

# Plenary Sessions and Workshops

## Program and Time Schedule



## PROGRAM OF PLENARY SESSIONS

### Genomes, function and emerging application

Date: Sunday 20 July 2008  
Chair: Prof. Dr. Bhanu Chowdary  
Co-chair: Prof. Dr. Tosso Leeb

8:45 - 9:25 Keynote speaker. Dr. Vivek Mittal, "RNAi in mammalian systems", CSHL, Cold Spring Harbor, USA.

9:25 - 10:00. Dr. Fiona McCarthy, "GOing from "OMICS" data to biological knowledge in livestock", Department of Basic Sciences, Mississippi State University, USA

10.00 - 10.30 Break

10.30 - 11:05 Dr. George Liu, "Genomic Variations and Functional Elements in the Bovine Genome", USDA Bovine Functional Genomics Laboratory, Beltsville MD, USA

11:05 - 11:40 Dr. Carole Charlier, "Highly effective SNP based association mapping and management of recessive defects in livestock", University of Liège, Liège, Belgium

11:40 - 12:15 Dr. Leif Andersson, "Harvesting time for chicken genomics", Uppsala University, Uppsala, Sweden.

### Genetics of Immune Response

Date: Monday 21 July 2008  
Chair: Prof. Dr. Susan Lamont  
Co-chair: Dr. Inger Edfors

9:00 - 10:00 Keynote speaker. Dr. W. Wiersinga, "Genetics of autoimmune thyroid disease in humans", Dept of Endocrinology and Metabolism, Academic Medical Center, University of Amsterdam, the Netherlands

10:00 - 10:30 Break

10:30 - 11:00 Dr. Chris Tuggle, "Transcriptomic analysis of immune response to Salmonella infection in the pig", Department of Animal Science, Iowa State University, Ames, Iowa USA

11:00 - 11:30 Dr. James Wynn, "Molecular investigation of resistance to amoebic gill disease in Atlantic salmon", CSIRO Marine and Atmospheric Research, Hobart, Tasmania, Australia

11:30 - 12:00 Dr Rebecca Baxter, "Polymorphisms in *DRB3* binding pockets affect immune response to a FMDV peptide in cattle", The Roslin Institute and R(D)SVS, University of Edinburgh



## **Forensics, Legal Aspects and Technical Challenges in Low Copy Number DNA amplification**

Date: Wednesday 23 July 2008

Chair: Dr. Bruce Budowle, Co-chair: Dr. Paolo Garofano

09.00 - 10.00 Keynote speech: Dr. B. Budowle, "Low Copy Number DNA Typing and Considerations for Routine Laboratory Work". Federal Bureau of Investigation, Laboratory Division, Quantico, VA, USA.

10.00 - 10.25 Break

10.25 - 10.55 Dr. Paolo Garofano, "Interlaboratory experiences: From human cancer research to post-pharmacogenetics in animals". Coanan, Rome, Italy.

10.55 - 11.25 Dr. Mikko Koskinen, "High Performance PCR". Finnzymes Diagnostics, Espoo, Finland.

11.25 - 11.35 Yoshiyuki Miyazaki, "The validity of SNP markers for Bovine Parentage Test in Japan". Livestock Improvement Association of Japan inc., Maebashi-city, Japan.

11.35 - 11.45 Alessio Valentini, "Dynamic annotation of DNA sequences in agricultural species". Universita della Tuscia, Viterbo, Italy.

11.45 - 11.55 Baruch Karniol, "Development of a 25-plex SNP assay for traceability in cattle". Bactochem LTD, Ness-zion, Israel

11.55 - 12.05 Dr. Sree Kanthaswamy, "Canine Population Data Generated from a Multi-Plex STR Kit for Use in Forensic Investigation". University of California, Davis, USA.

## **Animal Models for Human Diseases**

Date: Thursday 24 July 2008

Chair: Prof.dr. Herman Raadsma, Co-chair: Prof.dr. Larry Schook

9:00 - 9:50 Keynote speaker. Dr Chand Khanna, "A comparative approach to identify and understand metastasis-associated genes in osteosarcoma". CCR National Cancer Institute, NIH, Rockville, MD, USA.

