Research on domesticated animals has important socio-economic impacts, including underpinning improvements in the livestock sector, contributions to medical research, animal health and welfare, the evolution of domestication and the understanding of natural animal populations.

The genomes of the major domesticated animal species have been sequenced and significant improvements in the contiguity of the reference genome sequences of farmed animals have been achieved recently. However, the characterisation and annotation of these genome sequences remains a work in progress. The number of alternative transcripts for protein coding genes is underestimated, non-coding RNA genes are poorly characterised and annotated and critically current annotation is almost devoid of regulatory sequences. Thus, significant investment is required to improve the functional annotation of these genomes in order to improve their utility for research and application.

The global launched “Functional Annotation of Animal Genomes” (FAANG) initiative aims to improve the functional annotation of animal genomes. This FAANG - Europe COST Action will facilitate the aims of the FAANG project

www.faang-europe.org

23 participant EU countries
3 non-EU partners, 1 EU organization
COST action duration April 2016-April 2020

Action Chair: Prof. Dr. Alan Archibald, Roslin Institute

Action Co-Chair: Dr. Elizabetta Giuffra, INRA

STSM coordinator: Dr. Andreia J. Amaral, FMV-UL
Improving the functional annotation of animal genomes is our key challenge

This COST action has created a network to address this challenge at European level creating new bridges between European researchers

COST Action CA15112 on "Functional Annotation of Animal Genomes - European Network" (FAANG-Europe) was set in the context of the global Functional Annotation of Animal Genomes (FAANG) initiative. The global FAANG initiative as well as CA15112 COST Action aim to facilitate cooperation between researchers in Europe as well to provide the means for capacity building towards the common objective of improving genomic prediction by identifying the functional sequences within domesticated animal genomes. The Action runs from 2016-2020 and is organized in 5 Working Groups (WG) aiming at building a European community of researchers and stakeholders sharing the interests in the scientific and/or socio-economic relevance of the FAANG initiative. Efforts are in place to promote knowledge exchange and the development of a joint research agenda.

FAANG-Europe
Capacity building for the annotation of livestock genomes

# | WG Leader | Country |
---|-----------|---------|
WG1 | Dr Elena Sarropoulou sarris@hcmr.gr | Greece |
WG2 | Dr Frank Panitz frank.panitz@mbg.au.dk | Denmark |
WG3 | Prof. Dr Jan Gorodkin mailto:gorodkin@rth.dk | Denmark |
WG4 | Prof Peter Dovc peter.dovc@bf.uni-lj.si | Slovenia |
WG5 | Dr Ramona Pena romi.pena@ca.udl.cat | Spain |
Capacity building

Objectives

To train research scientists and students in a) assays by sequencing, b) analysis of functional sequence data, c) use of annotated genome sequences and functional annotation data.

To identify and facilitate the sharing of biological resources for functional genomics in domesticated animals.

To identify and facilitate the sharing of bioinformatics resources for functional genomics in domesticated animals.

STSM Program

Training for research scientists has been delivered through Short Term Scientific Missions (STSMs). This COST Action has enabled a total of seven STSMs, two to Early Career Researchers (up to 8 years after PhD) and the remaining five to PhD candidates. The Action has been successful in stimulating the participation of female researchers that account for 42% of the STSMs. The STSMs have facilitated both training in the analysis of functional sequence data as well as in assays by sequencing (e.g. Chromatin Immuno-precipitation Sequencing, ChIP-Seq).

Hackathons

In November 2016, the first Hackathon was organized by Jan Gorodkin in Copenhagen. In this event the goal was to get together researchers in Bioinformatics and Genomics in order to develop pipelines and analyses that would enable contributions to the aim of FAANG, the annotation of animal genomes, using public available data. In this hackathon PhD candidates, postdocs and staff researchers from 8 different countries participated and two working groups were established. one focusing on small ncRNAs (mainly micro RNAs) and one on long ncRNAs. For each of these groups there have been regular TCs ensuring the further coordination of the efforts. A key focus has been to identify the proper data sets for benchmarking suitable program for the different steps ranging from QC to complete

Elena Kirsanova
PhD candidate, first year
Norwegian University of Life Sciences

“The results obtained during the STSM will contribute to better functional annotation of the bovine genome”.

Aroa Suarez Vega, PhD
Affiliation during the STSM: Universidad de Léon, Spain
Currently at University of Guelph, Canada

“The exchange visit funded by the STSM COST Action has allowed me to increase my expertise on the analytical approaches implemented for the annotation of functional elements on RNA-Seq” data.”
Continued

ncRNA transcripts and genes. The efforts has also been disseminated both at the non-coding RNA workshop at the PAG meeting 2018 (both groups) as well as at the RNAcentral meeting 2017 in Hinxton.

A second Hackaton of FAANG-Europe was held in March 2017 in Toulouse, France. Its was organized by Sarah Djebeli, Sylvain Foissac and Christophe Klopp from INRA. It aimed at evaluating the impact of the sequencing depth on the evolution of various QC criteria for three different types of analysis: a) Gene expression; b) Gene modeling; c) ATAC-seq. At this event researchers from 11 different countries participated. As a result metrics were established for different types of analysis of functional data.

The third Hackaton of FAANG-Europe was held in Copenhagen in September 2018. Its was organized by Jan Gorodkin as follow-up of the workings groups that were previously established. The aim was to develop the outline of the dissemination papers that are currently under preparation as a result of this joint effort.

International training school on ChIP-seq (wet-lab) and basic functional animal genome analysis

Wageningen University & Research, Animal Breeding and Genomics did organize a training school from 25-29 of June, 2018 about functional annotation. The training school was a combination of wet-lab experiments (hands on ChIP-seq), data analysis (genome annotation) and a seminar with international guest speakers. The strength of this training school was the combination of wet-lab and data analysis and presentations on applications on functional annotation. Within the training school we worked with a team of international trainers on data analysis and wet-lab ChIP-seq of cultured chicken fibroblast cells and porcine liver tissue in close collaboration with Diagenode. Nuclei from cultured cells or harvested from disaggregated liver tissue were isolated followed by DNA-protein crosslinking, chromatin shearing and immunoprecipitation. Quantitative PCR was used to check for final enrichment. The data analysis part was divided in building blocks (modules) including a module on working with command line software (Linux), data quality checks, data and analysis of whole genome sequence, expression and ChIP-seq data. In total 17 participants from 8 countries and 3 continents participated in this training school. We were able to
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