

Animal Epigenetics Workshop

Organised by a Standing Committee: YES NO

Meeting information

Date: July 4, 2023

Time: 1-5:30pm CDT

Number of participants: 95 simultaneous participants; 2021 online meeting numbers: 125

Chair

Name: George Liu acting for Kyle M. Schachtschneider

Affiliation: United States Department of Agriculture, USA

Contact email: George.Liu@usda.gov

Co-Chair (optional)

Name:	
Affiliation:	
Contact email:	



Agenda

Agenda	1			
Animal Epigenetics (orals) Chair(s): George Liu, USDA/ARS and Luciana Correia de Almeida Regitano, Embrapa Brazil				
	_	ntion assigned)		
		esday, July 4, 2:00 PM - 5:30 PM		
2:00 PM	89542	Annotation of functional variations in four livestock genomes utilizing cisregulatory elements datasets. (Prerecorded) Ruixian Ma*1, Renzhuo Kuang¹, Mingyang Hu¹, Yaping Guo¹, Daoyuan Wang¹, Honghong Zhou¹, Zheyu Han¹, Linmi Li¹, Zhixiang Xu¹, Yan Zhang¹, Yunxiao Zhao¹, Xinyun Li¹,², and Shuhong Zhao¹,², ¹Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministryof Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, 430070, China., ²Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan ,430070, China.		
2:15 PM	89723	DNA methylation alteration patterns in repeat elements are similar during subclinical mastitis caused by Staphylococcus chromogenes and Staphylococcus aureus. Mengqi Wang ^{1,2} , Nathalie Bissonnette ¹ , Mario Laterrière ³ , David Gagné ³ , and Eveline M. Ibeagha-Awemu* ¹ , ¹ Sherbrooke Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Québec, Canada, ² Département des sciences animales, Université Laval, Québec, Québec, Canada, ³ 3Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Québec, Québec, Canada.		
2:30 PM	89520	Extending Ensembl regulatory annotation to farmed animals. G.R. Ilsley*, G.A. Merino, P.R. Branco Lins, M. Perry, D. Urbina-Gomez, and P. Harrison, European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, Cambridge, UK.		
2:45 PM	89381	Genome-wide acetylation modification of H3K27ac in bovine rumen cell following butyrate exposure. Xiaolong Kang ^{1,2} , Chenglong Li ² , Ransom L Baldwin ¹ , George Liu ¹ , and Congjun Li* ¹ , ¹ ARS, USDA, Beltsville, MD, USA, ² Ningxia University, Yinchuan, Ningxia, China.		
3:00 PM	89757	Long-term selection impacts the rewiring of chromatin structure in chickens. Dailu Guan ¹ , Ying Wang ¹ , Samuel Aggrey ² , Ron Okimoto ³ , Rachel Hawken ³ , and Huaijun Zhou* ¹ , ¹ University of California, Davis, Davis, CA, USA, ² University of Georgia, Athens, GA, USA, ³ Cobb-Vantress Inc., Siloam Springs, AR, USA.		
3:15 PM	89422	M6A demethylase ALKBH5 regulates PRRSV replication by manipulating host immune response. (Could not make it due to the visa) Qiuju Su*1, Xiangge Meng¹, Bang Liu¹,², and Xiang Zhou¹,², ¹Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural		