9.50 - 10.10 Dr Emanuelle Bourneuf, "The pig as a biomedical model for human melanoma", UMR INRA-CEA LREG, Domaine de Vilvert, bat 320, Jouy-en-Josas, France.

10:10 - 10:40 Break

10.40 - 11.20 Prof Larry Schook, "Large animal models for human diseases", University of Illinois, 1203 W. Gregory Drive, Urbana, USA

11.20 - 12.00 Dr Imke Tammen, "Animal models for Neuronal Ceroid Lipofuscinosis (NCL)", Reprogen, Faculty of Veterinary Science, University of Sydney, Camden, Australia

**ISAG2008**



## WORKSHOP PROGRAM

The following workshop program is scheduled:

### Sunday July 20

#### 13.30 -17.30 ISAG-FAO Advisory Group on Animal Genetic Diversity

Chair: Hans Lenstra [J.A.Lenstra@uu.nl](mailto:J.A.Lenstra@uu.nl)

Venue: RAI Auditorium

- 13.30-14.00 Steffen Weigend, Friedrich-Loeffler-Institute, Neustadt, Germany  
Assessment of population structure and genetic diversity in chickens based on molecular markers
- 14.00-14.30 Paolo Ajmone Marsan, Università Cattolica del S. Cuore, Piacenza, Italy  
A global view of livestock biodiversity and conservation
- 14.30-15.00 Tad S. Sonstegard, Agricultural Research Service, Beltsville, MD, USA  
SNP analysis and population structure in cattle breeds
- 15.00-15.30 Ottmar Distl, University of Veterinary Medicine Hannover, Germany  
Genetic diversity in horse breeds
- 15.30-15.45 Break
- 15.45-16.00 Paul Boettcher, FAO-AGAP, Rome, Italy  
The role of the ISAG-FAO Advisory Group in the implementation of the global plan of action for animal genetic resources
- 16.00-16.15 Johannes A. Lenstra, Utrecht University, Utrecht, The Netherlands  
Metaanalysis of microsatellite data allows a molecular classification of European cattle (poster 5041)
- 16.15-16.30 Christoff Knorr, University of Göttingen, Göttingen, Germany  
Admixture analysis of European and Chinese pig breeds (poster 5006)
- 16.30-16.45 Ercan Kurar, Selcuk University, Konya, Turkey  
In vitro conservation and preliminary molecular characterization of some Turkish native domestic animal genetic resources-I (TURKHAYGEN-I) (poster 5025)
- 16.45-17.00 Pam Wiener, Roslin Institute, Roslin, UK  
Patterns of genetic diversity near genes under selection in cattle (poster 5011)
- 17.00-17.15 Miika Tapio, ILRI, Nairobi, Kenya  
Molecular estimation of effective population size – a new perspective for the assessment of risk status of livestock breeds (poster 5027)

#### 13.30 -17.30 Poultry Gene Mapping

Chair: Richard Crooijmans [Richard.Crooijmans@wur.nl](mailto:Richard.Crooijmans@wur.nl)

Venue: RAI Room A

No agenda provided.

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## Sunday July 20 (continued)

### 13.30 -17.30 Satellite workshop: Domestic Animal Epigenetics

Chair: Ikhide Imumorin [iimumorin@spelman.edu](mailto:iimumorin@spelman.edu)

Co-chair: Hasan Khatib [hkhatib@wisc.edu](mailto:hkhatib@wisc.edu)

