and H. Mannen[1], [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. Sasazaki[1], M. Lwin[2], H. Moe[3], T. Shimogiri[3], and H. Mannnen[1], [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. Bolívar[3], M. A. Galindo-Pellicena[2], J. L. Arsuaga[2], C. Ginja[1], 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-ISCIII 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. Castaneda[1], R. Juras*[1], T. Raudsepp[1], I. Randlaht[2], and E. G. Cothran[1], [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. Martinez*[1,2] and B. Consortium[1], [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. Yildirim[1], M. Nizamlioglu[1], M. D. Oncu[2], E. K. Bastanlar[2], 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. Carlsson[2], and D. Berry[3], [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. 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]*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. Librado[1], A. Fages[1,2], C. Gaunitz[1], N. Khan[1], K. Hanghøj[1,2], C. Gamba[1], C. Der Sarkissian[1], M. Leonardi[1], M. Schubert[1], 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. Weigend[1], D. Malomane[2], and H. Simianer[2], [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. McCabe[1], A. K. Kelly[2], D. A. Kenny[1], P. Cormican[1], and S. M. Waters[1], [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. Estellé[3], M. Revilla[1,2], L. Criado-Mesas[1,2], Y. Ramayo-Caldas[3], C. Óvilo[4], A. I. Fernández[4], M. Ballester[5], 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-Caldas[1], F. Levenez[2], G. Lemonnier[1], C. Denis[1], M. Berri[3], M.-J. Mercat[4], Y. Billon[5], J. Doré[2], C. Larzul[1,6], P. Lepage[2], and C. Rogel-Gaillard[1], [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-BIOPORC, 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. Stewart[1], A. Warr[1], T. Snelling[3], M. Auffret[2], A. Walker[3], R. Wallace[3], and R. Roehe[2], [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. Pedersen[1], N. Canibe[2], P. Kiilerich[3], K. Kristiansen[3], and M. Fredholm[1], [1]*Department of Veterinary and Animal Science, Faculty of Health & Medical Sciences, University of Copenhagen, Frederiksberg, Denmark;* [2]*Department of Animal Science, Aarhus University, Tjele, Denmark;* [3]*Department of Biology, Faculty of Science, University of Copenhagen, Copenhagen, Denmark.*

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

Pig Genetics and Genomics

MT243 **Quantitative trait loci (QTL) mapping of growth and conformation traits in F_2 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. Garrayo[3], A. Fernandez[3], Y. Nuñez[3], R. Benitez[3], C. Garcia-Contreras[3], M. Vazquez-Gomez[1], B. Isabel[1], A. Fernandez[3], A. Rey[1], A. Golzalez-Bulnes[4], C. Lopez-Bote[1], and C. Ovilo[3], [1]*Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense, Madrid, Spain;* [2]*Applied Veterinary Morphology, Department of Veterinary Sciences, University of Antwerp, Wilrijk, Antwerp, Belgium;* [3]*Departamento de Mejora Genética Animal, INIA, Madrid, Spain;* [4]*Comparative Physiology Lab SGIT-INIA, Madrid, Spain.*

MT246 **Investigating the genomic basis of pigs that have died in transit.**
F. Bertolini*[1], K. Zurbrigg[2], T. van Dreumel[2], T. O'Sullivan[2], and M. F. Rothschild[1], [1]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*University of Guelph, Guelph, Ontario, Canada.*

MT247 **GWAS on coat color in wuzhishan pig using the Porcine SNP80 BeadChip.**
X. Qiao* and F. Meiying, *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. Rawat[1], W. SS[1], P. Kumar[1], S. Qureshi[1], A. Kumar[1], S. Kumar[1], and B. Bhushan[1], [1]*ICAR-Indian Veterinary Research Institute, Izatnagar, UP, India;* [2]*ICAR-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. Fang[2], J. Wang[2], C. Zhang[2], R. Zhang[2], D. Liu[4], Y. Zhao[1,2], X. Hu[2,3], and N. Li[2], [1]*Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University, Beijing, China;* [2]*State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, China;* [3]*National Engineering Laboratory for Animal Breeding, China Agricultural University, Beijing, China;* [4]*Institute of Animal Industry, Heilongjiang Academy of Agricultural Sciences, Harbin, Heilongjiang, China.*

MT250 **Transcriptome analysis reveals long intergentic 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. Heuß[1], C. Große-Brinkhaus[1], H. Henne[2], A. K. Appel[2], K. Schellander[1], and E. Tholen[1], [1]*Institute of Animal Science, University of Bonn, Bonn, Germany;* [2]*BHZP 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. Rau[3], Y. Ramayo-Caldas[3], J. Estellé[3], A. Castelló[1,2], A. I. Fernández[4], M. Ballester[5], and J. M. Folch[1,2], [1]*Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, 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 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), 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. Fernández[3], M. Ballester[4], and J. M. Folch[1,2], [1]*Plant and Animal Genomics, Centre de Recerca en Agrigenòmica (CRAG), Consorci CSIC-IRTA-UAB-UB, Campus UAB, Bellaterra, Barcelona, Spain;* [2]*Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain;* [3]*Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain;* [4]*Departament 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. Alves[2], L. Silió[2], C. Rodriguez[2], F. Sánchez-Esquiliche[3], J. M. García-Casco[1,2], and M. Muñoz[1,2], [1]*Centro de I+D en Cerdo Ibérico, INIA, Zafra, Badajoz, Spain;* [2]*Departamento de Mejora Genética Animal, INIA, Madrid, Spain;* [3]*Sánchez-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. Miller[1], [1]*USDA-ARS-NADC, Ames, IA, USA;* [2]*ORISE-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. Casiró[1], Y. B. Rubio[2], R. Bates[1], N. Raney[1], J. Steibel[1,3], and C. Ernst[1], [1]*Department of Animal Science, Michigan State University, East Lansing, MI, USA;* [2]*Department of Epidemiology and Biostatistics, Michigan State University, East Lansing, MI, USA;* [3]*Department 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. Oluwole[3], M. O. Oladele-Bukola[3], Olorungbounmi[3], B. A. Boladuro[3], S. C. Olaogun[4], L. M. Nneji[1], O. J. Sanke[5], P. M. Dawuda[6], O. G. Omitogun[7], L. Frantz[8], R. W. Murphy[1,9], H.-B. Xie[1,2], M.-S. Peng[1,10], Y.-P. Zhang[1,11], [1]*State Key Laboratory of Genetic Resources and Evolution & Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China;* [2]*Sino-Africa Joint Research Center, Chinese Academy of Sciences, Kunming, China;* [3]*Institute of Agricultural Research and Training, Obafemi Awolowo University, Ibadan, Nigeria;* [4]*Department of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria;* [5]*Taraba State Ministry of Agriculture and Natural Resources, Jalingo, Taraba State, Nigeria;* [6]*Department of Veterinary Surgery and Theriogenology, College of Veterinary Medicine, University of Agriculture Makurdi, Makurdi, Benue State, Nigeria;* [7]*Department of Animal Sciences, Obafemi Awolowo University, Ile-Ife, Nigeria;* [8]*The Palaeogenomics and Bio-Archaeology Research Network, Research Laboratory for Archaeology, University of Oxford, Oxford, UK;* [9]*Centre for Biodiversity and Conservation Biology, Royal Ontario Museum, Toronto, Canada;* [10]*Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China;* [11]*State 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], [1]*Inner Mongolia Agricultral University, Hohhot, Inner Mongolia, China;* [2]*The Ministry of Agriculture Key Laboratory of animal genetics and breeding of sheep, Hohhot, Inner Mongolia, China;* [3]*Inner Mongolia Key Laboratory of animal genetics, breeding and reproduction, Hohhot, Inner Mongolia, China;* [4]*Inner 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. Wurmser[1], G. Dahinten[2], K.-U. Götz[2], D. Seichter[3], and I. Russ[3], [1]*Lehrstuhl für Tierzucht, TU München, Freising, Germany;* [2]*Institut für Tierzucht, Bayerische Landesanstalt für Landwirtschaft, Poing, Germany;* [3]*Tierzuchtforschung e.V. München, Poing, Germany;* [4]*Animal Genomics, Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland*.

