



# ISAG . 2019

37th International Society for  
Animal Genetics Conference

July 7 - 12, 2019 - Lleida, Spain

## Comparative & Functional Genomics

Organised by a standing committee: YES

### Meeting information

Date: Thursday 11 July 2019

Time: 14:30-17:45

Number of participants: 80-120

### Chair

Name: Fiona McCarthy

Affiliation: University of Arizona

Contact email: fionamcc@email.arizona.edu

### Agenda

## Comparative and Functional Genomics

### SYMPOSIA AND ORAL SESSIONS

**Comparative and Functional Genomics (THURSDAY AFTERNOON) (orals)**

Chair(s): **Fiona McCarthy**

Location: **Auditorium 1**

Date & Time: **Thursday, July 11, 2:30 PM - 6:00 PM**

2:30 PM 80192 **FAANGMine: A Genomic Data Mining Warehouse for Domesticated Animal Species.**

CG Elsik\*, M Shamimuzzaman, DA Triant, JJ Le Tourneau, and AT Walsh,

*University of Missouri, Columbia, MO, USA.*

2:45 PM 79942 **High-order gene-by-gene and gene-by-environment interactions: is there a need to consider them when dissecting the genetic basis of complex traits?**

Örjan Carlborg\* and Yanjun Zan, *Department of Medical Biochemistry and Microbiology, Uppsala, Sweden.*

3:00 PM 79823 **Evaluation of RNA-Sequencing pipelines for optimized power and accuracy of SNP and INDEL identification.**

S. Lam\*<sup>1</sup>, F. Miglior<sup>1</sup>, J. Zeidan<sup>1</sup>, I. Gómez-Redondo<sup>1,2</sup>, A. Suárez-Vega<sup>1</sup>, P. A. S. Fonseca<sup>1</sup>, and F. Schenkel<sup>1</sup>, <sup>1</sup>*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada,* <sup>2</sup>*Spanish National Institute for Agriculture and Food Research and Technology, Madrid, Spain.*

3:15 PM 79482 **Genetic control of temperament traits across species: association of autism spectrum disorder genes with cattle temperament.**

Roy Costilla\*<sup>1,2</sup>, Kathryn Kemper<sup>1</sup>, Enda Byrne<sup>1</sup>, Laercio Porto-Neto<sup>4</sup>, Roberto Carneiro<sup>5</sup>, Donagh Berry<sup>6</sup>, Deidre Purfield<sup>6</sup>, Jenny Doyle<sup>6</sup>, Stephen Moore<sup>2</sup>, Naomi Wray<sup>1</sup>, and Ben Hayes<sup>2</sup>, <sup>1</sup>*Institute for Molecular Bioscience. The University of Queensland, Brisbane. Australia.,* <sup>2</sup>*Queensland Alliance for Agriculture and Food Innovation. The University of Queensland., Brisbane. Australia.,* <sup>3</sup>*Queensland Brain Institute. The University of Queensland., Brisbane. Australia.,* <sup>4</sup>*Commonwealth Scientific and Industrial Research Organization (CSIRO), Agriculture and Food, Brisbane. Australia.,* <sup>5</sup>*School of Agricultural and Veterinarian Sciences, Sao Paulo State University, Sao Paulo. Brasil.,* <sup>6</sup>*Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co, Cork, Ireland.*

3:30 PM 79064 **Copy number variants reveal traces of recent selection in two dairy cattle breeds.**

Y.L. Lee\*<sup>1</sup>, A. Bouwman<sup>1</sup>, M.A.M. Groenen<sup>1</sup>, E. Mullaart<sup>2</sup>, R.F. Veerkamp<sup>1</sup>, and M. Bosse<sup>1</sup>, <sup>1</sup>*Wageningen University & Research, Animal Breeding and Genomics, P.O. Box338, 6700 AH, Wageningen, the Netherlands,* <sup>2</sup>*CRV B.V., P.O. Box 454, 6800 AL, Arnhem, the Netherlands.,*

3:45 PM 79626 **Chromatin accessibility conservation across four livestock species.**

Sarah Djebali\*<sup>1</sup>, Sylvain Foissac<sup>1</sup>, Nathalie Vialaneix<sup>2</sup>, Kylie Munyard<sup>3</sup>, Andrea Rau<sup>4</sup>, Thomas Faraut<sup>1</sup>, Sandrine Lagarrigue<sup>5</sup>, Hervé Acloque<sup>4</sup>, Elisabetta Giuffra<sup>4</sup>, and FR-AgENCODE consortium<sup>1,4</sup>, <sup>1</sup>*GenPhySE, University of Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France,* <sup>2</sup>*MIAT, INRA, Castanet Tolosan, France,* <sup>3</sup>*Curtin University, School of Biomedical Sciences, CHIRI Biosciences, Perth, Australia,* <sup>4</sup>*GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France,* <sup>5</sup>*UMR PEGASE, INRA, 35042 Rennes, France and UMR PEGASE, AGROCAMPUS OUEST, Rennes, France.*