Venue: RAI Room B

- Chromatin Remodeling in Porcine Embryos  
R.A. Cabot, Purdue University, West Lafayette, USA
- Epigenomic Characterization of Cloned Cattle  
A. Eggen, INRA, France
- The Mouse H19ICR: DNA Methylation and Beyond  
C. Gebert, NIH-NICHD, Bethesda, MD. USA
- Imprinted Genes in Bovine Embryo-Fetal Development  
S. Hiendleder, U of Adelaide, Adelaide, Australia.
- Comparative *In Silico* Analysis of Some Imprinted Regions in Cattle  
I.G. Imumorin, Spelman College, Atlanta, USA.
- Sequence Characteristics of Imprinted Genes in Cattle  
H. Khatib, University of Wisconsin, Madison, USA.
- Epigenetic Regulation of Short Chain Fatty Acids in Ruminants  
C-J. Li, USDA-ARS, Beltsville, MD, USA.
- Epigenetic Case Studies in Agricultural Animals  
G. Liu, USDA-ARS, Beltsville, MD, USA.
- Epigenetic Variation in Cloned Swine  
P. Piedrahita, North Carolina State University, Raleigh, USA.
- Molecular Characterization of M16iX Myostatin in Mouse  
J.M. Reecy, Iowa State University, Ames, USA.
- Interaction of H19 and IGF2 on Carcass Traits in Beef Cattle  
S.M. Schmutz, U of Saskatchewan, Saskatoon, Canada.
- MicroRNA-26a Targets Histone Methyltransferase Enhancer of Zeste homolog 2 during Myogenesis  
R. Tellam, CSIRO Livestock Industries, Australia.

### 13.30 -15.30 Applied Genetics Committee of Companion Animals

Chairs: Leslie Lyons [lalyons@ucdavis.edu](mailto:lalyons@ucdavis.edu)

Cindy Harper [cindy.harper@up.ac.za](mailto:cindy.harper@up.ac.za)

Venue: RAI Room C

No agenda provided.

### 13.30 -16.30 Comparative MHC Steering Committee

Chair: Shirley Ellis [Shirley.ellis@bbsrc.ac.uk](mailto:Shirley.ellis@bbsrc.ac.uk)

Venue: RAI Room D

- Shirley Ellis: Institute for Animal Health, Compton, UK  
Comparative MHC committee: what have we achieved since 2002?
- Steven Marsh: Anthony Nolan Research Institute, London, UK  
IPD-MHC: a database for MHC sequences
- Rebecca Baxter: The Roslin Institute and R(D)SVS University of Edinburgh, UK  
Annotation of the bovine MHC
- Don Miller: Cornell University, Ithaca, USA  
Polymorphism and genomic organisation of the equine MHC class II region

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## Sunday July 20 (continued)

### Comparative MHC Steering Committee (continued)

- Keith Ballingall: Moredun Research Institute, Edinburgh, UK  
Signatures of species hybridisation contributing to MHC diversity in domestic sheep
- Chris Davies: Utah State University, Logan, USA  
The non-classical MHC class I genes of cattle
- Mike Stear: University of Glasgow, UK  
Immunogenetic analysis of nematode infections in sheep
- Joan Lunney: USDA, Beltsville, USA  
Update on SLA genes and their impact on immune and disease interactions

### 15.30 – 17.30 Genetics of Immune Response

Chair: Herman Raadsma [h.raadsma@usyd.edu.au](mailto:h.raadsma@usyd.edu.au)

Venue: RAI Room C

1530 - 1535	Herman Raadsma, introduction to workshop
1535 - 1542	Marcos Vinicius Silva, A whole-genome association study of major determinants for parasitic infection in Angus breed.
1545 - 1552	Guiguigbaza Kossigan, Detection of signature of selection among 14 cattle European and African populations in genomic regions associated to trypanotolerance
1555 - 1602	Nicholas N Jonsson, Selecting cattle for host resistance to tick ( <i>Rhipicephalus microplus</i> ) infestation – natural and human-directed selection.
1605 - 1612	Eduardo Casas, A putative quantitative trait locus on chromosome 20 associated with bovine pathogenic disease Incidence
1615 - 1622	Natasha Ellis, Fine mapping of QTL for parasite resistance in sheep
1625 - 1632	Tracy Hadfield, High-Resolution RH Mapping of a Potential QTL Region on Sheep Chromosome 9 (OAR9)
1635 - 1642	Jens Tetens, Expression of antimicrobial peptides in different localisations of the bovine udder.
1645 - 1652	R.J. Leach, The quantification of genetic components controlling observed variability to immunisation with a peptide derived from Foot and Mouth disease Virus
1655 - 1702	H. Murua Escobar, Establishment of an in vivo model for canine prostate cancer and development of an AAV mediated gene therapeutic approach
1705 - 1712	Yu Gao, The SLA-immune long oligonucleotide set: a new tool for functional studies of immunity and disease resistance in pig
1715 - 1722	S Mashima, Immunological Parameters of the Chicken Lines selected for the response in <i>Graft-versus-host reaction in ovo</i>
1725 - 1732	Chang-Chun Li, Understanding <i>Haemophilus Parasuis</i> Infection in Porcine Spleen Through Transcriptomics Approach
1735 - 1742	Oliver Jann, comparative genomics of Toll-like receptor signalling reveals candidate genes for disease resistance traits
1745 - 1800	Raadsma Herman, Election workshop committee