MT262 **Genetic dissection of mechanisms underlying heat adaptation in pigs.**
J. Riquet*[1], H. Gilbert[1], K. Fève[1], Y. Labrune[1], R. Rose[2], Y. Billon[3], M. Giorgi[2], T. Loyau[2], J. Gourdine[2], and D. Renaudeau[4], [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. Stuczynska[2], and K. Zukowski[1], [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. Szmatola, 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-Prendes[1], R. Quintanilla[2], A. Zidi[1], Y. R. Caldas[2], T. F. Cardoso[1,4], A. Manunza[1], A. Canovas[3], A. Castello[1], 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. Quintanilla[2], T. F. Cardoso[1,3], J. Tibau[4], O. González-Rodríguez[2], R. González-Prendes[1], M. Ballester[2], and M. Amills[1], [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. Quintanilla[3], J. Tibau[4], M. Gil[4], E. Mármol-Sánchez[1], O. González-Rodríguez[3], R. González-Prendes[1], and M. Amills[1], [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. Fernández[1], J. Segura[2], R. Benítez[1], J. Olivas[3], J. Viguera[4], C. López-Bote[2], L. Calvo[3], and C. Óvilo[1], [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. Hamill[1], H. Reyer[2], N. Trakooljul[2], P. G. Lawlor[3], and K. Wimmers[2], [1]*Teagasc, Food Research Centre, Ashtown, 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. Reyer[2], K. Wimmers[2], N. Trakooljul[2], P. G. Lawlor[3], and R. M. Hamill*[1], [1]*Teagasc, Food Research Centre, Ashtown, 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. Schiavo[1], F. Bertolini[1,4], G. Galimberti[5], A. B. Samorè[1], S. Dall'Olio[1], 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. Beiki[1], M. Schroyen*[1,2], A. Rakhshandeh[3], N. Gabler[1], J. Dekkers[1], and C. Tuggle[1], [1]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*Département AgroBioChem, Université de Liège, Gembloux, Belgium;* [3]*Department 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-Montes[2], Y. Núñez[2], A. Fernández[2], J. Folch[3,4], and A. Fernández[2,5], [1]*Centro de I+D en Cerdo Ibérico INIA-Zafra, Zafra, Badajoz, Spain;* [2]*Departamento Mejora Genética (INIA), Madrid, Madrid, Spain;* [3]*CRAG, Plant and Animal Genomics, Bellaterra, Barcelona, Spain;* [4]*Universitat Autònoma de Barcelona, Departament de Ciència Animal i dels Aliments, Bellaterra, Barcelona, Spain;* [5]*Hospital 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. Tor[1], F. Vilaró[2], R. Ros-Freixedes[1], J. Álvarez-Rodríguez[1], L. Bosch[3], J. Reixach[4], and J. Estany[1], [1]*Department of Animal Science, University of Lleida - Agrotecnio Center, Lleida, Spain;* [2]*Scientific- Technical Services, DATCEM, University of Lleida - Agrotecnio Center, Lleida, Spain;* [3]*Departament d'Enginyeria Química, Agrària i Tecnologia Agroalimentària, University of Girona, Girona, Spain;* [4]*Selección Batallé S.A, Riudarenes, Spain*.

MT278 **Genetic architecture of a QTL for teat number on porcine chromosome 7.**

M. van Son[1], M. S. Lopes[2], J. Kongsro[1], L. E. Gangsei[3], E. Grindflek[1], E. F. Knol[2], and B. Harlizius*[2], [1]*Norsvin SA, Hamar, Norway;* [2]*TopigsNorsvinResearch Center, Beuningen, the Netherlands;* [3]*Animalia, Oslo, Norway*.

MT279 **Genome wide association of changes in feeding behavior due to heat stress in pigs.**

A. J. Cross[1], B. N. Keel[2], T. M. Brown-Brandl[2], and G. A. Rohrer*[2], [1]*South Dakota State University, Brookings, SD, USA;* [2]*US Meat Animal Research Center, USDA Agriicultural Research Service, Clay Center, NE, USA*.

MT280 **Identification of SNPs associated with meat pHu in Italian Duroc pigs.**

R. Davoli[1], P. Di Battista[2], M. Zappaterra[1], and P. Zambonelli*[1], [1]*Department of Agricultural and-Food Sciences (DISTAL), Bologna University, Bologna, Italy;* [2]*Centro 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. Bressan[3], C. Bettencourt[3], J. Almeida[3], J. Sá[2], M. Gama-Carvalho[2], J. Santos-Silva[3], A. Belo[3], H. Bovenhuis[4], O. Moreira[3], R. Bessa[5], and L. Gama[5], [1]*Instituto de Medicina Molecular, Lisbon, Portugal;* [2]*BioISI- Biosystems and Integrative Sciences Institute, Lisbon, Portugal;* [3]*Instituto Nacional de Investigação Agrária e Veterinária, Santarém, Portugal;* [4]*Animal Breeding and Genomics Centre, Wageningen, Netherlands;* [5]*Faculdade de Medicina Veterinária, Lisbon, Portugal*.

MT282 **Heterospermic fertility index applied to frozen and refrigerated swine semen.**

C. Previtali[1], G. Bongioni*[1], and A. Galli[2], [1]*Istituto Sperimentale Italiano Lazzaro Spallanzani, Rivolta d'Adda, Cremona, Italy;* [2]*Centro 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. Ponsuksili[1], and K. Wimmers[1,2], [1]*Institute for Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;* [2]*Leibniz 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. Maroilley[1], M. Berri[2], D. Esquerré[3], C. Chevaleyre[4], G. Lemonnier[1], J. J. Leplat[1,4], S. Vincent-Naulleau[1,4], M. J. Mercat[5], Y. Billon[6], P. Lepage[7], C. Rogel-Gaillard[1], and J. Estellé*[1], [1]*GABI, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France;* [2]*ISP, INRA, Université de Tours, Nouzilly, France;* [3]*GenPhySe, INRA, INP, ENSAT, Université de Toulouse, Castanet-Tolosan, France;* [4]*CEA, DSV, IRCM, Laboratoire de Radiobiologie et Etude du Génome, Jouy-en-Josas, France;* [5]*IFIP-BIOPORC, Pôle génétique, Le Rheu, France;* [6]*GENESI, INRA, Surgères, France;* [7]*MICALIS, 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. Castelló[1], M. Montfort[2], J. Hecht[2], J.-E. Rodríguez-Gil[3], A. Sánchez[1], and À. Clop[1], [1]*Center for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB, Bellaterra, Spain;* [2]*Center for Genomic Regulation (CRG), Barcelona Biomedical Research Park (PRBB), Barcelona, Spain;* [3]*Unit 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. Schwind[1], K. A. Darfour-Oduro[2], Y. Liu[2,3], S. Mäkeläinen[4,5], A. K. De[2], L. A. Rund[2], O. Madsen[4], M. A. M. Groenen[4], R. C. Gaba[1], and L. B. Schook[1,2], [1]*Department of Radiology, University of Illinois at Chicago, Chicago, IL, USA;* [2]*Department of Animal Sciences, University of Illinois, Champaign-Urbana, IL, USA;* [3]*Department of Animal Genetics and Breeding, Sichuan Agricultural University, Chengdu, China;* [4]*Wageningen University & Research, Animal Breeding and Genomics, Wageningen, The Netherlands;* [5]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

MT287 **Updated pig genome resources in Ensembl.**
T. Hourlier*[1], L. Eory[2], K. Billis[1], C. García Girón[1], L. Haggerty[1], O. Izuogu[1], D. N. Murphy[1], R. Nag[1], F. J. Martin[1], A. L. Archibald[2], B. Aken[1], and P. Flicek[1], [1]*European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridgeshire, UK;* [2]*The 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. Yang[1], X. Han[1], Y. Gao[1], X. Li[1,2], S. Xie[1,2], and S. Zhao[1,2], [1]*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, Chin;* [2]*The 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. Acloque[1], M. Zytnicki[2], D. Robelin[1], S. Djebali[1], N. Villa-Vialaneix[2], O. Madsen[3], Y. Lahbib-Mansais[1], D. Esquerré[1], F. Mompart[1], L. Liaubet[1], M. Groenen[3], M. Yerle-Bouissou[1], and S. Foissac[1], [1]*GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France;* [2]*MIAT, University of Toulouse, INRA, Castanet Tolosan, France;* [3]*Animal 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. Ribani[1], V. J. Utzeri[1], F. Bertolini[1,4], G. Schiavo[1], 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*.

