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Epigenetic Variation Influences on Livestock Production and Disease Traits

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Deadline for manuscript submissions:
closed (15 December 2022)

Message from the Guest Editors

Dear Colleagues,

Accumulating evidence shows that epigenetic marks (including DNA methylation, chromatin remodeling, histone modifications, and other molecules that can transmit epigenetic information) can influence livestock species in gene expression and phenotypic outcomes. The data currently available show that epigenetic factors play an important role in the expression of imprinting genes, cellular processes, fat metabolism, and the development of muscle tissue in livestock. Meanwhile, there is already compelling evidence that various additives in the diet have the ability to induce epigenetic modifications of phenotypic variability. There is growing pressure to increase livestock production in light of an expanding human population and environmental challenges, but the related epigenetic data on livestock to complement genomic information and support advances in improvement breeding and health management is limited. In this Special Issue, we will examine the recent discoveries on epigenetic processes due to DNA methylation, histone modification, and chromatin remodeling and their impacts on disease traits and production traits in livestock.

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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