ISAG INTERNATIONAL SOCIETY FOR ANIMAL GENETICS

Joint workshop

Comparative and Functional Genomics

Organised by a Standing Committee: ☑ YES NO

Meeting information

Date: 24/07/2025 (24th July 2025)
Time: 13:30 to 18:00
Number of participants: ~ 120 participants

Chair

Name: Christa KUEHN
Affiliation: Friedrich-Loeffler-Institute, Germany
Contact email: christa.kuehn@fli.de

Co-Chair (optional)

Name: Cristina Ovilo
Affiliation:
Contact email:

Agenda

1:30 to 3.00 PM – Presentation of selected communications

1:30 PM OP197 Decoding the bovine regulatory landscape: Genome-wide high-resolution mapping of regulatory elements in cattle.

R. Zhao*[1], R. Owen[1], L. Pagie[2], M. Marr[1], K. Jensen[1], V. Bisht[2], T. Connelley[1], L. Morrison[1], J. van Arensbergen[2], M. Hassan[1], and J. Prendergast[1], *[1]Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, United Kingdom, [2]Annogen B.V., Science Park 406, 1098XH, Amsterdam, The Netherlands.*

2:00 PM OP198 An atlas of gene expression in goats.

M. J. Wang*[1,2], A. Noce[1], M. Luigi Sierra[1], D. Vargas[1], E. Mármol-Sánchez[1], K. Wang[1], E. Petretto[1], S. Olvera Maneu[3,4], P. Serres[4], J. Gardela[4], M. López Béjar[4], and M. Amills[1,2],
[1]Centre de Recerca Agrigenòmica (CRAG), CSIC-IRTA-UAB-UB, Campus Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, [3]Department of Veterinary Medicine, University of Nicosia, School of Veterinary Medicine, Nicosia, Cyprus, [4]Department of Animal Health and Anatomy, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.

2:18 PM OP199 Cross-species integration of single-cell RNA sequencing reveals conserved mechanisms in bovine and ovine placentation.

M. L. Leavitt[1], W. C. Warren[2,3], T. E. Spencer[2,4], and K. M. Davenport*[1]
[1]Department of Animal Sciences, Washington State University, Pullman, WA, USA, [2]Division of Animal Sciences, University of Missouri, Columbia, MO, USA, [3]Institute for Data Science and Informatics, University of Missouri, Columbia, MO, USA, [4]Department of Obstetrics, Gynecology, and Women's Health, University of Missouri, Columbia, MO, USA.

2:36 PM OP200 ISAG Bursary Award: RNA-editing, a potential mechanism to influence gene expression, is regulated by genomic variation in Bos taurus and Bos indicus cattle.

M. S. Tahir*[1], M. Goddard[1,4], B. Hayes[2], C. Van der Jagt[1], R. Xiang[1], B. Mason[1], M. Forutan[2], E. Ross[2], L. T. Nguyen[2], I. van den Berg[1], S. Meier[3], C. Phyn[3], C. Burke[3], and A. Chamberlain[1]
[1]AgriBio Center, Agriculture Victoria Research, Bundoora, Victoria, Australia, [2]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Queensland, Australia, [3]DairyNZ, Newstead, Hamilton, New Zealand, [4]University of Melbourne, Parkville, Victoria, Australia, [5]School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia.

2:54 PM OP201 Chromosome-level genome assembly of Korean long-tailed chicken and pangenome of 40 Gallus gallus assemblies.

H. D. Shin*[1], W. Park[2], H. Chai[2], Y. Lee[1], J. Jung[1], BJ Ko[3], and H. Kim[1,3]
[1]Interdisciplinary Program in Bioinformatics, Seoul National University, Seoul, Republic of Korea, [2]Animal Genomics & Bioinformatics Division, National Institute of Animal Science, RDA 1500, Wanju, Republic of Korea, [3]Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.

3:12 PM OP202 Identification of goat molQTL based on large-scale transcriptome data.

Min Tian[1], Meiwen Song[1], Zhen Zhang[1], Yifan Li[1], Xueqing Han[1], Jun Luo[1], Lingzhao Fang[2], and Cong Li*[1]
[1]College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China, [2]Center for Quantitative Genetics and Genomics, Aarhus University, Aarhus, Denmark.

3:30 PM Coffee Break.

4.00 PM to 5.48 PM – Presentation of selected communications

4:00 PM OP203 A comprehensive miRNA resource for livestock genomics.

K. Pokharel*[1], A. J. Amaral[2], B. Liang[3], C. Anthon[3], G. Corsi[3], S. Marthey[4], A. Hoffman[5], J. Lagnel[6], F. Haack[7], O. Palasca[3], S. Seemann[3], L. T. Gama[2], M. A. M. Groenen[8], J. Kantanen[1], R. P. M. A. Crooijmans[8]

[1]Natural Resources Institute Finland (Luke), Jokioinen, Finland, [2]Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, [3]Center for Noncoding RNA in Technology and Health, Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark, [4]GABI, AgroParisTech, INRA, Université Paris Saclay, Jouy-en-Josas, France, [5]Bioinformatics Group, Department of Computer Science, University of Leipzig, Leipzig, Germany, [6]INRA PACA, Montfavet Cedex, France, [7]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [8]Wageningen University & Research, Wageningen, the Netherlands, [9]Veterinary Integrative Biosciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA, [10]Veterinary Science Department, Martin-Gatton College of Agriculture, Food, and Environment, Lexington, KY, USA.

4:18 PM OP204 Deep learning deciphers the regulatory grammar of transcription initiation in non-model immune cells.

