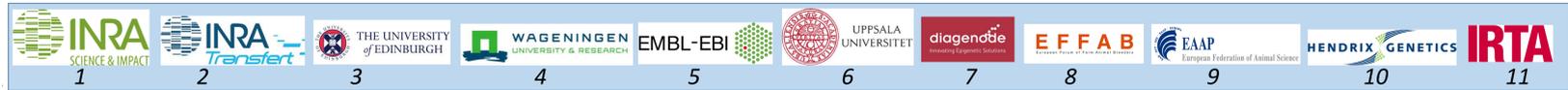


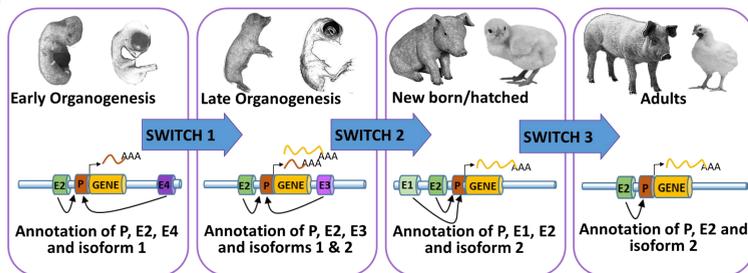
Elisabetta Giuffra, GENE-SWitCH Consortium[§]

[§]Executive Committee: Elisabetta Giuffra¹, Hervé Acloque¹ (deputy coordinator), Camille Bénard², Léa Tourneur², Mick Watson³, Alan Archibald³, Mario Calus⁴, Jerry Wells⁴, Guy Cochrane⁵, Fergal Martin⁵, Celine Sabatel⁷, Cagla Kaya⁸, Duru Eroglu⁸, Andrea Rosati⁹, Marco Bink¹⁰



The H2020 project GENE-SWitCH (2019-2023) aims to deliver new underpinning knowledge on the functional genomes of two main monogastric farm species (pig and chicken) in the framework of the Functional Annotation of Animal Genomes (FAANG) initiative and to enable immediate translation to the pig and poultry sectors. The consortium brings together partners representing pan-European excellence and world-leading animal breeding and biotech industry in a true co-creation effort. INRA coordinates the Consortium and is in charge of the management of project and ethical aspects.

Functional Annotations across tissues and developmental stages



High-quality, richly annotated maps of pig and chicken genomes

- **Developmental stages:** fetus/embryo at 30 and 70 days post-fertilization, and newborns.
- **Biological replicates:** 2 males and 2 females.
- **Tissues:** liver, skeletal muscle, small intestine, cerebellum, dorsal epidermis, lung and kidney.
- **Assays:** ATAC-seq; CHIP-seq: H3K4me3, H3K4me1, H3K27me3, H3K27Ac, CTCF; RNA-seq: mRNA-seq; small RNAseq, lRNA-seq; DNA methylation: RRBS and WGBS, Hi-C: Capture Hi-C; whole genome sequences.

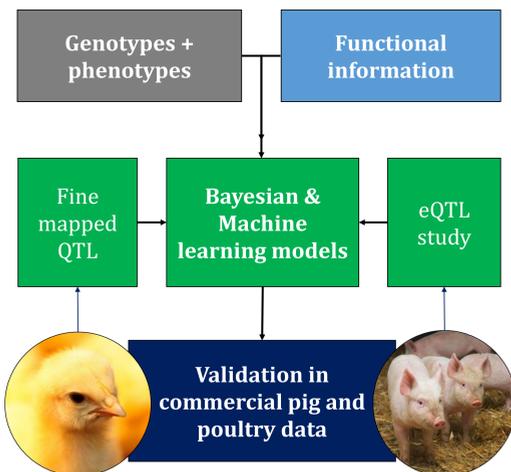
- **Development and deployment of bioinformatic pipelines and analyses:** i) generate and integrate new annotations with existing FAANG data in adult animals to detect developmental gene switches, unravel the evolutionary dynamic of putative functional elements and infer their patterns of conservation and variation by comparative analyses; ii) deliver the annotations via the Ensembl Genome Browser.
- **The new pipelines will be used for the analyses of data from larger animal cohorts by relying on the enriched annotations.**

