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Genome-Wide Association Analysis of Cattle

Guest Editor:

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Deadline for manuscript submissions:
closed (15 September 2021)

Message from the Guest Editor

Genome-wide association studies (GWAS) using SNP chip data have significantly contributed to efforts in deciphering Mendelian and complex traits in many livestock species, particularly in cattle. SNP chips cover bovine genes and genomes at a limited resolution, whereas genome-sequencing data offer a high coverage of genomes as well as a much high number of genetic and structural variants. Along with GWAS, new statistical analysis methods were developed to model population structure and relatedness among individuals—multiple simultaneous SNP analyses instead of SNP-by-SNP association studies, meta-analyses with large independent datasets, and methods to estimate and partition genetic variance due to segregating variants.

This Special Issue in Genes on “Animal Genetics and Genomics” will highlight the advances of understanding the biological consequences of variants tagging complex traits. Research articles and short communications are invited to provide recent developments and the translation of GWAS discoveries into the biological understanding of complex traits.

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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