A European infrastructure
for farmed animal genotype to phenotype research

Deliverable 7.2
Report on possible collaboration between EuroFAANG and ESFRI infrastructures

Grant agreement no°: 101094718
Due submission date
2025-August 31
Actual submission date
2025-August-29

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Sensitive: NO

This project has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No 101094718. The content of this report reflects only the author's view. The European Commission is not responsible for any use that may be made of the information it

DOCUMENT CONTROL SHEET

Deliverable name	Report on possible collaboration between EuroFAANG and ESFRI infrastructures
Deliverable number	7.2
Partners providing input to this Deliverable	EMBL-EBI, EFFAB
Draft final version circulated by lead party to: On date	27.08.2025
Approved by (on date)	FBN as coordinator on 29.08.2025
Work package no	7
Dissemination level	PU

REVISION HISTORY

Version number	Version date	Document name	Lead partner
Vs1	2025/08/26	D7.2_v0	INRAE
Vs2	2025/08/27	D7.2_v1	INRAE
Vs3	2025/08/28	D7.2_v2	INRAE
Vs4			
Vs5			

Changes with respect to the DoA (Description of Action)

None

Dissemination and uptake

This is a public deliverable

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1. Executive Summary

Background	As reported in MS19, we identified a number of Research Infrastructures on the ESFRI roadmap with which EuroFAANG could develop collaborations. The first one is ELIXIR, for bioinformatics and data services. There is a set of biobanking infrastructures likely to also offer cellular models, with BBMRI, EMBRC, MIRRI, and a set of phenotyping infrastructures with INFRAFRONTIER (mouse models), EMPHASIS (plant phenotyping), METROFOOD (food quality measurement) as well as AnaEE-Europe for sustainable ecosystems.
Objectives	To identify synergies and prospects for collaboration with these ESFRI infrastructures. The scope of these consultations has been enlarged since the inclusion of EuroFAANG into the GenoPHEnix proposal submitted to the ESFRI roadmap in April 2025.
Methods	Regarding ELIXIR, we have set up a focus group following the roadmap presented in D7.1, in order to prepare an application for a community. Regarding the other infrastructures, we conducted interviews (reported in MS19) and sent a request for a Letter of Support to the GenoPHEnix proposal. Finally, we invited BBMRI and INFRAFRONTIER, to a research infrastructure workshop that EuroFAANG has organised during the 76th EAAP conference in Innsbruck on Aug 27.
Results & implications	As reported in D7.1, the title of the ELIXIR focus group is 'Domestic Animal Genomes and Phenomes'. Monthly online meetings have been organised to develop a white paper, listing the challenges, the expectations from a community and the possible synergies with other communities. These have been presented at the Elixir All Hands meeting on June 2-4, 2025. The white paper and the roadmap have been submitted to ELIXIR on August 14, 2025. We expect an answer from the Heads of Nodes by November 2025. In the frame of the submission of GenoPHEnix proposal, seven letters of Support have been collected from AnaEE-Europe, EMBRC, EMPHASIS, IBISBA, INFRAFRONTIER, LifeWatch and MIRRI. Their content is summarized in this deliverable. BBMRI and INFRAFRONTIER representatives each presented a talk at the EAAP session organised by EuroFAANG on August 27, 2025, entitled 'European Research Infrastructure to Support Livestock Science: Whom and How?'. The session was attended by 30 people from various institutions, including some non-partners in EuroFAANG. Issues and suggestions made at the final discussion of this session are reported in this deliverable.

1. Introduction

Any new Research Infrastructure has to demonstrate its added value as compared to existing RIs as well as to develop collaborations with existing RIs in order to exploit synergies.

For that aim, we distinguish ELIXIR from other RIs of the Health and Food domain, considering the major challenges for data curation and data sharing in EuroFAANG. We planned from the beginning of the project to set up a community for animal science, as described in D7.1. Progress in this endeavour is presented in this deliverable.

Then, we have exploited the discussions previously reported in milestones 19 and 20, in order to formalize our connections with oth ESFRI RIs. This was done in the frame of the preparation of the GenoPHEnix proposal, as reported in D1.5. We obtained letters of support from five ESFRI landmarks and two ESFRI projects that will be reported here.

Finally, to engage the animal science community and develop synergies with existing projects or ESFRI landmarks, we have organised a dedicated session on Research Infrastructures at the 76th annual meeting of the European Federation of Animal Science, held in Innsbruck, from August 25 to August 29, 2025

2. Application for an ELIXIR community

Following the recognition of a Focus Group by ESFRI, monthly on-line meetings were organised by E. Clark, now a staff member of EMBL-EBI, with 38 participants from 19 Elixir nodes (20 countries total and EMBL-EBI). A leading team has been established with representatives of 3 ELIXIR nodes (E. Clark for ELIXIR-UK and EMBL-EBI, Ole Madsen for ELIXIR-NL and Catherine Larzul for ELIXIR-FR) with the support of Physilia Chua, the ELIXIR hub liaison.

The Focus Group was presented first at the ELIXIR All-Hands meeting in Dublin in 2024. At the ELIXIR All-Hands meeting on June 2-4th, 2025, E. Clark and members of the Focus Group led a workshop focused on expanding the FAANG Data Portal to include phenotyping data, including speakers from the ELIXIR plant sciences community. Several other activities are planned including an ELIXIR aquaculture Industry Day in Oslo, Norway, and an ELIXIR BioHackathon in Berlin in 2025.

The progress of the Focus group was presented to ELIXIR Heads of Nodes in May 2025 (annex 1) and an invitation to submit documents to become a community was received as feedback on the progress of the Focus Group so far was very positive.

The proposed community is entitled “Domestic Animal Genomes and Phenomes” (DAGP).

The goals of DAGP are the following:

- To seek membership, and scope future community needs in different ELIXIR Nodes.
- To coordinate discussions and explore potential for data/technology solutions for addressing key issues in welfare, behaviour, health, infectious diseases, metabolism and nutritional efficiency and preservation of genetic diversity and environment.

- To develop data standards, coordination, workflows and visualisation for key developing areas of pangenomics, functional genomics, genome editing, phenotyping and bio-banking, which are needed to enhance data analyses.
- To develop FAIR data management guidelines, standards and ontologies and promote best practices in data coordination and archiving.
- To organise tools and data training and knowledge transfer events.

Discussions with some of the 18 ELIXIR communities were initiated to demonstrate complementarities with the new community we are proposing.

DAGP will contribute directly to the five broad objectives of the Biodiversity, Food Security and Pathogens (BFSP) priority area within ELIXIR strategy (Federation, FAIR Data, Analysis, Standards, Training). These contributions are described in the White paper submitted to ELIXIR on August 14, 2025 (annex 2).

For the Focus group to evolve towards a Community, a Roadmap has also to be submitted to the other ELIXIR communities and steering committee for feedback. This was done on August 14, 2025 (annex 3). The roadmap shows the objectives of the future Community and the 6 tasks to be undertaken to have it operational. The next step is to address the feedback and then formally submit these documents to the ELIXIR Heads of Nodes in November 2025 to decide on the focus group becoming a community.

The DAGP Community is also expected to operate as a component of the GenoPHEnix RI, if it is accepted as an ESFRI project, which is strategically linked with ELIXIR priorities.

