OPINION ARTICLE

Establishing the ELIXIR Domestic Animals Genome and Phenome Community

[version 1; peer review: 1 approved]

Emily L Clark[1,2], Andreia Amaral[3], Damir Baranasic[4,5], Endre Barta[6], Geena Cartick[7], Physilia Chua[8], Jose Espinosa-Carrasco[9], Lingzhao Fang[10], Daniel Fischer[11], Sarah O Fischer[12], Sylvain Foissac[13], Gareth Gillard[14], Elisabetta Giuffra[15], Tina Hartwig[12], Katharina F Heil[8], Christiaan Henkel[14], Haja N. Kadarmideen[10], Tomas Klingström[16], David E MacHugh[17,18], Brenda M Murdoch[19], Cedric Notredame[9], John O-Grady[17,18], Joseph Robertson[14], Patrick Ruch[20], Alexey Sokolov[1], Ilma Tapio[11], Michèle Tixier-Boichard[15], Robert M Waterhouse[20], Klaus Wimmers[12], Ole Madsen[21], Catherine Larzul[13]

[1]European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, CB10 1SD, UK
[2]The Roslin Institute, The University of Edinburgh, Roslin, Scotland, EH25 9RG, UK
[3]MED—Mediterranean Institute for Agriculture, Environment and Development and CHANGE – Global Change and Sustainability Institute, University of Évora, Polo da Mitra, Ap. 94, 7006-554, Évora, Portugal, Portugal
[4]Ruđer Bošković Institute, Bijenička Cesta 54, 10000, Zagreb, Croatia
[5]Imperial College London Section of Cell Biology and Functional Genomics, London, England, SW7 2AZ, UK
[6]Hungarian University of Agriculture and Life Sciences, Gödöllő, Páter Károly u. 1, 2100, Hungary
[7]European Forum for Farmed Animal Breeders, Rue de Trèves 61, 1040 Brussels, Belgium
[8]ELIXIR Hub, South Building, Wellcome Genome Campus, Hinxton, Cambridge, CB10 1SD, UK
[9]Centre for Genomic Regulation, The Barcelona Institute of Science and Technology, Dr. Aiguader 88, Barcelona, 08003, Spain
[10]Aarhus University, Aarhus, 8000, Denmark
[11]LUKE Natural Resources Institute, 29 A 31600 Jokioinen, Finland
[12]Research Institute for Farm Animal Biology, Wilhelm-Stahl-Allee 2, 18196, Dummerstorf, Germany
[13]GenPhySE, Université de Toulouse, INRAE, ENVT, 31326 Castanet-Tolosan, France
[14]Centre for Integrative Genetics (CIGENE), Norwegian University of Life Sciences, Ås, NO-1432 Ås, Norway
[15]Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France
[16]Department of Animal Biosciences, Swedish University of Agricultural Sciences, Box 7023, Uppsala, 750 07, Sweden
[17]UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin, D04 V1W8, Ireland
[18]University College Dublin Conway Institute of Biomolecular and Biomedical Research, Dublin, Leinster, Ireland
[19]Department of Animal, Veterinary, and Food Sciences, Bioinformatics and Computational Biology, University of Idaho, Moscow, Idaho, USA
[20]SIB Swiss Institute of Bioinformatics, 1227 Geneva, Switzerland, Switzerland
[21]Wageningen University and Research, , Droevendaalsesteeg 4, 6708 PB, Wageningen, The Netherlands

v1 **First published:** 02 Mar 2026, **15**(ELIXIR):339
https://doi.org/10.12688/f1000research.177500.1

Latest published: 02 Mar 2026, **15**(ELIXIR):339
https://doi.org/10.12688/f1000research.177500.1

Open Peer Review

Approval Status ✓

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) Community supports genome-to-phenome analyses for farmed and companion animal species. Its aim is to coordinate, discuss, and explore the potential of data technology solutions to address key issues in animal welfare, behaviour, health, infectious diseases, metabolism, nutritional efficiency, and the 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 FAIR data principles and leverage established ontologies 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 available for domestic animal genomics and phenomics, and presents community-led plans and priorities to 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: i) expanding the FAANG Data Portal for phenotype data with ELIXIR Data Platforms; ii) supporting submissions of new data types across ELIXIR Core Data Resources , including proprietary data from industry partners; and iii) strengthening connections to existing ELIXIR Communities and international consortia. This article provides a set of priorities for a Domestic Animals Genome and Phenome Community in ELIXIR and outlines the next steps to engage across stakeholders and to consolidate data for domestic animal science in Europe.

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

	1
version 1 02 Mar 2026	✔ view

1. **Muhammad Farhab**, Yangzhou University, Yangzhou, China

Any reports and responses or comments on the article can be found at the end of the article.

This article is included in the ELIXIR gateway.

This article is included in the EMBL-EBI collection.

Corresponding author: Emily L Clark (eclark@ebi.ac.uk)

Author roles: Clark EL: Writing – Original Draft Preparation; **Amaral A**: Writing – Review & Editing; **Baranasic D**: Writing – Original Draft Preparation, Writing – Review & Editing; **Barta E**: Writing – Review & Editing; **Cartick G**: Writing – Review & Editing; **Chua P**: Project Administration, Writing – Review & Editing; **Espinosa-Carrasco J**: Writing – Original Draft Preparation, Writing – Review & Editing; **Fang L**: Writing – Review & Editing; **Fischer D**: Writing – Review & Editing; **Fischer SO**: Writing – Original Draft Preparation, Writing – Review & Editing; **Foissac S**: Writing – Review & Editing; **Gillard G**: Writing – Original Draft Preparation, Writing – Review & Editing; **Giuffra E**: Writing – Original Draft Preparation, Writing – Review & Editing; **Hartwig T**: Writing – Review & Editing; **Heil KF**: Writing – Review & Editing; **Henkel C**: Writing – Review & Editing; **Kadarmideen HN**: Writing – Review & Editing; **Klingström T**: Writing – Original Draft Preparation, Writing – Review & Editing; **MacHugh DE**: Writing – Original Draft Preparation, Writing – Review & Editing; **Murdoch BM**: Writing – Original Draft Preparation, Writing – Review & Editing; **Notredame C**: Writing – Original Draft Preparation, Writing – Review & Editing; **O-Grady J**: Writing – Review & Editing; **Robertson J**: Writing – Original Draft Preparation, Writing – Review & Editing; **Ruch P**: Writing – Review & Editing; **Sokolov A**: Writing – Original Draft Preparation, Writing – Review & Editing; **Tapio I**: Writing – Review & Editing; **Tixier-Boichard M**: Writing – Original Draft Preparation, Writing – Review & Editing; **Waterhouse RM**: Writing – Review & Editing; **Wimmers K**: Writing – Review & Editing; **Madsen O**: Writing – Original Draft Preparation, Writing – Review & Editing; **Larzul C**: Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This work was funded through the Horizon Europe EuroFAANG Research Infrastructure Project under Grant Agreement No. 101094718 and UK Research and Innovation Grant 10068653. It was also supported by ELIXIR, the research infrastructure for life science data and the European Union's Horizon 2020 Research and Innovation Programme under Grant Agreement No. 817923 (AQUA-FAANG), No. 817998 (GENE-SWitCH), No. 815668 (BovReg), No. 101000226 (Rumigen), No. 101000213 (Holoruminant) and No. 101000236 (GEroNIMO). Participants were also supported by the Project PCI2025-167077-2 funded by MICIU /AEI /10.13039/501100011033 / FEDER, UE (JCE and CN); FCT—Foundation for Science and Technology under Projects UIDB/05183 and CEEC 4th edition (2021.02058. CEECIND) (AJA); NFDI4Biodiversity - NFDI4Biodiversity is funded by the German Research Foundation (DFG) within the framework of an agreement between the Federal Government and the Länder on the establishment and funding of the National Research Data Infrastructure (NFDI) of 26 November 2018 (Grant Number 442032008) (SF); Research Ireland Centre for Research Training in Genomics Data Science (grant no. 18/CRT/6214) (JFO'G and DM); Department of Agriculture, Food, and the Marine (DAFM) project award (TB-ORNOT-TB: grant no. 2023RP902) (DM); the BReIF project funded by AgroEcoNum high priority programme (PEPR) of the France 2030 initiative (MTB); Stiftelsen Seydlitz MP bolagen and Formas – a Swedish Research Council for Sustainable Development (Grant Number 2021-01608) (TK); Agriculture of Data (IMAP-Dairy) project EU Research Executive Agency under grant agreement No 101197332 (HK); USDA NIFA Animal Breeding-RCN:Farm Animal Genomics Collective Project Number UTA-01798 (BM); PigWeb project EU Horizon 2020 Research and Innovation Programme under Grant Agreement No 101004770 (CL); Biotechnology and Biological Sciences Research Council Awards BB/W018772/1, BBW019108/1 and BBS/E/RL/230001B (ELC).
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

