

Conference Program

August 20 (Sunday)

August 20 (Sunday) at Room X

Plenary Session 1: Biodiversity research: understanding the past, designing the future.

Chair: Henner Simianer, *Inst. Animal Breeding & Genetics, Germany*

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| 10:00-12:00 | <ul style="list-style-type: none">▪ The value of diversity rational concepts on how to assess diversity and develop global strategies to maintain it - <i>Martin Weitzman, Department of Economics, Harvard University, USA</i>▪ The history of the molecular diversity of livestock genetic resources: overview of our current knowledge - <i>Olivier Hanotte, International Livestock Research Institute, Kenya.</i>▪ Conservation genetics in a megadiversity country – <i>Fabrcio R. Santos, Universidade Federal de Minas Gerais, Brazil.</i> |
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10:00-15:30 Poster mounting (all sessions)

12:00-13:30 Lunch Time

15:30-16:15 Coffee break

15:30-18:15 Poster exhibition

18:15-19:45 Welcome reception

August 20 (Sunday) at Room X

Workshop 1: Pig Gene Mapping and Applied Genetics.

Chair: Gary Rohrer, *USDA-MARC, Clay Center, NE, USA*

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| 13:30-15:30 | Session 1: Status of Pig Genomic Research |
| Coffee break | <ul style="list-style-type: none">▪ Welcome [5'] |
| 16:15-18:15 | <ul style="list-style-type: none">▪ Overview of Pig QTL and Identification of QTN [25']▪ An integrated RH map of the porcine genome with more than 5000 anchoring points on the human genome provides a framework for the sequencing of the pig - <i>Denis Milan, INRA/Laboratoire de Génétique Cellulaire, France</i> [20'/25' – abstr 520]▪ Construction of pig gene catalog: determination and application of porcine full-length cDNA sequences - <i>Hirohide Uenishi, National Institute of Agrobiological Sciences, Japan</i> [20'/25' – abstr 283]▪ Genetics of porcine Geneexpression - <i>Christian Bendixen, Danish Institute of Agricultural Sciences, Denmark</i> [20'/25' – abstr 444]▪ Sequencing the Pig Genome using a BAC by BAC approach - <i>Sean Humphray, The Wellcome Trust Sanger Institute, UK</i> [20'/25' – abstr 404] |
| | Session 2: Highlights of Posters |
| | <ul style="list-style-type: none">▪ Improved annotation of the porcine Affymetrix GeneChip(R) and functional comparison to QIAGEN-NRSP8 oligonucleotide array data - <i>Oliver Couture, Iowa State University, Ames, USA</i> [12'/15' – abstr 246]▪ Microsatellite and chromosome Y sequence analysis of wild boar and autochthonous pig breeds from Asia, Europe, South America and Africa - <i>Oscar Ramirez, Universitat Autònoma de Barcelona, Spain</i> [12'/15' – abstr 320]▪ QTL scan for physiological variables related to vitality in newborn piglets - <i>Anna Tomas, UAB, Spain</i> [12'/15' – abstr 347]▪ Characterization of the aldo-keto reductase 1C gene cluster on pig chromosome 10 and association with age of puberty and ovulation rate - <i>Dan Nonneman, USDA/ARS/US Meat Animal Research Center, Clay Center, USA</i> [12'/15' – abstr 277]▪ Confirmation of QTL for the inverted teat defect in porcine dam lines - <i>Klaus Wimmers, Research Institute for the Biology of Farm Animals (FBN Germany)</i> [12'/15' – abstr 299]▪ Refined linkage mapping of the Escherichia coli F4ac receptor gene on pig chromosome 13 - <i>David Joller, Institute of Animal Sciences, Switzerland</i> [12'/15' – abstr 512]▪ Business meeting and election of new committee [30'] |

August 20 (Sunday) at Room X

Workshop 2: Applied Genetics Committee of Companion Animals

Chair: *Hein van Haeringen, Dr. Van Haeringen Laboratorium B.V, Wageningen, The Netherlands*