MT292 **Dietary vitamin A differentially affects fat desaturation in porcine stearoyl-CoA desaturase genotypes.**
J. Estany*[1], S. Gol[1], M. Tor[1], L. Bosch[2], J. Reixach[3], and R. Pena[1], [1]*Departament of Animal Science, University of Lleida, Agrotecnio Center, Lleida, Spain;* [2]*Departament of Agriculture Engineering and Food Technology. University of Girona, Girona, Spain;* [3]*Selección 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. Fernández[1], M. Muñoz[1], F. García[1], Y. Núñez[1], C. Geraci[2], A. Crovetti[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]*INIA, Madrid, Spain;* [2]*UNIBO, Bologna, Italy;* [3]*UNIFI, Firenze, Italy;* [4]*KIS, Ljubljana, Slovenia;* [5]*INRA, Toulouse, France;* [6]*IFIP, 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. Cesar[2], L. Geistlinger[3], P. Tizioto[2], P. Oliveira[3], J. Afonso[1], M. Rocha[1], A. Lima[1], C. Buss[1], L. Coutinho[2], and L. Regitano[3], [1]*Departament of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil;* [2]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil;* [3]*Embrapa 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. Fang[1], Z. Zhao[1], G. Li[2], X. Yu[3], Z. Wei[2], H. Yu[1], and R. Yang*[1], [1]*College of Animal Science, Jilin University, Changchun, Jilin Province, China;* [2]*The Key Laboratory of National Education Ministry for Mammalian Reproductive Biology and Biotechnology, Inner Mongolia University, Hohhot, Inner Mongolia Autonomous Region, China;* [3]*Department 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. Mukiibi*[1], M. Vinsky[2], C. Fitzsimmons[1,2], S. M. Waters[3], P. Stothard[1], and C. LI[1,2], [1]*Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada;* [2]*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, Alberta, Canada;* [3]*Animal 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. Arends[1], M. Reissmann[1], A. S. Ahmed[1], K. Wimmers[3], H. Reyer[3], and G. A. Brockmann[1], [1]*Albrecht Daniel Thaer-Institut für Agrar- und Gartenbauwissenschaften, Humboldt-Universität zu Berlin, Berlin, Germany;* [2]*Department of Dairy Production, Faculty of Animal Production, University of Khartoum, Khartoum North, Sudan;* [3]*Leibniz-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. Fukazawa[1], F. Kawaguchi[1], T. Matsuhashi[2], S. Maruyama[3], K. Oyama[4], S. Sasazaki[1], and H. Mannen[1], [1]*Graduate School of Agricultural Science, Kobe University, Kobe, Japan;* [2]*Institute of Advanced Technology Kindai University, Wakayama, Japan;* [3]*Gifu Prefectural Livestock Research Institute, Takayama, Japan;* [4]*Food 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. Matsumoto[1], F. Kawaguchi[1], Y. Uemoto[2], E. Kobayashi[3], M. Fukushima[4], E. Iwamoto[5], E. Yoshida[5], T. Akiyama[4], N. Kohama[4], K. Oyama[6], T. Honda[6], H. Mannen[1], and S. Sasazaki[1], [1]*Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Japan;* [2]*National Livestock Breeding Center, Fukushima, Japan;* [3]*Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, Tsukuba, Japan;* [4]*Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, Asago, Japan;* [5]*Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, Kasai, Japan;* [6]*Food 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. Muchadeyi[1], M. Malesa[1,2], P. Soma*[3], and E. Dzomba[2], [1]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, South Africa;* [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa;* [3]*Agricultural 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. Wang[2], D. Wang[1], H. Liu[1], J. Liu[1], and L. L. Guan[2], [1]*Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, China;* [2]*Department 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. Nakajima[1], Y. Uemoto[2], M. Fukushima[3], E. Yoshida[4], E. Iwamoto[4], T. Akiyama[3], N. Kohama[3], E. Kobayashi[5], K. Oyama[6], and H. Mannen[1], [1]*Graduate School of Agricultural Science, Kobe University, and Kobe, Hyogo, Japan;* [2]*National Livestock Breeding Center, and Nishigo, Fukushima, Japan;* [3]*Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, and Asago, Hyogo, Japan;* [4]*Hyogo Prefectural Technology Center of Agriculture, Forestry and Fisheries, and Kasai, Hyogo, Japan;* [5]*Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, and Tsukuba, Ibaraki, Japan;* [6]*Food 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. Kigoshi[1], A. Nakajima[1], Y. Matsumoto[1], Y. Uemoto[2], M. Fukushima[3], E. Yoshida[3], E. Iwamoto[3], T. Akiyama[3], N. Kohama[3], E. Kobayashi[4], T. Honda[5], K. Oyama[5], H. Mannen[1], S. Sasazaki[1], [1]*Graduate School of Agricultural Science, Kobe University, and Kobe, Japan;* [2]*National Livestock Breeding Center, and Fukushima, Japan;* [3]*Northern Center of Agricultural Technology, General Technological Center of Hyogo Prefecture for Agriculture, Forest and Fishery, and Asago, Japan;* [4]*Animal Breeding and Reproduction Research Division, NARO Institute of Livestock and Grassland Science, and Tsukuba, Japan;* [5]*Food 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. Agaba[1], [1]*Nelson Mandela African Institution of Science and Technology, and Arusha, Tanzania;* [2]*Mkwawa 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. Tarekegn*[1,2], F. Meutchieye[3], J. Mwacharo[4], A. Djikeng[2], M. Raphael[5], B. Liu[6], W. Zhang[7], O. A. Mwai[5], T. Dessie[8], C. Mutai[2], S. Osama[9], P. Wouobeng[3], K. S. Jaures[3], and J. Birungi[2], [1]*Department of Animal Production and Technology, Biotechnology Research Institute, Bahir Dar University, Bahir Dar, Ethiopia;* [2]*Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub, Nairobi, Kenya;* [3]*Faculty of Agronomy and Agriculture, University of Dschang, Dschang, Cameroon;* [4]*Small Ruminant Genetics and Genomics Group, International Centre for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia;* [5]*International Livestock Research Institute (ILRI), Nairobi, Kenya;* [6]*Nei Mongol BioNew Technology Co. Ltd, Hohhot, China;* [7]*College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China;* [8]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia;* [9]*The 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. Albayati[3], A. Essa[3], and O. Hanotte[1], [1]*School of Life Sciences, The University of Nottingham, Nottingham, UK;* [2]*College of Veterinary Medicine, University of Baghdad, Baghdad, Iraq;* [3]*Animal Genetics Resources Department, Ministry of Iraqi Agriculture, Baghdad, Iraq*.

MT314 **Congenital mandibular prognathia in Droughtmaster cattle.**
S. A. Woolley*[1], E. R. Tsimnadis[1], M. S. Khatkar[1], C. E. Willet[2], B. A. O'Rourke[3], and I. Tammen[1], [1]*Sydney School of Veterinary Science, The University of Sydney, Camden, NSW, Australia;* [2]*Sydney Informatics Hub, Core Research Facilities, The University of Sydney, Sydney, NSW, Australia;* [3]*The 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. Liu[1], R. A. Harris[1], X. Qin[1], S. Richards[1], J. Rogers[1], Y. Han[1], Q. Meng[1], T. P. Smith[2], B. P. Dalrymple[3], S. N. White[4], B. Murdoch[5], J. Kijas[6], N. E. Cockett[7], D. M. Muzny[1], K. C. Worley*[1], [1]*Baylor College of Medicine, Houston, TX, USA;* [2]*USDA Agricultural Research Service, U.S. Meat Animal Research Center, Clay Center, NE, USA;* [3]*University of Western Australia, Institute of Agriculture, Perth, Western Australia, Australia;* [4]*Washington State University, Veternary Microbiology and Pathology, Pullman, WA, USA;* [5]*University of Idaho, Animal and Veternary Science, Moscow, ID, USA;* [6]*CSIRO, St. Lucia, Australia;* [7]*Utah 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. Nishimura[2], H. Hara[1], Y. Sugimoto[2], and K. Hanzawa[1], [1]*Tokyo University of Agriculture, Funako, Atsugi, Kanagawa, Japan;* [2]*Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Nishi-shirakawa, Fukushima, Japan*.

