Annual Report 2025

Task Force: FarmGTEx
— Farm Animal Genotype-Tissue Expression (FarmGTEx) Task Force

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FarmGTEx TF priorities

Most genomic variants control complex phenotypes through modulating intermediate molecular phenotypes (e.g., gene expression and alternative splicing). The systematic characterization of regulatory variants across diverse biological contexts (i.e., tissue, cell, sex and development) is essential for dissecting the genetic architecture underlying complex traits of economic importance, interpreting adaptive evolution and domestication, and optimizing genetic improvement programs in farm animals. The Farm Animal Genotype-Tissue Expression (FarmGTEx) Task Force aims to provide a comprehensive public resource of regulatory variants in diverse biological and environmental contexts across farmed animal species. In the past 8 years, by pulling together public data, the pilot phase of FarmGTEx reports millions of genetic regulatory effects across a range of tissues in major farm animals, including cattle, pigs, sheep, and chickens. However, substantial gaps still remain, and a global effort is thus urgently needed. In the beginning of this year, we thus published the white paper of FarmGTEx in Nature Genetics (https://www.nature.com/articles/s41588-025-02121-5) to summarize the current achievement and discuss the future development. The purpose of this TF will be to define the current gaps, propose potential solutions, and facilitate global collaborations. We list additional priorities besides the ones that already on the website (https://www.faang.org/tf?name=FarmGTEx).

1. *Building the Farm animal tissue biobanks for both primary tissues and in vitro systems, such as cell lines and organoids, in a range of farmed animal species*

2. *Investing the impact of rare variants and complex structural variants on genome function by generating paired whole-genome sequencing and functional genome data (such as RNA-seq and ATAC-seq)*
3. *Expanding to the discovery of context-specific regulatory effects, such as development, sex, diet and immune-responsive regulatory effects*

Summary of Activities:

1) In the beginning of 2025, we invited speakers from human genetics and computational biology at the FarmGTEx workshop at PAG.
2) We had FarmGTEx workshop and round-table discussion on the National conference of animal genetics and breeding on 10th July, 2025, Harbin, China.
3) We had a bi-monthly online meeting on updating the FarmGTEx project at 13th Nov, 2025
4) We will have a FarmGTEx and domesticated workshop at The Fourth AsiaEvo Conference on 10th Dec. 2025, Kunming, China
5) At the coming PAG 2026, the FarmGTEx workshop will have another five invited talks (such as DeepMind group on AlphaGenome), followed by discussion on future directions and collaborations with other existing consortia in other species, including humans.
6) In the past year, we have published the pilot ChickenGTEx resource, the white paper of FarmGTEx, and the pilot SheepGTEx resource.
7) The FarmGTEx consortium is currently working on other farmed species, including goat, yak, horse, and duck.
8) The FarmGTEx consortium is currently developing tissue biobanks, particularly for ruminants and pigs. For example, we collected 100 tissues of 1000 adult cattle, and 100 tissues of 600 pigs from four developmental stages, 70 tissues of 1000 sheep from nine developmental stages.
9) We are working on sex and development GTEx for pigs, sheep, and chickens

Challenges:

There are several challenges in the FarmGTEx TF: 1) grant opportunities for the next phases of FarmGTEx, 2) advanced computational methods and platforms that are suitable for farm animal specific data structure, 3) developing primary and *in vitro* tissue biobank in farmed animals, 4), application of FarmGTEx resource in genomic prediction and genome editing, 5) close collaborations with consortia from human and biodiversity projects,

Future Directions:

- To include more types of genomic variants in the molQTL mapping, including SNPs and SVs at different allele frequency: somatic, rare, and common
- To fill the gaps detected in the pilot phase of FarmGTEx, e.g., under-represented tissues, cells, and biological and environmental conditions (e.g., embryonic development, immune response, and heat/cold tolerance).
- To develop more advanced bioinformatics and AI pipelines for defining more informative molecular phenotypes (pan-transcriptome phenotypes) from RNA-Seq and other omics data

- To figure out the funding opportunities for the next phase of FarmGTEx to study the genetic regulatory effects in more specific biological and environmental contexts and evolution times
- To develop a close collaboration network with GTEx projects from other species, including human (e.g., IGVF and developmental GTEx), non-human primate species and model organisms (e.g., rat and fruit fly)