13:30-15:30	<ul style="list-style-type: none">▪ Welcome▪ Comparison test: Comments from Duty Laboratory South Africa; Comments from Computing Laboratory The Netherlands; Discussion▪ ISAG panels: Do they work well? How many laboratories are using these panels in the routine? Do we need changes? Standard / Reference samples?▪ Nomenclature: Is there a need to change or do we continue?▪ Next Comparison test: Do we need another one? If so, when? Duty laboratory; Computing laboratory▪ Cat Phenotypic and Health Information Registry (PHIR): Presentation by Leslie Lyons▪ Elections: Hein van Haeringen will step down; Matthew Binns and Andrea Rosati have changed their position▪ Any other business▪ Closing remarks
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August 20 (Sunday) at Room X

Workshop 3: Equine Genetics and Parentage Testing Standardization

Chair: *E. Gus Cothran, Texas A & M University, College Station, TX, USA*

16:15-18:15	<ul style="list-style-type: none">▪ Introduction.▪ Horse Comparison Discussion▪ Duty Lab Report▪ Analysis Lab Report▪ Discussion of Results▪ Short Presentations (to be announced)▪ Election of Committee▪ Other Business▪ Close ▪ Diversity and performance of a standard set of 17 microsatellites for paternity testing in Brazilian Crioulo, Campolina and Thoroughbred horses - <i>Dario Grattapaglia, Genomax/ Heréditas Tecnologia em Análise de DNA, Brasília, DF, Brazil</i> [10' – abstr 352]▪ Equine Genotyping: Minimizing the risk of parentage errors - <i>Wim A van Haeringen, Dr. Van Haeringen Laboratorium BV, Wageningen, The Netherlands</i> [10' – abstr 375]▪ Development of mutagenically-separated PCR assays for equine genetic screening - <i>Ann E.O. Trezise, Australian Equine Genetics Research Centre & School of Biomedical Sciences, University of Queensland, Australia</i> [10' – abstr 377]▪ Molecular and evolutionary study of genetic variability in Equids DRA gene - <i>Silvina Díaz CIGEB, Facultad Ciencias Veterinarias. Universidad Nacional de La Plata. Argentina</i> [10' – abstr 536]
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August 21 (Monday)

August 21 (Monday) at Room X

Workshop 4: Animal Forensic Genetics – Part 1

Chairs: *Wim van Haeringen, Dr. Van Haeringen Laboratorium B.V, Wageningen, The Netherlands and Sree Kanthaswamy, University of California-Davis, USA.*

10:00-12:00	<ul style="list-style-type: none">▪ Resequencing microarray technology for nucleotide sequence analysis of the entire mitochondrial genome - <i>Matthew C Lorence</i>▪ Wildlife DNA forensics in the UK: a partnership approach - <i>Ross McEwing</i>▪ Improved Genomic Typing for Animal Identification and Breed Estimation - <i>Peter Kesners</i>
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12:00-13:30 Lunch Time

15:30-16:15 Coffee break

15:30-19:15 Poster exhibition

August 21 (Monday) at Room X	
Workshop 5: Cattle Molecular Markers and Parentage Testing	
Chair: Marie-Yvonne Boscher, Labogena, France	
16:15-18:15	<ul style="list-style-type: none"> ▪ Welcome Introduction. ▪ Comparison test: Comments from Duty Laboratory; Comments from Computing Laboratory ▪ Discussion of Results : STR and genes, ▪ Next comparison test ▪ Other Business: Advance in the use of SNPs for cattle identification, need for accreditation ▪ Election of Committee ▪ Close

