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EDITORIAL by Elisabetta GIUFFRA

GENE-SWitCH was conducted with an ambitious goal: to provide new fundamental knowledge on the functional genomes of two major meat sources (pig and chicken) and to enable its immediate translation to the pork and poultry industries.

Our final conference (Article #2) has showcased our efforts and achievements over these 4.5 years and can be entirely watched from our website. In addition to scientific presentations and the discussions that followed with a worldwide audience, you will have the opportunity to listen to two wonderful invited talks and to the presentations and roundtables held for the celebration of the 10y anniversary of the Functional Annotation of Animal genomes initiative.

We propose here three articles to summarise in simpler terms the main themes on which we have focused most of our efforts. First, we have pioneered open science for these two monogastric species (Article #3). All datasets have been produced in full compliance with FAANG standards, under the principles of international collaboration and open science, and in coordination and synergy with the other FAANG projects in the EU and worldwide working on other species. Second, we made a strong scientific effort to use the new genome annotations for the goal of precision breeding through two complementary approaches. One approach focused on improving genomic tools to enable sustainable breeding and production (Article #4). Genomic prediction models were extended by incorporating various functional and overlapping annotations and, after several tests, validated in commercial populations of both species. In another 'pilot' approach a large-scale animal experiment was conducted to assess the epigenetic effects on the functional genome induced by diet, an important environmental factor that can be easily manipulated for farm animals (Article #5).

A movie summarizing the rationale and achievements of GENE-SWitCH has been produced (Article #6) to illustrate the project's contribution to making animal production more sustainable and efficient, while still meeting the increasing demand for meat from a growing global population.

One project ends and several others follow... GERONIMO will continue to study the same species, using the results and tools of GENE-SWitCH and tackling new objectives to move forward. We dedicated the last day of our final conference to a joint discussion on policy and ethics in our field (Article #7). We discussed the challenges posed by existing legislation, misinformation and the importance of nuanced communication in shaping public perceptions, ultimately emphasizing the urgent need for stakeholder engagement in ethical debates.

Goodbye to our readers! With many thanks for having followed us.

Elisabetta Giuffra



GENE-SWitCH final Conference: Bridging the gap between genomic research and applications

The final conference of GENE-SWitCH, a Horizon 2020 project, was held as a hybrid event at the University Foundation in Brussels between 6 and 8 November 2023.

The conference showcased a comprehensive 2-day agenda to report the achievements and impacts of the project, celebrate the 10 years of the Functional Annotation of Farm ANimal Genomes initiative (FAANG), and host Policy and Ethics workshops addressing stakeholders.

The conference began with Session 1, titled "Identification and Characterisation of Functional Genomic Elements". The five presentations illustrated the identification and temporal dynamics of the pig and chicken functional elements across development and how richly annotated genome annotation maps have become available to the whole community.

Session 2, titled "Implementing FAANG innovation for precision breeding", featured two presentations on the epigenetic effects of maternal diets rich in fibres on pig offspring (fetuses and piglets), followed by six presentations on the development and validation of predictive models able to exploit the new annotation maps for the genomic selection of these species.

Session 3 - "Celebrating 10 years of FAANG: From FAANG to Fork: Highly annotated genomes as resources to improve farmed animal production" aimed at emphasising the transformative role of highly annotated genomes in advancing farmed animal sciences decade of international through а collaborative progress. It included five presentations (an opening talk and four summary talks on GENE-SWitCH main outcomes).





The following round table was structured in three parts: Genome annotations across developmental phases (Session 1), the epigenetic impact of diets (Session 2) and Genomic selection of swine and poultry (Session 3). The attending representatives from the main pig and poultry breeding companies (Hendrix Genetics, Topigs Norsvin, Genus-PIC and Cobb) provided their views on the applied interest and future potentials of these themes for the precision breeding of these species.

Two distinguished invited speakers, Jack C. M. Dekkers (Iowa State University) and Laurent Frantz (Ludwig Maximilian University) offered novel perspectives and angles of discussion with two main talks: "Genetics and genomics of potential indicator traits for disease resilience of grow-finish pigs" (J.C.M. Dekkers) and "Ancient DNA, Extinction, Domestication and the Cost of Modern Farming" (L. Frantz).

