ISAG . 2019
37th International Society for Animal Genetics Conference
July 7 - 12, 2019 - Lleida, Spain

Domestic Animal Sequencing and Annotation

Organised by a standing committee: **YES** NO

Meeting information

Date: July 9, 2019

Time: 14:30 – 16:00 and 16:30 – 18:00

Number of participants: There were approximately 180 individuals in each session

Chair

Name: James Reecy

Affiliation: Iowa State University

Contact email: jreecy@iastate.edu

Agenda

14:30 OP118 Invited Workshop Presentation: Navigating the genome with epigenome maps: Profiling cis regulatory elements at high-throughput and single-cell resolution. J. Chiou1 , J. Y. Han2 , C. Zheng3 , F. Cheng2 , M. Schlichting3,4, S. Huang3,4, J. Wang3,4, Y. Sui3,4, A. Deogaygay3 , M.-L. Okino3 , Y. S. Sun3 , P. Kudtarkar3 , R. Fan3 , M. Sander3,4, K. Galton3,5, S. Preissl2,4, and D. Gorkin*2,4, 1 Biomedical Graduate Studies Program, University of California San Diego, La Jolla, CA, 2 Center for Epigenomics, University of California San Diego, La Jolla, CA, 3 Department of Pediatrics, University of California San Diego, La Jolla, CA, 4 Department of Cellular and Molecular Medicine, University of California San Diego, La Jolla, CA, 5 Institute for Genomic Medicine, University of California San Diego, La Jolla, CA.

15:15 OP119 Update on the functional annotation of the equine genome project with a focus on histone modifications across tissues. R. R. Bellone*1 , 2 , J. L. Petersen3 , N. B.

Kingsley2 , C. Creppe4 , S. Peng1 , E. N. Burns1 , T. Kalbfleisch5 , C. Kern6 , H. Zhou6 , J.N. MacLeod5 , and C. J. Finno1 , 1 University of California-Davis, School of Veterinary Medicine, Department of Population Health and Reproduction, Davis, CA, USA, 2 University of California-Davis, School of Veterinary Medicine, Veterinary Genetics Laboratory, Davis, CA, USA, 3 University of Nebraska-Lincoln, Department of Animal Science, Lincoln, NE, USA, 4 Diagneode, Liège, Belgium, 5 University of Kentucky, Gluck Equine Research Center, Lexington, KY, USA, 6 University of California-Davis, Department of Animal Science, Davis, CA, USA.

15:30 OP120 The Ovine FAANG Project: A high-resolution atlas of transcription start sites in the new Rambouillet sheep genome. E. L. Clark*1 , M. Salavati1 , I. Gazova1 , R. Clark2 , T. P. Smith3 , K. C. Worley4 , N. E. Cockett5 , A. L. Archibald1 , and B. Murdoch6 , 1 The Roslin Institute, University of Edinburgh, Edinburgh, UK, 2 Clinical Research Facility, University of Edinburgh, Edinburgh, UK, 3 USDA, ARS, USMARC, Clay Center, NE, USA, 4 Baylor College of Medicine, Houston, TX, USA, 5 Utah State University, Logan, UT, USA, 6 University of Idaho, Moscow, ID, USA.

15:45 OP121 Genome-wide identification of functional DNA elements in the pig genome. Z. Yunxia1 , H. Mingyang1 , H. Ye1 , X. Yueyuan1 , Z. Huanhuan1 , F. Yuhua1 , Y. Hongbo2 , Y. Feng2 , L. Xinyun1 , and Z. Shuhong*1 , 1 Key Lab of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan, China, 2 Department of Biochemistry and Molecular Biology, College of Medicine, The Pennsylvania State University, University Park, PA, USA.

16:30 OP122 The impact of the 1000 Bull Genomes Project and its future. A. J. Chamberlain*1 , C. J. Vander Jagt1 , R. Xiang2 , M. E. Goddard1 , 2 , I. M. MacLeod1 , R. D. Schnabel3 , B. J. Hayes4 , and H. D. Daetwyler1 , 5 , 1 Agriculture Victoria, Centre for AgriBiosciences, Bundoora, Victoria, Australia, 2 Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville, Victoria, Australia, 3 Division of Animal Sciences, Informatics Institute, University of Missouri, Columbia, MO, USA, 4 Centre for Animal Science, The University of Queensland, St Lucia, Queensland, Australia, 5 School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia.

16:45 OP123 Analysis of alternative splicing events across cattle tissues by genome-wide integration of PacBio Iso-seq and RNASeq data. H. Beiki, J. Koltes, Z.-L. Hu, and J. Reecy*, Iowa State University, Ames, IA, USA.