August 21 (Monday) at Room X	
Workshop 6: ISAG-FAO Advisory Group on Animal Genetic Diversity	
Chair: Henner Simianer, Institute of Animal Breeding & Genetics, Germany	
16:15-19:15	<ul style="list-style-type: none"> ▪ Report on activities of FAO and the working group on Animal Genetic Diversity - <i>I. Hoffmann and H. Simianer</i> [20'] ▪ A mitochondrial survey of South American goat breeds reveals the existence of an ancient Canarian genetic signature - <i>Marcel Amills, Universitat Autònoma de Barcelona, Spain</i> [15' – abstr 240] ▪ Genetic variation at 23 STRs loci in five Brazilian populations of Santa Inês hair sheep breed <i>Carla A. Souza, Embrapa Genetic Resources and Biotechnology, Brazil</i> [15' – abstr 467] ▪ Mitochondrial DNA sequences reveal a putative East Asian ancestry for old Chilean chickens - <i>Jose Alcalde, Pontificia Universidad Catolica de Chile, Chile.</i> [15' – abstr 443] ▪ Phylogeography of three stocks of the Amazonian fish Peacock bass (<i>Cichla</i> - Pisces) introduced in Minas Gerais State, southeast Brazil - <i>Daniel Cardoso de Carvalho, Universidade Federal de Minas Gerais, Brasil</i> [15' – abstr 276] <p>Break</p> <ul style="list-style-type: none"> ▪ Microsatellites and Y-chromosomal haplotypes of European and Middle-Eastern cattle, sheep and goats: geographic clines, clusters, male introgression and conflicting views on diversity - <i>J.A. Lenstra, Utrecht University, The Netherlands</i> [15' – abstr380] ▪ Genome-wide SNP analyses of Holstein Friesian cattle reveal new insights into Australian and global population variability - <i>Kyall R. Zenger, The University of Sydney, Australia</i> [15' – abstr 481] ▪ Estimation of genetic distances from two partly overlapping microsatellite marker data sets <i>Helge Taeubert, Trinity College Dublin, Ireland</i> [15' – abstr 238] ▪ Weitzman's approach and the diversity within and between chicken populations - <i>Tamina Pinet, Georg-August-University, Germany</i> [15' – abstr 574] ▪ Accounting for concurrence between breeds in the derivation of conservation priorities based on Weitzman's diversity concept - <i>Henner Simianer, Georg-August-University, Germany</i> [15' – abstr 187]

August 22 (Tuesday)

August 22 (Tuesday) at Room X	
Plenary Session 2: Genomics and biodiversity.	
Chair: Harris A. Lewin, Department of Animal Sciences, University of Illinois, USA.	
10:00-12:00	<ul style="list-style-type: none"> ▪ Evolution Highway: large-scale analysis of vertebrate chromosomal evolution - <i>Denis Larkin, University of Illinois, USA.</i> ▪ Combined technologies of assisted reproduction, cloning and the state-of-the-art of microarray analysis - <i>Jerry Yang, University of Connecticut, USA.</i> ▪ Gene Identification Signature (GIS) analysis: a novel cloning technology using paired-end 5' and 3' tags to characterize mammalian transcriptome and genome – <i>Ruan Yijun, Genome Institute of Singapore, Singapore.</i>

12:00-13:30	Lunch Time
15:30-16:15	Coffee break
15:30-19:15	Poster exhibition

August 22 (Tuesday) at Room X

Workshop 7: Horse Genome Mapping

Chair: *Telhisa Hasegawa, Laboratory of Molecular and Cellular Biology, Equine Research Institute, Japan*

13:30-15:30
Coffee break
16:15-18:15

Session 1: Whole Genome Mapping and Sequencing

- Whole genome linkage maps - *Domenico Bernoco, Professor Emeritus, Dept of Population Health and Reproduction, University of California, USA*
- Integrated map - *Kao Castle, University of Sydney, Australia* [15' – abstr 553]
- Y chromosome BAC contig - *Terje Raudsepp, Texas A & M University, USA* [15' – abstr 410]
- BAC end sequencing - *Tosso Leeb, University of Berne, Switzerland & University of Veterinary Medicine Hannover, Germany* [15' – abstr 233]
- Whole Genome Sequencing - *Ernest Bailey, University of Kentucky, USA* [15' – abstr 551]
- **Discussion**

Session 2: Mapping traits

- QTL mapping for OC - *Catherine Wittwer*
- Whole genome LD analysis - *Teruaki Tozaki, Laboratory of Racing Chemistry, Utsunomiya, Japan* [15' – abstr 37]
- Mapping Grey coat colour – *Gerli Pielberg, Uppsala University, Sweden* [15' – abstr 371]
- Mapping silver coat color - *Sofia Mikko, Swedish University of Agricultural Sciences, Sweden* [15' – abstr 357]
- ECA3 inversion in Tobiano - *Samantha Brooks, University of Kentucky, USA* [15' – abstr 170]
- Brindle color and chimerism - *M. Cecilia T. Penedo, University of California, USA* [15' – abstr 521]
- **Discussion**