3. Collaboration with ESFRI infrastructures in the frame of GenoPHEnix proposal

A template for a support letter was provided in order to standardize the expression of support (annex 4).
We will present here the specific contect of the support letter describing possible collaboration with GenoPHEnix, and consequently with EuroFAANG.
The letter also mentioned the interest of each signatory to be kept informed of the progress made by the GenoPHEnix project towards its operational phase, which should start in 2033, even though some services may be accessible earlier. Furthermore, the signatory organisation would be interested to participate to the future GenoPHEnix Open Innovation Forum, to be created in 2027.

4.1 Collaboration with ESFRI projects

EMPHASIS
EMPHASIS is the European Infrastructure for multi-scale Plant Phenomics and Simulation for food security in a changing climate. It submitted its step 1 Eric in October 2024. EMPHASIS was mentioned in the ESFRI Gap analysis as a potential solution to develop animal phenotyping services. However, this suggestion was not supported by the leadership of EMPHASIS who stated the need for collaboration with GenoPHEnix on technological developments and data integration: « *The establishment of an institutional framework ensuring long-term access to farm animal*

genetic resources and phenotyping capacities will address a significant gap in the European research landscape. In this context, GenoPHEnix will enable fundamental and transformative research, contributing to solutions for the challenges facing the Agri-Food sector, including population growth, climate change, environmental concerns, disease, geopolitical uncertainties, and rising societal expectations regarding product quality, production methods, and animal health and welfare.

Given the specific requirements of an infrastructure dedicated to phenotyping studies in animals, such services are not currently part of the EMPHASIS portfolio. However, EMPHASIS and GenoPHEnix present significant potential for synergies and collaboration in key areas, such as technological advancements in phenotyping and the integration and processing of data. Additionally, exchanging experiences, expertise, and lessons learned in access provision and business model development will be mutually beneficial. »

IBISBA

IBISBA is a pan-European distributed Research Infrastructure dedicated to Industrial Biotechnology and Biomanufacturing, included in the ESFRI roadmap since 2018.

The director of IBISBA mentioned that the activities of the GenoPHEnix project are of direct interest and relevance for IBISBA, and identified opportunities for creating links between GenoPHEnix and IBISBA services. Some examples are listed below:

Topic of interest for IBISBA	GenoPHEnix services
Bioproduction of functional or neutraceutical feed (for example omega-3-rich oils issued from microalgae or other bioprocesses)	▪ Animal feed technology ▪ In vivo phenotyping of nutritional efficiency and emissions through gold standard methods ▪ In vivo phenotyping of production performances
New proteins (for example single cell protein) Functional characterisation of proteins	▪ Animal feed technology, ▪ In vivo phenotyping of nutritional efficiency and emissions through biomarkers and proxies

Complementarities with *in vitro* phenotyping is also expected.

4.2 Collaboration with ESFRI landmarks

AnaEE-Europe

AnaEE-ERIC (Analysis and Experimentation on Ecosystems) is a distributed infrastructure established in 2022. Its installations manipulate the environment and management methods of all type of continental ecosystems and provide support to the research in experimental and functional ecology.

« Our organisation would benefit from collaborating with GenoPHEnix. AnaEE-ERIC focusses mostly on ecosystems, including agro-ecosystems and freshwater aquaculture; there is an obvious complementarity with the study of farm animals and their impact on biodiversity and climate. »

EMBRC

Since a risk of overlap with GenoPHEnix may exist in the aquaculture domain, it was particularly important to get an expression of interest from EMBRC, which is covering the entire domain of

marine biological resources. The need to avoid duplication is addressed in the support letter signed by the director of EMBRC, in order to pave the way to fruitful collaboration :
« *An RI dedicated to the field of animal phenotyping and genotyping is welcome and will be able to support important research and the private sector in Europe. GenoPHEnix focuses on large farm animals, poultry, and fish destined for consumption. In terms of the marine component, Europe already has an RI dedicated to marine biological resources, EMBRC-ERIC. EMBRC offers a substantial catalogue of services for aquaculture and does not focus exclusively on fish, but covers the three main groups: fish, shellfish, and algal aquaculture. It covers a broader scope of aquaculture, including genotyping and phenotyping, exploration of new species for culture, improved production and environmental practices through experimental facilities and advanced platforms (e.g. imaging).*
GenoPHEnix offers a strong rationale for combining farmed animals and expertise for phenotyping and genotyping under one roof. However, it would be essential to establish, as part of GenoPHEnix' preparatory phase, how its services are articulated with those of EMBRC to avoid a substantial overlap and duplication of services and facilities.
GenoPHEnix promises to provide significant expertise on improving farmed animals, incorporating advanced techniques and technologies. EMBRC welcomes this focus on improving the biological resources and see a substantial opportunity to work closely with GenoPHEnix in support of aquaculture in Europe. »

INFRAFRONTIER
INFRAFRONTIER is the European Research Infrastructure for Modelling Human Diseases. It contributse to human health by advancing disease prevention and therapies through appropriate models. This represents an interesting parallel with *the in vitro* models that EuroFAANG will develop that could be used to study resistance to viral diseases for instance.

The director of INFRAFRONTIER stated that
« *Scope and activities of the GenoPHEnix project are of direct interest and relevance for INFRAFRONTIER ERIC and we see a lot of complementarities and high potential for synergistic developments between GenoPHEnix and INFRAFRONTIER.* »

LifeWatch
LifeWatch ERIC provides e-Science research facilities to scientists investigating biodiversity and ecosystem functions and services in order to support society in addressing key planetary challenges.
Lifewatch Director stated *a* great interest to collaborate with GenoPHEnix « *in the domain of data services, such as the FAANG data portal, Ensembl Genome Browser, data repositories, (Biosamples, Biostudies, ENA, Expression Atlas, Metabolights), imaging technologies for aquaculture species and BioImage Archive database. ».*

MIRRI
Established as an ERIC in 2022, MIRRI ERIC has developed services, and supports research in several Microbiology domains, namely health and food, agrofood and environment and energy, at the pan-European level.
The director of MIRRI stated that

« The activities of the GenoPHEnix project are of direct interest and relevance for the European Research Area and complementary to those of MIRRI-ERIC, namely in topics related to One Health, Agrofood and Climate Change. »

Thus, we could find specific topics of interest to develop future collaboration between GenoPHEnix and seven European Research Infrastructure in the Health and Food domain.
All signatories declared their interest in participating to the future GenoPHEnix Open Innovation Forum, which creates the basis for regular networking events.

4. Session on Research Infrastructures at EAAP, August 27, 2025

The session was proposed to the Genetics Commission of EAAP in order to be included into the official programme of the Conference.

The motivations for such a session were presented to EAAP as follows:

Research Infrastructures (RIs) are gathering expertise and top-quality equipments to support research on the long-term. By pooling unique resources, they offer services to researchers, they improve current methodologies, in particular to facilitate comparison across laboratories and countries. Among their services, they provide access to equipments and expertise as well as training to new techniques and methods. They offer the possibility to perpetuate and share new tools and methods developed from research projects. Thus, they are in constant interactions with scientists. European countries recognize the need for RIs by establishing a list of high priority infrastructures also called the ESFRI roadmap, which the European Commission can support by opening calls for funding. The ESFRI roadmap features RIs in life sciences, physics, social sciences…Within the life sciences domain, temporary projects have been funded for RIs aimed at phenotyping cattle, pigs and fish species, but there is no sustainable RI for livestock science. This is a major gap.