The conference concluded with Policy and Ethics workshops, jointly organised by GENE-SWitCH and GEroNIMO; it summarised the complementarity, achievements and progress of each project to their stakeholders, followed by an interactive session on the main ethical issues faced by the animal breeding sector, including researchers and companies, and action points to address these.

All video presentations of the conference are available here.



Pioneering open science for a more accessible and collaborative scientific landscape in monogastric breeding

The GENE-SWitCH project has embarked on an ambitious journey to transform the scientific ecosystem in monogastric breeding through the principles of open science.

This collaborative effort has yielded significant contributions. In this article, we delve into the project's remarkable achievements, focusing on their commitment to enhancing the FAIR Guiding Principles for scientific data management and stewardship (Findable, Accessible, Interoperable and Reusable) in monogastric genomics.

The Problem

The scientific community is grappling with challenges related to data accessibility, transparency, and reproducibility. Research data, often scattered across various platforms and in diverse formats, remains underutilised. This fragmentation hinders the full potential of scientific research and innovation.

GENE-SWitCH is stepping up to address these challenges by providing:

- Open access data for both scientific and commercial communities, fostering global collaboration.
- · A user-friendly platform for accessing and visualising genotype-to-phenotype data of
- monogastric species.
- Data in interoperability and standardised formats to enable interdisciplinary research and
- innovation.
- Standardised and enhanced data concepts and categories for the monogastric community.

Looking ahead, we aim to:

- Support the continuation and expansion of data collection and integration.
- Facilitate public-private partnerships.
- Develop Open Science Infrastructure and Tools.

Read the full article here:





Transforming precision breeding with novel technologies

Using innovative technologies, the GENE-SWitCH project has embarked on a cutting-edge journey to advance precision breeding in monogastric animals. In this article, we explore the remarkable contributions of the project, focusing on our efforts to address critical issues in the realm of genomics, environmental impact, and predicting animal performance.

The Problem

Precision breeding is confronted with several challenges, including limited genomic data, environmental impact, and the prediction of complex traits that are relevant to sustainability.

GENE-SWitCH is making significant contributions to overcome these challenges:





- Enhancing genomic information availability through Ensembl, providing a variety of data for researchers.
- Developing cutting-edge tools that combine genomic and functional data to predict relevant phenotypes.
- Investigate the complex interplay between the environment and the genome by studying the epigenetic impact of maternal diets in pigs.
- Our future goals include:
- Expanding the availability of genomic information.
- Enhancing the prediction of animal performance.
- Deepening the understanding of environmental impact.
- Fostering and supporting public-private partnerships to increase collaboration and knowledge
- uptake.
- Exploring the application of precision genome editing technology.

Read the full article here:





Transforming health & well-being through diet

The GENE-SWitCH project, with its innovative focus on diets, has opened new avenues for enhancing health and well-being across species; we explore the project's remarkable contributions that pertain to critical issues in animal health and sustainable food practices. Health and well-being are interlinked, and dietary interventions play an important role through their effect on the microbiota. In tackling this topic, GENE-switch has addressed the broad goals of sustainable food practices and animal health and welfare.



The Problem

Health and well-being are intimately connected, and dietary interventions play a pivotal role through their epigenetic effects.

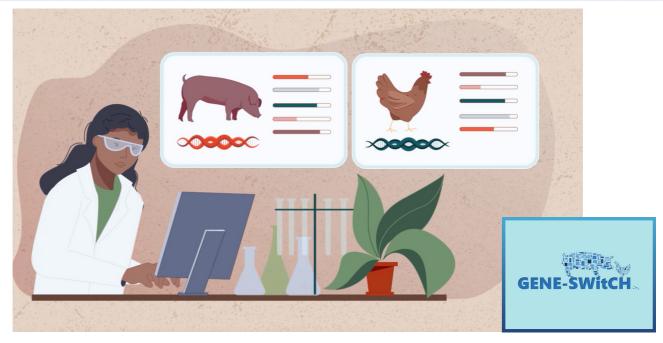
GENE-SWitCH is making significant strides in this area by:

- Implementing the use of high-fibre maternal feed to enhance piglet health and welfare.
- Uncovering positive human health implications of findings on the effects of high-fibre diets on
- liver and muscle metabolism and the immune system. Moving forward, our goals include:
- · Expanding in-depth studies on the influence of dietary fibre on host and offspring health.
- Promoting research into the effects of dietary interventions on animal welfare.
- Assessing the impact of fibre-enriched feed on animal health, growth performance, and product
- quality.
- Exploring sustainable fibre sources from waste streams, contributing to circular economy
- practices
- Using livestock to evaluate the effects of high-fibre diets on human health.
- Promoting interdisciplinary research between animal health, human health, and sustainable food
- production.

Read the full article here:







GENE-SWitCH Movie: Deciphering the functional genome of pigs and chickens

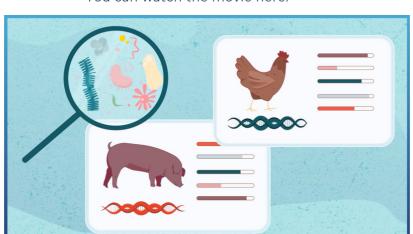
As the global human population is projected to reach 9 billion by 2050, significant challenges are posed for the food production system, particularly in the livestock sector. The farming sector is expected to become more sustainable and environmentally friendly, necessitating the development of new breeding technologies.

The European Union-funded GENE-SWitCH project aims to provide new insights into the functional genomes of pigs and chickens to make them healthier and more efficient. This is achieved through genomic selection, a process that allows the prediction of how a given mate selection will impact the performance of their progeny.

Unlike the DNA sequence, which is the same in all cells of an organism, the functional genome can change throughout our lives due to various environmental factors. These changes, known as epigenetic modifications, can sometimes be passed down to future generations.

The GENE-SWitCH project has explored whether the maternal diet of pigs and chickens can cause epigenetic changes in the genomes of their offspring, potentially affecting their health, body composition, and other desirable traits.

In summary, deciphering and exploiting the functional genome of pigs and chickens is vital for improving breeding programs for sustainable animal production. The GENE-SWitCH project has developed new technologies and results that will enable the farming sector to become more sustainable and efficient while still meeting the increasing demand for meat from the growing global population.



You can watch the movie here:





GENE-SWitCH and GEroNIMO projects showcase groundbreaking achievements and ethical discourse in genomic research

In a significant stride towards the future of genomic research, the GENE-SWitCH and GEroNIMO projects have unveiled ground-breaking achievements. The final conference of the GENE-SWitCH project, held in Brussels on November 30, 2023, showcased the project's accomplishments in decoding pig and chicken genomes. Led by Elisabetta Giuffra, the project has provided open-access data, innovative tools for precision breeding, and functional annotations. These tools have broad-ranging impacts on the pig and poultry sectors, marking a new era in genomic understanding.

The conference also introduced the GEroNIMO project, led by Tatiana Zerjal and Mario Calus. This venture, involving 21 partners from 11 countries, focuses on the impact of environmental changes on early life stages, welfare, and feed quality efficiency. It aims to provide breeders with new knowledge and tools to promote innovative genome and epigenome-enabled selection methods.

An insightful policy and ethics workshop was conducted during the conference, emphasising the need for stakeholder engagement in ethical debates. Attendees delved into the societal implications of enhancing efficiency in animal agriculture, recognising its global significance in addressing food security and environmental impact.

The session brought to light the collective responsibility of stakeholders, emphasizing the necessity for collaboration with local communities to tailor solutions. High-tech solutions like genome editing and the ethical use of animals in experimentation were explored, emphasizing the challenges posed by existing legislation, misinformation, and the importance of nuanced communication in shaping public perception.

In conclusion, the GENE-SWitCH and GEroNIMO projects are pioneering the future of genomic research with their ground-breaking achievements and ethical discourse. Their work is set to shape the future of the pig and poultry sectors and potentially revolutionise the field of animal breeding. This marks a significant milestone in the field of genomic research, setting the stage for future advancements in this domain.



