

Workshop 2014

Epigenomic Toolbox: from Methods to Models

Las Palmas, Spain, 07 - 09 May 2014

PROGRAMME

Day 1

Wednesday 07 May 2014

- 16:00 – 19:00 Meeting Registration
- 19:00 – 20:30 Welcome Reception
- 20:30 – 23:00 Dinner

Day 2

Thursday 08 May 2014

- 08:00 – 08:45 Breakfast
- 08:45 – 09:00 **Opening of Meeting**
Welcome Address
- 09:00 – 09:40 **What's in the Epigenomic Toolbox?**
Claude Robert, Laval University, Canada
Integrating the DNA methylome and transcriptome to better define the long term impacts of assisted reproductive technologies.
- 09:40 – 10:20 **Andre Eggen, Illumina, United States**
Last generation tools for the study of the genome and the epigenome.
- 10:20 – 10:35 **Gavin Kelsey, Babraham Institute, United Kingdom**
Profiling DNA methylation genome-wide at base-pair resolution in single oocytes.
- 10:35 – 10:50 **Dafni Anastasiadi, Institute of Marine Sciences, Spain**
Genome-wide alterations of DNA methylation in European sea bass (*Dicentrarchus labrax*) subjected to different environments.
- 10:50 – 11:20 Coffee
- 11:20 – 11:35 **Analyse your Data!**
Laszlo Tecsı, University of Sheffield, United Kingdom
Rules of Travel Reimbursements
- 11:35 – 12:15 **Christoph Bock, Research Centre for Molecular Medicine, Austria**
Methods for sequencing-based mapping and bioinformatics analysis of DNA methylation.
- 12:15 – 12:55 **Ana Conesa, Principe Felipe Research Centre, Spain**
The STATegra project: new statistical tools for analysis and integration of diverse omics data.

12:55 – 14:15	Lunch
14:15 – 14:55	Epigenetic Regulation of Development Valentina Lodde, University of Milan, Italy Oocyte large-scale chromatin configuration re-modelling: state of the art and perspectives.
14:55 – 15:35	Philippe Collas, Oslo University Hospital, Norway Microchip assay and epigenetics of embryonic genome activation and early development.
15:35 – 15:50	Ramiro Alberio, University of Nottingham, United Kingdom Paracrine effects of embryo-derived FGF4 and BMP4 during pig trophoblast elongation.
15:50 – 16:05	Karolien Desmet, University of Antwerp, Belgium Elevated non-esterified fatty acid concentrations during bovine embryo culture influence DNA methylation patterns in blastocysts.
16:05 – 16:35	Tea
16:35 – 19:00	Epigenomic Toolbox: from Methods to Models Poster Presentation
19:00 – 23:00	Gala Dinner

Day 3

Friday 09 May 2014

08:00 – 09:00	Breakfast
09:00 – 09:40	Epigenetic Reprogramming Manel Esteller, Bellvitge Biomedical Research Institute, Spain Cancer Epigenetics: from knowledge to applications.
09:40 – 09:55	Marisol Izquierdo, University of Las Palmas, Spain <i>Sparus aurata</i> as a model for nutritional reprogramming of marine fish: Effectiveness of different developmental windows.
09:55 – 10:10	Aneta Andronowska, Institute of Animal Reproduction and Food Research, Poland Does the presence of an embryo in the uterus prevent induction of luteolytic chemokines and chemokine receptors mRNA in the porcine CL?
10:10 – 10:25	Antonio Gonzalez-Bulnes, Spanish National Institute for Agricultural and Food Research and Technology, Spain Modification of adiposity and metabolic features by trans-generational developmental programming in swine with thrifty genotype.
10:25 – 10:40	Catherine Labbe, French National Institute for Agricultural Research, France DNA methylation pattern in fish spermatozoa after cryopreservation: a species specific alteration in cyprinids.
10:40 – 11:10	Coffee
11:10 – 12:00	Roundtable
12:00 – 13:00	Application to Horizon 2020

Closing of Meeting

13:00 – 13:15 Farewell Address

13:15 – 14:30 Lunch

15:00 – 18:00 Sightseeing Tour

20:30 – 23:00 Dinner

Day 4

Saturday 10 May 2014

08:00 – 09:00 Breakfast

10:00 – 14:00 Excursion