**Monday July 21 (continued)**

**13.30-15.00 Satellite workshop: Informal Meeting regarding DNA technology in Llama and Alpaca**

Chair: Cecilia Penedo [mctorrespenedo@ucdavis.edu](mailto:mctorrespenedo@ucdavis.edu)  
**Venue: RAI Room C**

No agenda provided.

**15.30-17.30 Comparative Genomics**

Chair: Chris Tuggle [cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)  
**Venue: RAI Auditorium**

- 15.30 – 15.40 Welcome and introduction
- 15.40 – 16.00 Oliver Jann – Comparative genomics of Toll-like receptor signalling
- 16.00 – 16.20 Tomasz Zabek – Phylogeny relationship of GDF5 in mammals
- 16.20 – 16.30 Comparative Genomics Workshop discussion
- 16.30 – 16.50 Shuhong Zhao – Discovery of miRNAs through comparative genomics
- 16.50 – 17.10 Strozzi and Williams – Analysis of non-orthologous genes between genomes
- 17.10 – 17.30 Denis Larkin – Chromosome rearrangements in amniote evolution

**15.30-17.30 Cattle Molecular Markers and Parentage Testing**

Chair: Leanne van de Goor [lgo@vhladmin.nl](mailto:lgo@vhladmin.nl)  
**Venue: RAI Room A**

- Welcome
- Comparison Test 2007-2008
- Next Comparison Test 2009-2010
- Use of SNPs for Parentage Testing or Identification – Brent Woodward, Merial Limited, USA
- Other business
- Election of Committee
- Close

**15.30-17.30 Satellite workshop: Aquaculture Genomics and Genetics**

Chair: Sylvie Quiniou [Sylvie.Quiniou@ARS.USDA.GOV](mailto:Sylvie.Quiniou@ARS.USDA.GOV)  
**Venue: RAI Room B**

- 15:30 - John Benzie, Shrimps genomics today.
- 15:50 - Marlies Rise, The Atlantic Cod Genomics and Broodstock Development Project.
- 16:10 - Pierre Boudry, Recent Advances in the development of genomic resources in *Crassostrea gigas*: towards the sequencing of the Pacific oyster genome.
- 16:30 - Filip Volckaert, Genomic tools for breeding, fisheries and evolutionary biology of European Sea Bass.
- 16:50 - Thomas Moen, QTL for resistance against Infectious Pancreatic Necrosis in Atlantic salmon.
- 17:10 - Mathew Baranski, Use of SNP-chips and selective DNA pooling for identifying disease resistance markers in Atlantic salmon.
- 17:30 - Sylvie Lapegue, Mapping QTL for disease or stress resistance in oysters.



## Monday July 21 (continued)

### 15.30-17.30 Dog Genome Mapping

Chair Kathryn Graves

[ktgraves@email.uky.edu](mailto:ktgraves@email.uky.edu)

Venue: RAI Room C

- Leif Andersson "Genome-wide association analysis - a powerful method for finding genes underlying phenotypic diversity in the dog." 45-60 minute presentation
- Poster Presentations: 15 minutes each plus question time
- - Alan Wilton Poster 2178 Disease Gene Identification in Dogs: Use of SNP arrays and candidate genes
- Barbara Zangerl Poster 2130 CFA9 association study to identify potential modifier loci for progressive rod-cone degeneration (PRCD) in the dog.
- Cord Drögemüller Poster 2193 Positional cloning of the canine hairless mutation reveals an essential role for the FOXI3 gene in ectodermal development

