Comparative and Functional Genomics

STANDING COMMITTEES / WORKSHOPS   Information will be posted online

Organised by a standing committee   yes

Date and meeting time: July 20, 2017; 16:30 – 18:00

Chair name and contact email: Fiona McCarthy, fionamcc@emailarizona.edu

Agenda / programme: attached below

Number of participants at meeting: approx. 170

Summary of the meeting including votes, decisions taken and plans for future conferences

The meeting covered presentations about (1) functional genomics studies related to specific traits and pathways, and (2) studies related to functional genome annotation including an update by Dr Huaijun Zhou about current FAANG (Functional Annotation of Animal Genomes) efforts to identify regulatory elements in livestock species. During the business meeting the chair informed 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 the excellent talks and active contributions to interesting discussions.

Committee members:
Chair: Fiona McCarthy (2016- present)

Fiona McCarthy	2012 – 2019	fionamcc@email.arizona.edu
Paolo Zambonelli	2014 – 2017	paolo.zambonelli@unibo.it
Guisheng Liu	2014 – 2017	guisheng_liu1964@yahoo.com
Yangfang Wang	2014 – 2017	yanfangw@hotmail.com
Christa Kühn	2016 – present	kuehn@fbn-dummerstorf.de
Christina Ovilo	2016 – present	ovilo@inia.es
Carl J Schmidt	2016 – present	schmidtc@udel.edu

Comparative and functional genomics Workshop schedule:

Comparative and functional Genomics (orals)
Chair(s): **Fiona McCarthy, The University of Arizona**
Location: **George Moore Auditorium, O'Brien Science Building**
Date & Time: **Thursday, July 20, 2:30 PM - 6:00 PM**

2:30 PM		**Welcoming Remarks.**
2:30 PM	71642	**Identification of Regulatory Elements in Livestock Species.**
		H Zhou*[1], P Ross[1], C Kern[1], P Saelao[1], Y Wang[1], M Halstead[1], K

Chanthavixay[1], I Korf[1], ME Delany[1], HH Cheng[2], JF Medrano[1], AL Van Eenennaam[1], CK Tuggle[3], and C Ernst[4], *University of California, Davis, Davis, CA, USA*, [2]*USDA-ARS, Avian Disease and Oncology Laboratory*, *East Lansing, MI, USA*, [3]*Iowa State University, Ames, IA, USA*, [4]*Michigan State University, East Lansing, MI, USA*.

3:00 PM	71665	**Transcription factor binding sites enrichment in ruminant and cetartiodactyl specific conserved non-coding elements.** Laura Buggiotti*, Marta Farrè, and Denis Larkin, *Royal Veterinary College, London, United Kingdom.*
3:15 PM	70387	**Gene regulation in sheep alveolar macrophages: Genome-wide identification of active enhancers.** AT Massa*[1], MR Mousel[2,1], B Murdoch[3], and SN White[2,1], [1]*Washington State University, Pullman, WA, USA*, [2]*United States Department of Agriculture-ADRU, Pullman, WA, USA*, [3]*University of Idaho, Moscow, ID, USA.*
3:30 PM	71645	**The reconstruction and evolutionary history of eutherian chromosomes.** J. Kim[1], M. Farre[2], L. Auvil[3], B. Capitanu[3], J. Ma[4], H.A. Lewin[5], and D.M. Larkin*[1], [1]*Department of Biomedical Science and Engineering, Konkuk University, Seoul, Korea*, [2]*Royal Veterinary College, University of London, London, UK*, [3]*Illinois Informatics Institute, University of Illinois at Urbana-Champaign, Urbana, IL, USA*, [4]*Computational Biology Department, School of Computer Science, Carnegie Mellon University, Pittsburgh, PA, USA*, [5]*Department of Evolution and Ecology, University of California, Davis, CA, USA.*
3:45 PM	70141	**iTRAQ-based proteomic analysis reveals key proteins affecting muscle growth and lipid deposition in pig.** Z Wang*[1], P Shang[1,2], Q Li[3], L Wang[1], H Zhang[1], and C Wu[1], [1]*China Agricultural University, Beijing, China*, [2]*Tibet Agriculture and Animal Husbandry University, Linzhi, China*, [3]*Anhui Academy of Agricultural Sciences, Hefei, China.*
4:00 PM		**Coffee/Tea Break.**
4:30 PM	71284	**Hypothalamus transcriptome during the early rise in LH secretion related to puberty age in bull calves.** JP Liron[1], ME Fernández*[2], A Prando[3], A Baldo[3], and G Giovambattista[2], [1]*Center of Veterinary Research (CIVETAN, CONICET), Faculty of Veterinary Sciences, UNCPBA, Tandil, Buenos Aires, Argentina.*, [2]*Institute of Veterinary Genetics (IGEVET, CONICET), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina*, [3]*Cátedra de Zootecnia Especial (II Parte)), Faculty of Veterinary Sciences, National University of La Plata, La Plata, Buenos Aires, Argentina.*
4:45 PM	71396	**Integrative genomics of human and bovine tuberculosis.** K. E. Killick*[1,2], M. P. Mullen[3], T. Hall[1], N.C. Nalpas[4], I.W. Richardson[5], D.A. Magee[1], C.N. Correia[1], J.A Browne[1], D.P. Berry[6], D. Bradley[7], V. Naranbhai[8], A Hill[8], E. Gormley[9], S.V. Gordon[2,9], D.E. MacHugh[1,2],

		[1]*University College Dublin, UCD College of Health and Agricultural Sciences, University College Dublin, Dublin 4, Ireland,* [2]*University College Dublin, UCD Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Ireland,* [3]*Athlone Institute of Technology, Department of Life and Physical Sciences, Athlone Institute of Technology, Athlone, N37 HD68, Ireland.,* [4]*University of Tübingen, Quantitative Proteomics and Proteome Centre Tübingen, Interfaculty Institute for Cell Biology, University of Tübingen, 72076 Tübingen, Germany.,* [5]*IdentiGEN Ltd, IdentiGEN Ltd., Blackrock Business Park, Blackrock, Dublin, D04 W6F6, Ireland.,* [6]*Teagasc, Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Cork, P61 C996, Ireland.,* [7]*Trinity College, Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin 2, Ireland.,* [8]*University of Oxford, Wellcome Trust Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, Oxford, OX3 7BN, UK.,* [9]*University College Dublin, UCD School of Veterinary Medicine, University College Dublin, Belfield, Dublin, D04 W6F6, Ireland.*
5:00 PM	71407	**Circulating microRNAs as potential novel biomarkers to diagnose *Mycobacterium avium* subsp *paratuberculosis* infection in cattle.** K Zhao[1], S Hendrick[2], and LL Guan*[1], [1]*Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada,* [2]*Coaldale Veterinary Clinic, Lethbridge, Canada.*
5:15 PM	71652	**Generating customized integrated functional annotation datasets with BovineMine.** CG Elsik*, DR Unni, A Tayal, and DE Hagen, *University of Missouri, Columbia, Missouri, USA.*
5:30 PM	71488	**The vertebrate gene nomenclature committee (VGNC).** P Denny*, B Yates, S Tweedie, B Braschi, K Gray, R Seal, and E Bruford, *European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Hinxton, Cambridgeshire, UK.*
5:45 PM		**Workshop Business Meeting**