



Editorial: Multi-Omics Approaches to Study Complex Traits in Domestic Animals

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Keywords: multi-omics approach, domestic animals, complex traits, gut microbiota, machine learning

Editorial on the Research Topic

Multi-Omics Approaches to Study Complex Traits in Domestic Animals

INTRODUCTION

Domestic animals are important for human society as they provide the principal protein source in many people's diets. There are notable advantages to dissecting domestic animals' genetic basis for complex traits, as we have access to more details of phenotype records than other animals. The population of domestic animals has a rich collection and mutation of affected phenotypic traits (Andersson and Georges, 2004). Research on domestic animals has entered a post-genomic era, which is difficult for scientists to study and understand because complex traits are influenced by many genetic and environmental factors. After a decade of genome-wide association studies, fundamental questions on domestic animal genetics, such as the extent of pleiotropy across the genome and variation in genetic architecture across complex traits, are still unanswered.

Multi-omics is a powerful technology to understand the interaction between genotype, environment, and life in a concerted way and illustrates these complex traits and diseases. The omics field has been driven largely by technological advances that have made cost-efficient, high-throughput analysis of biological molecules possible. Such omics data are derived from diverse biological sources and include metagenomics, genomics, transcriptomics, epigenomics, proteomics, metabolomics, and so on. The integration of omics data provides a better understanding of how a genotype influences a complex phenotype, as well as the molecular mediators at the multiscale that regulate the underlying pathway mechanisms of complex traits in domestic animals. The Research Topic on "Multi-omics Approaches to Study Complex Traits in Domestic Animals" in Frontiers in Genetics includes a series of four articles that discuss recent advances regarding the underlying regulation mechanisms of complex traits in domestic animals and highlight challenges and outstanding questions that need to be addressed in future research.

MULTI-OMICS WITHIN DOMESTIC ANIMALS

After a decade of genome-wide association studies, a large number of genetic variants associated with specific traits have been discovered. However, the difficulty of detecting GWAS results for

OPEN ACCESS

Edited and reviewed by:

Rongling Wu,
The Pennsylvania State University
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Specialty section:

This article was submitted to
Integrative Genetics and Genomics,
a section of the journal
Frontiers in Systems Biology

Received: 06 September 2021

Accepted: 27 September 2021

Published: 15 October 2021

Citation:

Wu J, Li X and Xu X (2021) Editorial:
Multi-Omics Approaches to Study
Complex Traits in Domestic Animals.
Front. Syst. Biol. 1:771644.
doi: 10.3389/fsysb.2021.771644

complex traits may be influenced by the pleiotropic nature of these traits. Integrating other types of data such as intermediate molecular phenotypes to identify associations could overcome these limitations. Liu et al. performed a genome-wide association study and RNA sequencing analyses to detect candidate genes for the feather rate in Shouguang chicken. Two overlapping genes (SPEF2 and PRLR) between the results of GWAS and differential expression analysis were identified, which provide possible candidate genes for the formation of the chicken feathering phenotype. Wu et al. investigated clinical ketosis-associated metabolomic and proteomic changes using statistical analyses. Ketosis altered a wide range of metabolic pathways, such as metabolism, metabolism of proteins, gene expression and post-translational protein modification, vitamin metabolism, signaling, and disease-related pathways. Integration of Multi-omics was utilized in the future study to 1) investigate the extent of pleiotropy at complex traits, and 2) to characterize the hub molecular (gene, SNP, and gene-set levels gene or metabolite) trait-associated variants and crosstalk among different regulation levels of biological functionality of complex traits.

MULTI-OMICS BETWEEN DOMESTIC ANIMALS AND GUT MICROBIOTA

The review by Patil et al. (2020) discusses the interactions between host and gut microbiota in domestic animals. The microbiome plays a critical role in maintaining metabolic homeostasis, neurological and immunological functions, including protection from pathogens and digestion of food materials. Seika and Theresa also review microbiome genomic data across domestic species and highlight the common occurrence of gut microbiome dysbiosis during idiopathic intestinal inflammation in multiple species. Domestic animals represent important resources for understanding the shared mechanisms underlying complex natural diseases that arise due to both genetic and environmental factors. The gut microbiota also plays a critical role in the digestion of food materials, especially for a ruminant. Wu et al. used Multi-omics techniques to analyze the nutritional value of different lamb feed from the microbiome, transcriptome, metabolome, and fatty acid profiles. They found that there was potential cross-talk between the four omics data layers, which helps to further understanding of the mechanism by which feed affects the meat quality of lamb (Wu et al., 2020). While deeper analyses of different levels of omics data in a host, coupled with microbiome molecular analyses in the digestion track are

needed, comparative studies across domestic species can reveal shared microbial alterations and regulatory mechanisms that will improve understanding of complex traits in domestic animals.

FUTURE PERSPECTIVES

Multi-omics approaches derive a holistic understanding of the regulation mechanism under complex traits in domestic animals with its share of challenges. On the one hand, Multi-omics data are generated from different platforms with various data formats. How to integrate the different data layers of Multi-omics as a system should be considered. It is a challenge to combine machine learning in the data preprocessing of Multi-omics and to improve accuracy and inject biological information. On the other hand, the genetic dissection of complex traits, such as meat quality and residual feed intake, are challenging because of the small effect of each locus and the interaction of environmental factors that can affect the phenotype. A systematic analysis of Multi-omics data and an experimental design are critical components of the genetic dissection of complex traits and new systems biology tools and pipelines for Multi-omics need to be developed to address these challenges in the next decade.

AUTHOR CONTRIBUTIONS

XL and XX polished this manuscript. JW compiled the contributions from all authors. All authors contributed to the article and approved the final version of the manuscript.

FUNDING

This work was supported by the National Natural Science Foundation of China (31560623), the Doctoral Scientific Research Foundation of Inner Mongolia University for Nationalities (BS527), and the Key Science-Technology Project of Inner Mongolia (2021GG0008).

ACKNOWLEDGMENTS

We would like to thank all authors for their contributions to the Research Topic and the reviewers for their time and effort. We also greatly appreciate the Chief Editor and Editorial Office of *Frontiers in Genetics* for their support during the process of processing the manuscript.

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