Implementing FAANG innovation for animal breeding

Improving predictive models for genomic selection

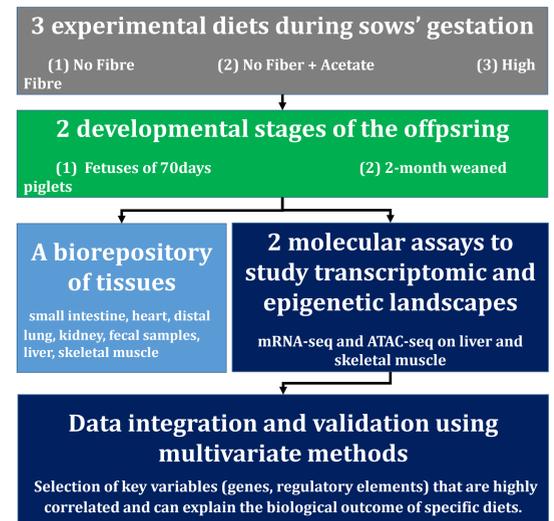
Develop and validate new genomic prediction models that use functional information on top of the commonly used phenotypic and genotypic data.

Pigs: eQTL data generated within GENE-SWitCH as phenotypes (300 animals, 3 target tissues: small intestine, skeletal muscle, liver). Chicken: use of existing high-resolution growth QTL identified in an experimental Advanced Intercross Lines.



Influence of maternal diet on the epigenetic programming of pig offspring

A "diet x epigenetics" study to explore the transcriptional and epigenetic effects triggered by maternal diets differing in fibre contents on the pig fetus, and the possible persistence of such effects until the post-weaning stage. Porcine liver and skeletal muscle will be profiled by RNA-seq and ATAC-seq and data analyzed in light of the enriched annotation maps.



Standardization of data and processes, dissemination and outreach

- The new annotation maps will be integrated in the **FAANG Data Coordination Centre (DCC)**. Data coordination, curation, validation, archiving, dissemination and publication through the European biological data archives and the FAANG Data Portal (data.faang.org).
- Extensive dissemination, communication and training activities will ensure interactions with stakeholders and the scientific community and **facilitate uptake of the GENE-SWitCH outcomes**.
- A European node of the DCC (EU FAANG DCC) has been established in collaboration with the two other H2020-SFS30 funded projects (BovReg and AQUA-FAANG) to facilitate collaboration ("clustering") and **coordinate our efforts within the global FAANG action**.

First achievements and perspectives



A biorepository of 3120 samples is almost completed (Jan. 2020) - DNA and RNA extraction have started; CHIP-seq and ATAC-seq optimization (for snap-frozen samples) are in progress - The Data Management Plan has been established - Prototype GENE-SWitCH cloud infrastructure has been established on the EMBL-EBI embassy cloud (www.embassycloud.org) - Reproducible, scale-able analysis workflows for data analysis are in progress (initial workflows to be released on FAANG GitHub accounts).

The sampling of 300 pigs for the eQTL study is completed, with RNA and DNA extraction of 900 samples in progress - Bayesian and machine learning models for genomic selection study is in progress - The pilot study for the diet x epigenetics study was completed and the final diet composition for the main trial established.

The project identity package has been completed - The project website (www.gene-switch.eu) and the Twitter account (@GeneSwitch) are established - The GENE-SWitCH project data portal slice of the FAANG data portal (data.faang.org) is being completed (as well as for the other H2020 projects) - The first version of the plan for outreach, dissemination, and training is available - The Knowledge Exchange Platform (KEP) and Stakeholder Advisory Board (SAB) are being established.

*More clustering activities will be implemented for the harmonized development of annotation and evolutionary and comparative analyses of genomes and for developing new genomic prediction models. We anticipate that GENE-SWitCH results will identify several putative functional elements acting across tissues and development, thus leading to new hypotheses on their role to determine phenotypes. In this context, INRA (GABI Unit: GeMS and @Bridge teams) is collaborating with Wageningen Univ. to create a porcine organoid biorepository from GENE-SWitCH samples from intestine portions, liver and lung and in order to represent the fetal, newborn and adult stages. This common resource represent a potentially interesting *in vitro* biological system for the next validation of GENE-SWitCH predictions.*