This session first aim is to popularize the concept of RIs for the scientific community working on livestock, whatever the discipline (genetics, physiology, pathology). It will feature current RIs projects of interest to the community (PIGWEB, AQUAEXCEL, ISIDORe, EuroFAANG, AGROSERV), as well as some established RIs to illustrate their added value, for instance in data science (ELIXIR) or model species (INFRAFRONTIER). The session will collect feedback from the scientific community which represents current or potential users of a new RI in preparation to support livestock science, that will join phenotyping with functional annotation of the genome in order to bridge the gap from genotype to phenotype in terrestrial as well as aquatic species.

The agenda of the session (annex 5) was elaborated by contacting colleagues from infrastructures we had been in touch previously: BBMRI, INFRAFONTIER and the animal phenotyping infrastructures. A representative from EU was invited to present the ESFRI landscape. Mihaela CONSTANTIN provided a set of introductory slides to be presented by E. Clark. Then the

GenoPHEnix proposal will be presented by the coordinator, René Baumont, and specific issues related to data sharing and public-private partnership will be addressed.

The session ended with a discussion covering several interesting points. The questions and answers raised in the discussion as summarised below.

<u>Questions and Answers from Infrastructures Workshop at EAAP August 27th 2025</u>

What if GenoPHEnix is not successful? What is needed to improve the proposal?

- If not successful, then we hope the ESFRI panel and/or the European Commission (EC) present us with an alternative to work. Already €20 million investment by the EC.
- If we can't enter the ESFRI RoadMap, then hopefully there will be a suitable alternative.
- Support from additional countries and member states is important, we continue our efforts to recruit countries to GenoPHEnix.
- Communicate as much as possible with the project officers and EC, support from European Partnership in Animal Science and the EPAHW.

Do data have to be encrypted in the same way in the same platform to be combined?

- Sharing data from two countries/groups each group would have their own key, when data is combined they would all receive the same results using their key.

A lot of time spent on working on EC research proposals, how can we better make use of research infrastructures in these proposals? How can EAAP be made use of in research infrastructures?

- Projects being prepared to be submitted in RIA topic calls can mention in their proposals that they would be willing to use the infrastructure and how the proposal would utilise services, how this would save money etc.
- The proposals can explicitly state if there was an infrastructure called GenoPHEnix how would they use it.
- Linking across projects can be helpful on both sides, needs to be convincing with good examples. Providing these examples/use cases and circulating to the community would be helpful.
- For EAAP it is a slightly different story as they receive money from EC projects, their main purpose could be in raising awareness, EAAP could be a good vehicle for that.
- EAAP facilitates the dialogue on important issues, but they require funds to do that.
- We did invite someone from the EC to the session to discuss but they could not travel.
- Proposing a session at EAAP conference has several hurdles but this could be the first infrastructure workshop and continued annually.
- Infrastructures must be multidisciplinary which is a big challenge, EAAP can help facilitate this bringing researchers together across disciplines.
- The infrastructure funding calls are very different INFRA-DEV concept development is very different to INFRAIA for example.

In the context of benchmarking and biobanking, agriculture is the perfect environment for doing large-scale genetics, it captures complex phenotypes - is there any benchmarking of agricultural data relative to human data, what could be done with agricultural data to inform human research, how close are they in terms of resources, could we work more with BBMRI?

- Difficult to answer, in agriculture we don't have as much data.

- One issue with animal breeding populations is the LD, it is why we need the omics resources, e.g. from EuroFAANG, to point to causative genes.
- Dairy cattle data collection infrastructure, pay to access data. More investment in infrastructure could facilitate this.
- How to tap into biomedical research funding.

What about critical mass? It is larger for INFRAFRONTIER and BBMRI? Way to ensure GenoPHEnix is pan-European?

- For ESFRI need to have a strong credibility, so have a small consortium at this stage.
- Over the preparatory stage until finalisation as an ERIC gives us time to expand the consortium and add new partners.
- There is sufficient critical mass across Europe, further recruitment of countries including ITC's is important, the EU-LI-PHE COST Action can help facilitate this.

What is the potential to increase profit to breeding companies that the RI could bring? Can the breeding companies co-fund it? Animal breeding companies will only buy into it if they get something from it.

- Very strong interest from feed companies in SmartCow and PigWeb services, industry can access services for free, collaborate with academia and test products.
- Companies come and develop trials, as they want to use experimental facilities.
- Issue is often accessibility of the data produced, successful collaborations already, needs proper guidelines on how data will be shared.
- Provide some examples of successful collaborations with industry from PigWeb and SmartCow.
- Value of the data to the whole sector is one thing but at the same time industry stakeholders need to see a profit.
- FAANG Data Portal is a place all the data can be accessible. We know industry stakeholders utilise the portal. Commercial data request portal as for AG2P-DISC could be an option.
- Some data has been released e.g. Corteva for plant breeding, and PIC for breeding data. There are also genome assemblies for two Cobb poultry breeding lines.
- One option is to use the encryption methods presented by UC Davis/Iowa State so only encrypted data is available publicly, threshold/risk for involvement gets lowered and industry may buy in.
- There has been a lot of collaboration between academia and industry but there is increased competition between industry whereas pressure comes from academia to share data publicly.
- Public funding can also be useful for industry for example to collect additional phenotypes.
- Need to propose something that industry couldn't do without us.
- RIs enable rather than fund research.
- RI will still be there after 4-8 years so there is good longevity which could be attractive for industry.
- EU Farmbook to collect all results from agriculture projects funded by the EU. Aims to keep track of the projects to show what is new and minimise duplicated effort.

How does BBMRI deal with data and the data sharing ethics?

- Key of being an RI is that you network well and have convincing arguments to join.

- Build national nodes then the national nodes do the local networking to collaborate and see the joint vision.
- Matter of ownership is key so not just a top-down approach, the data collectors doing the work need to have a sense of ownership of the RI and join vision.
- 10-year roadmap, co-creation approach, includes the wishes and vision of all to provide opportunities for feedback.
- Include all people in countries networking on behalf of the RI in developing the vision.

Can we coordinate the update of animal facilities across Europe?

- Can GenoPHEnix help promote the next step to be an excellent centre for animal phenotyping?
- Future proofing the farmed animal facilities across Europe is essential as many require updating.
- Better coordination is required of facilities on site and investment in the updating of these.
- Important issue and goal to have some optimisation of facilities at European level.
- However, each distributed institute wants to have its own facilities.
- This has different considerations to the investment in upgrading large telescopes for example where only one exists and several institutions invest in it.
- There is no point to have an infrastructure with technologies being developed independently, we also need a synergistic approach where appropriate.

5. Conclusion

As a concept development, we can see that EuroFAANG has successfully set the basis for long-term cooperation with RIs of the ESFRI roadmap.

While we are still expecting the final approval of the creation of the Domestic Animal Genomes and Phenomes ELIXIR community, we are fairly optimistic on the possibility to launch it before the end of EuroFAANG grant.

Furthermore, we have identified areas of cooperation between GenoPHEnix as a whole and a set of Research Infrastructures of the ESFRI roadmap. Data services, technological developments and cellular models proposed by EuroFAANG for *in-vitro* phenotyping offer various opportunities to build sustainable links with other RIs interested in biodiversity, ecology, marine biology, plant production, microbiology and biotechnologies.

The infrastructure session at EAAP brought additional ideas to enrich this perspective.

