

Highlights of special issue on Animal Science

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Animal husbandry is a pillar industry of agriculture in China. Farm animals provide the meat, egg, milk, fur and wool that meet the needs of the people's everyday life. China has witnessed unprecedented development of animal husbandry over recent decades, greatly contributing to increasing improvements in our life. It is undeniable that an important part of this development has been built on new and innovative techniques for the efficient genetic improvement of farm animals. These techniques have been successfully established on the basis of the growing knowledge of genomics, transcriptomics, proteomics, epigenomics, genome editing, sophisticated statistics and the like, which have had profound effects on Chinese and global animal husbandry. This special issue is a collection of ten papers related to the topics of animal genetics and breeding, with the authors aiming to present the enduring advances in this vital research area.

Historically, the breeding value of farm animals were estimated using linear modeling (BULP) and the information on pedigree and phenotypes. This method has been revolutionized by genomic selection (GS) that predicts breeding value using phenotypes and genetic markers across the genome. GS is now recognized as a next-generation breeding tool not only for farm animals but also for plants. In this special issue, Kang et al. introduce several commonly used GS statistical methods and make a comparison of these methods in terms of their prediction accuracy. They also discuss factors affecting the accuracy of prediction and briefly describe the current status of GS implemented in the breeding programs for dairy cattle, pigs and poultry. The information presented in this paper will benefit the GS schemes developing in these and other species in China and the world.

The sheep industry is an indispensable part of global animal husbandry, especially for the economic development of rangeland areas such as in northwest China. Over the last decade, genome-wide association studies (GWAS) have been extensively conducted on a range of species and have identified a huge number of genetic variants associated with diverse phenotypic traits in these species including sheep. Of note, a handful of causative mutations have been painstakingly and unequivocally shown to affect specific traits in sheep. Xu et al. summarize a list of genes and variants that were recently characterized to be associated with economically important traits in sheep via high-resolution screening technologies. Through in-depth literature mining, they present a comprehensive review of candidate genes, genetic variants, miRNA and signaling pathway potentially involved in the formation of these important traits. This review is of particular value for the reader in the field of ovine genetics and breeding, and will benefit future studies aiming to dissect the molecular basis of phenotypic traits in sheep.

The domestication of wild horses is a groundbreaking event in animal husbandry, which has deeply influenced human history because the domestication of horses accelerated human civilization, revolutionized warfare and promoted agricultural production. Also, human-driven artificial selection has resulted in diverse horse breeds with various phenotypes and has shaped the genome of these breeds. Liu et al. describe the recent progress in the field of horse genomics, focusing on those genes and genomic regions under positive selection for five categories of phenotypic traits, including coat color, gait, stature, racing performance and local adaptation. These traits have been artificially or naturally selected during and after the domestication of the horse. This mini-review will help us better understand the genetic architecture of complex traits in and beyond this domestic species.

Muscle growth is a longstanding target for selection of meat-producing animals. Skeletal muscle, a major component of muscle, is important for movement, strength, body posture and meat production of farm animals. Using the chicken as a

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model animal, Luo et al. summarize the currently characterized genetic factors affecting skeletal muscle development. These factors include candidate genes, genetic variants, non-coding RNAs, epigenetic markers and transcription factors involved in the development of chicken skeletal muscle. They also point out the shortcomings of the current findings and suggest directions for future studies. The cutting-edge knowledge of this review enables us to better understand the genetic regulation of skeletal muscle development in farm animals.

The tremendous development of genomics has driven the transition of sparse marker-based studies to high-density marker dependent researches not only in farm animals but also in aquatic animals. As in farm animals, aquatic animals are now becoming part of the genomic era. In this special issue, Xu et al. present an overview of the history of development of genetic analyses in aquatic animals, including construction of linkage and physical maps, screening of quantitative trait loci (QTL) and characterization of genes for economically important traits, and identification of genetic markers associated with important traits and their application in breeding programs for aquatic animals. They also describe decoded genomes of aquatic animals and discuss the potential effect of genome editing, genomic selection and multi-omics on aquatic animal industries. This review gives the reader a broad picture of progress and prospects of genomics and genetic breeding in aquatic animals.

China's farm animals represent a rich genetic resource. About one-third of global pig breeds are found in China. These diverse breeds are renowned for desirable traits related to reproduction, disease resistance, docility and meat quality, providing valuable germplasm supporting the sustainable development of the pig industry. The Rongchang pig is a representative indigenous breed in China, which has a unique, solid white coat phenotype. To dissect the genetic basis of the special features of Rongchang pigs, Chen et al. used a range of approaches including Z-transformed population differentiation (Fst) and nucleotide variability (Hp) statistics to identify genomic regions and candidate genes under selection in the genome of Rongchang pigs in comparison with Chinese wild boars. Their findings advance our understanding of the evolution forces shaping so-called "domestic traits" in pigs, and also provide insights into evolutionary genomic studies on indigenous Chinese domestic pigs.