17:00 OP124 BovReg: An international consortium for functional annotation of the bovine genome. C. Kühn*1 , J. Vanselow1 , C. Notredame2 , D. Rocha3 , D. Boichard3 , D. Allaer4 , C. Charlier5 , H. Pausch6 , Y. deHaas7 , M. Lund8 , J. Vilkki9 , H. Taniguchi10, F. Meijboom11, D. Zerbino12, A. Rosati13, G. Plastow14, E. Clark15, J. Prendergast15, A. Bruce15, M. Schmicke16, A. Chamberlain17, H. Daetwyler17, V. Blanquet18, A. J. Amaral19, and D. Bruce20, 1 Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, 2 Centre for Genomic Regulation (CRG), Barcelona, Spain, 3 Institut National de Recherche Agronomique (INRA), Jouy-en-Josas, France, 4 DIAGENODE, Liege, Belgium, 5 GIGA, Université de Liège, Liege, Belgium, 6 Eidgenoessische Technische

Hochschule, Zuerich, Switzerland, 7 Stichting Wageningen Research, Wageningen, Netherlands, 8 Aarhus University, Foulum, Denmark, 9 Natural Resources Institute Finland (LUKE), Jokioinen, Finland, 10Institute of Genetics and Breeding, Jastrebiec, Poland, 11University Utrecht, Utrecht, Netherlands, 12European Molecular Biology Laboratory (EMBL-EBI), Hinxton, UK, 13European Association for Animal Production, Rome, Italy, 14University of Alberta, Edmonton, Canada, 15The University of Edinburgh, Edinburgh, UK, 16Stiftung Tieraerztliche Hochschule Hannover, Hannover, Germany, 17Agriculture Victoria, Centre for Agribiosciences, Bundoora, Australia, 18University of Limoges, Limoges, France, 19Centre for Interdisciplinary in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, 20Edinethics Ltd., Edinburgh, UK.

17:15 OP125 Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. M. Farré1 , J. Kim2 , A. A. Proskuryakova3,4, Y. Zhang5 , A. I. Kulemzina3 , Q. Li6 , Y. Zhou6 , Y. Xiong6 , J. L. Johnson7 , P. L. Perelman3,4, W. E. Johnson8,9, W. Warren10, A. V. Kukekova7 , G. Zhang6,11,12, S. J. O'Brien13, O. A. Ryder14, A. S. Graphodatsky3,4, J. Ma5 , H. A. Lewin15, D. M. Larkin*1,16, 1 Royal Veterinary College, University of London, London, UK, 2 Konkuk University, Seoul, Korea, 3 Institute of Molecular and Cellular Biology, Novosibirsk, Russia, 4 Novosibirsk State University, Novosibirsk, Russia, 5 Carnegie Mellon University, Pittsburgh, PA, USA, 6 BGI-Shenzhen, Shenzhen, China, 7 University of Illinois at Urbana-Champaign, Urbana, IL, USA, 8 Smithsonian Conservation Biology Institute, Front Royal, VA, USA, 9 Smithsonian Institution, Suitland, MD, USA, 10Washington University School of Medicine, St. Louis, MO, USA, 11Kunming Institute of Zoology, Kunming, China, 12University of Copenhagen, Copenhagen, Denmark, 13St. Petersburg State University, St. Petersburg, Russian Federation, 14San Diego Zoo, Escondido, CA, USA, 15University of California, Davis, Davis, CA, USA, 16The Federal Research Center Institute of Cytology and Genetics, Novosibirsk, Russia.

17:30 OP126 eMIRNA: A comprehensive pipeline for discovery and annotation of microRNAs in multiple species. E. Mármol-Sánchez*1 , S. Cirera2 , R. Quintanilla3 , A. Pla4 , and M. Amills1 , 5 , 1 Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, 2 Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark, 3 Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Spain, 4 Department of Medical Genetics, University of Oslo, Oslo, Norway, 5 Departament de Ciència Animal I dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.

17:45 Workshop Business Meeting.

Summary of the meeting

Marina Navel-Sanchez was nominated to serve on the organizing committee. Her membership on the committee was approved by unanimous vote.

Committee chair (the new chair)

Chair: George Liu

Term of service: Through 2021

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

E-mail address: George.Liu@USDA.GOV

Committee members (the new committee)

Other members	Term of service	E mail address
Brenda Murdoch	Through 2023	bmurdoch@uidaho.edu
Sarah Djebali	Through 2023	sarah.djebali-quelen@inra.fr
Marina Naval-sanchez	Through 2025	Marina.Navalsanchez@csiro.au
Lin Jiang	Through 2025	jianglin@caas.cn

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