## Tuesday July 22

### 08.30- 12.00 Cattle, Sheep and Goat Gene Mapping

Chair: Eduardo Casas

[Eduardo.Casas@ARS.USDA.GOV](mailto:Eduardo.Casas@ARS.USDA.GOV)

Venue: RAI Auditorium

- Welcome and Business meeting (E. Casas, USDA, ARS, Clay Center, Nebraska, USA).
- The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution (H. Lewin, Institute for Genomic Biology, Urbana, Illinois, USA).
- Dutch Milk Genomics Initiative (A. Schennink, Animal Breeding and Genomics Centre, Wageningen University, The Netherlands).
- Genome wide association study of feed efficiency in beef cattle (L. Sherman, University of Alberta, Alberta, Canada).
- Genomic signatures of artificial selection in US Holstein cows (T. Sonstegard, USDA, ARS, Beltsville, Maryland, USA).
- FecXr, a deletion in the BMP15 locus associated to increased prolificacy in the Rasa Aragonesa (L. Monteagudo, University of Zaragoza, Zaragoza, Spain).
- Gene expression profiles in CNS of naturally scrapie-affected sheep (I. Martin-Burriel, Universidad de Zaragoza, Zaragoza, Spain).
- Using a 1.5K ovine SNP array to expand the sheep linkage map (J. Maddox, University of Melbourne, Victoria, Australia).
- Gene discovery for reproduction rate in tropically adapted Australian beef cattle (R. Hawken, CSIRO St Lucia, Australia).
- Profile of circulating DNA in healthy cattle (J. Beck, Chronix Biomedical GmbH, Goettingen, Germany).
- Functional analysis of the c.1892+19 T>C SNP of the PPARGCIA gene which is associated with variation in milk fat yield (R. Fuerbass, Research Institute for the Biology of Farm Animals, Dummerstorf, Germany).
- Analysis of gene expression in horned and polled tissue from Brahman cattle using Agilent bovine microarray (M. Mariasegaram, CSIRO St. Lucia, Australia).
- Goat mammary expressed genes representative of immunity function during pregnancy before acquisition of its secretory phenotype (F. Faucon, INRA Jouy en Josas, France).





**Tuesday July 22 (continued)**

**08.30- 12.00 Avian Immunogenetics**

Chair: Janet Fulton

[JFulton@hyline.com](mailto:JFulton@hyline.com)

**Venue: RAI Room A**

No agenda provided.

**08.30- 12.00 Animal Forensics**

Chair: Sree Kanthaswamy

[skanthaswamy@ucdavis.edu](mailto:skanthaswamy@ucdavis.edu)

**Venue: RAI Room B**

- Present Guidelines from Budowle et al. 2005
- Forensic and non- forensic testing
- Inter-lab collaboration
- Proficiency tests v. Comparison tests
- Accreditation/Certification
- Databases
- Nominate new standing committee members
- Other business

**08.30- 12.00 Meeting of the Editorial Board of Animal Genetics**

Moderator: The Editor [Chris.Moran@vetsci.usyd.edu.au](mailto:Chris.Moran@vetsci.usyd.edu.au)

**Venue: RAI Room C**

No agenda provided.

**15.30 – 17.30 Applied Genetics in Sheep and Goats**

Chair: Jill Maddox

[Jillm@rubens.its.unimelb.edu.au](mailto:Jillm@rubens.its.unimelb.edu.au)

**Venue: RAI Room B**

15:30 Sandy Sgorlon, poster 2208: Nutrigenomics studies in sheep using a custom microarray platform

15:45 Amparo Martínez Martínez, poster 2231: Genetic relationships between native goat populations from Spain, Portugal and America

16:00 José Antonio Bouzada Rey, poster 2152: High exclusion probability in ovine genealogical control through 18plex and 20plex PCR

16:15 Jill Maddox on behalf of Mike Heaton and the ISGC "Update on developing sheep SNP markers for parentage testing from the ovine genome project" and "Update on the Sheep HapMap project"

16:30 Susan Dileanis ISAG 2008 Goat Comparison Test Results

16:50 Jill Maddox ISAG 2008 Sheep Comparison Test Results

17:20 General discussion and election of new committee

17:30 End of session



**Tuesday July 22 (continued)**

**15.30 – 17.30 Equine Genetics and Thoroughbred Parentage Testing**

Chair: Alan Guthrie [alan.guthrie@up.ac.za](mailto:alan.guthrie@up.ac.za)

**Venue: RAI Room A**

No agenda provided.