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		University, Wuhan, China, ² Hubei Hongshan Laboratory, Wuhan, China.
3:30 PM		Tea/Coffee Break, Exhibition and Poster Viewing.
4:00 PM	89610	Relationship between spleen and uterus gene expression and DNA methylation according to developmental stages of pigs. B Ahn*1, M Kang¹, M Choi¹, L Rund³, L Shook³, and C Park¹, ¹Department of Stem Cell and Regenerative Biotechnology, Konkuk University, Seoul, Korea, ²Living Systems Institute, University of Exeter, Exeter, United Kingdom, ³Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, USA.
4:15 PM	89405	RNA Methylation as a Mechanistic Link Between EpiGenotype and Phenotype. S Xie ¹ , B Murdoch ¹ , and S McKay* ^{2,3} , ¹ University of Idaho, Moscow, Idaho, USA, ² University of Vermont, Burlington, VT, USA, ³ University of Missouri, Columbia, MO, USA.
4:30 PM	89439	Super-accessible chromatin regions are associated with increased gene transcription and regulation of cell differentiation in mammals. (Prerecorded) Mingyang Hu*1, Yunxia Zhao1, Xiaolong Qi1, Honghong Zhou1, Yaping Guo1, Linmi Li1, Renzhuo Kuang1, Ruixian Ma1, Ge Sun4, Li Li4, Mengjin Zhu1,3, Xinyun Li1,3, and Shuhong Zhao1,2, 1Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China, Hubei, China, The Cooperative Innovation Center for Sustainable Pig Production, Wuhan, Hubei, China, College of Biomedicine and Health, Huazhong Agricultural University, Wuhan, Hubei, China.
4:45 PM	89457	Beyond the genome: establishing molecular phenotypes to accelerate adaptation to a changing environment. A. Caulton* ¹ , R. Brauning ¹ , K. M. McRae ¹ , K. G. Dodds ¹ , C. Couldrey ² , P. L. Johnson ¹ , and S. M. Clarke ¹ , ¹ AgResearch, Invermay Agricultural Centre, Mosgiel, Otago, New Zealand, ² Livestock Improvement Corporation, Hamilton, New Zealand.
5:00 PM	87670	African swine fever infection enhances the host transcriptional regulation of membrane protein-encoding genes mediated by changes in chromatin state. Xiaolong Qi*1, Yue Xiang¹, Limeng Sun³, Lingyu Xing³, SaiXian Zhang¹, Qiulin Zhao¹, Lu Zhang¹, Jingjin Li¹, Peng Zhou¹, Zhuqing Zheng¹, Xinyun Li¹, Liangliang Fu¹, Guiqing Peng³, and Shuhong Zhao¹, **Ikey Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education and Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China, **The Cooperative Innovation Center for Sustainable Pig



Production, Wuhan, China, ³State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, HuazhongAgricultural University, Wuhan, China, ⁴State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, HuazhongAgricultural University, Wuhan, China.

5:15 PM

Business meeting.

Summary of the meeting

This workshop included eleven invited speakers representing different areas of epigenetics spanning multiple species. Speakers were selected to represent different species, institutions, geographic locations, and disciplines. Eight presentations were presented in person and two were prerecorded with the exception of one speaker (Qiuju Su; abstract #89422) who was unable to attend the workshop due to the visa issue and did not present. To fill this spot, presentations and Q&A sessions were allowed to run long as opposed to inserting a new presentation into that time slot.

A business meeting was held at the end of the workshop. As all the previous committee members and the Chair were elected in the 2019 meeting, new elections were required. Changes in the committee: Dr. Kyle Schachtschneider and Dr. Luca Fontanesi retired from this committee, after their active involvement and leadership in the committee for the last few conferences. The other current members sought reelection for another term. Dr. Alex Caulton and Dr. Kun Han were nominated to serve on the organizing committee. Their memberships on the committee were approved by unanimous votes. Dr. George Liu was elected as the new chair and Dr. Luciana Correia de Almeida Regitano was elected as the new Co-Chair.

New Committee chair

Chair: George Liu

Term of service: 2019-2027

Affiliation: United States Department of Agriculture, USA

E-mail address: George.Liu@usda.gov

Co-Chair: Luciana Correia de Almeida Regitano

Term of service: 2019-2027

Affiliation: Embrapa Brazil

E-mail address: luciana.regitano@embrapa.br

Committee members (the new committee)

Other members	Term of service	E mail address
Hasan Khatib	2019-2027	hkhatib@wisc.edu
Congjun Li	2019-2027	Congjun.Li@ARS.USDA.GOV
Siriluck Ponsuksili	2019-2027	ponsuksili@fbn-dummerstorf.de
Alex Caulton	2023-2027	Alex.Caulton@agresearch.co.nz
Kun Han	2023-2027	hankun@mail.hzau.edu.cn

COMPARISON TEST (2020-2021) YES NO

SIGNATURES

Chair