August 22 (Tuesday) at Room X

Workshop 8: Poultry Gene Mapping

Chair: *Richard Crooijmans, Wageningen Univ, Anim. Breeding & Genetics Group, The Netherlands*

13:30-15:30
Coffee break
16:15-19:15

Chicken genome (Topics)

- Genome Sequence update - *Richard Crooijmans*
- Use of large scale SNPs (Genetic maps, LD) - *Richard P.M.A. Crooijmans, Wageningen University, The Netherlands* [10' – abstr 389]
- RH-maps - *A. Vignal, INRA Laboratoire de Génétique Cellulaire, France* [10' – abstr 466]
- (Fine) mapping QTLs
 - QTL mapping for resistance - *Marie-Helene Pinard-Van Der Laan, UMR INRA/INA-PG Génétique et Diversité Animales, France* [10' – abstr 465]
 - SNP allele frequencies between lines - *Chris M. Ashwell, North Carolina State University, USA* [10' – abstr 197]
 - Candidate genes of myogenic factors - *Helena J. Alves, Animal Biotechnology Laboratory USP/ESALQ* [10' – abstr 518]
 - Differential expression - *Anna K. Bennett, Iowa State University, Ames, IA USA* [10' – abstr 168]
- Regulation
 - MicroRNAs - *Hongtao Xu, China Agriculture University, China* [10'-abstr 103]
 - MircoRNA prediction- *Shu-Hong Zhao, Huazhong Agricultural University, China* [10' – abstr 434]

MHC (Chair Janet Fulton)

- MHC haplotypes - *Janet E. Fulton, Hy-Line International, USA* [10' – abstr 543]
- Genotyping MHC class-I locus BF1 - *Bertrand Bed'Hom, UMR INRA / INA-PG Génétique et Diversité Animale, France* [10' – abstr 456]
- Genomic analysis of the MHC in turkey – *Lee D. Chaves, University of Minnesota, USA* [10' – abstr 333]
- Quail genome
- Update genetic resources – *Alain Vignal* [10']

Duck genome

- Update genetic resources – *Ning Li* [10']
- Genetic relationships among Chinese ducks - *Ning Yang, China Agricultural University, China.* [10' – abstr 211]

Turkey Genome

- Update genetic resources *Edward Smith* [10']
 - Candidate genes - *Edward J. Smith, Virginia Tech, USA* [10' – abstr 221]

August 22 (Tuesday) at Room X

Workshop 9: Applied Genetics in Sheep and Goats

Chair: *Liliana Di Stasio, Dipartimento di Scienze Zootecniche, Italy*

13:30-15:30	<ul style="list-style-type: none">▪ Comparison test: report from the Duty Laboratory (LABOGENA, France)▪ Discussion of results▪ Poster presentation▪ Election of Committee▪ Any other business▪ Close▪ Novel Y Chromosomal Haplotypes Reveal Wild and Domestic Sheep Diversity - <i>Jennifer R. S. Meadows, CSIRO Livestock Industries, Australia</i> [15' – abstr 70]▪ Enhanced mapping tools for the sheep genome – BACs, SNPs and the virtual map - <i>Jillian F. Maddox, University of Melbourne, Australia</i> [15' – abstr 507]
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August 23 (Wednesday)

09:00-12:00	Conference tour
09:00-15:30	Poster exhibition
12:15-13:30	Lunch Time
13:30-15:30	Poster viewing
15:30-16:15	Coffee break
15:30-18:15	Poster removing

August 23 (Wednesday) at Room X

Workshop 10: Comparative Genomics

Chair: *Christopher Tuggle, Department of Animal Science, Iowa State University, USA*