How to cite this article: Clark EL, Amaral A, Baranasic D *et al.* **Establishing the ELIXIR Domestic Animals Genome and Phenome Community [version 1; peer review: 1 approved]** F1000Research 2026, **15**(ELIXIR):339 https://doi.org/10.12688/f1000research.177500.1

First published: 02 Mar 2026, **15**(ELIXIR):339 https://doi.org/10.12688/f1000research.177500.1

Introduction

Domestic animals are defined as having been bred and adapted to meet human needs. They meet the needs of humans in many ways, including as sources of food, workforce, transportation, leisure, companionship, and as key components of many human cultures. They also contribute to agroecosystems by shaping rural landscapes, enhancing soil fertility by producing manure and maintaining biodiversity on marginal and grazing lands.

Domestic animals face several challenges across different contexts:

- **Sustainable animal production in a changing climate:** Animal-based food production represents a significant challenge to climate change mitigation because livestock, particularly ruminants, contribute to greenhouse gas emissions. They are also vulnerable to drought and heat stress caused by the changing climate, and modern breeding programmes must mitigate these effects. However, with a rapidly growing human population, the demand for animal-derived protein and other food products is increasing. The challenge is now to produce the same amount of food from fewer animals more sustainably, i.e., from a lower number of highly productive animals that require less input, reducing environmental cost.

- **Emerging diseases and the need for genomic resilience:** Global climate change has led to an increased risk of contagious and vector-mediated diseases, some of which are zoonoses; and when, coupled with increased antimicrobial resistance, understanding the genomic drivers of disease resilience for all domestic animals is essential to mitigate the threat of future disease outbreaks.

- **Robustness is a key trait for future livestock:** In addition to improving resilience, improving robustness is a common objective for all animal farming systems, including those based upon workforce and transportation, which are still important in many regions of the world. Robust animals that can survive extreme events, such as disease outbreaks or drought, and go on to reproduce, represent valuable genetic resources.

- **Welfare challenges from breeding and management practices:** A range of welfare issues also pose challenges for domestic animals, including the preferential selection of extreme traits due to skewed breeding objectives, and pressure to rapidly change housing, management systems, or breeding programmes in response to climate-related impacts.

- **Maintaining genetic diversity:** Several companion animal breeds exhibit high levels of inbreeding and founder effects, which increase the frequency of genetic diseases leading to increased morbidity or early mortality. This phenomenon has also been observed in several highly selected livestock breeds, including the widely used Holstein-Friesian dairy cattle.

- **Aligning animal production with societal expectations:** Domestic animal welfare and health are a priority in Europe, to a greater extent than in many regions of the world. However, meeting societal expectations is a challenge for animal producers, scientific researchers and associated stakeholders across the domestic animal sectors worldwide.

- **Implementing the 3Rs in scientific research:** In scientific research, the widespread adoption of the 3Rs (Replacement, Reduction and Refinement) principle for the use of live animals necessitates the timely adoption of advanced *in silico, in vitro,* and *in vivo* methodologies, which involve complex technology and protocol development.

Opportunities to address these challenges include:

- Developing data infrastructure according to the FAIR data principles (Findable, Accessible, Interoperable, Reproducible),[1] through resources including the FAANG Data Portal.[2]

- Breeding for increased feed efficiency and reduced rumen size in ruminants[3] to lower input use and greenhouse gas emissions.

- Integrating microbiome profiling into breeding strategies to improve animal health and performance.

- Conserving genetic diversity by supporting locally adapted and resilient breeds.

- Introducing genetic screening and genomic evaluation in species where these tools are not yet used, to reduce the accumulation of deleterious alleles.
- Using advanced paleogenomics techniques with zooarchaeological samples for understanding the origins, history, and evolution of domestic animals.[4]
- Developing cellular technologies to link genome and phenome data across *in vitro* and *in vivo* systems, from cell to whole-animal scale.
- Applying genome-wide CRISPR screens *in vitro* to identify targets for genome editing that improve disease resistance[5–7] and welfare traits.[8]
- Using sensor data and high-throughput phenotyping with genetics to enable informed, efficient, and sustainable breeding decisions.[9]

Genome sequencing technologies and steady improvements in functional annotation of domestic animal genomes[10–12] have advanced our understanding of genetic diversity and how the genome is expressed and regulated in different species, breeds and populations. Yet, much still needs to be done to link genome information to real-world outcomes such as trait improvement. Better integration of genome and phenome information in domestic animals is essential and underpinned by efficient use of data and data resources. As a community of researchers, we need to shift our focus from being descriptive to being predictive; this is a primary objective of data science, which is expected to extract new knowledge from big data.

To meet the challenges described above, productive new collaborations need to be developed across fields, including genetics, biochemistry, microbiology, physiology, nutrition, immunology, and disciplines relevant to data science such as quantitative biology, statistics, computer science, and mathematics. Thus far, a holistic approach has proven difficult with limited sharing of data, data tools and resources across fields. A dedicated ELIXIR community of scientists focused on domestic animal genomics and phenomics will help address the data resource and management challenges towards a shared goal of sustainably managing and maintaining healthy populations of companion animals and productive and sustainable farmed animals.