**15.30 – 17.30 Satellite workshop: Coat Colour Genetics**

Chair: Sheila Schmutz [Sheila.schmutz@usask.ca](mailto:Sheila.schmutz@usask.ca)

**Venue: RAI Auditorium**

- 13:30 White patterns in Horse and Cattle  
Tosso Leeb, Switzerland
- 13:50 White and Belt Phenotypes in Chinese Pigs (*KIT*)  
Lusheng S Huang, China
- 14:10 The Beta-Defensin Gene in Dogs – Black and Brindle  
Greg Barsh, USA
- 14:30 The Mutation for Progressive Gray in Horses  
Leif Andersson, Sweden
- 14:50 Lavender plumage colour phenotype in Quail and Chicken : same *MLPH* gene but very different mutations.  
Bertrand Bed'Hom, France
- 15:10 Dilute Phenotypes in Cattle (*SILV*)  
Sheila Schmutz, Canada

**Wednesday July 23**

**15.30- 17.30 Domestic Animal Sequencing**

Chair: Lawrence Schook [Schook@uiuc.edu](mailto:Schook@uiuc.edu)

**Venue: RAI Auditorium**

- 15:30 to 15:45 Call to order, Review of Previous Meeting and Workshop Objectives, Larry Schook
- 15:45 to 16:00 Harris Lewin, Bovine Genome Project
- 16:00 to 16:15 Richard Crooijmans, Chicken Genome Project
- 16:15 to 16:30 Jill Maddox, Ovine Genome Project
- 16:30 to 16:45 Ed Smith, Turkey Genome Project
- 16:45 to 17:00 Alan Archibald, Pig Genome Sequencing Project
- 17:00 to 17:15 Jim Reecy, QTLdb
- 17:15 to 17:30 Discussion and Business Meeting
- Transition from sequencing to annotation and bioinformatics
  - Animal phenotypes



**Wednesday July 23 (continued)**

**15.30- 17.30 Horse Genome Mapping**

Chair: Imke Tammen

[itammen@camden.usyd.edu.au](mailto:itammen@camden.usyd.edu.au)

**Venue: RAI Room A**

- 15.30 **Leif Andersson\*** and Claire Wade on behalf of the Equine Genome Sequencing Consortium  
Preliminary analysis of the equine genome  
20min + 5 min discussion
- 15.55 **Terje Raudsepp\***, Nandina Paria and Bhanu P. Chowdhary  
Sequencing-ready physical map of the horse Y chromosome  
15min + 5 min discussion
- 16.15 Suzanne Eivers, Beatrice McGivney, David MacHugh, Cormac Taylor, Katie Mason, James MacLeod, Lisa Katz and **Emmeline Hill\***  
Exercise-induced gene expression in equine skeletal muscle.  
10min + 5min discussion
- 16.30 **Virgine Lampe\***, Claudia Dirks and Ottmar Distl  
Insights into equine osteochondrosis based on genetic markers in Hanoverian warmblood horses  
10min + 5min discussion
- 16.45 **Sarah Blott\***, L.Y. Fox-Clipsham, E. Temperton, J.E. Swinburne and M. Vaudin  
Single nucleotide polymorphism (SNP) density and predicted mapping resolution of complex trait genes in the Thoroughbred horse  
10min + 5min discussion
- 17.00 Brief updates  
**Ottmar Distl** - Equine BAC – physical map  
**Bhanu Chowdhary** - Expression arrays
- 17.10 General discussion and group updates
- 17.20 Election of chair and steering committee
- \* = presenting author

**15.30- 17.30 Pig Gene Mapping and Applied Genetics**

Chair: Gary Rohrer

[Gary.Rohrer@ARS.USDA.GOV](mailto:Gary.Rohrer@ARS.USDA.GOV)

**Venue: RAI Room C**

No agenda provided.

