



Domestic Animal Sequencing and Annotation

Organised by a Standing Committee: YES NO

Meeting information

Date: July 28, 2021

Time: 13:00 - 16:30

Number of participants: There were approximately 110 individuals

Chair

Name: George Liu

Affiliation: United States Department of Agriculture; Beltsville, Maryland, USA

Contact email: George.Liu@ USDA.GOV

Co-Chair (optional)

Name: Brenda Murdoch

Affiliation: University of Idaho

Contact email: bmurdoch@uidaho.edu

Agenda

1:00 PM	85421	<p>Bovine genome annotation using integration of multi-omics data. Hamid Beiki¹, Clare Gill², Honglin Jiang³, Wansheng Liu⁵, Zhihua Jiang⁴, Stephanie McKay⁶, Brenda M. Murdoch⁷, James Koltes¹, Monique Rijnkels², Tim P.L. Smith⁸, Pablo Ross⁹, Huaijun Zhou⁹, and James Reecy*¹, ¹<i>Iowa State University, Ames, IA, USA</i>, ²<i>Texas A&M University, College Station, TX, USA</i>, ³<i>Virginia Tech University, Blacksburg, VA, USA</i>, ⁴<i>Washington State University, Pullman, WA, USA</i>, ⁵<i>Penn State University, State College, PA, USA</i>, ⁶<i>University of Vermont, Burlington, VT, USA</i>, ⁷<i>University of Idaho, Moscow, ID, USA</i>, ⁸<i>US Meat Animal Research Center, Clay Center, NE, USA</i>, ⁹<i>University of California - Davis, Davis, CA USA</i>.</p>
1:15 PM	85416	<p>BovReg: a high resolution functional annotation of the cattle genome using novel breeds/crosses. Gabriel Costa Monteiro Moreira*¹, Sébastien Dupont¹, Doreen Becker², Mazdak Salavati³, Richard Clark⁴, Emily L. Clark³, Graham Plastow⁵, Christa Kühn^{2,6}, Carole Charlier¹, and on behalf of the BovReg consortium⁶, ¹<i>Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium</i>, ²<i>Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany</i>, ³<i>The Roslin Institute, University of Edinburgh, Edinburgh, UK</i>, ⁴<i>Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK</i>, ⁵<i>Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada</i>, ⁶<i>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany</i>.</p>
1:30 PM	85398	<p>Annotation of transcription start sites in the bovine genome reveals novel breed specific complexity. Mazdak Salavati*¹, Richard Clark², Doreen Becker³, Christa Kühn^{3,4}, Graham Plastow⁵, Gabriel Costa Monteiro Moreira⁶, Carole Charlier^{6,7}, Emily L. Clark¹, and on behalf of the BovReg consortium⁴, ¹<i>The Roslin Institute, University of Edinburgh, Edinburgh, UK</i>, ²<i>Genetics Core, Edinburgh Clinical Research Facility, The University of Edinburgh, Edinburgh, UK</i>, ³<i>Faculty of Agricultural and Environmental Sciences, University Rostock, Rostock, Germany</i>, ⁴<i>Institute of Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany</i>, ⁵<i>Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada</i>, ⁶<i>Unit of Animal Genomics, GIGA Institute, University of Liège, Liège, Belgium</i>, ⁷<i>Faculty of Veterinary Medicine, University of Liège, Liège, Belgium</i>.</p>
1:45 PM	85436	<p>The Functional Annotation of the Ovine Genome. Brenda Murdoch*¹, Kimberly Davenport¹, Mazdak Salavati², Emily Clark², Alan Archibald², Alisha Massa Marie Herndon³, Michelle Mousel⁴, Stephen White⁴, Kim Worley⁵, Suraj Bhattarai Stephanie McKay⁶, Alex Caulton⁷,</p>