MT320 **Melatonin target scondary hair follicle by RORα 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], [1]*Inner Mongolia Agricultral University, Hohhot, Inner Mongolia, China;* [2]*The Ministry of Agriculture Key Laboratory of Animal Genetics and Breeding of Sheep, Hohhot, Inner Mongolia, China;* [3]*Inner Mongolia Key Laboratory of Animal Genetics, Breeding and Reproduction, Hohhot, Inner Mongolia, China;* [4]*Inner 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 Jagt[1], M. Goddard[1,2], C. Reich[1], C. Prowse-Wilkins[1], B. Mason[1], H. Daetwyler[1,3], and B. Hayes[1,4], [1]*Agriculture Victoria, Centre for AgriBiosciences, Bundoora, VIC, Australia;* [2]*Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville, VIC, Australia;* [3]*School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia;* [4]*Centre 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. McWilliam[1], S. Harburg[2], S. A. Lehnert[1], and A. Reverter[1], [1]*CSIRO Agriculture & Food, Brisbane, QLD, Australia;* [2]*North Australian Pastoral Company, Brisbane, QLD, Australia*.

MT323 **A missense mutation of *ADAMTS3* causes pulmonary hypoplasia and anasarca (PHA) syndrome in Cika cattle.**
N. Wiedemar[1], T. Svara[2], V. Cociancich[3], K. Sest[4], M. Gombac[2], T. Paller[2], J. Staric[4], V. Jagannathan[1], and C. Drögemüller*[1], [1]*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland;* [2]*Institute of Pathology, Wild Animals, Fish and Bees, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia;* [3]*National Veterinary Institute, Veterinary Faculty, University of Ljubljana, Ljubljana, Slovenia;* [4]*Clinic 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. Bishop[1], A. Allen[2], S. McBride[2], R. Skuce[2,3], D. Bradley[4], D. Berry[5], M. Coffey[6], G. Banos[6,1], M. Mrode[6], J. Woolliams[1], and E. Glass[1], [1]*The Roslin Institute and R(D)SVS, The University of Edinburgh, Easter Bush, UK;* [2]*Agri-Food and Biosciences Institute Stormont, Stoney Road, Belfast, UK;* [3]*Queen's University Belfast, Medical Biology Centre, Belfast, UK;* [4]*Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin, Ireland;* [5]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Co. Cork, Ireland;* [6]*Scotland'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. Goszczynski[1], A. Molina[2], G. Giovambattista*[1], H. Morales Durand[1], and S. Demyda-Peyras[1], [1]*Instituto 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;* [2]*Departamento de Genética, Universidad de Córdoba, Córdoba, Spain*.

MT327 **Liver transcriptome profiling of beef steers divergent in feed intake or growth rate phenotype.**
R. Mukiibi[1], M. Vinsky[2], C. Fitzsimmons[1,2], S. M. Waters[3], P. Stothard[1], and C. Li*[1,2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada;* [2]*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, Alberta, Canada;* [3]*Animal 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. Ammermüller[1], A. Heldmann[1], and R. Fries[1], [1]*Chair of Animal Breeding, TUM, Freising, Germany;* [2]*Animal 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. Szmatola, 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], [1]*Inner Mongolia Agricultral University, Hohhot, Inner Mongolia, China;* [2]*The Ministry of Agriculture Key Laboratory of animal genetics and breeding of sheep, Hohhot, Inner Mongolia, China;* [3]*Inner Mongolia Key Laboratory of animal genetics, breeding and reproduction, Hohhot, Inner Mongolia, China;* [4]*Inner 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. Hadlich[1], H. M. Hammon[1], D. Frieten[2], C. Gerbert[3], C. Koch[3], G. Dusel[2], and C. Kühn[1,4], [1]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany;* [2]*University of Applied Sciences, Bingen, Germany;* [3]*Educational and Research Centre for Animal Husbandry, Hofgut Neumühle, Münchweiler, Germany;* [4]*University 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. Fair[2], P. Cormican[1], C. Byrne[1,3], S. M. Waters[1], and D. A. Kenny[1,3], [1]*Animal and Bioscience Research Department, Teagasc, Grange,, Dunsany, Co. Meath, Ireland;* [2]*Laboratory of Animal Reproduction, Department of Biological Sciences, School of Natural Sciences, Faculty of Science and Engineering, University of Limerick, Limerick, Ireland;* [3]*School 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. Strillacci[1], E. Gorla[1], M. C. Cozzi[1], M. Vevey[2], F. Bertolini[3,4], L. Fontanesi[3], and A. Bagnato*[1], [1]*Department of Veterinary Medicine, University of Milan, Milano, Italy;* [2]*Associazione Nazionale Allevatori Bovini Razza Valdostana, Gressan, Italy;* [3]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy;* [4]*Department 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. Dammann[2], W. M. Wemheuer[3], W. E. Wemheuer[1], A. Chilla[1], A. Tipold[4], W. J. Schulz-Schaeffer[3], J. Beck[5], E. Schütz[1,5], and B. Brenig[1], [1]*Institute of Veterinary Medicine, University of Goettingen, Goettingen, Germany;* [2]*Prion and Dementia Research Unit, Department of Neuropathology, University Medical Center Goettingen, University of Goettingen, Goettingen, Germany;* [3]*Institute of Neuropathology, University of the Saarland, Germany;* [4]*Dept. Small Animal Medicine and Surgery, University of Veterinary Medicine Hannover, Hannover, Germany;* [5]*Chronix Biomedical, Goettingen, Germany.*

MT337 **Allele-specific gene expression in liver of Nelore cattle extremes for feed efficiency.**
M. Rocha*[1], M. de Souza[1], A. Zerlotini-Neto[2], P. Tizioto[3], P. de Oliveira[4], A. de Lima[1], J. Afonso[1], L. Coutinho[3], L. Regitano[4], and S. Niciura[4], [1]*Departament of Genetics and Evolution, Federal University of São Carlos/UFSCar, São Carlos, São Paulo, Brazil;* [2]*Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil;* [3]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Bazil;* [4]*Embrapa 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. Perkins[4], J. Genho[5], R. Ferretti[2], M. Wells[2], R. J. Tait[2], S. Bauck[2], and G. J. M. Rosa[1], [1]*University of Wisconsin, Madison, WI, USA;* [2]*GeneSeek (An Neogen company), Lincoln, NE, USA;* [3]*University of Nebraska, Lincoln, NE, USA;* [4]*International Brangus Breeders Association, San Antonio, TX, USA;* [5]*Livestock Genetic Services LLC, Woodville, VA, USA.*

MT339 **Gene mapping and genomic prediction of sire conception rate in US dairy cattle.**
F. Peñagaricano*[1], Y. Han[1], P. Nicolini[1,2], G. Morota[3], and R. Abdollahi-Arpanahi[1,4], [1]*University of Florida, Gainesville, FL, USA;* [2]*Universidad de la República, Tacurembó, Uruguay;* [3]*University of Nebraska-Lincoln, Lincoln NE, USA;* [4]*University of Tehran, Tehran, Iran.*