16:15-19:15	<ul style="list-style-type: none">▪ Combining mouse mammary gene expression and comparative mapping for the identification of candidate genes for QTL of milk production traits in dairy cattle – <i>Ron Micha, Agricultural Research Organization, Israel</i> [30' – abstr 317]▪ A procedure to finemap mouse QTLs using dense SNP data – <i>Gudrun A Brockmann, Humboldt-Universität zu Berlin, Germany</i> [15' – abstr 402]▪ Comparative Functional Genomics: Endometrial gene expression profiling during the estrous cycle and early pregnancy of Yorkshire gilts using the Affymetrix porcine GeneChip – <i>Shu-Hong Zhao, Huazhong Agricultural University, China & Department of Animal Science, Iowa State University, USA</i> [15' – abstr 263]▪ Comparative profiles of gene expression of <i>Bubalus bubalis</i> and <i>Bos taurus</i> – <i>Maria Paula Schneider, Universidade Federal do Pará, Brazil</i> [15' – abstr 548] <p>Break</p> <ul style="list-style-type: none">▪ Systematic identification of regulatory elements in cattle - <i>George E. Liu, USDA, ARS, ANRI, Bovine Functional Genomics Laboratory, BARC-East, USA</i> [15' – abstr 448]▪ Evolutionary analyses of housekeeping and tissuespecific genes reveal common selection for economy and specialization – <i>Yiqiang Zhao, China Agricultural University, China</i> [15' – abstr 105]▪ Phylogenetic relationships among wild boar (<i>Sus scrofa</i>) populations in Italy – <i>Longeri et al. Maria Longeri, University of Milan, Italy.</i> [15' – abstr 308]▪ FUGATO - Functional Genome Analysis in Animal Organisms – <i>Kirsten Sanders, Managing office FUGATO, Germany,</i> [30' – abstr 328]▪ Open discussion regarding possible collaborative projects, 2008 Workshop format, new election of Committee members [15']
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August 23 (Wednesday) at Room X

Workshop 11: Comparative MHC: levels of diversity and mechanisms involved in its generation

Chair: Shirley Ellis, Institute for Animal Health, UK

16:15-18:15	<ul style="list-style-type: none">▪ Welcome and introduction – Shirley Ellis, IAH, UK [10’]▪ Update on Immuno Polymorphism Database – Steven Marsh, Anthony Nolan Research Institute, UK [20’]▪ Disease associations with MHC in farm animals – Mike Stear, Glasgow University, UK [20’]▪ What can we learn from examination of MHC diversity in non-human species? Shirley Ellis, IAH, UK [15’]▪ Pig MHC haplotypes – Hirohide Uenishi, STAFF-Institute, Japan [15’]▪ Microsatellite diversity within the SLA region of homozygous and heterozygous samples - Asako Ando, Tokai University School of Medicine, Isehara, Japan [15’ – abstr 229]▪ Polymorphism and gene organization of Bubalus bubalis MHC-DQB show homology to BoLA DQB region - Leonardo Sena, Instituto de Estudos Superiores da Amazônia, Brazil [10’ – abstr 313]▪ Analysis of MHC class II genes in Scottish Blackface sheep - Lisa Murphy, Glasgow University Veterinary School, Scotland, UK [10’ – abstr 321]
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August 23 (Wednesday) at Room X

