



# ISAG . 2019

37th International Society for  
Animal Genetics Conference

July 7 - 12, 2019 - Lleida, Spain



## Animal Epigenetics

Organised by a standing committee:      YES      NO

### Meeting information

Date: July 8, 2019

Time: 14:30 to 18:00

Number of participants:

### Chair

Name: Stephanie McKay

Affiliation: University of Vermont

Contact email: Stephanie.mckay@uvm.edu

### Agenda

14:30 OP4 Comparative analyses of cattle DNA methylome provide insights into tissue specific patterns, epigenomic evolution, and complex traits. G. Liu\*, Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, USA.

14:50 OP5 Identification of orthologous tissue-specific enhancer-gene pairs across chicken, pig and cattle. M. M. Halstead\*<sup>1</sup>, C. Kern<sup>1</sup>, Y. Wang<sup>1</sup>, X. Xu<sup>1</sup>, G. Chanthavixay<sup>1</sup>, P. Saelao<sup>1</sup>, S. M. Waters<sup>1</sup>, J. F. Medrano<sup>1</sup>, A. L. Van Eenennaam<sup>1</sup>, M. E. Delany<sup>1</sup>, H. H. Cheng<sup>2</sup>, C. K. Tuggle<sup>3</sup>, C. W. Ernst<sup>4</sup>, H. Zhou<sup>1</sup>, P. J. Ross<sup>1</sup>, <sup>1</sup> University of California Davis, Davis, CA, USA, <sup>2</sup> USDA, ARS, ADOL, East Lansing, MI, USA, <sup>3</sup> Iowa State University, Ames, IA, USA, <sup>4</sup> Michigan State University, East Lansing, MI, USA.

15:08 OP6 Whole genome DNA methylation profiles in the central nervous system of sheep naturally infected with scrapie. A. Hernaiz\*<sup>1</sup>, S. Sentrel<sup>1</sup>, R. Bolea<sup>2</sup>, O. López-Pérez<sup>1, 2</sup>, A. Sanz<sup>1</sup>, P. Zaragoza<sup>1</sup>, J. J. Badiola<sup>2</sup>, J. M. Toivonen<sup>1</sup>, H. Filali<sup>2</sup>, and I. Martín-Burriel<sup>1, 2, 1</sup>



## INTERNATIONAL SOCIETY FOR ANIMAL GENETICS

LAGENGIO, Faculty of Veterinary, IA2, University of Zaragoza, Zaragoza, Spain, 2 CIEETE, Faculty of Veterinary, IA2, University of Zaragoza, Zaragoza, Spain.

15:26 OP8 The genome-wide RNA-chromatin interactions revealed by GRID-seq in skeletal muscle of three pig breeds. L. Fu, J. Li\*, Y. Liao, P. Zhou, X. Li, and S. Zhao, Key Laboratory of Pig Genetics and Breeding, MOA China, Huazhong Agricultural University, Wuhan, Hubei Province, China.

15:44 OP9 Tissue-specific characterization of the ovine methylome. A. J. Caulton\*<sup>1, 2</sup>, R. Brauning<sup>2</sup>, B. M. Murdoch<sup>3</sup>, and S. M. Clarke<sup>2, 1</sup> University of Otago, Dunedin, New Zealand, 2 AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand, 3 University of Idaho, Moscow, ID, USA.

16:32 OP10 Regulatory polymorphisms associated with allele-specific expression (aseQTL) in Nelore (*Bos indicus*) muscle. J. J. Bruscin<sup>1, 2</sup>, M. M. de Souza<sup>3</sup>, K. S. de Oliveira<sup>1</sup>, A. Zerlotini Neto<sup>4</sup>, and L. C. A. Regitano\*<sup>1</sup>, 1 Embrapa Southeast Livestock, São Carlos, São Paulo, Brazil, 2 Graduate Program on Evolutionary Genetics and Molecular Biology, Federal University of São Carlos, São Carlos, São Paulo, Brazil, 3 Department of Animal Science, Iowa State University, Ames, IA, USA, 4 Embrapa Informatics Agriculture, Campinas, SP, Brazil, 5 Department of Animal Science, University of São Paulo, Piracicaba, São Paulo, Brazil.

16:52 OP11 Can we predict an animal's biological age: A study on DNA methylation from bovine tail hair and liver tissues? L. T. Nguyen\*, E. M. Ross, and B. Hayes, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, QLD, Australia.

17:11 OP12 Allele-specific chromatin accessibility and histone modifications in an F1 cross of MD resistant and susceptible chicken lines. C. Kern\*<sup>1</sup>, Y. Wang<sup>1</sup>, P. Saelao<sup>1</sup>, K. Chanthavixay<sup>1</sup>, M. E. Delany<sup>1</sup>, H. H. Cheng<sup>2</sup>, P. Ross<sup>1</sup>, and H. Zhou<sup>1</sup>, 1 Department of Animal Science, University of California, Davis, CA, USA, 2 USDA-ARS, Avian Disease and Oncology Laboratory, East Lansing, MI, USA.

17:30 OP13 Epigenome-wide skeletal muscle DNA methylation profiles at the background of distinct metabolic types and ryanodine receptor variation. S. Ponsuksili\*<sup>1, 2</sup>, N. Trakooljul<sup>1, 2</sup>, S. Basavaraj<sup>1, 2</sup>, F. Hadlich<sup>1, 2</sup>, E. Murani<sup>1, 2</sup>, and K. Wimmers<sup>1, 2</sup>, 1 Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2 Institute for Genome Biology, Dummerstorf, Germany

17:50 Business Meeting

### **Summary of the meeting**

The workshop included nine invited speakers representing different disciplines of animal epigenetics. Speakers were selected to represent different species, different institutions and different disciplines of animal epigenetics. A business meeting was held at the end of the workshop and a new committee and a new chair were elected. The number of participants in the meeting ranged from 145-188 people.

**Committee chair** (the new chair)

Chair: Kyle Schachtschneider
Term of service: 2019-2022
Affiliation: University of Illinois at Chicago
E-mail address: kschach2@uic.edu

**Committee members** (the new committee)

Other members	Term of service	E mail address
Hasan Khatib	2019-2022	hkhatib@wisc.edu
Congjun Li	2019-2022	Congjun.Li@ARS.USDA.GOV
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