MT340 **The Ovine Functional Annotation Project.**
B. Murdoch*[1], S. White[2,3], M. Mousel[2], A. Massa[3], K. Worley[4], A. Archibald[5], E. Clark[5], B. Dalrymple[6], J. Kijas[7], S. Clarke[8], R. Brauning[8], T. Smith[9], T. Hadfield[10], and N. Cockett[10], [1]*University of Idaho, Moscow, ID, USA;* [2]*USDA, ARS, Animal Disease Research Unit, Pullman, WA, USA;* [3]*Washington State University, Pullman, WA, USA;* [4]*Baylor College of Medicine, Houston, TX, USA;* [5]*The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, Scotland;* [6]*University of Western Australia, St Lucia, Queensland, Australia;* [7]*CSIRO Agriculture, St Lucia, Queensland, Australia;* [8]*AgResearch, Invemay Agricultural Centre, Mosgiel, New Zealand;* [9]*USDA, ARS U.S. Meat Animal Research Center, Clay Center, NE, USA;* [10]*Utah 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. Jarczak[1], M. Czopowicz[2], D. Sloniewska[1], K. Horbanczuk[1], W. Jarmuz[1], J. Kaba[2], L. Zwierzchowski[1], and E. Bagnicka[1], [1]*Institute of Genetics and Animal Breeding PAS in Jastrzebiec, Magdalenka, Poland;* [2]*Warsaw 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. Jarczak[1], M. Czopowicz[2], D. Sloniewska[1], M. Mickiewicz[2], K. Horbanczuk[1], W. Jarmuz[1], J. Kaba[2], L. Zwierzchowski[1], and E. Bagnicka[1], [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. Zalewska[1], D. Reczynska[1], E. Kosciuczuk[1], D. Sloniewska[1], S. Marczak[1], W. Jarmuz[1], and E. Bagnicka[1], [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. Megens[1], V. Silva[1,2], V. Marleen[1], M. Groenen[1], and R. Crooijmans[1], [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. Artesi[1], V. Hahaut[1], N. Rosewick[1,2], P. Griebel[3], N. Arsic[3], A. Burny[2], M. Georges[1], 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, Universite 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. Yudin[1], A. Yurchenko[1], R. Aitnazarov[1], P. Plysnina[1], 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. Durkin[1], A. Marçais[3], V. Hahaut[1], P. Griebel[4], N. Arsic[4], A. Burny[2], C. Charlier[1], O. Hermine[3], M. Georges[1], 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'hematologie, Hopital 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. Waters[1], J. Evans[1], P. Cormican[1], D. Doyle[1], 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. Waters[1], K. Keogh[1], R. Porter[2], and D. Kenny[1], [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. Cambuli[1], R. Puglisi[1], F. Fusi[2], L. Bertocchi[2], A. Galli[3], G. Bongioni*[1], and M. Montedoro[1], [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 Ubertini*, *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. Afonso[1], P. Tizioto[2], P. Oliveira[3], W. Diniz*[1], A. Lima[1], M. Souza[1], M. Rocha[1], J. Silva[1], C. Buss[1], C. Gromboni[4], G. Mourão[2], A. Nogueira[3], L. Coutinho[2], and L. Regitano[3], [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. Buss[1], W. Diniz[1], B. Andrade[3], M. Rocha[1], A. Lima[1], L. Geistlinger[3], J. Afonso[1], R. Tullio[3], P. Tizioto[2], J. Petrini[2], L. Coutinho[2], J. Wolf[4], G. Mourão[2], and L. Regitano*[3], [1]*Department of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil;* [2]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil;* [3]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil;* [4]*Department of Biology & Biochesmistry, 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. Novosel[1], V. Brajkovic[1], S. Krebs[2], J. Sölkner[3], D. Salamon[1], S. Ristov[4], S. Triviziaki[5], I. Bizelis[6], M. Ferenčaković[1], S. Rothammer[7], E. Kunz[7], M. Simčič[8], P. Dovč[8], G. Bunevski[9], H. Bytyqi[10], B. Marković1[1], M. Brka[12], K. Kume[13], S. Stojanović[14], V. Nikolov[15], N. Zinovieva[16], M. Cacic[17], I. Curik[1], and I. Medugorac[7], [1]*Faculty of Agriculturae, University of Zagreb, Zagreb, Croatia;* [2]*Laboratory for Functional Genome Analysis, Gene Center, Ludwig Maximilians University Munich, Germany;* [3]*Division of Livestock Sciences, University of Natural Sciences and Life Sciences, Vienna, Austria;* [4]*Ruder Boškovic Institute, Zagreb, Croatia;* [5]*Institute of Animal Genetic Improvement, Thessaloniki, Greece;* [6]*Department of Animal Breeding and Husbandry, Faculty of Animal Science and Aquaculture Agricultural University of Athens, Athens, Greece;* [7]*Chair of Animal Genetics and Husbandry, LMU Munich, Munich, Germany;* [8]*Department of Animal Science, Biotechnical Faculty, University of Ljubljana, Domžale, Slovenia;* [9]*Faculty of Agricultural Sciences and Food, University Ss. Cyril and Methodius, Skopje, Macedonia;* [10]*Department of Animal Science, Faculty of Agriculture and Veterinary, University of Prishtina, Prishtina, Kosovo;* [11]*Department of Livestock Science, Biotechnical Faculty, University of Montenegro, Podgorica, Montenegro;* [12]*Institute of Animal Sciences, Faculty of Agriculture, University of Sarajevo, Sarajevo, Bosnia and Herzegovina;* [13]*ALBAGENE Association, Tirana, Albania;* [14]*Ministry of Agriculture and Environmental Protection, Beograd, Serbia;* [15]*Executive Agency for selection and reproduction in Animal Breeding, Sofia, Bulgaria;* [16]*Center of Biotechnology and Molecular Diagnostics of the L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation;* [17]*Croatian 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. Schenkel[1], V. Kroezen[1], A. Fleming[1], M. Sargolzaei[1,2], C. Baes[1], J. Squires[1], and F. Miglior[1,3], [1]*Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, Ontario, Canada;* [2]*The Semex Alliance, Guelph, Ontario, Canada;* [3]*Canadian Dairy Network, Guelph, Ontario, Canada.*

MT357 **Association of candidate SNPs with feed efficiency in Israeli-Holstein lactating cows.**
M. Cohen-Zinder*[1], J. Miron[2], Y. Ben-Meir[2], E. Lipkin[3], and A. Shabtay[1], [1]*Dept. of Ruminant Science, Agricultural Research Organization, Newe-Ya'ar Research Center, Ramat Yishay, Israel;* [2]*Dept. of Ruminant Science, Institute of Animal Science, Agricultural Research Organization, Beit Dagan, Israel;* [3]*Dept. of Genetics, Silberman Life Sciences Institute, The Hebrew University of Jerusalem, Jerusalem, Israel.*

MT358 **Production of goat milk lacking an allergenic protein (αs1-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. Rosen[1], O. Hanotte[2], T. Sonstegard[3], and C. Van Tassell[1], [1]*USDA/ARS/AGIL, Beltsville, MD, USA;* [2]*U of Nottingham/School of Life Sciences, Nottingham, UK;* [3]*Acceligen of Recombinetics, St Paul, MN, USA.*

MT362 **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]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*LASIG, EPFL, Lausanne, Switzerland;* [3]*INRA, Castanet-Tolosan, France;* [4]*DIMEVET, University of Milan, Milan, Italy.;* [5]*PTP, Lodi, Italy.*

MT363 **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]*Istituto di Zootecnica, Universitá Cattolica del Sacro Cuore, Piacenza, Italy;* [2]*Recombinetics Inc., St. Paul, Minnesota, USA.*

MT364 **The ruminant biology and evolution revealed by a flock of ruminant *de novo* genomes.**
W. Wang[1], Q. Q. Qiu[1], G. Zhang[3,4], R. Heller[3], H. R. Siegismund[3], 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*.

MT365 **Genotyping by sequencing for genomic selection in dairy goats (*Capra hircus*).**
S. Clarke*[1], K. Dodds[1], R. Brauning[1], T. Van Stijn[1], R. Anderson[1], M. Wheeler[2], B. Foote[3], A. Cameron[4], and J. McEwan[1], [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*.

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 diarrhea virus in F_2 and F_3 Nellore-Angus halfblood steers.**
K. M. Sarlo Davila*[1], A. D. Herring[1], J. E. Sawyer[1], J. F. Ridpath[2,3], and C. A. Gill[1], [1]*Texas A&M University, College Station, TX, USA;* [2]*National Animal Disease Center, Ames, IA, USA;* [3]*Ridpath 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. Durkin[1], M. Artesi[1], L. Karim[1,3], N. Cambisano[1,3], M. Deckers[1,3], N. Tamma[1,3], E. Mullaart[4], W. Coppieters[1,3], M. Georges[1], 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*.

