



CONFERENCE/WORKSHOP ORGANISER'S REPORT

“International Symposium of Animal Functional Genomics”

The opinions expressed and arguments employed in this report are the sole responsibility of the authors and do not necessarily reflect those of the OECD or of the governments of its Member countries.

Brief Description of what the conference/workshop was about

ISAFG2015 convened prominent scientists from all over the world to define the state of the art of technologies and strategies available for investigating livestock biology. Topics discussed included genome architecture and regulation, the role of microbes in health and production, and the best use of new technologies for improving livestock sustainability in developed and developing countries.

Participation – details of total number of participants, countries they came from, backgrounds (academia, industry, etc.

A total of 150 participants from 22 different countries (Australia, Brazil, Canada, Denmark, Egypt, Finland, France, Germany, Greece, Korea, Ireland, Israel, Italy, Poland, Portugal, Romania, Spain, South Africa, The Netherlands, Czech Republic, United Kingdom, United States) participated at ISAFG2015. The majority were from academia, but representatives of biotech industries and breeding organizations were also present.

Major highlights from the presentations

ISAFG2015 started with a brief welcome of the organizer (Paolo Ajmone Marsan) and an introduction of OECD organization and goals (Rafael Blasco). The scientific program followed up. The main concepts arising from the presentations and the lively discussion were the following:

- 1) EU framework programmes had an important role in fostering cooperation between countries by funding a number of successful projects on livestock sustainability and welfare; many involving advanced technologies (Jean Charles Cavitte). Horizon 2020 offers new funding opportunities.
- 2) Genomic technologies are mature to be applied in the field. Genomic selection based on arrays of markers is already applied in dairy cattle worldwide. Whole genome sequencing (WGS) greatly facilitates the identification of causative mutations responsible for genetic defects negatively affecting animal welfare and production, and for beneficial characteristics (Jerry Taylor; Tad Sonstegard).
- 3) The identification and use of genes controlling complex traits is still more elusive. Genes are identified but their cumulative effect on traits is small (Nicole Soranzo). One option is to tag the so called “intermediate phenotypes” (Ben Hayes), that is individual components of complex traits, as the concentration of specific compounds in milk that contribute to milk quality and yield or immune repertoire profiling (Tim Smith).
- 4) WGS permits also the reconstruction of species and breed origin, demography and admixture and to identify genomic region under positive and balancing selection and therefore carrying relevant genes for production and adaptation (Martien Groenen).
- 5) The use of genomics and other –omic technologies in developing countries is greatly dependent on the type of husbandry system and level of organization of animal breeding (Kathiravan Peryasami, José Fernando Garcia). In no case the genomic selection model as applied in the developed world seems the most appropriate.
- 6) The next step in livestock genomic is the investigation of gene regulation mechanisms and the consequent annotation of livestock genomes with regulatory important sites. The FAANG (Functional Annotation of



Animal Genomes) initiative is guiding this endeavor and includes hundreds researchers worldwide that agree in producing according to shared standards and immediately open to the public functional data (Alan Archibald) adapting to livestock the model set by the human ENCODE project.

- 7) Understanding the epigenetic control of gene expression and the biological mechanisms taking from the genotype to the phenotype is still very challenging. MicroRNAs have been proven to influence livestock and human disease status by post-transcriptionally controlling gene expression (John Williams). However their mechanisms of recruitment, regulation, and action are still not completely understood (Amy Pasquinelli). The control of gene expression by DNA methylation appears extremely important during embryo development and a major case of failure in embryos developed *in vitro* (Pasqualino Loi).
- 8) Finding connections and eventually make sense of millions data produced by different –omic technologies is a difficult task requiring a significant amount of time and effort by the scientific community. Computational and systems biology together with system genetics bioinformatics are exploring novel strategies of data analysis and solutions, as new network analysis and visualization tools, to support data exploration and interpretation. These new approaches are efficient in investigating traits important for humans as well as livestock as response to vaccination, obesity, fertility and feed efficiency (Haja Kadarmideen, David Lynn).
- 9) The gut microflora has an important role in animal and human health and in nutrient absorption, likely influencing feed efficiency and obesity (Lorenzo Morelli). Animal-microbes interaction is particularly important in ruminants. Rumen microbioma permits animals to survive on a high fiber diet by fermenting cellulose, but produces carbon dioxide and methane that have a greenhouse effect. The interaction between the rumen microbioma and the genetics of animals is presently under investigation, to explore the opportunity of improving ruminants for low methane emission and high feed efficiency. (John Wallace)
- 10) Advances in technologies drive advances of science. Reliability, accuracy, throughput and affordability of genomic and post genomic technologies is improving, but needs further development that is possible only with a close collaboration between biotech industries and the research community (Affimetrix, Illumina, Agilent, Recombinetics, Flowmetric).

Major outcomes/conclusions in terms of policy relevance

ISAFG2015 discussed the state of the art and the role of genomic and post-genomic technologies in better understanding livestock biology. New technologies have the potential to speed up and precisely guide selection and to customize animal management to increase livestock efficiency, welfare and animal product quality while decreasing the environmental impact of breeding. Conclusions drawn during the symposium are:

- 1) Further research is needed to exploit the full potential of -omic information.
 - a. Reference genomes are still imprecisely assembled and their annotation is largely incomplete. In addition sequencing cost is still too high for sequencing large populations, while large numbers are needed for sound statistical analyses.
 - b. Phenotypes are presently limited to a few traits, sometimes exceedingly complex, so new and better phenotypic data are needed,
 - c. Better methods of data analysis are desirable on the one side to estimate the effect of structural variations, on the other to integrate genomic with other -omic data.



- d. Other –omic technologies (transcriptomics, proteomics, metabolomics, epigenomics) are fundamental for understanding animal biology, the interaction between genes and the environment and the functional annotation of genomes.
 - e. The collection, management and interpretation of billions –omic data makes biostatistics and bioinformatics a real need for the scientific community. Novel models of analysis, open source software, storage and calculus capacity are key issue for the future of research in the field.
 - f. Understanding the interaction between livestock and gut micro-organisms appears fundamental to fully understand animal biology.
 - g. New technologies for targeted genetic editing have been developed. Once identified a favorable allele in a breed, these permit to quickly introduce favorable alleles in animals from other breeds. These technologies are very interesting and do not involve transfer of genes between species or between animals, as in the debated GMO technology.
- 2) International collaboration and public availability of data are fundamental for the quick progress of knowledge and its translation in practical applications.
- a. Partnership and coordination between public funders, research and industry within and across country is the way to proceed.
 - b. National support and resources integrated within a regional (e.g. EU) or global strategy, avoid duplications and exploit synergies.
 - c. Open source of data and software improves the efficiency and efficacy of research directed to address both global and local problems.
 - d. Fostering internationalization through collaborative projects and young and experience researcher exchange reinforces existing and creates new networks, trigger cooperation and improve local knowledge

Relevance to CRP theme(s)

The topic of the Symposium is extremely relevant to the CRP Food Chain theme. Across the globe, livestock are a major source of human food with high nutritional value. Genomic and post-genomic technologies will play a key role in better understanding livestock biology and hence more effectively directing selection for genetic improvement and guiding animal management to increase efficiency and quality while decreasing environmental impact

Website for further details – please also indicate if the presentations are/will be available on the website

For further details, please visit the ISAFG2015 website (WWW.ISAFG2015.it). A .pdf version of the presentations will be available soon.