Oral Presentations of Selected Papers

Chair: Ernest Bailey, University of Kentucky, USA

16:15-18:15	<ul style="list-style-type: none">▪ Alleles of a bovine <i>DGATI</i>-promoter variable number of tandem repeat associated with a milk fat QTL at chromosome 14 can stimulate gene expression - Fürbass R¹, Winter A², Fries R², Kühn C¹. (¹Research Unit Molecular Biology, Research Institute for the Biology of Farm Animals, Dummerstorf, Germany; ²Lehrstuhl für Tierzucht der Technischen Universität München, Freising, Germany). [20’ - abstr. 186]▪ Preliminary results on the genetic background of meat quality differences between two muscles in Avileña Negra-Ibérica calves, using cDNA microarrays - Moreno-Sánchez N¹, Rueda J², Carabaño MJ, González C¹, Wang Y-H³, Reverter A³, Díaz C¹. (¹Departamento de Mejora Genética Animal, INIA (Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria), Madrid, Spain; ²Departamento de Genética, Universidad Complutense, Madrid, Spain; ³CSIRO Livestock Industries and Cooperative Research Centre for Cattle and Beef Quality, Brisbane, Australia). [20’ - abstr. 311]▪ Fine-mapping of a bovine QTL for marbling on BTA 4 using association study - Yokouchi K¹, Mizoguchi Y¹, Iwamoto E², Maruta S³, Ogino A⁴, Watanabe T¹, Takasuga A¹, Sugimoto Y¹. (¹Shirakawa Institute of Animal Genetics, Japan, ²Hyogo Prefectural Institute of Agriculture, Forestry & Fisheries, Japan, ³Nagasaki Prefectural Beef Cattle Improvement Centre, Japan, ⁴Livestock Improvement Association of Japan, Japan). [20’ - abstr. 557]▪ Myosin heavy chain isoform transcript abundance and muscle fiber type distribution of <i>Longissimus Dorsi</i> in high and low performing pigs and in different pig breeds - Ngu NT¹, Jennen DGJ¹, Ponsuksili S², Murani E², Hoelker M¹, Tholen E¹, Juengst H¹, Tesfaye D¹, Schellander K¹, Wimmer K². (¹Institute of Animal Science, Animal Breeding and Husbandry Group, University of Bonn, Endenicher Allee 15, 53115 Bonn; ²Research Institute for the Biology of Farm Animals (FBN), 18196 Dummerstorf, Germany). [20’ - abstr. 272]▪ Transcript profiling of chondrocytes in a porcine impact injury model of osteoarthritis - Ashwell MS¹, O’Nan AT¹, Mente PL². (¹Department of Animal Science, ²Department of Biomedical Engineering, North Carolina State University, Raleigh, NC USA). [20’ - abstr. 198]
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August 24 (Thursday)

August 24 (Thursday) at Room X

Plenary Session 3: The functional genome.

Chair: Luiz Lehmann Coutinho, Department of Animal Science, Universidade de São Paulo, Brazil.

10:00-12:00	<ul style="list-style-type: none">▪ Functions of microRNAs in <i>C. elegans</i> development and human cancer - Eric Miska, Dept. Biochemistry, University of Cambridge, United Kingdom.▪ The population genomics approach: case studies, potentialities, limitations - Gordon Luikart, University Joseph Fourier, Grenoble, France.▪ Physiological genomics Identifying genes for endoparasite resistance - Allan Crawford, AgResearch, New Zealand
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12:00-13:30 Lunch Time

13:30-15:30 ISAG gen business meeting

15:30-16:15 Coffee break

20:00-24:00 Banquet

August 24 (Thursday) at Room X

Workshop 4: Animal Forensic Genetics – Part 2

Chairs: Wim van Haeringen, Dr. Van Haeringen Laboratorium B.V, The Netherlands and Sree Kanthaswamy, University of California-Davis, USA.

16:15-18:15	<ul style="list-style-type: none">▪ An STR Forensic Typing System in the Domestic Cat and Population Genetic Database in 38 Cat Breeds – <i>Marilyn Menotti-Raymond</i>▪ Development of STR assays for identification and forensic testing - <i>Mikko T. Koskinen</i>▪ Round Table Discussion - Recommendations for Animal DNA Forensic and Identity Testing
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August 24 (Thursday) at Room X