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. Mayes[1], J. Williams[1], E. Fritz-Waters[1], E. Downey[2], R. Tait[3], A. Woolums[4], C. Chase[5], J. Ridpath[6], and J. Reecy[1], [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*.

MT371 **Sheep parchment as a genetic resource.**
M. Teasdale*, *Trinity College Dublin, Dublin, Ireland*.

MT372 **SheepGenomesDB: Towards 1000 Genomes.**
S. McWilliam*[1], R. Brauning[2], S. Clarke[2], A. McCulloch[2], N. Cockett[3], G. Saunders[4], M. N. Sanchez[1], H. Daetwyler[5,6], and J. Kijas[1], [1]*CSIRO, St Lucia, QLD, Australia;* [2]*AgResearch Ltd, Invermay Mosgiel, New Zealand;* [3]*Utah State University, Logan, UT, USA;* [4]*EMBL-EBI, Cambridge, UK;* [5]*Department of Economic Development, Jobs, Transport and Resources, Bundoora, VIC, Australia;* [6]*La Trobe University, Bundoora, VIC, Australia*.

MT373 **The water buffalo gene expression atlas.**
R. Young*[1], L. Lefevre[1], S. Bush[1], J. Williams[2], S. Gokhale[3], S. Kumar[4], A. Archibald[1], and D. Hume[1], [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*.

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. Marelli[1], A. Picchi[1], F. Danelli[1], J. Riva[2], E. Moretti[2], A. Talenti[1], G. Gandini[1], G. Pagnacco[1], M. Polli[1], and P. Crepaldi[1], [1]*Department of Veterinary Medicine, University of Milan, Milan, Lombardy, Italy;* [2]*Vetogene - 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. Radko[1], W. Nizanski[2], J. Kochan[3], A. Nowak[3], and M. Bugno-Poniewierska[1], [1]*National Research Institute of Animal Production, Department of Animal Genomics and Molecular Biology, Balice, Cracow, Poland;* [2]*Wroclaw University of Environmental and Life Sciences, Faculty of Veterinary Medicine, Department of Reproduction and Clinic of Farm Animals, Wroclaw, Poland;* [3]*University 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. Dreger[2], F. Danelli[1], S. Frattini[1], B. Coizet[1], S. P. Marelli[1], G. Pagnacco[1], G. Gandini[1], M. Polli[1], R. Caniglia[3], M. Galaverni[3], E. A. Ostrander[2], and P. Crepaldi[1], [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*.

WT6 **Can-ID: The genetic Identification system for Canine samples based on SNPs.**
O. Ramírez*[1], A. Cuscó[1], A. Sánchez[2], O. Francino[2], and L. Altet[1], [1]*Vetgenomics, Barcelona, Spain;* [2]*Molecular Genetics Veterinary Service (SVGM), 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. Mohsin[2], A. N. Khosa[1], N. Bangulzai[1], and I. B. Marghazani[1], [1]*Lasbela University of Agriculture, Water and Marine sciences, UThal, Balochistan, Pakistan;* [2]*Livestock 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-Sunesson[1], E. Jonas[1], S. Mikko[1], and A. Johansson[1], [1]*Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine and Animal Science, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [2]*UFR 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. Wang[1], R. Di[1], Q.-Y. Liu[1], W.-P. Hu[1], X.-Y. He[1], X.-H. Cao[1], and M.-X. Chu[1], [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. Arranz[1], A. Suarez-Vega[1], M. Martínez-Valladares[2,3], and B. Gutiérrez-Gil[1], [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. Oliveira[2], M. R. Mousel[1,4], M. V. Gonzalez[2,5], M. A. Highland[1], J. B. Taylor[6], 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. Serrano[2], A. Martinez-Royo[1], B. Lahoz[1], P. Sarto[1], A. Ibañez-Deler[1], J. Folch[1], and J. L. Alabart[1], [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. Molaee, 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. Sebastiani[1], M. Torricelli[1], M. Ciullo[1], G. Vaccari[2], E. Lasagna[3], F. Sarti[3], S. Ceccobelli[3], N. D'Avino[1], M. Paniccià[1], 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. Eshghabadi[1], A. A. Masoudi*[1], H. Emrani[2], and S. Amirina[2], [1]*Tarbiat Modares University, Tehran, Tehran, Iran;* [2]*Animal Sciene Research Institute, Tehran, Tehran, Iran.*

WT21 **Detecting selection footprints from production system-driven genomic divergence of South African sheep breeds.**
E. Dzomba*[1], M. Snyman[2], M. Chimonyo[1], and F. Muchadeyi[3], [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. Borkova[2], A. Svitakova[1], J. Kyselova[1], and T. Kott[1], [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. Latifah[1], D. A. Priyadi[1], K. Kustantinah[2], 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. Slate[1], J. Pemberton[2], C. Berenos[2], J. Pilkington[2], and S. Johnson[2], [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. Chitneedi[1], A. Suarez-Vega[1], P. Wiener[2], C. Esteban-Blanco[1], and J. J. Arranz[1], [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. Pena[1], C. Huau[1], D. Marcon[2], Y. Bourdillon[2], and D. Allain[1], [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. Mirkena[3], G. Duguma[2], S. Gizaw[2], M. Wurzinger[4], J. Solkner[4], O. Mwai[2], T. Dessie[2], A. Abebe[6], M. Mamiru[8], T. Tadesse[7], R. N. B. Lobo[5], and B. Rischkowsky[1], [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. Yang[1], N. Gorkhali[1], Y. Ma[1], 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. 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]*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. Crouse[1], R. A. Cushman[2], K. J. McLean[3], C. R. Dahlen[1], P. P. Borowicz[1], L. P. Reynolds[1], and J. S. Caton[1], [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-Contreras[2], R. Benítez[2], Y. Nuñez[2], A. Fernández[2], A. Gónzalez-Bulnes[2], B. Isabel[1], and C. Óvilo[2], [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], [1]*Key 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;* [2]*The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China;* [3]*Department of Biostatistics, University of Michigan, Ann Arbor, MI, USA;* [4]*Center for Statistical Genetics, University of Michigan, Ann Arbor, MI, USA*.

WT37 **Characterization of perirenal fat transcriptome from suckling lambs.**
A. Suárez-Vega*[1], J. Arranz[1], J. Mateo[2], and B. Gutiérrez-Gil[1], [1]*Department of Animal Production, Faculty of Veterinary Sciences, University of León, León, Castilla y León, Spain;* [2]*Department 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 Consortium[2], [1]*Royal Veterinary College, London, UK;* [2]*Names 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. McQuillan[1], E. Finlay[1], C. O'Farrelly[3], S. Fair[4], and K. G. Meade[1], [1]*Animal & Bioscience Research Department, Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co Meath, Ireland;* [2]*Vet sciences centre, School of agriculture, UCD, Dublin, Ireland;* [3]*Comparative Immunology Group, School of Biochemistry and Immunology, Trinity Biomedical Sciences Institute, Trinity College Dublin, Dublin, Ireland;* [4]*Laboratory 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. Ortillés[2], A. de Torre[2], M. E. Lebrero[2], P. Zaragoza[1], and C. Rodellar[1], [1]*LAGENBIO, Departamento de Anatomía, Embriología y Genética Animal, Facultad de Veterinaria, Universidad de Zaragoza, Zaragoza, Spain;* [2]*Departamento 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-Contreras[1], O. Madsen[2], M. Vázquez-Gómez[3], S. Astiz[1], R. Benítez[1], Y. Núñez[1], A. Rey[3], B. Isabel[3], M. Groenen[2], A. González-Bulnes[1], and C. Óvilo*[1], [1]*INIA, Madrid, Spain;* [2]*WUR, Wageningen, Netherlands;* [3]*UCM, 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. Voillet[1], Y. Lippi[2], N. Iannuccelli[1], C. Lascor[1], Y. Billon[3], M. San Cristobal[1], and L. Canario[1], [1]*GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France;* [2]*Toxalim (Research Centre in Food Toxicology), Université de Toulouse, INRA, ENVT, INP-Purpan, UPS, Toulouse, France;* [3]*INRA 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. Flach[3], E. Ashley[1], R. Shave[4], and A. Boswood[2], [1]*Stanford University, Stanford, CA, USA;* [2]*Royal Veterinary College, London, UK;* [3]*Zoological Society London, London, UK;* [4]*Cardiff 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. McLoughlin[1], C. N. Correia[1], N. C. Nalpas[2], D. A. Magee[1], J. A. Browne[1], K. Rue-Albrecht[3], H. M. Vordermeier[4], B. Villarreal-Ramos[4], E. Gormley[5], 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*.