ELIXIR is a European life sciences infrastructure which supports the management of public research data and coordinates access to life science resources, helping researchers maximise the impact of life science research on public health, the environment, and the economy.[13]

The ELIXIR domestic animal genome and phenome community

Organisational opportunities and the role of ELIXIR

Until relatively recently, the research landscape for domestic animals was highly divided, mostly by specialisation on a single species. From 2018, six H2020 projects, with the common aim of providing genomic resources to inform precision breeding in farmed animals, came together under the umbrella of the 'EuroFAANG' (https://eurofaang.eu) and were the first to connect species-specific projects (https://data.faang.org/projects). Collectively, the projects produced very large omics datasets for pig and chicken (GENE-SWitCH and Geronimo), cattle (BovReg and Rumigen), six teleost fish species (AQUA-FAANG) and the ruminant microbiome (Holoruminant). The concerted efforts of these projects demonstrate what is possible in terms of data analysis, integration and development of shared resources and expertise by working together as one community under the EuroFAANG umbrella. The EuroFAANG projects led to further community infrastructure development, including the nf-core special interest group in animal genomics (https://nf-co.re/special-interest-groups/animal-genomics), and the Horizon Europe INFRA-DEV EuroFAANG Research Infrastructure (EuroFAANG RI) concept development project (https://eurofaang.eu). The EuroFAANG RI Project led to further integration between the farmed animal genome and phenome communities and was co-developed into a proposal, submitted to the 2026 update of the ESFRI Road Map, entitled GenoPHEnix (https://genophenix-ri.eu/), merging the concepts of EuroFAANG with existing H2020 INFRAIA infrastructures for farmed animal phenotyping, PigWeb (https://www.pigweb.eu), SmartCow (https://smartcow.eu/) and AquaExcel 3.0 (https://aquaexcel.eu). The involvement of ELIXIR nodes in these projects (Table 1) provides opportunities to build on ELIXIR networks to link and expand collaboration within and between projects and develop shared data management strategies based on the foundation provided by ELIXIR core data resources.

Table 1 highlights the scope and diversity of projects and the informatics and data management needs facing the domestic animal science research space, particularly in terms of infrastructure and resources.

Table 1. A selection of transnational and national projects related to the area of domestic animals in which ELIXIR Nodes are involved.

Project title	ELIXIR node/Funder	Summary details/Description
Functional Annotation of Animal Genomes (FAANG) initiative	Multiple across Europe, national, European Commission, US FAANG and international	Global initiative working to discover basic functional knowledge of genome function to decipher the genotype-to-phenotype (G2P) link in farmed animals with 3 main aims: 1. Standardize core assays and experimental protocols 2. Coordinate and facilitate data sharing through its Data Portal 3. Establish suitable infrastructures for data analysis
EuroFAANG H2020 Projects - GENE-SWitCH, BovReg, AQUAFAANG, HoloRuminant, Geronimo, Rumigen	Multiple across Europe, European Commission Horizon 2020	Generation of multi-omics datasets to inform precision breeding of farmed animals.
INFRAIA farmed animal phenotyping infrastructures – PigWeb, SmartCow and AquaExcel 3.0	Multiple across Europe, European Commission Horizon 2020 INFRAIA	Infrastructures providing transnational access to facilities for farmed animal phenotyping.
MuDiS4LS	IFB, France, under ANR	Improving data services for life sciences: case study on integrating data for the holobiont.
BReIF	IFB collaborator, France, ANR	Data FAIRNESS for animal and plant biobanks, pipelines for pangenome analysis.
EB^2 Engineering Biology Hub	UK, BBSRC, Gates Foundation, Roslin Foundation	Building resources such as genome-wide CRISPR screens to link genotype to phenotype in domestic animals.
Ensembl in a new era	UK, EMBL, UKRI BBSRC BBR Fund	Providing deep annotation of domestic animal genomes, including pangenomes and breed-specific assemblies in the Ensembl Genome Browser.
EuroFAANG RI Concept Development Project	UK, France, Norway, Netherlands, Germany HORIZON- INFRA-DEV	Developing a concept for a research infrastructure to build capacity for genotype to phenotype research for farmed animals in Europe. Provided the foundation for establishing the Domestic Animals Genome and Phenome Focus Group.
NFDI	DFG-funded/Multiple German ELIXIR nodes	NFDI systematically indexes and networks valuable scientific and research data for the entire German scientific system and makes it available for sustainable and qualitative use. Until now, they have mostly been available on a decentralised, project-related or temporary basis, especially for the life sciences through the consortia-NFDI4Biodiversity.
EU-LI-PHE	EU COST Action CA22112, including multiple ELIXIR nodes, e.g. UK, Ireland, France …	Focused on phenomics in livestock animals. EU-LI-PHE will create a Europe-centred multidisciplinary, interconnected and inclusive community of experts in livestock phenomics.
Insect-IMP	EU COST Action CA22140, including multiple ELIXIR nodes, e.g. UK, Slovenia.	The Insect-IMP network aims to support insect genetic improvement to enhance food security and sustainability while reducing environmental impact.

Table 1. *Continued*

Project title	ELIXIR node/Funder	Summary details/Description
GenoPHEnix	Multiple, submission as a proposal to ESFRI RoadMap	A research infrastructure for farmed animal science in Europe to generate readiness to meet future challenges to the Agri-Food sector. Combines funded INFRAIA infrastructures PigWeb, SmartCow and AquaExcel 3.0 for farmed animal phenotyping and the EuroFAANG RI INFRA-DEV concept development project. Proposal submitted for inclusion as an infrastructure project on the ESFRI Road Map in 2026.
SalmoCode	Norway, Norwegian Seafood Research Fund (FHF)	Utilising single-cell RNA sequencing to screen developing salmon from a range of production conditions and thereby building a salmon map of organs and cells for the optimal development of embryos.
SalmoStrong - Drivers of Salmon Robustness	UK, BBSRC Prosperity partnership between the Roslin Institute (University of Edinburgh) and Mowi Scotland	Advancing scientific understanding that will facilitate enhanced robustness of salmon, with the long-term goal to reduce current mortality levels by 50% during seawater production over the next ten years, establishing fish populations highly adapted to Scottish farming conditions.
DoGA Consortium Expression Atlas	Finland, Sweden, UK, Finnish national funding	A promoter and gene expression atlas with interactive, open data resources, including a data coordination center and genome browser for the domestic dog.

As part of the process of maturing from a Focus Group to a Community, we aim to initiate community activities including: (1) cataloguing ELIXIR Services that support domestic animal genomics and phenomics research; (2) developing recommendations for connecting genomics and phenomics research infrastructures for domestic animals through ELIXIR; and (3) coordinating ELIXIR Node participation in Horizon Europe (HE) infrastructure project proposals such as GenoPHEnix (https://genophenix-ri.eu), the HE cluster 6 topic calls, EU COST Actions and the topics of the future European Commission's work programme.