6. Annex 1 – Presentation at ELIXIR All Hands meeting

Domestic Animals Genome and Phenome

ELIXIR Focus Group Progress and Updates

Emily Clark (EMBL-EBI)

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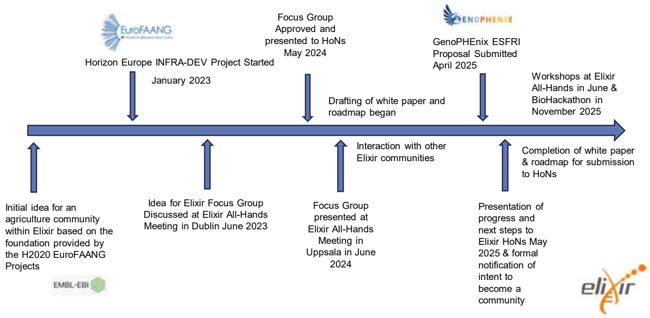
Process to date and next steps



Initial idea for an agriculture community within Elixir based on the foundation provided by the H2020 EuroFAANG Projects

Horizon Europe INFRA-DEV Project Started January 2023

Idea for Elixir Focus Group Discussed at Elixir All-Hands Meeting in Dublin June 2023

Focus Group Approved and presented to HoNs May 2024

Focus Group presented at Elixir All-Hands Meeting in Uppsala in June 2024

Drafting of white paper and roadmap began

Interaction with other Elixir communities

GenoPHEnix ESFRI Proposal Submitted April 2025

Presentation of progress and next steps to Elixir HoNs May 2025 & formal notification of intent to become a community

Workshops at Elixir All-Hands in June & BioHackathon in November 2025

Completion of white paper & roadmap for submission to HoNs

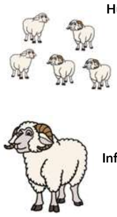
ELIXIR focus group: Domestic Animals Genome and Phenome

Aim: To build a case for an Elixir community to support genotype and phenotype analysis for farmed and companion animal species, and develop a coordinated, open and standardised data life cycle.

https://elixir-europe.org/focus-groups/domestic-animals-genome-phenome

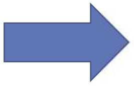
Biodiversity, food security and pathogens

Chief among the improvements required in animal breeding and management in the coming decade is the ability to more accurately use an animal's genetic code (genome) to predict its characteristics (phenome)



Thousands of genetic differences ("G")
Hundreds of different characteristics ("P")

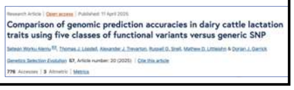
Associate genetic code with characteristics ("G to P")



Inform genomic selection, genome editing, fundamental biology

Breed the 'best' animals for:

- Disease resistance
- Reduced environmental impact
- Adaptation to changing environments



Research Article | Open access | Published: 11 April 2025

Comparison of genomic prediction accuracies in dairy cattle lactation traits using five classes of functional variants versus generic SNP

Genetics Selection Evolution 57, Article number: 20 (2025) | Cite this article

776 Accesses | 3 Altmetric | Metrics

Tier	SCIENCE Enable scientists to access and analyse life science data		
Strategic Priorities	Cellular and molecular research	Biodiversity, food security and pathogens	Human data and translational research
Ambitions	1.1 Connect the latest developments and established data resources to realise the potential of cellular and molecular biology	1.2 Mobilise and integrate molecular data to support transnational research programmes in biodiversity, food security and pathogens	1.3 Provide the infrastructure to support the discovery, access, sharing and analysis of human genomics data and linked phenotypic/other data on a massive scale

Outcomes

In the areas of biodiversity, food security and pathogens:

- A coordinated and comprehensive portfolio of activities is built via ELIXIR Communities (existing and newly created) and externally funded projects (national and transnational)
- Nodes broker biomolecular data into accessible reference collections for the research community
- Nodes are established as integral components of national data management programmes
- Nodes run a suite of services allowing molecular, cellular and imaging data to be routinely mobilised, connected and analysed
- Large and well-curated datasets are available for artificial intelligence analysis, high performance computing service use and advanced analytics
- Collaborations link to other disciplines and infrastructures to facilitate seamless data management, connectivity and analysis for the research community

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Addresses key ELIXIR Societal challenges

Disease prevention

Climate change

Diminishing biodiversity

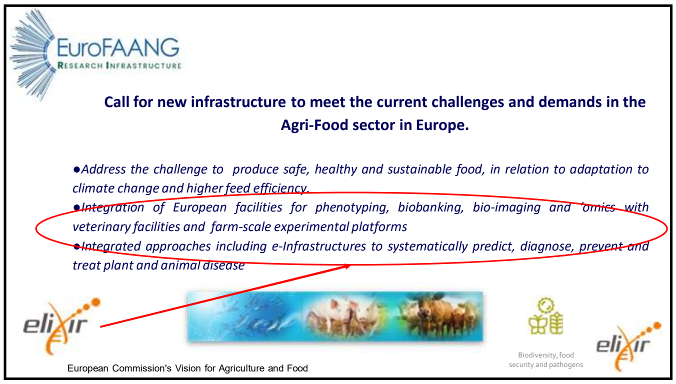
Disease diagnosis

Sustainable food production

Pandemic preparedness

Cancer

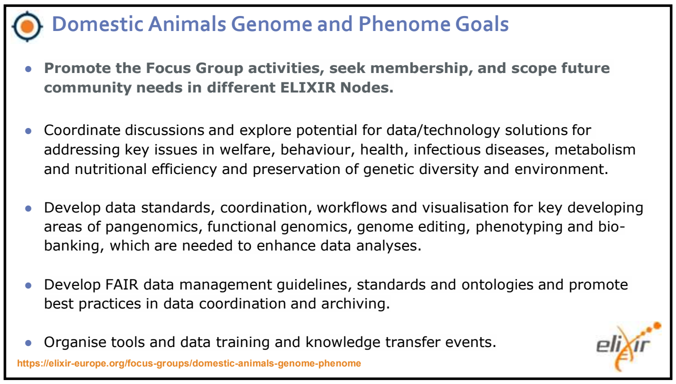
Impact of climate & geopolitics on farming



Call for new infrastructure to meet the current challenges and demands in the Agri-Food sector in Europe.

- *Address the challenge to produce safe, healthy and sustainable food, in relation to adaptation to climate change and higher feed efficiency.*
- *Integration of European facilities for phenotyping, biobanking, bio-imaging and 'omics with veterinary facilities and farm-scale experimental platforms*
- *Integrated approaches including e-Infrastructures to systematically predict, diagnose, prevent and treat plant and animal disease*

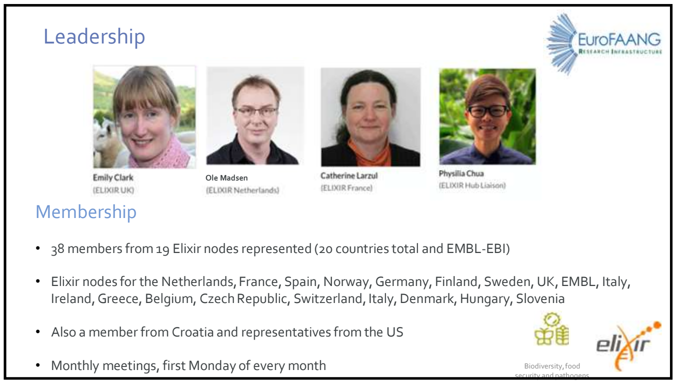
European Commission's Vision for Agriculture and Food