Oral Presentations of Selected Papers

Chair: Ernest Bailey, University of Kentucky, USA

16:15-18:15	<ul style="list-style-type: none">▪ Genomic characterization of a defensin gene cluster on ECA 27q17 – <i>Looft C¹, Paul S², Philipp U³, Regenhard P², Kuiper H³, Distl O³, Chowdhary BP⁴, Leeb T⁵</i>. (¹Department of Animal and Veterinary Basic Sciences, The Royal Veterinary and Agricultural University, Denmark; ²Institute of Animal Breeding and Husbandry, Christian-Albrechts-University of Kiel, , Germany; ³Institute of Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Germany; ⁴Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, , USA; ⁵Institute of Genetics, Vetsuisse Faculty, University of Berne, , Switzerland. [20' - abstr. 242]▪ Analysis of novel equine defensins and psoriasin as another antimicrobial peptide - <i>Bruhn O¹, Regenhard P¹, Paul S¹, Groetzinger J², Thaller G¹, Kalm E¹</i>. (¹University of Kiel, Institute of Animal Breeding and Husbandry, Germany; ²University of Kiel, Biochemical Institute, Germany. [20' - abstr.174]▪ mtDNA sequences shows Japanese native chickens have multiple origins - <i>Oka T¹, Ino Y¹, Nomura K¹, Kuwayama T¹, Hanada H¹, Amano T¹, Takada M², Takahata N³, Hayashi Y⁴, Fumihito A⁵</i>. (¹ Tokyo University of Agriculture, Kanagawa, Japan; ² The Research Institute of Evolutionary Biology, Tokyo, Japan; ³ The Graduate University for Advanced Studies, Kanagawa, Japan; ⁴ The University of Tokyo, Tokyo, Japan; ⁵ Yamashina Institute of Ornithology, Chiba, Japan). [20' - abstr.209]▪ Evidence for a separate lineage of the insulin gene in tetrapods and fish - <i>Waldbieser GC, Clay LA, Peterson BC</i>. (USDA, ARS, Catfish Genetics Research Unit, Stoneville, Mississippi, USA). [20' - abstr. 441]▪ An intronic insertion in <i>KPL2</i> results in abnormal gene expression and causes the immotile short tail sperm defect in Finnish Large White - <i>Sironen A¹, Thomsen B², Andersson M³, Ahola V⁴, Vilkki J¹</i>. (¹MTT, Biotechnology and Food Research, Animal Genomics, Jokioinen, Finland; ²Danish Institute of Agricultural Sciences, Department of Genetics and Biotechnology, Tjele, Denmark; ³University of Helsinki, Department of Clinical Veterinary Sciences, Helsinki, Finland). [20' - abstr. 289]
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August 25 (Friday)

August 25 (Friday) at Room X

Workshop 12: Cattle, Sheep and Goat Gene Mapping

Chair: Eduardo Casas, Molecular Genetics Research Unit, US Meat Animal Research Center, ARS-USDA, USA

10:00-12:00 Lunch time 13:30-15:30	<ul style="list-style-type: none">• Welcome and introduction - <i>Eduardo Casas</i>• Development of an ovine 20K SNP chip and its use to construct an ovine HapMap - <i>James Kijas, CSIRO, Australia</i> [30']• Differential gene expression in the muscle of callipyge sheep - <i>Chris Bidwell, Purdue University, USA</i> [15']• A bovine whole genome long oligonucleotide expression array - <i>Chris Elsik, Texas A&M University, USA</i> [15']• Linkage disequilibrium: Why do we care and now what? - <i>Stephanie McKay, University of Alberta, Canada</i> [15']• Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues – <i>Luiz Coutinho, University of Sao Paulo, Brazil</i> [15']• Characterization and validation of in silico developed SNP mapping to three different bovine genomic regions on 15 different cattle breeds - <i>Mathieu Gautier, INRA, France</i>• Validation of molecular markers: the industry's perspective – <i>Brent Woodward, Merial Limited</i> [15']• Business meeting [30']• An overview of the bovine HapMap project - <i>Curt Van Tassell, ARS-USDA, USA</i> [30']• The bovine gene atlas - <i>Tad Sonstegard, ARS-USDA, USA</i> [15']• Genomics approaches to genetic disorders in France : Identification of a doublet mutation responsible for Syndactyly in Holstein cattle and primary localisation of an Hypoplasia syndrome in Montbeliard cattle - <i>André Eggen, INRA, France</i> [15']• Allelic variation in gene expression is correlated with phenotypic variation - <i>Hasan Khatib, University of Wisconsin, USA</i> [15']• Prediction of putative imprinted genes influencing birth weight in the bovine genome- <i>Ikhide Imumorin, Spelman College</i> [15']
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12:00-13:30 Lunch Time