Connections with ELIXIR platforms and communities

Since its establishment in 2024, the Domestic Animals Genome and Phenome (DAGP) Focus Group has been developing connections with the ELIXIR platforms and communities, which are summarised in Table 2. In addition, synergies with the activities of the communities for Biodiversity, Plant Sciences, Single-cell Omics and Federated Human Data are well established through shared activities and described in more detail below.

Developing shared phenotyping metadata and minimal reporting standards with the plant sciences and biodiversity communities

In domestic animal populations, data recording standards for phenotyping studies, e.g., longitudinal observational studies, are minimal and require improvement. To achieve this, we are working with the Plant Science Community to align with their commonly used ISA standardisation[14] efforts for minimal information recording, as well as working with the biodiversity community to adapt the ABCD (Access to Biological Collection Data) standard for domestic animals.

Supporting data interoperability through the single-cell omics community

Members of the DAGF Community will contribute high-quality single-cell RNA-seq (scRNA-seq) data to open, standardised infrastructures. However, direct community submission to the Single Cell Expression Atlas (scEA) (https://www.ebi.ac.uk/gxa/sc/home) is not yet supported, and metadata gaps limit interoperability with other ELIXIR resources. To remedy this, we have discussed aligning metadata standards between resources such as Annotare (https://www.ebi.ac.uk/fg/annotare/login/) and the FAANG Data Portal (https://data.faang.org) pre-archiving, to facilitate easier data ingestion. This will enhance FAIR practices, support multimodal data integration and interoperability by evaluating how existing metadata standards align in practice to identify concrete opportunities for harmonisation across FAANG and the scEA.

Table 2. Examples of links between the ELIXIR domestic animals genome & Phenome community and other ELIXIR platforms and communities.

ELIXIR Platform/ community	Shared activities	Planned/proposed joint activities
Data	Enhancing the discoverability of image data and defining a suitable repository for observational data.	Mapping across repositories, serving data to the community via the FAANG Data Portal
Interoperability	Facilitating multi-modal data submissions across ELIXIR core database repositories.	Single-cell case study ingestion of data into the single cell Expression Atlas (scEA)
Tools	Benchmarking activities	Development of minimal information standards for animals, e.g., equivalent of the ELIXIR plant community tool MIAPPE
Training	Development of Learning Paths	Metadata and data submission via the FAANG Data Portal to ELIXIR core databases via training workshops
Biodiversity	Integration of omics data with phenotype, e.g., observational data. Multi-modal data submissions across the ELIXIR core database repositories	Development of standards to promote best practices, FAIR data checking workflows and expansion of the FAANG Data Portal to incorporate phenotype data
Federated Human Data	Development of data encryption to facilitate the sharing of proprietary data	Development of standards to promote best practices, and expansion of the FAANG Data Portal to incorporate encrypted data Homomorphic data encryption case study
Food and Nutrition	Facilitating further community interaction across domains	Network with relevant stakeholders
Galaxy	Workflow and pipeline development, scalability and deployment	Links with the animal science nf-core community
Human copy number variation	Pangenome methodology, analysis and workflow development.	Interaction with EVA and other ELIXIR archives. Particularly for structural variants from pangenome analysis and functional consequences, e.g., Ensembl VEP
Metabolomics	Development of appropriate metadata standards and submission guidelines.	Sharing of metabolomic data from animals through ELIXIR database repositories, e.g., Metabolights
Microbiome	Shared goals/stakeholders, linked ELIXIR core data resources, e.g., MGnify	Community efforts to catalogue MAGs from ruminants, e.g. to facilitate research in greenhouse emissions Shared goals/stakeholders relating to AMR and antibiotic use in domestic animals
Plant Sciences	Development of minimal information requirements for phenotyping experiments, e.g., MIAPPE	Integrate reproducible workflows. Shared biohackathon to provide minimal information requirements for animals
Research Data Management	Interoperability, multimodal data submissions, standards	Multimodal data submissions for omics data from domestic animals across ELIXIR Core Database Resources, identification of gaps in metadata limiting interoperability
Single Cell Omics	Interoperability, multimodal data submissions, standards	Shared goals/stakeholders across resources, including Expression Atlas and BioImage Archive. Integrate workflows. Shared proposals to facilitate multi-modal data submissions across resources
Systems Biology	Scalability, standards	Development of metadata standards for in vitro systems and workflows high-content screens. Integration of workflows

Exploring the potential of data encryption for G2P data sharing based on frameworks developed by the Federated human data community

Genome-to-phenome (G2P) research in domestic animals is constrained by industry reluctance to share genotype and phenotype data due to intellectual property and privacy concerns. This limits data reuse and joint analysis across sectors, undermines FAIR data sharing principles and is slowing progress in food security-relevant genomics. We are addressing this challenge by evaluating data encryption as a technical and community-ready solution for secure G2P data sharing, linking with similar activities led by the Federated Human Data community.

Contribution to the ELIXIR biodiversity, food security and pathogens priority area

The DAGP community 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 detail in the sections below.

FAIR Data – 'The FAANG Data Portal' supporting direct download from multiple ELIXIR core data resources to enable seamless access to all FAANG data

The FAANG Data Portal currently supports the domestic animal genomics community through open sharing of data, following the FAIR principles,[1] complete with standardised rich metadata. The Data Portal is described in detail in Harrison et al. 2021,[2] briefly: FAANG projects produce a standardised set of multi-omic assays with resulting data placed into ELIXIR core database resources (https://elixir-europe.org/platforms/data/core-data-resources). 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 Data Portal supports direct download from multiple ELIXIR data and metadata repositories, including the European Nucleotide Archive (ENA) and BioSamples, to enable seamless access to all FAANG data from within the portal itself. The portal provides a range of predefined filters, powerful predictive search, a catalogue of sampling and analysis protocols and automatically identifies publications associated with any dataset. To ensure all FAANG data submissions are high-quality, the portal includes powerful contextual metadata validation and data submissions brokering to the underlying ELIXIR data repositories. 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. Through the DAGP Focus Group, we have explored options to provide data via the FAANG Data Portal for emerging species, including insects, and encrypted proprietory genotype and phenotype data.

A key strategic aim for the emerging DAGP community is to expand the FAANG Data Portal to include observational data types, including phenotypic measurements and image data, bringing new ELIXIR archives, including BioStudies and the BioImage Archive, into the portal infrastructure. This will empower agrobiodiversity and food security-relevant research by reducing the need for observational data submissions to disparate repositories, promoting FAIR principles to enhance data reuse and joint analysis across sectors, and providing a highly standardised data submission system for all animal agriculture data. To facilitate this, appropriate metadata standards for recording animal phenotype information in BioSamples will need to be developed, building on the published FAANG, Vertebrate Breed Ontology and ELIXIR Plant Science Community standards and ensuring compatibility and interoperability across resources for multi-modal submissions across ELIXIR Core Data Resources. We will also co-develop mechanisms with data producers that facilitate the capturing of key information during data production to facilitate easier pre-archive processing, curation and ingestion. In parallel, we plan to explore expanding the functionality of the FAANG Data Portal to provide a searchable and unified view of phenotypic measurement and image data, providing a powerful resource to integrate omics technologies with complementary observation data, enabling solutions to the grand challenges outlined in the BFSP strategy.