Domestic Animals Genome and Phenome Goals

- **Promote the Focus Group activities, seek membership, and scope future community needs in different ELIXIR Nodes.**
- Coordinate discussions and explore potential for data/technology solutions for addressing key issues in welfare, behaviour, health, infectious diseases, metabolism and nutritional efficiency and preservation of genetic diversity and environment.
- Develop data standards, coordination, workflows and visualisation for key developing areas of pangenomics, functional genomics, genome editing, phenotyping and bio-banking, which are needed to enhance data analyses.
- Develop FAIR data management guidelines, standards and ontologies and promote best practices in data coordination and archiving.
- Organise tools and data training and knowledge transfer events.

https://elixir-europe.org/focus-groups/domestic-animals-genome-phenome



Leadership

Emily Clark
(ELIXIR UK)

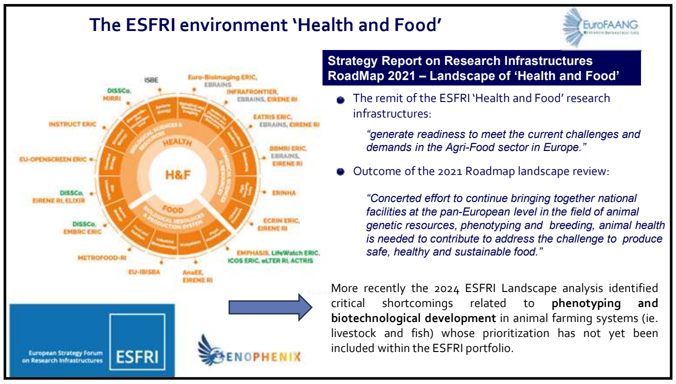
Ole Madsen
(ELIXIR Netherlands)

Catherine Larzul
(ELIXIR France)

Physilia Chua
(ELIXIR Hub Liaison)

Membership

- 38 members from 19 Elixir nodes represented (20 countries total and EMBL-EBI)
- Elixir nodes for the Netherlands, France, Spain, Norway, Germany, Finland, Sweden, UK, EMBL, Italy, Ireland, Greece, Belgium, Czech Republic, Switzerland, Italy, Denmark, Hungary, Slovenia
- Also a member from Croatia and representatives from the US
- Monthly meetings, first Monday of every month



The ESFRI environment 'Health and Food'

Strategy Report on Research Infrastructures RoadMap 2021 – Landscape of 'Health and Food'

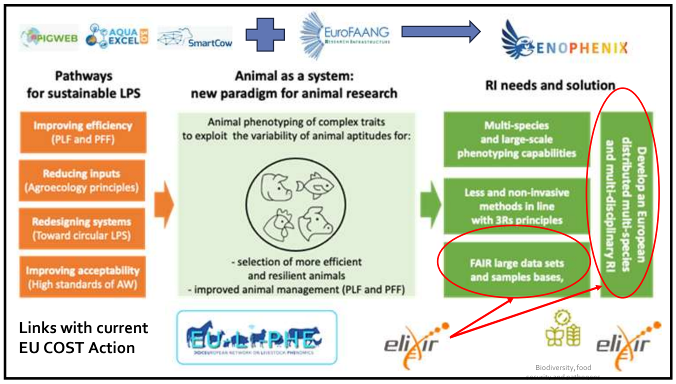
- The remit of the ESFRI 'Health and Food' research infrastructures:

  "generate readiness to meet the current challenges and demands in the Agri-Food sector in Europe."

- Outcome of the 2021 Roadmap landscape review:

  "Concerted effort to continue bringing together national facilities at the pan-European level in the field of animal genetic resources, phenotyping and breeding, animal health is needed to contribute to address the challenge to produce safe, healthy and sustainable food."

More recently the 2024 ESFRI Landscape analysis identified critical shortcomings related to **phenotyping and biotechnological development** in animal farming systems (ie. livestock and fish) whose prioritization has not yet been included within the ESFRI portfolio.



Pathways for sustainable LPS

- Improving efficiency (PLF and PFF)
- Reducing inputs (Agroecology principles)
- Redesigning systems (Toward circular LPS)
- Improving acceptability (High standards of AW)

Animal as a system: new paradigm for animal research

Animal phenotyping of complex traits to exploit the variability of animal aptitudes for:

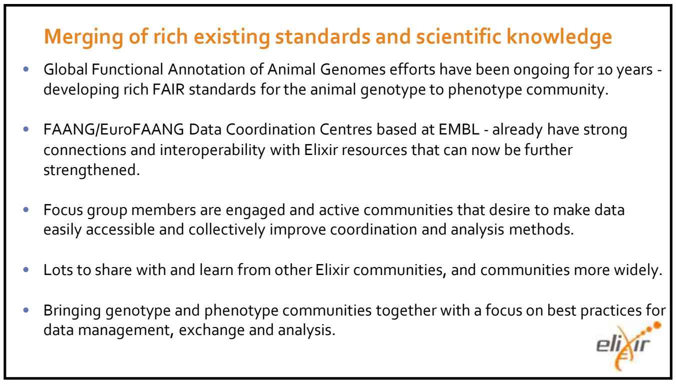
- selection of more efficient and resilient animals
- improved animal management (PLF and PFF)

RI needs and solution

- Multi-species and large-scale phenotyping capabilities
- Less and non-invasive methods in line with 3Rs principles
- FAIR large data sets and samples bases,

Develop an European distributed multi-species and multi-disciplinary RI

Links with current EU COST Action



Merging of rich existing standards and scientific knowledge

- Global Functional Annotation of Animal Genomes efforts have been ongoing for 10 years - developing rich FAIR standards for the animal genotype to phenotype community.
- FAANG/EuroFAANG Data Coordination Centres based at EMBL - already have strong connections and interoperability with Elixir resources that can now be further strengthened.
- Focus group members are engaged and active communities that desire to make data easily accessible and collectively improve coordination and analysis methods.
- Lots to share with and learn from other Elixir communities, and communities more widely.
- Bringing genotype and phenotype communities together with a focus on best practices for data management, exchange and analysis.

EMBL-EBI

Benefit to the entire farmed animal research community:

The FAANG data coordination center

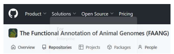
https://data.faang.org/home, at the moment financially supported by the EuroFAANG RI project


FAANG
Functional Annotation of Animal Genomes

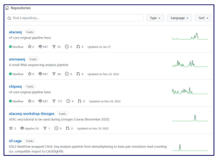
Data Portal

FAANG is the Functional Annotation of Animal Genomes project. We are working to understand the genotype to phenotype link in domesticated animals.

This data portal will help find and browse FAANG's data. Let us know what you think at faang-dcc@ebi.ac.uk.



- **Downloads**
  - Data sets
  - Files
  - Analyses
  - Protocols
  - Publications
- **Visualization**
  - Track hubs (beta version)
- **Project environments**
  - BovReg
  - Gene-SWitCH
  - Aqua-FAANG
  - Geronimo
  - Rumigen
  - HoloRuminant
- **Ontology improver**
- *https://github.com/orgs/FAANG/repositories*



atacseq Public
nf-core original pipeline here:

smrnaseq Public
A small-RNA sequencing analysis pipeline

chipseq Public
nf-core original pipeline here:

atacseq-workshop-limoges Public
ATAC-seq tutorial to be used during Limoges Course (November 2022)

nf-cage Public
DSL2 NextFlow wrapped CAGE-Seq analysis pipeline from demultiplexing to base pair resolution read counting (i.e. compatible import to CAGEfightR)

Funded by
the European Union

https://elixir-europe.org/focus-groups/domestic-animals-genome-phenome

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Expanding the FAANG Data Portal for GenoPHEnix through Focus Group Discussions

Community need to maintain the FAANG Data Portal for brokered submission of omics datasets, metadata and ontologies.

