

# Field Day: Quantitative multi-omics to unravel G2P in crops and livestock



Agricultural Genome to Phenome Initiative



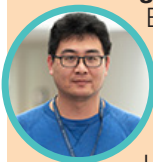
## Farm animal Genotype-Tissue Expression (FarmGTEx) project: a public multi-tissue atlas of regulatory variants in farm animals

The systematic discovery and characterization of regulatory variants (i.e., eQTLs and sQTLs) is essential for dissecting the genetics of complex traits, understanding adaptive evolution and domestication, optimising genetic improvement programmes and allowing cross-species mapping studies in farm animals. The Farm Animal Genotype-Tissue Expression (FarmGTEx) project, an international collaborative endeavour, aims to provide a comprehensive public resource of tissue-specific gene expression and genetic regulation in farm animal species. The pilot phase of FarmGTEx reports millions of such regulatory variants, and provides direct evidence of their associations with complex traits of economic value. We believe that findings from this global effort will have unprecedented influences and impacts on the livestock science research.

## Unraveling Signaling Networks using Integrated Omic Profiling

Quantitative multi-omic datasets enable systems biology approaches aimed at understanding biological phenomena. In this half of the field day, Dr. Justin Walley will discuss the generation and integration of a large-scale transcriptome, proteome, and phosphoproteome data in maize and Arabidopsis.

### About the presenters:



**Lingzhao Fang** is a Post Doctoral Researcher at The University of Edinburgh. He completed his Ph.D. on quantitative genetics at Aarhus University and China Agricultural University jointly. Subsequently, he did his first postdoc research on bioinformatics and quantitative genetics in USDA and University of Maryland. After that, he joined the group of Albert Tenesa at the Institute of Genetics and Cancer at University of Edinburgh as a Train@Ed Research Fellow.



**Justin Walley** is Associate Professor, Department of Plant Pathology and Microbiology. He obtained his Ph.D. from U.C. Davis. Using systems biology, his lab integrates proteomics with other types of omics datasets, such as transcriptome profiling, to generate hypotheses to test using various biochemical and genetic approaches.

**June 15, 2022**  
**10:30 AM–12:00 PM**  
(Central Time, UTC–5)

**Purpose:** Discuss infrastructure, opportunities and bottlenecks in linking various omics data to phenotype.

**Register for this Zoom virtual meeting:**

<https://tinyurl.com/AG2PI-FD19>

Upon registration, you will receive a confirmation email with information about joining the meeting.

A recording will be available at a later date at: [ag2pi.org/](https://ag2pi.org/)



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