Analysis - Provision of consolidated computational tools and pipelines for genomic analysis

An increasing amount of domestic animal-related data is now being produced through sequencing. Sequencing provides access to genetic diversity and sheds essential light on key molecular processes. These include gene expression levels and various epigenetic analyses that help improve our understanding of the dynamics of gene expression and its intricate relationship with genetic diversity. The substantial advancements in sequencing technology mean that these fundamental questions can now be addressed using high-throughput sequencing, with the raw data effectively represented as counts mapped onto a reference genome.

Of course, the devil is in the details, and a wide variety of sequencing technologies now co-exist at multiple levels, including acquisition methodologies and interpretation algorithms. Yet, achieving seamless integration across datasets, experiments, and species is often crucial for maximising the potential of these data. This is why ENCODE[15] and similar large-scale distributed projects were initially presented as major models in the initial FAANG white paper.[11] Indeed, one of the main achievements of ENCODE is arguably the capacity to generate enormous amounts of data perfectly comparable across sites and assays for human and mouse.

In the meantime, the landscape of large-scale genomics analysis has significantly evolved, particularly for biodiversity. Domestic animal genomics is now closely connected to a broader global effort aimed at characterising the genomes of all animal species on Earth, as exemplified by the Earth BioGenome Project (https://www.earthbiogenome.org). While the specific needs of domestic animal research may differ from those of strictly ecological studies, there are compelling reasons why data generated by the animal genomics community and the domestic animal genomics community should remain interoperable. One key reason is the identification of evolutionary constraints. From an evolutionary perspective, genomic data can provide crucial insights into the emergence of traits in wild species and their subsequent harnessing through domestication, particularly with the integration of paleogenomics data across time transects e.g.[4] Similarly, studying the genomics of closely related wild species can enhance our understanding of disease resistance across species and improve strategies for managing genetic diversity.[16] One example is the DoGA Atlas project for the domestic dog (https://www.doggenomeannotation.org/), which provides an expression atlas of promoters and genes for 100 tissues from both domestic dog breeds and wolves, enabling high resolution disease mapping.[17] These considerations explain why the domestic animal genomics community has a strong interest in developing computational tools within a framework that ensures the highest level of interoperability—not just within its research community but also across related fields with similar goals.

In recent years, an increasing number of scientific communities have adopted FAIR principles for software development and implementation. In the context of animal genomics, one of the most advanced European initiatives is the Darwin Tree of Life (DToL) (https://www.darwintreeoflife.org), which utilises Nextflow technology to implement pipelines following the nf-core standard.[18] More recently, the six H2020 projects under the EuroFAANG umbrella have joined forces to adopt the nf-core standard collectively. The adoption process is detailed in the recently published nf-core update,[19] which highlights both the necessity of the FAIRification process for pipelines and the feasibility of a gradual transition. This transition ensures that fragmented ecosystems remain functional while progressing toward greater interoperability. Given that large-scale funding for a uniform transition to a unified computational framework is unlikely, the DAGP Community must propose a pragmatic path toward computational FAIRification while maximising integration with minimal constraints.

The computational framework associated with EuroFAANG is a cornerstone of its long-term sustainability. This framework serves four primary purposes:

1. It provides practical solutions for the community to manage and maximise the value of generated data.
2. It ensures that datasets can be compared and interoperated across consortia and species, enabling data consolidation for the most informative analyses.
3. It guarantees long-term data interoperability while addressing two conflicting realities: on the one hand, sequencing technologies will continue to improve, becoming more precise and affordable; on the other hand, older datasets—produced under less advanced standards—will still contain key information essential for improving newer datasets.
4. It is designed to be compatible with industrial developments.

These objectives can be effectively met through the implementation of robust standards. Establishing community-wide standards will therefore be a key mission of the DAGP Community, ensuring that these emerging standards align with the outlined objectives through active community participation.

A community-driven approach is particularly effective for fostering the emergence of standards in a bottom-up manner. This strategy was successfully demonstrated in the development of nf-core standards[19] and FAANG community metadata standards,[20] which were initially defined collaboratively and refined over time.

Standards - Providing data resources, standards and FAIR data sharing for *in vitro* systems that link cell, tissue and whole animal scale knowledge

The ability to predict biological outcomes at the cell, tissue, and organismal level (i.e., the genotype-to-phenotype challenge, G2P) relies on the timely adoption and integration of *in silico*, *in vitro*, and *in vivo* technologies. *In vitro* systems include immortalised cell lines, primary cells, stem cell lines and organoids (miniaturised and simplified versions of organs produced in three dimensions, “3D”, derived from adult or embryonic stem cells), and more complex microphysiological systems such as Organ-on-Chip (OoC), that are microfluidic cell culture devices inhabited by living cells arranged to simulate tissue- and organ-level physiology.[21] *In vitro* systems are amenable to an extensive array of biochemical perturbation and genetic modification (such as genome editing) techniques for fundamental and translational research and can be phenotyped by existing assays such as bulk and single-cell omics and imaging. Among 3D models, organoids have been developed and used across the main farm animal species for a wide range of scientific goals,[22,23] while the development of OoCs, is still in its infancy.

Widespread use of 3D and complex cell models in farm animal sciences is hindered by the need to adapt existing lab methodologies across different species and to improve reproducibility. A primary challenge is the rapid pace of evolution of methods, coupled with the need to control the biological and technical variation inherent to these systems. For example, one relevant feature for G2P research in farm animals is the interest in cryopreserving "*in vitro* populations" by the implementation of adequate cryobanking of non-sterile tissues still enabling organoid derivation.[24] On the other side, immortalised cell lines have been instrumental in validating specific molecular hypotheses from *in vivo* studies and in generating new hypotheses. CRISPR screens[25] can be used to identify genetic determinants of host response to important infectious diseases, nutrient uptake or other environmental challenges. This approach facilitates insight into the mechanisms regulating traits that, especially in the case of infectious diseases, are virtually impossible to study *in vivo* e.g.[7,26] or that constitute extremely complex traits well studied *in vivo*, such as feed efficiency.[27] The limitations of immortalised cell lines remain their limited physiological representation of the physiology of the target tissue, and the non-representation of the genetic background between individuals within and between populations.

The improvement of metadata requirements and the progressive standardisation of protocols and processes, from biobanking to FAIR data production and sharing (see "Consolidated computational tools and pipelines for genomic analysis"), is an essential prerequisite for exploiting the full potential of these models for linking cell, tissue and whole animal scale knowledge. Currently, the FAANG Data Portal rule sets include the metadata requirements for "purified cells", "cell culture", "cell lines" and "organoid" that link each cell model to the original organism and tissue, and to the data generated at all levels. This expansion and improvement of metadata rules is an ongoing process relying on the progressive adaptation of existing metadata requirements defined in other species (e.g., Organoid network of the Human Cell Atlas portal: https://data.humancellatlas.org/hca-bio-networks/organoid).