C. Zhu*, R. Owen, T. Connelley, L. Morrison, M. Hassan, D. Macqueen, R. Zhao, and J. Prendergast

Roslin Institute, The Royal (Dick) School of Veterinary Studies, The University of Edinburgh, Edinburgh, Scotland, UK.

4:36 PM OP205 Chromatin activation direct asymmetrical gonadal development in female but not male chickens.

Z. L. Peng*, Y. Q. Jiang, Y. L. Liao, X. Y. Li, and H. Wang

Huazhong Agricultural University, Wuhan, Hubei, China.

4:54 PM OP206 Comparison of pig, human, and mouse transcriptomes: Implications for complex traits and disease modeling.

Jingwen Dou*[1], Xin Huang[1], Jingjin Li[1], Hong Liu[1], Yong Liao[1], Yue Wang[1], Jingya Xu[1], Zhengshuang Tang[1], Xinyun Li[1,2], Shuhong Zhao[1,2], Xiaolei Liu[1,2], and Yuhua Fu[1]

[1]Key Laboratory of Agricultural Animal Genetics, Breeding and Reproduction, Ministry of Education, Huazhong Agricultural University, Wuhan, Hubei 430070, PR China, [2]Frontiers Science Center for Animal Breeding and Sustainable Production, Wuhan, Hubei 430070, PR China, [3]Hubei Hongshan Laboratory, Wuhan, Hubei 430070, PR China.

5:12 PM OP207 European Network on Livestock Phenomics: An international initiative to enhance genome to phenome integration in all livestock species for applications in animal breeding.

Luca Fontanesi*1, Tomas Norton[2], and EU-LI-PHE Consortium

[1]Animal and Food Genomics Group, Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy, [2]M3-BIORES Research Group, Division of Animal and Human Health Engineering, Department of Biosystems, KU Leuven, Leuven, Belgium.

5:30 PM OP208 Enrichment of fertility-related quantitative trait loci in regulatory regions of the bovine placenta.

M. D. Wagle*[1], H. L. Neibergs[1], T. E. Spencer[2,3], and K. M. Davenport[1]
[1]Department of Animal Sciences, Washington State University, Pullman, Washington, United States of America, [2]Division of Animal Sciences, University of Missouri, Columbia, Missouri, United States of America, [3]Department of Obstetrics, Gynecology, and Women's Health, University of Missouri, Columbia, Missouri, United States of America.

5:48 PM Business meeting.

Summary of the meeting

The Comparative and Functional Genomics poster session featured 28 posters covering nine species and also several (seven) multispecies posters underlining the across-species focus of this workshop. The quality of abstracts and subsequently the poster on display at the conference were of high scientific quality, particularly those from early-career scientists.

From the submitted abstracts 12 posters were presented as oral presentations in the workshop. The number of submissions cancelled before the conference was low, also an indicator of the strong interest of colleagues in the topic of the workshop.

The presentations were a good representation of the wide range of abstract topics. They ranged from overviews on European network projects on multispecies efforts for improved resources to novel laboratory and bioinformatic methods to characterize regulatory elements in livestock genome transcription. The mostly early career scientists presenting their work demonstrated that they had included comprehensive novel tools e.g. single cell sequencing, CRISPR and epigenomic assays, for characterization of genome function and its relation to complex traits.

Both parts of the workshop were well-attended until the end of the last presentation. The discussions of the presentations included questions as to the potential application of the new knowledge, the benefits of new methods and questions how to join the networks presented.

In the business meeting, the recent activities since the last workshop were summarized. The discussion from the last C&F Genomics workshop in Cape Town 2023 was taken up on the question, whether to merge with one of the other existing FAANG related workshops of ISAG (Epigenomics, Domestic Animal Sequencing). There was agreement that the 2025 ISAG contributions and the workshop program for each of the three workshops demonstrated a specific feature for each of the three. This was presumably the result of interaction between the three workshop standing committees with the ISAG secretary and ongoing FAANG actions before the conference. The large audience to the C&F Genomics workshop also proved the relevance of the workshop for livestock animal genomics. Thus, there was an agreement between workshop attendees to keep the workshop in its current structure.

New Committee chair

Chair: Emily Clark
Term of service: first year in second term
Affiliation: European Molecular Biology laboratory, Hinxton/UK
E-mail address: Emily Clark <eclark@ebi.ac.uk>

New Committee co-chair (optional)

Chair: Eveline Ibeagha-Awemu
Term of service : first year in second term
Affiliation: McGill University, Agriculture and Agri-Food Canada, Sherbrooke, Canada
E-mail address: Ibeagha-Awemu, Eveline (AAFC/AAC) <eveline.ibeagha-awemu@AGR.GC.CA>

Note: One term runs for two bi-annual conferences (i.e. four years)

Committee members

Other committee members	First term of service (from year to year)	Second term of service (from year to year)	Email address
Emily Clark		2025-2029	Emily Clark eclark@ebi.ac.uk
Lingzhao Fang		2025-2029	Lingzhao.fang@ed.ac.uk

Eveline Ibeagha-Awemu		2025-2029	eveline.ibeagha-awemu@agr.gc.ca
Stephanie McKay		2025-2029	Stephanie.McKay@missouri.edu
Maria Munoz	2025-2029		mariamm@inia.csic.es
Kimberley Davenport	2025-2029		kimberly.davenport@wsu.edu
Marta Godia	2025-2029		Marta.godia@wur.nl

COMPARISON TEST (2026-2027) YES ☑ NO (If no delete the rest of this page)

SIGNATURE

Chair (outgoing)