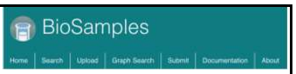
Example scale of the data per project:
421 samples
4 assay types (RNA-Seq, ATAC-Seq ChIP-Seq, WGS)
7Tb total

Build capacity for genome-wide CRISPR screens

Expand the FAANG Data Portal capacity for phenotype data

- images of different types, computer vision, in vitro imaging
- qualitative phenotype data e.g. trait-specific measurements
- new data should add new information
- consider if data is dynamic and multi-dimensional
- new metadata standards

Estimating the amount of data is difficult as currently phenotype data is submitted to various different non-standardized repositories.



Consolidating community resources and objectives

The nf-core Animal Genomics Special Interest Group brings together developers working towards collaborative genomics analysis tools.

Our aim is to collaborate with this group on standards, best practice and wider adoption in the wider domestic animal genome and phenome communities.

https://nf-co.re/special-interest-groups/animal-genomics nf-core


AgBioData

Toward enhanced genomics, genetics, and breeding research outcomes through standardization of practices and protocols across agricultural databases

https://www.agbiodata.org/

The Vertebrate Breed Ontology: Towards Effective Breed Data Standardization

Kathleen R Mullen [1], Imke Tammen [2], Nicolas A Matentzoglu [3], Marius Mather [2], Christopher J Mungall [4], Melissa A Haendel [5], Frank W Nicholas [2], Sabrina Toro [5]; Vertebrate Breed Ontology Consortium

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Intention to become an Elixir community

- **Elixir Activities**
- Attendance at cross-community workshops for biodiversity, food security and pathogens, and cellular and molecular resources.
- Workshops at Elixir All Hands meeting in June on expanding the FAANG Data Portal for Phenotype Data , and at Elixir BioHackathon on livestock phenotyping.
- **Developing a white paper and a roadmap.**
- Currently we have a white paper in draft form and have begun developing a roadmap to becoming a community and exploring links with other communities, particularly biodiversity and microbiome.
- The white paper sets out the challenges faced by domestic animals, the scientific and bioinformatic priorities, and opportunities provided by Elixir.

The EuroFAANG Research Infrastructure Concept
Development Project is funded by Horizon Europe under
Grant agreement n°: 101094718

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8. Annex 2 – Outline and abstract of the white paper for DAGP

ELIXIR Domestic Animals Genome and Phenome Focus Group

Whitepaper

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Abstract

The well-being of farmed and companion animals is increasingly recognised as integral to sustainable agroecosystems, companionship, and the One Health approach, which emphasises the interconnected health of people, animals, and the environment. The ELIXIR Domestic Animals Genome and Phenome (DAGP) Focus Group supports genotype-to-phenotype analysis for farmed and companion animal species. Its aim is to coordinate, discuss, and explore the potential for data/technology solutions for addressing key issues in animal welfare, behaviour, health, infectious diseases, metabolism, nutritional efficiency, and preservation of genetic diversity and the environment. Through consolidating efforts to develop data standards, coordination, workflows, and visualisation, it will enhance the science underpinning rapidly growing fields in domestic animal genomics, including genome-enabled breeding, population genomics, pangenome analysis, functional genomics, genome editing, paleogenomics, phenotyping, and bio-banking. These standards will adhere to the data principles (Findable, Accessible, Interoperable, Reproducible) [1], leveraging established ontologies and metadata standards to promote best practices in data coordination and archiving.

This white paper, prepared by the ELIXIR DAGP Focus Group, summarises the current data infrastructure, resources, and tools that are available for domestic animal genomics and phenomics, and presents a set of community-led plans and priorities that will be implemented to meet the requirements of ELIXIR services and the animal science community. We describe how ELIXIR services can be applied in the domestic animal genomics and phenomics fields and how we can connect projects and infrastructures that are active in the animal sciences domain. We also discuss three key priority areas, including: i) expanding the FAANG Data Portal [2], for example to include phenotype data, in cooperation with the ELIXIR Platforms; ii) exploring submissions of new and linked data types across ELIXIR services including single cell data and provision of proprietary data from industry partners; and iii) strengthening connections to existing ELIXIR Communities and international consortia. As such, this article provides a blueprint for a Domestic Animals Genome and Phenome Community in ELIXIR and will be a catalyst to identify and involve new stakeholders in the field of animal science.

Keywords

White Paper, ELIXIR Strategy, Community Roadmap, EuroFAANG, FAANG, Domestic Animal Phenomics, Domestic Animal Genomics, Informatics, Data Science

9. Annex 3 – Roadmap towards an ELIXIR community

ELIXIR Domestic Animals Genome and Phenome RoadMap 2025-2030

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Introduction

The proposed ELIXIR Domestic Animals Genome and Phenome (DAGP) Community (see associated white paper) will support genotype to phenotype analysis for farmed and companion animal species. As a community we aim to coordinate, discuss and explore the potential for data/technology solutions to address key issues in animal welfare, behaviour, health, infectious diseases, metabolism, nutritional efficiency, and preservation of genetic diversity and the environment. This will consolidate efforts to develop data standards, coordination, workflows and visualisation, which are needed to enhance the science underpinning rapidly developing fields in domestic animal genomics, including pangenome analysis, functional genomics, genome editing, phenotyping, and bio-banking. The developed standards will be based on the FAIR principles (Findable, Accessible, Interoperable, Reproducible) [1], leveraging established

data and metadata sharing principles, standards and ontologies to promote best practices in data coordination, analysis and archiving, as well as promoting readiness for use of AI tools.
The RoadMap for the ELIXIR Domestic Animal Genomes and Phenomes Community 2025-2030 builds on the current data infrastructure, resources and tools that are available for domestic animal genomics and phenomics, particularly the global Functional Annotation of Animal Genomes (FAANG) Data Sharing Principles [2] and FAANG Data Portal [3], and provides a set of community-led objectives. These objectives describe how ELIXIR services can be applied in the field of domestic animal genomics to benefit the entire community. Some examples include: i) expanding the FAANG Data Portal to include phenotype data and additional species, in cooperation with the ELIXIR Platforms, ii) exploring submissions of new and linked data types across ELIXIR services, including single cell data, and provision of encrypted proprietary data from industry partners, and iii) strengthening connections to existing ELIXIR Communities, infrastructures and international consortia. We have established strong links, for example, with the Plant Science Community through the similar challenges faced for food and agriculture. Our objectives are designed to contribute directly to the ELIXIR Biodiversity, Food Security and Pathogens and of the Cellular and Molecular Research scientific priority areas.

Objectives

Enhance visibility, findability and sustainable access to data for domestic animals: Encourage the use of established archives and databases, utilising current metadata standards such as those established by the FAANG consortium, and develop or adapt standards for animal phenotyping data. Identify valuable resources and explore new opportunities to consolidate and utilise these for improving data management and sharing.

Facilitate data integration and interoperability by providing examples of expected use cases across different data types and platforms e.g. for ingestion of single cell data for domestic animals into the single cell Expression Atlas (scEA).

Deliver containerised bioinformatic workflows for data analysis through strategic links with the nf-core Animal Genomics Special Interest Group.

