Special Issue

Quantitative Genomics and Computational Systems Biology in Agricultural Species

Message from the Guest Editor

Dear colleagues, Quantitative genetics and epigenetics has seen a paradigm shift moving from microarray-based technologies to next generation sequencing (NGS)-based genomics/ epigenomics in studying (epi)genetic variation in quantitative traits and complex diseases. Furthermore, the phenotypic data collected in farms/breeding herds go well beyond conventional traits included in breeding goals. The current Special Issue calls for original articles, review papers, perspectives and/or opinion articles in quantitative topics including but not limited to:

- Genome-wide association studies (GWAS) using NGS based (epi)genomic data with phenotype/ disease data for quantitative traits and diseases;
- Genomic selection in any agricultural species (animal, plant, fish and poultry) with a focus on using high throughput phenotyping;
- AI/machine learning methods for analysis of genomic/ epigenomic datasets in any agricultural species (animal, plant, fish and poultry);
- Computational methods and tools for multiomics data integration and multiomics prediction models for quantitative traits and diseases;
- Network biology/systems biology for quantitative traits and diseases.

Guest Editor

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Deadline for manuscript submissions

closed (31 October 2020)

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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?

Editor-in-Chief

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