Vertebral number is an economically important trait in pigs as it is significantly associated with body size and pork production. The pig has naturally occurring phenotypic variation in vertebral number, offering an excellent opportunity to decipher the genetic architecture of this trait. Zhang et al. conducted a GWAS for the number of vertebrae in a Large White × Minzhu F₂ pig population and identified two major loci for this trait, one each on pig chromosomes (SSC) 1 and 7, confirming previous reports. Further, they provide evidence that the previously reported c. 748 C > T in the *NR6A1* gene is not likely to be the causal mutation for the QTL on SSC1, and highlight *TGFβ3* as a novel candidate gene for the QTL on SSC7. Their findings expand our knowledge of the developmental biology of vertebrae and provide a potential tool to improve pork production by increasing vertebral number and consequently body size.

Intramuscular fat (IMF) content is directly associated with meat quality and is increasingly attracting the attention of consumers. Elucidating the genetic basis of IMF content would enable us to develop novel molecular breeding tools for the genetic improvement of this trait in commercial populations. To achieve this goal, Wang et al. performed a genome-wide association study for IMF content in a European commercial pig population, Duroc. Notably, they identified a genome-wide significant locus on SSC8, and report three functionally plausible genes for IMF content around this locus. The finding offers a robust marker to efficiently improve IMF content in this Duroc population, and paves a road to ultimately identify the responsible gene and causative mutation for this locus.

Infectious diseases are a great threat to the pig industry, causing huge economic losses. Hence, there is a pressing need to enhance innate resistance to infectious diseases in pigs, which requires a deep understanding of the molecular mechanisms underlying the resistance. Neutrophils are critical in defense against invaded pathogens and neutrophil variation is closely related to individual antiviral capacity. Wang et al. selected two groups of pigs that showed extreme and moderate response to poly I:C (a synthetic analog of dsRNA virus) stimulation, and then searched for differentially expressed genes (DEGs) in peripheral blood before and after poly I:C stimulation in these two groups of pigs. They further compared DEG-enriched biological processes and pathways between extreme and moderate response pigs, shedding insights into the molecular basis of the congenital antiviral capacity in pigs and other farm animals.

Traditional Chinese medicines (TCMs) have a history of more than 2500 years, and are widely used in China and are becoming increasingly available in Europe and North America. Although the main components of TCMs are plants, some non-botanic substances, such as animal bone, are also used. Tongren Dahuoluo Wan is a famous TCM for treating wind-cold-dampness arthralgia-syndrome. Historically, leopard bone powder was used as a key element of this medicine. Due to the regulations of prohibiting the use of endangered animals, including leopards, zokar bone is now used as a substitute for leopard bone in this medicine. Wang et al. establish a reliable diagnostic method to discriminate these two substances in Tongren Dahuoluo Wan formulations using an mtDNA-based PCR detection approach. This provides a successful example of molecular authentication of TCMs.

The research on animal genetics and breeding includes a wide range of diverse disciplines, and covers an even wider

range of globally important topics. Consequently, it is a huge challenge to cover all these disciplines and topics in this special issue. Nevertheless, we sincerely hope that the reader enjoy the papers presented in this collection, which are to a degree representative of recent progress across this research area. Lastly, I greatly appreciate the endeavors of all contributors in this collection. It would have been impossible to present this special issue without their full support.



Jun Ren, guest editor of this special issue, graduated from Jiangxi Agricultural University, China in 1995 and obtained a PhD from the University of Goettingen, Germany in 2004. He is now a full professor of animal genetics and breeding and vice director of State Key Laboratory of Pig Genetic Improvement and Production Technology in Jiangxi Agricultural University, China. His research interests include dissection of the molecular basis of innate diseases and complex traits, evolutionary and functional genomics and molecular breeding in pigs. As the first author or corresponding author, he has published 41 peer-reviewed papers in international journals. He has won one Second Prize for National Science and Technology Progress Awards, one Second Prize for National Technology Invention Awards and four other first prizes at ministerial and provincial level. He also won several other distinguished awards including National Distinguished Young Scholar in China, National Award for Young Researchers of China, Chinese Youth (May 4) Medical, and National Leading Talents of Scientific and Technological Innovation. His work has expanded our understanding of the genetic basis underlying complex traits and has significantly contributed to the genetic improvements in pigs.