**15.30- 17.30 Early Career Scientist Workshop. Steps to publish a paper in Animal Genetics.**

Moderators

[Chris.Moran@vetsci.usyd.edu.au](mailto:Chris.Moran@vetsci.usyd.edu.au)

[Noelle.Cockett@usu.edu](mailto:Noelle.Cockett@usu.edu)

[Debbie.Wright@oxon.blackwellpublishing.com](mailto:Debbie.Wright@oxon.blackwellpublishing.com)

**Venue: RAI Room D**

No agenda provided.



**The following poster abstracts have been presented incorrectly in the abstract book:**

**Poster 2198, Maternal dietary methionine supplementation modulates foetal hepatic expression profiles**

Presenting Author: Klaus Wimmers, Research Institute for the Biology of Farm Animals (FBN), Research Unit 'Molecular Biology', 18196 Dummerstorf, Germany

Other authors (name only):

1. Eduard Murani
2. Wirawan Nuchchanart
3. Siriluck Ponsuksili

**Abstract:**

Impact of maternal nutrition during pregnancy on gene expression profiles and phenotypes of offspring was shown experimentally and in epidemiological studies in model animals and humans. The aim of the study is demonstrating of foetal programming in pigs, listing of genes sensitive to foetal programming and evidencing and quantifying of the role of DNA-methylation in this phenomenon. Therefore, 36 sows were fed methionine supplemented ('MET') vs. control ('CON') gestation diets. Liver samples of fetuses of three developmental stages (d35, d63, d91 p.c.) were subsequently monitored for diet-dependent differential gene expression by using Affymetrix micorarrays. Statistical and bioinformatics evaluation of the expression profiles revealed largest effect of gestation diets at late foetal stages (91 dpc) when more than 1600 transcripts were differentially regulated. Functional annotation clustering highlighted the GO terms biological quality, cellular and anatomical structure morphogenesis, and negative regulation of metabolic processes. Interestingly, members of the IGF axis were found being diet-dependent regulated that play a key role in prenatal growth and are sensitive to regulation by DNA-methylation. Quantification of the DNA methylation at these loci will shed light on the role of this epigenetic mechanism as the molecular basis of genotype-environment (diet) interactions.

**Poster 2236, Expression profiling and eQTL analysis reveal biological pathways and candidate genes affecting water holding capacity of muscle**

Presenting Author: Siriluck Ponsuksili, Research Institute for the Biology of Farm Animals (FBN), Research Group 'Functional Genome Analysis', 18196 Dummerstorf, Germany

Other authors (name only):

- |                  |                   |
|------------------|-------------------|
| 1. E. Jonas      | 5. C. Walz        |
| 2. E. Murani     | 6. M. Schwerin    |
| 3. C. Phatsara   | 7. K. Schellander |
| 4. T. Srikanchai | 8. K. Wimmers     |
| 5.               |                   |

**Abstract (maximum 200 words):**

There is considerable variation in the water holding capacity (WHC) of meat, which is an important economic factor in pork production. WHC depends of numerous genetic and environmental factors that affect muscle fibre properties and metabolic processes ante and post slaughter. We aimed to identify candidate genes for WHC by QTL mapping, expression profiling and expressionQTL (eQTL) analysis. Expression microarray analysis of M. longissimus dorsi RNAs of 74 F2 animals of a resource population showed 1,279 transcripts with trait correlated expression. Negatively correlated transcripts were enriched in functional categories and pathways of extracellular matrix, receptor interaction, and Ca-signalling; positively correlated transcripts dominantly represented oxidative phosphorylation, mitochondrial pathways, and transporter activity. A eQTL analysis of trait correlated transcripts revealed 897 eQTL, with 104 eQTL matching previously identified QTL for WHC; 96 transcripts were trans regulated and 8 had cis acting regulation. Based on these findings, a priority list of genes was established out of the orchestra of genes of biological networks relevant to the liability to elevated drip loss. The complex relationships between biological processes in live skeletal muscle and meat quality are mainly influenced by the energy reserves and their utilisation in the muscle and by the muscle structure itself.