WT48 **Selective genotyping for genome-enabled prediction in mice.**
R. P. Savegnago*[1], S. B. Ramos[2], A. P. Sbardela[1], G. B. Nascimento[1], L. A. Freitas[1], P. A. Bernardes[1], and D. P. Munari[1], [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. Garcia[2], F. Gálvez[3], R. Symonová[4], and A. Kovarík[1], [1]*Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic;* [2]*Institut Botànic de Barcelona (IBB-CSIC-ICUB), Barcelona, Catalonia, Spain;* [3]*Bioscripts - Centro de Investigación y Desarrollo de Recursos Científicos, Sevilla, Andalusia, Spain;* [4]*Research Institute for Limnology, Mondsee, 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-Martínez[1], N. Abendaño[1], J. Asín[2], M. Sistiaga-Poveda[1], R. Reina[3], D. de Andrés[3], L. Luján[2], 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. McLoughlin[1], N. C. Nalpas[2], D. A. Magee[1], J. A. Browne[1], K. Rue-Albrecht[3], H. M. Vordermeier[4], B. Villarreal-Ramos[4], 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. Isabel[2], A. Fernández[1], Y. Núñez[1], E. De Mercado[3], E. Gómez Izquierdo[3], J. García-Casco[1], C. López-Bote[2], and C. Óvilo[1], [1]*INIA, Madrid, Madrid, Spain;* [2]*UCM, Madrid, Madrid, Spain;* [3]*Centro Pruebas Procino Itacyl, Hontalbilla, Segovia, Spain*.

WT54 **Transcription factor binding sites enrichement 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. Mullen[3], T. Hall[1], N. C. Nalpas[4], I. W. Richardson[5], D. A. Magee[1], C. N. Correia[1], J. A. Browne[1], D. P. Berry[6], D. Bradley[7], V. Naranbhai[8], A. Hill[8], E. Gormley[9], 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. Liron[1], M. Fernández*[2], A. Prando[3], A. Baldo[3], and G. Giovambattista[2], [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. Ross[1], C. Kern[1], P. Saelao[1], Y. Wang[1], M. Halstead[1], K. Chanthavixay[1], I. Korf[1], M. Delany[1], H. Cheng[2], J. Medrano[1], A. Van Eenennaam[1], C. Tuggle[3], and C. Ernst[4], [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. Zhao[1], S. Hendrick[2], and L. Guan*[1], [1]*Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada;* [2]*Coaldale Veterinary Clinic, Lethbridge, Canada*.

WT61 **The reconstruction and evolutionary history of eutherian chromosomes.**
J. Kim[1], M. Farre[2], L. Auvil[3], B. Capitanu[3], J. Ma[4], H. A. Lewin[5], 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*.

WT62 **iTRAQ-based proteomic analysis reveals key proteins affecting muscle growth and lipid deposition in pig.**
Z. Wang*[1], P. Shang[1,2], Q. Li[3], L. Wang[1], H. Zhang[1], and C. Wu[1], [1]*China Agricultural University, Beijing, China;* [2]*Tibet Agriculture and Animal Husbandry University, Linzhi, China;* [3]*Anhui Academy of Agricultural Sciences, Hefei, China*.

WT63 **Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhancers.**
A. Massa*[1], M. Mousel[2,1], B. Murdoch[3], 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*.

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. Ning[1], Y. Yu[1], L. Jiang[1], Y. Dong[2], P. Zhao[1], H. Wang[3], and J. Liu[1], [1]*China Agricultural University, Beijing, China;* [2]*Haian County Agricultural Commission, Nantong, Jiangsu, China;* [3]*Yang 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. Harrison[1], L. Eory[2], R. Kuo[2], G. Cochrane[1], A. Archibald[2], D. Zerbino[1], and P. Flicek[1], [1]*European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK;* [2]*The Roslin institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edniburgh, UK*.

WT67 **Identification and characterization of miRNAs for milk protein in Chinese Holstein cows.**
W. Cai*, 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 F_2 Nellore-Angus cattle demonstrates multilocus influences.**
K. Scienski*, 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-AgENCODE"].**
K. Muret*[1], S. Djebali[2], T. Derrien[3], C. Cabau[2], C. Klopp[4], D. Esquerré[2,5], K. Munyard[6], G. Tosser-Klopp[2], H. Acloque[2], E. Giuffra[7], S. Foissac[2], and S. Lagarrigue[1], [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*.

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. Jehangir[1], A. Cardoso[1], G. T. Valente[2], and C. Martins[1], [1]*Department of Morphology, Institute of Biosciences, UNESP, São Paulo State University, Botucatu, SP, Brazil;* [2]*Bioprocess 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. Yáñez[2], S. Queiroz[1], J. Lhorente[3], and R. Caralheiro[1], [1]*School of Agricultural and Veterinarian Sciences, São Paulo State University (Unesp), Jaboticabal, São Paulo, Brazil;* [2]*Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile;* [3]*Aquainnovo S.A, Puerto Montt, Chile.*

WT73 **Predictive sexing of African catfish based on body and morphometric measurements using statistical discriminant methods.**
O. T. Abanikannda[1], L. A. Awosanya[1], A. O. Giwa[1], O. N. Ottun[2], K. Z. Awusinu[1], and F. H. Abanikannda*[2], [1]*Lagos State University, Ojo, Lagos, Nigeria;* [2]*University of Lagos, Akoka, Lagos, Nigeria.*

WT74 **Genome sequencing of Tasmanian Atlantic salmon used to characterize multiple sex determination loci.**
S. McWilliam*[1], M. N. Sanchez[1], B. Evans[2], H. King[3], P. Kube[3], K. Verbyla[4], M. Menzies[1], and J. Kijas[1], [1]*CSIRO, St Lucia, QLD, Australia;* [2]*SALTAS, Hobart, TAS, Australia;* [3]*CSIRO, Hobart, TAS, Australia;* [4]*Data61, Canberra, ACT, Australia.*

WT75 **Prediction of the genetic sex in *Seriola lalandi lalandi* using whole-genome sequencing.**
V. Martinez*[1], P. Dettleff[1], S. Escobar[1], and P. Zamorano[2], [1]*FAVET-INBIOGEN, Faculty of Veterinary Science, University of Chile, Santiago, Chile;* [2]*University 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. Fernández[1], J. Fernández[1], M. Toro[2], P. Martínez[3], A. Millán[4], M. Hermida[3], A. Blanco[3], S. Cabaleiro[5], A. Doeschl-Wilson[6], and B. Villanueva[1], [1]*Departamento de Mejora Genética Animal, INIA, Madrid, Spain;* [2]*Departamento de Producción Agraria, ETS Ingenieros Agrónomos, Madrid, Spain;* [3]*Departamento de Xenética, Facultade de Veterinaria, Universidade de Santiago de Compostela, Lugo, Spain;* [4]*Geneaqua SL, Lugo, Spain;* [5]*CETGA, Cluster de Acuicultura de Galicia, Aguiño-Ribeira, Spain;* [6]*Division 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. Henryon[2], [1]*SalmoBreed AS, Bergen, Norway;* [2]*Seges, 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. Cichero[2], and V. Martinez[1], [1]*FAVET-INBIOGEN-Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile;* [2]*Blue 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. Verleih[1], and A. Rebl[1], [1]*Leibniz Institute for Farm Animal Biology, Inst. f. Genome Biology, Dummerstorf, Germany;* [2]*University 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. Rothschild[1], and L. Fontanesi[2], [1]*Department of Animal Science, Iowa State University, Ames, IA, USA;* [2]*Department of Agricultural and Food Sciences, Division of Animal Sciences, University of Bologna, Bologna, Italy;* [3]*Biocomputing 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. Mohamed[1], S. McWilliam[1], B. Evans[2], H. King[3], P. Kube[3], and K. Verbyla[4], [1]*CSIRO, Brisbane, Queensland, Australia;* [2]*SALTAS, Hobart, Tasmania, Australia;* [3]*CSIRO, Hobart, Tasmania, Australia;* [4]*Data61, Canberra, ACT, Australia.*