Ensure long-term sustainability of domestic animal data resources, data portals and databases, including the FAANG Data Portal, by promoting best practices in data and metadata submission, validation, and archiving, and fostering alignment with global, national and European infrastructure initiatives, through securing continuous funding.

Support the development of machine learning and AI-driven approaches, such as large language models (LLMs), for data integration, curation and analysis to improve automation and scalability, and facilitate complex queries of the datasets through existing data portal infrastructure.

Build capacity for sample and data sharing between biobanks by developing a standard based on the frameworks provided by BrAPI in the plant domain or the BBMRI directory for human health contributing to conservation of genetic diversity.

Provide a framework for consolidating data and metadata recording and archiving practices for phenotyping data, through understanding current workflows and preferred deposition databases, and building on existing experience, particularly from the Plant Science Community.

Work with industry stakeholders on standards for measurements that can be applied at the point of data collection to facilitate prioritisation and conversion of the data from farming equipment into measured traits in collaboration with internationally recognised organisations like the International Committee For Animal Recording and the ISO Technical committee 347 for Data-driven agrifood systems.

Build joint activities within and beyond the Domestic Animals Genome and Phenome Community leveraging existing initiatives for domestic animals, such as FAANG, to encourage the adoption of data standards by researchers, data and metadata repositories, and in scientific publications.

Facilitate options for data sharing with industry stakeholders through data encryption, anonymisation and/or other methods for sharing proprietary data, such as infrastructure changes to existing resources.

Develop community recommendations, create an open dialogue and contribute to ELIXIR's resources, enabling their broad adoption through targeted training and industry-focused materials to support adoption by data holders and researchers.

Perform gap analysis to identify missing tools and resources to advance the goals of the Domestic Animal Genome and Phenome Community and address them through ELIXIR supported mechanisms.

Strengthen engagement with the Biodiversity, Food Security & Pathogens (BFSP) and Cellular & Molecular Research (CMR) scientific priority areas by actively involving new stakeholders from across communities, and fostering joint activities based on developing shared resources.

Ensure that the Domestic Animal Genome and Phenome Community activities meet the demands and recommendations of researchers through internal communication in the Community and external joint actions, such as through review or opinion publications, and participation in working groups, EU COST-Actions and conferences.

Support the development and sustainability of community-specific tools, data portals, and repositories, promoting their use and ensuring their continued relevance, usability, and integration within the ELIXIR concept.

Implement this roadmap through European and global collaborations, actively contributing to international projects, through coordination and delivery of activities, and securing their funding.

RoadMap Work Plan Overview

Over the coming five years we have six main tasks that encompass the objectives listed above. These are described below with some examples of how they could be achieved.

Task 1 Data Standards, Development and Dissemination

The increasing volume, complexity, and diversity of data sets in fields such as animal genomics and phenomics, along with the rise in open data and open science initiatives, necessitate standardised and comprehensive data descriptions. These descriptions are essential for the findability, retrievability, and interoperability of data and must be documented during the data generation process. The Domestic Animal Genome and Phenome Community has endorsed existing descriptions from previous and ongoing projects, such as the FAANG metadata standards [2] for omics datasets, and the Vertebrate Breed Ontology [4]. Additionally, we aim to enhance the descriptions for phenotyping metadata. To achieve this, we are collaborating closely with the Plant Science Community to align with their commonly used ISA (Investigation-Study-Assay [5], standardisation efforts in the upcoming BioHackathon [biohackathon-projects-2025/17.md at main · elixir-europe/biohackathon-projects-2025 · GitHub], as well as working with the biodiversity community to adapt the ABCD standard for farm animals [Use Cases – Our Pilot Projects - NFDI4Biodiversity]. To provide more semantic meaning mapping to other important linked data resources, such as AGROVOC [6] and continuously growing ontologies like ATOL, EOL, and AHOL (https://bioportal.bioontology.org/ontologies/ATOL?p=classes&conceptid=root) are also incorporated. Also, when considering automatic data exchange, the Global standard for livestock data ICAR, and especially the ADE (Animal data exchange) (https://github.com/adewg/ICAR), which is currently under development, should be considered for coming standardisation efforts. Eventually, this will be applicable to the databases for gene banks to go beyond data sharing towards sharing of biological samples contributing to conservation of local and national genetic diversity.

Task 2 Data Collection

To facilitate easier ingestion of data into the archives we are working with data producers to develop standards that can be applied at the point of data collection. For example, we are working with industry stakeholders using ISO/TC 347 Datadriven agrifood systems to take measurements from farming equipment (fat content, amount of milking each time a cow is milked etc) and convert them into measured traits like milk yield based on standards developed by breeding organisations and ICAR. On farm data often includes 100's of 1000's of data points and images collected over time from sensors or cameras, e.g. for observational time series data for behaviour studies and feed intake measured using automated feeders. Image data is often very large, and not all the data is sufficiently informative to require archiving. As such welldefined data standards established at the point of data collection make downstream prioritisation of the data much easier.

Task 3 Data Discoverability

The FAANG Data Portal [3] currently supports the entire domestic animal genomics community, through open FAIR sharing of data, complete with standardised rich metadata. FAANG projects produce a standardised set of multi-omic assays with resulting data placed into ELIXIR open data archives. To ensure this data is easily findable and accessible by the community, the portal automatically identifies and collates all submitted FAANG data into a single easily searchable resource. The portal also has the flexibility to incorporate new technical infrastructure to effectively deliver new data types and technologies to best fit the needs of the domestic animal science community. As a community, we plan to further explore options to expand the capacity of the FAANG Data Portal to deliver data for emerging species, including insects, encrypted data and phenotype data. In the longer term, large language models and other machine learning tools will allow much more complex dynamic data queries which will greatly enhance the discoverability potential provided by the portal infrastructure. Our aim over the coming five years is to ensure the sustainability of the FAANG Data Portal through funding applications to the European Commission, and through shared goals and objectives with the global FAANG initiative [7].

Task 4 Data Integration and Interoperability

One example of how we plan to maximise interpretability and reuse of domestic animal datasets, is to integrate them with model-organism resources, using zebrafish as a case study. Specifically, we will (i) harmonise metadata and ontologies with FAANG and incorporate zebrafish genomic and epigenomic resources, namely DANIO-CODE (https://danio-code-dcc.genereg.net/, [8]) data into the FAANG data portal; (ii) leverage orthology and synteny frameworks (e.g., Ensembl Compara [9] and Genomicus [10]) to transfer gene- and enhancer-level annotations across species; (iii) perform comparative non-coding genome analysis, including inference of conserved regulatory programs with information-preserving projection (IPP; [11]); and (iv) integrate multi-species single-cell atlases (embryogenesis, tissue regeneration) developed within DANIO-ReCODE (https://danio-recode.eu) to map cell-type and state correspondences. This integration will enable zebrafish to serve both as a comparative anchor and as an experimental validation system where transgenesis in domestic species is impractical (e.g., long generation times, seasonal breeding). The approach aligns with ELIXIR best practices for FAIR metadata, interoperable vocabularies, and reproducible workflows—ensuring that cross-domain resources can be queried jointly for hypothesis generation and validation. Another example we plan to pilot to maximise data integration is a homomorphic-encryption workflow using sensitive, proprietary, salmon aquaculture phenotype/trait data to test practical encrypted submission and joint G2P analysis via the FAANG Data Portal and evaluate the improvements in genetic testing with larger integrated datasets, all while protecting proprietary records.