Since 2023, one of the core objectives of the EuroFAANG RI project has been to prepare the communities of *in vitro* model users to exploit the full potential of these systems for advancing excellent open-science and to face the challenges of animal sciences in sustainable agriculture. To date, networking, training and dissemination activities have focused on:

- Promoting best practices (experimental protocols sharing, identification of new relevant metadata) by expanding the current community and connecting with relevant initiatives in the human and model animals' field.

- Mapping of European animal biobanks to coordinate and expand their range of services, including new sets of biobanking rules for the cryopreservation and sharing of tissues, germplasms, stem cells, as well as edited cell lines, in connection with other European initiatives.

- Facilitating bilateral competitive research for the breeding industry stakeholders.

- Documenting the state-of-the-art of technologies and approaches most relevant to tackle the *in vitro-in vivo* challenge.

In addition, digital twins provide AI based *in silico* models that add a further dimension to the *in vitro-in vivo* challenge. They are virtual models of individual animals, herds or populations that use real-time data from sensors, such as wearables, to monitor, analyse and predict phenotypes such as health, behaviour, and environmental conditions. The model provides simulations to test different management strategies before implementation to improve animal health, welfare and productivity. They can enable, for example, anticipation of disease outbreaks in poultry and optimisation of feeding strategies based on environmental variables such as pasture health in dairy cattle.[28] The concept enables a constant data exchange between the 'real' animal and *in silico* model, allowing management decisions to be made remotely in 'real-time' minimising costly *in vivo* management interventions and increasing productivity and sustainability.[28] As digital twins are data derived entities, they are highly dependent on accurate metadata, which can pose a challenge. The potential they offer though to link *in vivo, in vitro* and *in silico* to predict biological outcomes across multiple levels (cell, tissue, individual, herd/population) is exciting, particularly for minimising the need for costly and invasive *in vivo* research.

Providing real-world outcomes - e.g., leveraging omics data resources to understand the genomic drivers of resilience to pathogens

There are several real-world outcomes of relevance to the BFSP strategy that could be achieved in domestic animals through cross-community interactions and shared objectives. One example is leveraging FAIR data and data resources to understand the genomic drivers of resilience to pathogens. The applicability of functional and integrative genomics approaches to understanding host-pathogen interactions and the infection biology of important livestock diseases has been demonstrated over the last decade using in vitro macrophage infection models for the intracellular mycobacterial pathogens that cause bovine tuberculosis (bTB) and Johne's disease.[29,30] For example, integration of transcriptomics (RNA-seq, microRNA-seq) and epigenomics (ChIP-seq) data sets revealed mechanisms responsible for the profound reprogramming of bovine alveolar macrophages in response to infection with *Mycobacterium bovis*, the causative agent of bTB.[31–33] Multi-omics experiments, focusing on infectious diseases in livestock, have the potential to guide future breeding programmes aimed at enhancing disease resilience through biology-driven selection and genome editing, including using high-throughput CRISPR screens to identify functional variants.[5,6]

Other examples include the consolidation of genomic data resources for conserving biodiversity[34] at local and regional levels through developing data standards for biobanking, and tools and workflows for pangenome analysis and structural variant effect prediction in breeds and populations, such as Ensembl Compara.[35] Links with the microbiome community and resources such as MGNify and Ensembl microbes[35] can also inform agricultural sustainability, for example, providing resources to characterise the microbiome of low and high-methane-emitting ruminants. Datasets processed by these resources and provided to the community could facilitate industry stakeholders to breed for improved sustainability by selecting efficient, low-methane-emitting animals.

A global network of projects and infrastructures for domestic animal genomics and phenomics

The DAGP Focus Group included members from many European and global initiatives and these will expand further as the DAGP Community grows. For example, the GenoPHEnix proposal (https://genophenix-ri.eu) to the 2026 update of the ESFRI Road Map aims to build a consolidated infrastructure for farmed animal science and biobanking in Europe to generate readiness to meet future challenges to the Agri-Food sector and has the following five aims:

- To sustainably produce and manage healthier farmed animals, with the highest welfare standards.
- To more accurately exploit animal variability through enhanced phenotyping and genotyping capacity.
- To contribute to the 3Rs (Replacement, Reduction and Refinement) in animal research by providing suitable models for deep phenotyping in vitro as well as in vivo.
- To advance the analysis of genome function, combined with the collection of deep phenotype information at cell, tissue, animal and on-farm/population level resolution.
- To provide tools and knowledge, from the above four aims, for optimal and more precise breeding considering sustainable management practices, and conservation of genetic diversity.

The data infrastructure proposed for GenoPHEnix will expand the FAANG Data Portal to include phenotype data in line with ELIXIR BFSP strategic priorities to provide linked omics and phenotype data to the community.

Members of the DAGP Community also participate in international committees dedicated to developing standards for animal recording, such as the International Committee for Animal Recording (ICAR) (www.icar.org) and have strong links with consortia aiming to capture local and global genomic diversity, such as the Ruminant T2T genome Project[36] and Bovine PanGenome Project.[37] Several members are also on the steering committees of large-scale genomics initiatives for domestic animals, such as the FAANG[12] and FarmGTEx projects.[38] They are therefore ideally placed to ensure the needs of the emerging DAGP Community are represented globally. DAGP Focus Group activities, including a workshop at the 'ELIXIR All Hands' conference in 2025, led to discussions with the AG2PI initiative in the USA[39] around data encryption and methods for sharing of proprietary data from industry stakeholders. Over the coming five years there will also be potential to run shared training workshops and develop shared objectives with the Animal Breeding - RCN: Farm Animal Genomics Collective in the US (https://portal.nifa.usda.gov/web/crisproject-pages/1032104-animal-breeding-rcn-farm-animal-genomics-collective.html). In Europe two COST Actions, EU-LI-PHE, focused on livestock phenomics (https://eu-li-phe.eu), and Insect-IMP (www.cost-insectimp.eu), focused on improving insect breeding, provide networking opportunities and the potential to capture the needs of both additional domestic species and countries in Europe that are not currently represented in the ELIXIR DAGP Community.