		Shannon Clarke ⁷ , Rudiger Brauning ⁷ , Tracy Hadfield ⁸ , Timothy P.L. Smith ⁹ , Noelle Cockett ⁸ , ¹ <i>University of Idaho</i> , ² <i>The Roslin Institute and Royal (Dick) School of Veterinary Studies</i> , ³ <i>Washington State University</i> , ⁴ <i>USDA ARS, Animal Disease Research Unit</i> , ⁵ <i>Baylor College of Medicine-Human Genome Sequencing Center</i> , ⁶ <i>University of Vermont</i> , ⁷ <i>AgResearch</i> , ⁸ <i>Utah State University</i> , ⁹ <i>USDA, ARS, U.S. Meat Animal Research Center</i> .
2:00 PM	85410	AQUA-FAANG: genome functional annotation of the six major European farmed fish species. Daniel J. Macqueen* ¹ , Sigbjørn Lien ² , and AQUA-FAANG consortium ³ , ¹ <i>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, Scotland, UK</i> , ² <i>Centre for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway</i> , ³ <i>AQUA-FAANG consortium, Europe</i> .
2:15 PM	85464	The Farm Animal Genotype-Tissue Expression (FarmGTEx) Consortium. L Fang*, <i>The University of Edinburgh, Edinburgh, UK</i> .
2:30 PM		Break.
2:45 PM	85468	The Bovine Pangenome Consortium. B. D. Rosen* ¹ , D. M. Bickhart ² , T.P.L. Smith ³ , D. Boichard ⁴ , G.A. Brockmann ⁵ , A.J. Chamberlain ⁶ , C. Couldrey ⁷ , H.D. Daetwyler ⁶ , A. Djikeng ⁸ , C. Drögemüller ⁹ , S. Elzaki ⁵ , R.K. Gandham ¹⁰ , DE Hagen ¹¹ , O. Hanotte ¹² , M.P. Heaton ³ , ¹ <i>USDA ARS AGIL, Beltsville, MD, USA</i> , ² <i>USDA ARS DFRC, Madison, WI, USA</i> , ³ <i>USDA ARS MARC, Clay Center, NE, USA</i> , ⁴ <i>INRAE Animal Genetics and Integrative Biology, Jouy en Josas, France</i> , ⁵ <i>Humboldt-Universität zu Berlin, Berlin, Germany</i> , ⁶ <i>Agriculture Victoria, Melbourne, Victoria, AU</i> , ⁷ <i>LIC, Hamilton, New Zealand</i> , ⁸ <i>Centre for Tropical Livestock Genetics and Health, Midlothian, Scotland</i> , ⁹ <i>University of Bern, Bern, Switzerland</i> , ¹⁰ <i>National Institute of Animal Biotechnology, Hyderabad, India</i> , ¹¹ <i>Oklahoma State University, Stillwater, OK, USA</i> , ¹² <i>International Livestock Research Institute, Addis Ababa, Ethiopia</i> .
3:00 PM	85469	An improved, high-quality ovine reference genome to facilitate functional annotation of gene regulatory elements. Kimberly M. Davenport* ¹ , Derek M. Bickhart ² , Kim C. Worley ³ , Shwetha C. Murali ³ , Noelle E. Cockett ⁴ , Michael P. Heaton ⁵ , Timothy P.L. Smith ⁵ , Brenda M. Murdoch ¹ , and Benjamin D. Rosen ⁶ , ¹ <i>Department of Animal, Veterinary, and Food Sciences, University of Idaho, Moscow, Idaho, United States</i> , ² <i>US Dairy Forage Research Center, USDA-ARS, Madison, Wisconsin, United States</i> , ³ <i>Baylor College of Medicine, Houston, Texas, United States</i> , ⁴ <i>Utah State University, Logan, Utah, United States</i> , ⁵ <i>US Meat Animal Research Center, USDA-ARS, Clay Center, Nebraska, United States</i> ,

<p>⁶<i>Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, Maryland, United States.</i></p>	
3:15 PM 85390	<p>Annotation of full-length transcripts including alternative splicing from 19 chicken tissues using Oxford Nanopore long-read sequencing. D. Guan*¹, M.M. Halstead¹, A.D. Islas-Trejo¹, D.E. Goszczynski¹, H.H. Cheng², P. Ross¹, and H. Zhou¹, ¹<i>Department of Animal Science, University of California Davis, Davis, CA, 95616 USA</i>, ²<i>Avian Disease and Oncology Laboratory, USDA ARS, East Lansing, MI 48823, USA.</i></p>
3:30 PM 85460	<p>Uncovering abundant missing genes in the chicken reference genome solves the avian gene depletion puzzle. Ming Li*¹, Naiyi Xu¹, Peipei Bian¹, Xiaoxiang Hu², Yu Jiang¹, and Ning Yang³, ¹<i>Key Laboratory of Animal Genetics, Breeding and Reproduction of Shaanxi Province, College of Animal Science and Technology, Northwest A&F University, Yangling 712100, China</i>, ²<i>State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, 100193, China</i>, ³<i>National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture and Rural Affairs, China Agricultural University, Beijing, 100193, China.</i></p>
3:45 PM 85440	<p>Chromatin accessibility and regulatory vocabulary in indicine cattle. P Alexandre*¹, M Naval-Sánchez^{1,2}, M Menzies¹, L Nguyen³, L Porto-Neto¹, M Fortes⁴, and A Reverter¹, ¹<i>CSIRO Agriculture & Food, 306 Carmody Rd., QLD 4067, Australia</i>, ²<i>Institute for Molecular Bioscience, The University of Queensland, QLD 4072, Australia</i>, ³<i>Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, QLD 4072, Australia</i>, ⁴<i>School of Chemistry and Molecular Biosciences, The University of Queensland, QLD 4072, Australia.</i></p>
4:00 PM	<p>Workshop Business Meeting.</p>

Summary of the meeting

The virtual workshop was well attended, and all the presentations and went well and on time. When Q&A ran out of the time, virtual discussions were followed up using the chatbox and other channels.

Changes in the committee: Dr. George Liu is retiring from this committee, after his active involvement and leadership in the committee for the last a few conferences. Dr. Brenda Murdoch was elected from the Co-Chair to the new Chair. Dr. Sarah Djebali was elected as the new Co-Chair. Dr. Ben Rosen, Mr. Micah Wells, and Dr. Huaijun Zhou were nominated to serve on the organizing committee. Their memberships on the committee were approved by unanimous votes.

New Committee chair

Chair: Brenda Murdoch
Term of service: First term 2017-2021, Second term 2021-2025
Affiliation: University of Idaho
E-mail address: bmurdoch@uidaho.edu

New Committee co-chair (optional)

Chair: Sarah Djebali
Term of service: First term 2017-2021, Second term 2021-2025
Affiliation: Inserm, France
E-mail address: sarah.djebali@inserm.fr

New Committee members

Other committee members	First term of service (from year to year)	Second term of service (from year to year)	Email address
Marina Naval-Sanchez	2019-2023		m.navalsanchez@imb.uq.edu.au
Lin Jiang	2019-2023		jianglin@caas.cn
Ben Rosen	2021-2025		ben.rosen@usda.gov
Huaijun Zhou	2021-2025		hzhou@ucdavis.edu
Micah Wells	2021-2025		mwells@rapid-genomics.com