Task 5 Data Analysis

To guarantee that analysis results remain a long-term asset to the scientific community, it is essential that they are produced using bioinformatics pipelines that adhere to the FAIR principles. The nf-core community have established a set of standards to deliver reproducible and interoperable data analyses (FAIR) pipelines implemented with Nextflow as a workflow management system [12]. Implementing these standards ensures that computational workflows are not only reproducible and transparent but also facilitate seamless integration with other research efforts so that comparative analysis can be performed. In the framework of animal research, the EuroFAANG consortium, which works on decoding genotype-to-phenotype relationships of farm animals, has shown that the adoption of nf-core as its standard for analysis workflows has been instrumental in leading to more efficient and reproducible cross-institutional collaboration and analysis [13]. Based on this we plan to continue our collaboration with the nf-core community by leveraging their extensive library of modules, subworkflows and pipelines to progressively adopt FAIR principles for workflows. Within nf-core, there is an Animal Genomics Special Interest Group (https://nf-co.re/special-interest-groups/animal-genomics) and a dedicated Slack channel, which serve as key platforms for collaboration. Additionally, the Domestic Animals Genome and Phenome Focus Group has already established spaces to foster interaction between nf-core members and the animal genomics and phenomics community. The goal is to ensure that nf-core pipelines can be continuously improved to meet the specific needs of animal genomics / multi-omics and phenomics analyses, facilitating the development of high-quality, standardized workflows for animal research.

Task 6 Collaboration

Members of the community are involved in many European and global initiatives for domestic animals including the GenoPHEnix ESFRI proposal (https://genophenix-ri.eu) to build consolidated infrastructure for farmed animal science and biobanking in Europe. We also participate in international committees dedicated to developing standards for animal recording such as ICAR and have strong links with consortia aiming to capture local and global genomic diversity such as the Ruminant T2T project [14] and Bovine PanGenome Project [15]. With representation on the steering committees of large-scale genomics initiatives for domestic animals such as the FAANG [16] and FarmGTEx [17] projects we are ideally placed to ensure the needs of the Domestic Animals Genome and Phenome Community are represented globally. Over the coming five years we hope to facilitate training workshops and develop shared objectives with the Animal Breeding - RCN: Farm Animal Genomics Collective in the US (https://portal.nifa.usda.gov/web/crisprojectpages/1032104-animal-breeding-rcn-farm-animal-genomics-collective.html) and with the EU-LI-PHE COST-Action focused on livestock phenomics (https://eu-li-phe.eu/). To deepen engagement with industry, we will organize ELIXIR Industry Engagement Day events, starting with the Aquaculture Industry Engagement Day (October 2025), that convenes salmon producers and breeding companies with ELIXIR/EuroFAANG partners to set joint priorities.

Acknowledgements

The authors would like to thank all members of the Domestic Animals Genome and Phenome Focus group, the ELIXIR hub, and particularly the Plant Science Community for input into the development of this RoadMap.

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10. Annex 4 Template of Support letter from ESFRI landmarks and projects to GenoPHEnix

Template for the support letter :

To whom it may concern,

Established in [Insert the year of foundation of your organisation], our [Insert the name of your Infrastructure.] has [developed services and supported research in] [description of domain] at the pan-European level.
In my position of [Insert here your position within the organisation], I have met with [Name of your contact in the GenoPHEnix project] who introduced me to the GenoPHEnix project.
I understand that the GenoPHEnix project aims at setting up a new, pan-European research infrastructure of reference in the field of farm animal genomics and phenotyping.
I also understand that the primary goal of GenoPHEnix is to be the one-stop shop for researchers and professionals in the relevant field, designed and operated to grant users, access to rare, state-of-the-art resources, e.g. access to the facilities of partner institutions of GenoPHEnix, access to the expertise of their partner institution researchers, and access to data produced by researchers in partner institutions.
The activities of the GenoPHEnix project are of direct interest and relevance for our organisation. As I browsed through the GenoPHEnix catalogue of services, I understand that our organisation would benefit from collaborating with GenoPHEnix for the following services and related activities: Complete at our convenience.
For those reasons, I would like to be kept informed of the progress made by the project towards its operational phase, which I understand should start in 2033, even though some services may be accessible earlier. Also, my organisation would be interested to participate to the future GenoPHEnix Open Innovation Forum, to be created in 2027.
Eventually, by the present letter, my organisation is glad to affirm our support to the establishment of the GenoPHEnix-RI.
Yours sincerely,

[Insert prefix] [Insert first name and family name]
[Insert here the quality that empowers you to apply on behalf of your organisation, e.g. Member of the Board, Chairman, President, CEO, etc.]
[Insert the name of the organisational unit of the respondent]
[Insert the name of the organisation]
[Signature]

11. Annex 5 Agenda of the Research Infrastructure Session at EAAP, Aug. 27, 2025.

European Research Infrastructure to Support Livestock Science: Whom and How?

Congress Center | Room Seminar 1 & 2 | 14:30 - 18:05

	Activity	Speaker(s)	Description
Session 1: Setting the Stage			
14:30	**Opening & Welcome**	**Michèle Tixier-Boichard**	Brief introduction to the session goals and structure.
14:35	**Keynote: The Current Landscape of European Research Infrastructures: Where Do Livestock, Aquaculture, and Insect Science Fit In?**	**Emily Clark**	The current landscape of European Research Infrastructures: which place for livestock, aquaculture, and insect science?
Session 2: European Research Infrastructures in Practice			
14:55	**Biobanking for a Healthier World – Introducing BBMRI-ERIC**	**Johanna Kostenzer**	Lessons from human biobanking and potential applications for livestock science.
15:10	**INFRAFRONTIER: Cutting-Edge Human Disease Modelling**	**Yan Herault**	Phenotyping animal models and its relevance to livestock.
15:25	**SmartCow in the AgroServ project: Giving access to research services to advance the agroecological transition of cattle husbandry**	**René Baumont**	Achievements in aquaculture research and infrastructure integration.
15:40	**Open Science needs a more open livestock research community**	**Jaap van Milgen**	Insights from pig research infrastructure and coordinator's perspective on RIs.
15.55	**Coffee break (15 min)** Networking & discussion break		
16:10	**GenoPHEnix – a European research infrastructure to study genome and phenome interactions for sustainable animal production**	**René Baumont**	The future of integrated livestock research infrastructures.
Session 3: Data, Collaboration & Future Needs			

16.30	**Platforms & Methods for Sharing and Collaboration on Agricultural Genome-to-Phenome Using Public and Confidential Data**	**Jack Dekkers**	Presentation on secure data sharing strategies for agricultural research.
16.45	**Creating common structure and data access services for animal agriculture in Europe in collaboration with ELIXIR**	**Emily Clark (ELIXIR)**	Exploring best practices for secure and open data sharing in livestock research.
17.00	**Public-Private Sector Collaboration & Research Infrastructure Needs**	**Geena Cartick and Cagla Kaya**	How infrastructures can engage better with sector
17.15	**The EuroFAANG Research Infrastructure as platform to support new projects in farmed animal G2P research**	**Elisabetta Giuffra**	How past and ongoing research projects contribute to infrastructure development.
Session 4: Open Discussion & Next Steps			
17.35	**Q&A and Open Discussion**	**Michèle Tixier-Boichard and Geena Cartick**	Interactive discussion on future needs, funding, and collaboration.
18:00	**Closing Remarks & Next Steps**		Summary of key takeaways, future actions, and engagement opportunities