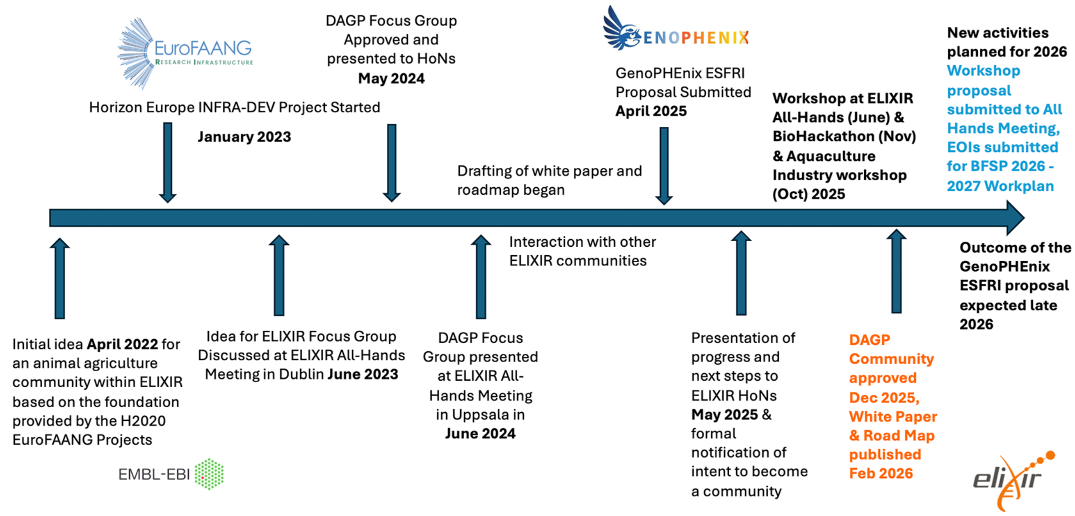

Figure 1. Timeline for establishing the domestic animals genome and phenome focus group and roadmap to becoming a community, including planned activities for 2025.

Conclusions: A vision for the ELIXIR domestic animals genome and phenome community going forward

A RoadMap for 2025-2030 for the DAGP Community is provided as a separate document describing the main objectives and examples of the tasks required to achieve them.[40] In Figure 1 below, the timeline for establishing the Community is shown, including the Focus Group activities.

Focus Group activities included a workshop held at the ELIXIR All Hands Meeting in June 2025 to expand the FAANG Data Portal, and a ELIXIR BioHackathon workshop to develop minimal reporting standards for farmed animals based on the Plant Science Community standards in November 2025. In addition, with ELIXIR Norway an ELIXIR industry day took place in Oslo in October 2025, focused on innovating the aquaculture sector with big data resources, which brought together participants from the aquaculture sector from industry and academia. These activities will help to plan community needs and determine which are the highest priority.

The ELIXIR DAGP Focus Group defined the following six initial key priorities for the ELIXIR DAGP Community:

1. Consolidation and standardisation of phenomic data and metadata, including standardised recording of longitudinal behavioural measurement data and image data into ELIXIR core data resources.

2. Consolidation of data/metadata across submission platforms to improve interoperability, access and sharing, e.g., single-cell data, and as a basis for adoption of new methodological standards.

3. Sharing of proprietary data from industry partners using secure data encryption methods.

4. Development and harmonising of best practices for bio-banking data and samples, building community best practices.

5. Establishing Persistent Unique Identifiers (PUIDs) for all data types related to a given animal.

6. Better integration of omics data with phenotype data, e.g. through expansion of existing resources to incorporate phenotyping data, such as the FAANG Data Portal (https://data.faang.org/home), to increase data visibility, accessibility, and interoperability.

To achieve these initial priorities, we are participating in ELIXIR implementation calls and BFSP Science Tier Work Programme development. We will also leverage other EU and international funding opportunities, and the GenoPHEnix proposal to the 2026 update of the ESFRI Road Map, to ensure continuous support for the community goals.

Data availability

There is no data associated with this manuscript.

References

1. Wilkinson MD, Dumontier M, Aalbersberg IJ, *et al.*: **The FAIR Guiding Principles for scientific data management and stewardship.** *Sci. Data.* 2016; **3**: 160018.
PubMed Abstract | Publisher Full Text | Free Full Text

2. Harrison PW, Sokolov A, Nayak A, *et al.*: **The FAANG Data Portal: Global, Open-Access, "FAIR", and Richly Validated Genotype to Phenotype Data for High-Quality Functional Annotation of Animal Genomes.** *Front. Genet.* 2021; **12**:639238.
Publisher Full Text

3. Åby BA, Bhatti MA, Steinheim G: **Rumen size of sheep: difference between a modern and a native Norwegian sheep breed.** *Acta Agric Scand Sect — Anim Sci.* 2024; **73**: 79–85. Taylor & Francis.
Publisher Full Text

4. Daly KG, Mullin VE, Hare AJ, *et al.*: **Ancient genomics and the origin, dispersal, and development of domestic sheep.** *Science.* 2025; **387**: 492–497. American Association for the Advancement of Science.
Publisher Full Text

5. Jin Z, Yi C, Zhou D, *et al.*: **Chicken genome-wide CRISPR library screen identifies potential candidates associated with Avian influenza virus infection.** *Int. J. Biol. Macromol.* 2025; **293**: 139267. Netherlands.
PubMed Abstract | Publisher Full Text

6. Guo G, Zhang M, Xu Z, *et al.*: **Genome-wide CRISPR screen reveals key role of sialic acids in PEDV and porcine coronavirus infections.** *MBio.* 2025; **16**: e0162825. United States.
PubMed Abstract | Publisher Full Text | Free Full Text

7. Pannhorst K, Carlson J, Hölper JE, *et al.*: **The non-classical major histocompatibility complex II protein SLA-DM is crucial for African swine fever virus replication.** *Sci. Rep.* 2023; **13**: 10342.
PubMed Abstract | Publisher Full Text | Free Full Text

8. Tait-Burkard C, Doeschl-Wilson A, McGrew MJ, *et al.*: **Livestock 2.0 – genome editing for fitter, healthier, and more productive farmed animals.** *Genome Biol.* 2018; **19**: 204.
PubMed Abstract | Publisher Full Text | Free Full Text

9. Koltes JE, Cole JB, Clemmens R, *et al.*: **A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock.** 2019.
Publisher Full Text

10. Giuffra E, Tuggle CK: **Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap.** *Annu. Rev. Anim. Biosci.* 2019; **7**: 65–88.
PubMed Abstract | Publisher Full Text

11. Andersson L, Archibald AL, Bottema CD, *et al.*: **Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project.** *Genome Biol.* 2015; **16**: 57.
PubMed Abstract | Publisher Full Text | Free Full Text

12. Clark EL, Archibald AL, Daetwyler HD, *et al.*: **From FAANG to fork: application of highly annotated genomes to improve farmed animal production.** *Genome Biol.* 2020; **21**: 285.
PubMed Abstract | Publisher Full Text | Free Full Text

13. Harrow J, Drysdale R, Smith A, *et al.*: **ELIXIR: providing a sustainable infrastructure for life science data at European scale.** *Bioinformatics.* 2021; **37**: 2506–2511. England.
PubMed Abstract | Publisher Full Text | Free Full Text

14. Rocca-Serra P, Brandizi M, Maguire E, *et al.*: **ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level.** *Bioinformatics.* 2010; **26**: 2354–2356.
PubMed Abstract | Publisher Full Text | Free Full Text

15. Birney E, Stamatoyannopoulos JA, Dutta A, *et al.*: **Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project.** *Nature.* 2007; **447**: 799–816.
PubMed Abstract | Publisher Full Text | Free Full Text

16. Xia X, Qu K, Wang Y, *et al.*: **Global dispersal and adaptive evolution of domestic cattle: a genomic perspective.** *Stress Biol.* 2023; **3**: 8.
PubMed Abstract | Publisher Full Text | Free Full Text

