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## Quantitative Genomics and Computational Systems Biology in Agricultural Species

Guest Editor:

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Deadline for manuscript  
submissions:

**closed (31 October 2020)**

### 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.



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# Special Issue



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## Editor-in-Chief

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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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