August 25 (Friday) at Room X

Workshop 13: Domestic Animal Genome SequencingChair: *Lawrence Schook*

10:00-12:00	<ul style="list-style-type: none">▪ Introduction and Call to Order - <i>Lawrence B. Schook, University of Illinois, USA</i>▪ Chicken Genome Project – <i>Richard Crooijmans, Wageningen University, The Netherlands</i>▪ Bovine Genome Project - <i>Curt Van Tassell, ARS-USDA, USA</i>▪ Porcine Genome Project - <i>Jane Rogers, The Wellcome Trust Sanger Institute</i>▪ Ovine Genome Project - <i>Noelle Cockett, Utah State University, USA</i>▪ Canine and Equine Genome Projects - <i>Matthew Binns, Royal Veterinary College, University of London, UK</i>▪ Closing Remarks
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August 25 (Friday) at Room X

Workshop 14: Dog Genome MappingChair: *Kathryn Graves, Equine Parentage Testing and Genetic Research Lab, University of Kentucky, USA*

13:30-15:30	<ul style="list-style-type: none">▪ Population structure and complex traits: methods for mapping in the dog genome - <i>Heidi G. Parker.</i>▪ Molecular characterization of the canine RAGE gene <i>Hugo Murua Escobar, University of Veterinary Medicine Hanover, Germany</i> [15' – abstr 415]▪ Two novel mutations in the canine bestrophin gene are associated with autosomal recessive multifocal retinopathy - <i>Karina E. Guziewicz, University of Pennsylvania, USA.</i> [15' – abstr 316]▪ Use of autozygosity mapping in dogs: Mapping the gene for Trapped Neutrophil Syndrome, an immune dysfunction in Border Collies - <i>Alan N. Wilton, University of New South Wales, Australia</i> [15' – abstr 318]
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August 25 (Friday) at Room X

Workshop 15: Immune Response and Disease ResistanceChair: *Herman Raadsma, ReproGen, University of Sydney, Australia*

13:30-15:30	<ul style="list-style-type: none">▪ Quantitative trait loci associated with parasitic infection in a bovine F2 population - <i>Marcos V. G. B. Da Silva, Embrapa Dairy Cattle Research Center, Brazil</i> [10' – abstr 348]▪ Putative QTL for Parasite Resistance in Sheep - <i>Tracy S. Hadfield, Utah State University, USA</i> [10' – abstr 407]▪ Quantitative <i>trait</i> locus affecting susceptibility to mycobacterium paratuberculosis infection identified on BTA 20 in US Holsteins - <i>Michael G. Gonda, University of Wisconsin, USA</i> [10' – abstr 472]▪ Genome scan for QTLs related to tick resistance in bovine - <i>Marco A. Machado, Embrapa Dairy Cattle Research Center, Brazil</i> [10' – abstr 267]▪ Fine mapping of QTL affecting mastitis resistance in Nordic dairy cattle - <i>Mogens S. Lund Danish Institute of Agricultural Sciences & MTT Agrifood Research Finland,</i> [10' – abstr 454]▪ Wide-response variation to <i>Babesia bovis</i> infection can be used to select babesiosis-resistant cattle - <i>Magda V. Benavides, Embrapa Sheep and Cattle Research Centre, Brazil.</i> [10' – abstr 458]▪ Comparative transcriptomic analysis of the immune response in Large White pigs differing by 20 years of selection - <i>Valentina Mariani, INRA CEA, Laboratoire de Radiobiologie et Etude du Génome, France</i> [10' – abstr 345]▪ Gene expression analysis in cattle resistant and susceptible to gastrointestinal nematode infections by real-time RT-PCR <i>Lilian G. Zaros, University of São Paulo/ESALQ, Brazil</i> [10' – abstr 66]▪ Lack of a strong NFkB-dependent transcriptional response during infection with <i>Salmonella enterica</i> serovar Typhimurium as compared to that observed in <i>S. Choleraesuis</i> infection – <i>Chris Tuggle, Iowa State University, USA</i> [10' – abstr 264]▪ Microarray analysis of host gene expression in response to bovine Leukemia Virus Infection <i>Rosane Oliveira, University of Illinois at Urbana-Champaign, USA</i> [10' – abstr 554]▪ Fine mapping of <i>trypanosomosis</i> resistance loci, Tir2 and 3, sequence and expression variation of TLR as candidate genes underlying the QTL - <i>Joseph Nganga, International Livestock Research Institute & Jomo Kenyatta University of Agriculture and Technology, Kenya</i> [10' – abstr 335]
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