17. Hörtenhuber M, Hytönen MK, Mukarram AK, *et al.*: **The DoGA consortium expression atlas of promoters and genes in 100 canine tissues.** *Nat. Commun.* 2024; **15**: 9082.
PubMed Abstract | Publisher Full Text | Free Full Text

18. Ewels PA, Peltzer A, Fillinger S, *et al.*: **The nf-core framework for community-curated bioinformatics pipelines.** *Nat. Biotechnol.* 2020; **38**: 276–278.
PubMed Abstract | Publisher Full Text

19. Langer BE, Amaral A, Baudement M-O, *et al.*: **Empowering bioinformatics communities with Nextflow and nf-core.** *Genome Biol.* 2025; **26**: 228.
PubMed Abstract | Publisher Full Text | Free Full Text

20. Harrison PW, Fan J, Richardson D, *et al.*: **FAANG, establishing metadata standards, validation and best practices for the farmed and companion animal community.** *Anim. Genet.* 2018; **49**: 520–526.
PubMed Abstract | Publisher Full Text | Free Full Text

21. Bhatia SN, Ingber DE: **Microfluidic organs-on-chips.** *Nat. Biotechnol.* 2014; **32**: 760–772.
Publisher Full Text

22. Kawasaki M, Goyama T, Tachibana Y, *et al.*: **Farm and Companion Animal Organoid Models in Translational Research: A Powerful Tool to Bridge the Gap Between Mice and Humans.** *Front. Med. Technol.* 2022; **4**: 895379. Switzerland.
PubMed Abstract | Publisher Full Text | Free Full Text

23. Gabriel V, Zdyrski C, Sahoo DK, *et al.*: **Adult Animal Stem Cell-Derived Organoids in Biomedical Research and the One Health Paradigm.** *Int. J. Mol. Sci.* 2024; **25**: 25. Switzerland.
PubMed Abstract | Publisher Full Text | Free Full Text

24. Beaumont M, Blanc F, Cherbuy C, *et al.*: **Intestinal organoids in farm animals.** *Vet. Res.* 2021; **52**: 33.
PubMed Abstract | Publisher Full Text | Free Full Text

25. Bock C, Datlinger P, Chardon F, *et al.*: **High-content CRISPR screening.** *Nat. Rev. Methods Primer.* 2022; **2**: 8.
Publisher Full Text

26. Xing C, Zhang C, Xu Z, *et al.*: **Genome-wide CRISPR screening identifies LRP1 as an entry factor for SFTSV.** *Nat. Commun.* 2025; **16**: 4036.
PubMed Abstract | Publisher Full Text | Free Full Text

27. da Silva MRG, Veroneze R, Marques DBD, *et al.*: **A meta-analysis of genome-wide association studies to identify candidate genes associated with feed efficiency traits in pigs.** *J. Anim. Sci.* 2025; **103**: skaf010.
PubMed Abstract | Publisher Full Text | Free Full Text

28. Neethirajan S, Kemp B: **Digital Twins in Livestock Farming.** *Animals.* 2021; **11**: 11.
PubMed Abstract | Publisher Full Text | Free Full Text

29. Casey ME, Meade KG, Nalpas NC, *et al.*: **Analysis of the Bovine Monocyte-Derived Macrophage Response to Mycobacterium avium Subspecies Paratuberculosis Infection Using RNA-seq.** *Front. Immunol.* 2015; **6**: 23. Switzerland.
Publisher Full Text

30. Nalpas NC, Magee DA, Conlon KM, *et al.*: **RNA sequencing provides exquisite insight into the manipulation of the alveolar macrophage by tubercle bacilli.** *Sci Rep.* 2015; **5**: 13629. England.
PubMed Abstract | Publisher Full Text | Free Full Text

31. Hall TJ, Mullen MP, McHugo GP, *et al.*: **Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria.** *BMC Genomics.* 2021; **22**: 343. England.
PubMed Abstract | Publisher Full Text | Free Full Text

32. Hall TJ, Vernimmen D, Browne JA, *et al.*: **Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Mycobacterium bovis Infection.** *Front. Genet.* 2019; **10**: 1386. Switzerland.
PubMed Abstract | Publisher Full Text | Free Full Text

33. Malone KM, Rue-Albrecht K, Magee DA, *et al.*: **Comparative'omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli.** *Microb. Genomics.* 2018; 4. England.
Publisher Full Text

34. Theissinger K, Fernandes C, Formenti G, *et al.*: **How genomics can help biodiversity conservation.** *Trends Genet.* 2023; **39**: 545–559. Publisher Full Text

35. Dyer SC, Austine-Orimoloye O, Azov AG, *et al.*: **Ensembl 2025.** *Nucleic Acids Res.* 2025; **53**: D948–D957. England. PubMed Abstract | Publisher Full Text | Free Full Text

36. Kalbfleisch TS, McKay SD, Murdoch BM, *et al.*: **The Ruminant Telomere-to-Telomere (RT2T) Consortium.** *Nat. Genet.* 2024; **56**: 1566–1573. United States. PubMed Abstract | Publisher Full Text

37. Smith TPL, Bickhart DM, Boichard D, *et al.*: **The Bovine Pangenome Consortium: democratizing production and accessibility of genome assemblies for global cattle breeds and other bovine species.** *Genome Biol.* 2023; **24**: 139. PubMed Abstract | Publisher Full Text | Free Full Text

38. Fang L, Teng J, Lin Q, *et al.*: **The Farm Animal Genotype–Tissue Expression (FarmGTEx) Project.** *Nat. Genet.* 2025; **57**: 786–796. PubMed Abstract | Publisher Full Text

39. Tuggle CK, Clarke J, Dekkers JCM, *et al.*: **The Agricultural Genome to Phenome Initiative (AG2PI): creating a shared vision across crop and livestock research communities.** *Genome Biol.* 2022; **23**: 3. PubMed Abstract | Publisher Full Text | Free Full Text

40. Clark E, Chua P, Heil K, *et al.*: **ELIXIR domestic animals genome and phenome community road map 2025-2030 [version 1; not peer reviewed].** *F1000Res.* 2026; **15**(ELIXIR): 229. (document). Publisher Full Text

Open Peer Review

Current Peer Review Status:

Version 1

Reviewer Report 05 May 2026

https://doi.org/10.5256/f1000research.195733.r468810

Muhammad Farhab
Yangzhou University, Yangzhou, China

The manuscript is scientifically sound, well-referenced, and appropriately positioned within the current literature. The authors accurately describe the landscape of domestic animal genomics, existing ELIXIR infrastructure, and international initiatives. Factual statements regarding projects, databases, and timelines are correct and adequately supported by the cited references.
My Recommendation: Accept as it is.

Is the topic of the opinion article discussed accurately in the context of the current literature?
Yes

Are all factual statements correct and adequately supported by citations?
Yes

Are arguments sufficiently supported by evidence from the published literature?
Yes

Are the conclusions drawn balanced and justified on the basis of the presented arguments?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Toxoplasma gondii

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.