4:00 PM		<b>Coffee/Tea Break.</b>
4:30 PM	80082	<p><b>Meta-analysis of differentially co-expressed gene modules for high- and sub-fertile beef cows.</b>  Pablo Augusto de Souza Fonseca*, Aroa Suárez-Vega, Stephanie Lam, Flavio S. Schenkel, Samir Id-Lahoucine, and Angela Canovas, <i>University of Guelph, Guelph, Ontario, Canada.</i></p>
4:45 PM	79754	<p><b>Broadening the miRNA catalogue in livestock species: a contribution to the functional annotation of animal genomes.</b>  Andreia Amaral*<sup>1</sup>, Christian Anthon<sup>2</sup>, Giulia Corsi<sup>2</sup>, Ana Vasconcelos<sup>1</sup>, Sylvain Marthey<sup>3</sup>, Anne Hoffman<sup>4</sup>, Fiete Haack<sup>5</sup>, Kisun Pokharel<sup>6</sup>, Stefan Seeman<sup>2</sup>, Luis Gama<sup>1</sup>, Martien Groenen<sup>7</sup>, Monique Rijnkels<sup>8</sup>, Elisabetta Giuffra<sup>3</sup>, Ole Madsen<sup>7</sup>, Jan Gorodkin<sup>2</sup>, <sup>1</sup><i>Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal,</i> <sup>2</sup><i>Center for noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark,</i> <sup>3</sup><i>INRA, UMR GABI, Jouy-en-Josas, France,</i> <sup>4</sup><i>Bioinformatics Group, Department of Computer Science University of Leipzig, Leipzig, Germany,</i> <sup>5</sup><i>Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany,</i> <sup>6</sup><i>Natural Resources Institute Finland, Jokioinen, Finland,</i> <sup>7</sup><i>Wageningen University, WAGENINGEN, Netherlands,</i> <sup>8</sup>, <i>Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&amp;M University, 400 Bizzell St, Texas USA.</i></p>
5:00 PM	80160	<p><b>Detection of long-non coding RNAs from the differential transcriptomic analysis of abomasal lymph node from resistant and susceptible sheep to the infection by <i>Teladorsagia circumcincta</i>.</b>  PK Chitneedi<sup>1</sup>, C Kühn<sup>2</sup>, R Weikard<sup>2</sup>, JJ Arranz<sup>1</sup>, M Martínez-Valladares<sup>3,4</sup>, and B Gutiérrez-Gil*<sup>1</sup>, <sup>1</sup><i>Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, Campus de Vegazana s/n, 24071, León, Spain,</i> <sup>2</sup><i>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), D-18196, Dummerstorf, Germany,</i> <sup>3</sup><i>Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, Campus de Vegazana s/n, 24071, León, Spain,</i> <sup>4</sup><i>Instituto de Ganadería de Montaña, CSIC-Universidad de León, 24346, Grulleros (León), Spain.</i></p>
5:15 PM	79722	<p><b>Circular RNA expression in turkey skeletal muscle and response to thermal challenge.</b>  Kent M. Reed*<sup>1</sup>, Kristelle M. Mendoza<sup>1</sup>, and Juan E. Abrahante<sup>2</sup>, <sup>1</sup><i>Department of Veterinary and Biomedical Sciences, University of Minnesota, St. Paul, MN, USA,</i> <sup>2</sup><i>University of Minnesota Informatics Institute, University of Minnesota, Minneapolis, MN, USA.</i></p>
5:30 PM	79882	<p><b>Functional analysis of G-protein-coupled receptors during porcine subcutaneous preadipocytes differentiation.</b>  Masaaki Taniguchi*<sup>1</sup>, Aisaku Arakawa<sup>1</sup>, Ikuyo Nakajima<sup>1</sup>, Hirohide</p>



## INTERNATIONAL SOCIETY FOR ANIMAL GENETICS

Uenishi<sup>2</sup>, and Satoshi Mikawa<sup>1</sup>, <sup>1</sup>*Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan*, <sup>2</sup>*Institute of Agrobiological Sciences, National Agriculture and Food Research Organization, Tsukuba, Ibaraki, Japan*.

5:45 PM

**Business Meeting.**

### **Summary of the meeting**

The organizers of the conference took up the recommendation from the previous conference and set up a program avoiding parallel sessions of the workshops on Epigenetics, Domestic Animal Sequencing and Comparative and Functional Genomics to enable complementary actions and attendance. Nevertheless, the Comparative and Functional Genomics session overlapped with the Microbiomes session, which could limit the attendance to both workshops which are of transversal nature and of interest to many scientists. This should be probably taken into account in future conferences.

The contributions to the Comparative and Functional Genomics workshop were selected out of all abstracts submitted to the conference with a preference to abstract allocated to the Functional and Comparative Genomics section by the members of the standing committee based on the rank sum of the individual scores.

The workshop meeting covered presentations about (1) functional genomics resources available to the community and (2) studies related to functional and comparative genomics across livestock species. During the business meeting the chair thanked attendees for their participation and the committee for their help and support. No new business was submitted for discussion. The chair closed the session by thanking all presenters and participants for their presentations to the working group.

**Committee chair (the new chair)**

Chair: Fiona McCarthy
Term of service: 2012-2021
Affiliation: University of Arizona
E-mail address: fionamcc@email.arizona.edu

**Committee members (the new committee)**

Other members	Term of service	E mail address
Cristina Ovilo	2016-2023	ovilo@inia.es
Christa Kühn	2016-2023	kuehn@fhn-dummerstorf.de
Guisheng Liu	2014-2021	guisheng_liu1964@yahoo.com
Paolo Zambonelli	2014-2021	paolo.zambonelli@unibo.it
Carl Schmidt	2016-2023	schmidtc@udel.edu
Yangfang Wang	2014-2021	yanfangw@hotmail.com

**COMPARISON TEST (2018-2019)      NO**