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From QTL Mapping to QTG and QTN Identification

Guest Editor:

Dr. Akira Ishikawa

Laboratory of Animal Genetics and Breeding, Department of Animal Sciences, Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya 464-8601, Japan

Deadline for manuscript submissions:

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Message from the Guest Editor

Most traits of great importance in medicine, agriculture and evolution are quantitative in nature. These traits include traditional quantitative traits (e.g., complex human diseases and livestock products) and molecular traits (e.g., gene expression, protein expression, DNA methylation and metabolites). These traits are controlled by many quantitative trait loci (QTLs), environmental factors and their interactions.

A great number of QTLs affecting a variety of quantitative traits have so far been mapped to almost all chromosomal regions of animals, including humans, model animals, livestock and poultry. Recent advances in QTL studies that are integrated with next-generation sequencing, multi-omics approaches and/or causality analysis have allowed us to identify the candidates of causal quantitative trait genes (QTGs) and causal quantitative trait nucleotides (QTNs). However, it is still challenging to identify true QTGs and QTNs, because common QTLs with relatively small phenotypic effects are usually located in noncoding genomic regions. In this Special Issue, any original and review articles related to QTL, QTG or QTN identification in animals are welcomed.



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Special Issue



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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan

Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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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Genes Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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