WT86 **Reconstructing the complex structure of the sex determination locus in Atlantic herring using SMRT sequencing.**
N. Rafati*[1], C.-J. Rubin[1], C. Feng[1], M. Petterson[1], A. Bario Martinez[2], S. Lamichhaney[1], I. Bunikis[3], and L. Andersson[1,5], [1]*Science for Life Laboratory, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden;* [2]*Science for Life Laboratory, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden;* [3]*Science for Life Laboratory, National Genomics Infrastructure, Uppsala University, Uppsala, Sweden;* [4]*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden;* [5]*Department 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. Mwacharo[3], H. Bahbahani[4], S. Mastrangelo[5], F. Pilla[6], E. Ciani[7], and O. Hanotte[1], [1]*School of Life Sciences, University of Nottingham, Nottingham, Nottinghamshire, UK;* [2]*Department of Zoology, Faculty of Sciences, Misurata University, Misurata, Libya;* [3]*Small Ruminant Genetics and Genomics Group, International Center for Agricultural Research in the Dry Areas (ICARDA), Addis Ababa, Ethiopia;* [4]*Department of Biological Sciences, Faculty of Science, Kuwait University, Safat, Kuwait;* [5]*Dipartimento di Scienze Agrarie e Forestali, University of Palermo, Palermo, Italy;* [6]*Dipartimento Agricoltura, Ambiente e Alimenti, Università degli Studi del Molise, Campobasso, Italy;* [7]*Dipartimento 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. Upadhyay[1], R. Mukiibi[2], E. Kanis[1], and R. Crooijmans[1], [1]*Wageningen University and Research Animal Breeding and Genomics, Wageningen, the Netherlands;* [2]*Department of Agriculture, Food and Nutritional Sciences (AFNS), Faculty of Agriculture, Life and Environmental Sciences University of Alberta, Alberta, Canada;* [3]*National Agricultural Research Organization (NARO), Entebbe, Uganda*.

WT89 **Genome-wide association study of growth traits in Nellore cattle.**
R. B. Costa*[1], A. P. N. Terakado[2], G. M. F. Camargo[1], R. Carvalheiro[2], and L. G. Albuquerque[2], [1]*Federal University of Bahia, Salvador, BA, Brazil;* [2]*Sao 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. Flores[2], C. Gondro[3], and J. H. van der Werf[3], [1]*Philippine Carabao Center-University of the Philippines College, Laguna Philippines;* [2]*Philippine Carabao Center National Headquarters, Muñoz, Nueva Ecija, Philippines;* [3]*School 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. Muchadeyi[2], [1]*University of Pretoria, Pretoria, Gauteng, South Africa;* [2]*Biotechnology 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. Dzomba[2], K. Mdladla[1,2], P. Soma[3], and F. Muchadeyi[1], [1]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, South Africa;* [2]*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa;* [3]*Agricultural Research Council, Animal Production Institute, Irene, South Africa*.

WT93 **Genetic characterization of Argentine and Bolivian creole cattle using HD SNPs microarray.**
M. Fernandez[1], M. Ortega Masague[2], J. Orellana[3], F. Valdez[4], S. Peña[5], A. Rogberg Muñoz[1,6], L. Gutierrez[2], M. Baudoin[5], D. M. Posik[1], E. E. Villegas Castagnasso[1], I. P. Manrique Osinaga[3], F. D. Holgado[2], J. P. Lirón[7], D. E. Goszczynski[1], P. P. García[1], C. Bomblat[5], E. Salas[4], J. A. Pereira Rico[3], and G. Giovambattista[*1], [1]*Instituto de Genética Veterinaria (IGEVET), CCT La Plata CONICET - Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata, La Plata, Buenos Aires, Argentina;* [2]*Instituto de Investigación Animal del Chaco Semiárido (IIACS – INTA Leales), Leales, Tucumán, Argentina;* [3]*Facultad de Ciencias Veterinarias, Universidad Autónoma Gabriel René Moreno, Santa Cruz de la Sierra, Santa Cruz, Bolivia;* [4]*Centro de Investigación Agrícola Tropical (CIAT), Santa Cruz de la Sierra, Santa Cruz, Bolivia;* [5]*CEASIP, Fundación Simón I Patiño, Santa Cruz de la Sierra, Santa Cruz, Bolivia;* [6]*Departamento de Producción, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina; INPA–Unidad Ejecutora UBA CONICET de Investigaciones en Producción Animal, CABA, Argentina;* [7]*Center 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. Grobler[1], K. Ehlers[1], K. Ncube[3], F. C. Muchadeyi[3], and N. O. Mapholi[2], [1]*University of Free State, Department of Genetics, Bloemfontein, Free State, South Africa;* [2]*Agricultural Research Council-Animal Production Institute, Irene-Pretoria, Gauteng, South Africa;* [3]*Agricultural 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], [1]*The University of Nottingham, Nottingham, Nottinghamshire, UK;* [2]*International 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. Missohou[1], K. Marshal[2], S. F. Tebug[2], J. Juga[4], and M. Tapio*[5], [1]*Interstate School of Veterinary Science and Medicine of Dakar, Dakar, Senegal;* [2]*International Livestock Research Institute, Nairobi, Kenya;* [3]*University of Ngaoundere, Ngaoundere, Cameroon;* [4]*University of Helsinki, Helsinki, Finland;* [5]*Natural 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. Kim[3], R. Mrode[2], B. Salim[5], N. Oyekanmi[4], H. Kim[3], and O. Hanotte[1,2], [1]*School of life Sciences, University of Nottingham, Nottingham, United Kingdom;* [2]*International Livestock Research institute (ILRI), Nairobi, Kenya;* [3]*C&K genomics, Seoul National University Research Park, Seoul, South Korea;* [4]*National Biotechnology Development Agency, Lugbe, Abuja, Nigeria;* [5]*Department 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. Campos[2], C. C. Gulias-Gomes[1], B. P. Sollero[1], and A. R. Caetano[3], [1]*Embrapa Pecuária Sul, Bagé, RS, Brazil;* [2]*Universidade Federal de Pelotas, Pelotas, RS, Brazil;* [3]*Embrapa 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. Huson[3], M. Wurzinger[1], J. Burgstaller[4], S. Gizaw[5], A. Haile[6], B. Rischkowsky[6], G. Brem[4], S. A. Boison[1], G. Mészáros[1], A. O. Mwai[7], 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*.

WT101 **Matching breeds to production clusters using high-density SNP arrays: The case of East Africa.**
F. D. N. Mujibi*[1], E. K. Cheruiyot[2], T. Dusingizimana[3], M. Chagunda[4], J. Ojango[5], 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, UK;* [5]*International Livestock Research Institute, Nairobi, Kenya*.

WT102 **Genomic selection based on current status in developing countries.**
R. Mrode*[1], J. Ojango[1], O. Mwai[1], and J. M. Mwacharo[2], [1]*Animal Biosciences, International Livestock Research Institute, Nairobi, Kenya;* [2]*Small 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. Holl[2], D. Miller[3], S. Abdalla[4], B. Shykind[4], J. Malek[4], Y. Mohamoud[4], K. Pasha[5], A. Khalili[5], D. F. Antczak[3], and S. Brooks[1], [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*.

WT105 **Delineating Indian native cattle specific allelic variants and haplotypes in lactoferrin gene: A potential candidate for disease resistance.**
A. Sharma*[1,2], M. Sodhi[2], P. Jain[1], M. Kumar[2], and M. Mukesh[2], [1]*University Institute of Engineering & Technology, Kurukshetra, Haryana, India;* [2]*National Bureau of Animal Genetics Resources, Karnal, Haryana, India*.

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Author Index

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