Special Issue

Pig Genomics and Genetics

Message from the Guest Editors

The pig (Sus scrofa) is the most common large mammal in the world. Since the draft reference genome sequence of S. scrofa was assembled in 2012, the processes of identification of genes related to important phenotypic traits and of search of genetic markers for pig selection have been significantly refined. In addition, the newest wide-range high-throughput techniques, including microarrays, next-generation sequencing, and the recent PacBio sequencing platform providing ultra-long sequencing reads, allow identifying gene mutations and gene candidates throughout the whole genome, transcriptome, or epigenome and estimating quantitative traits important for breeding as well as the genetic backgrounds of inherited diseases.

In this Special Issue, we will present the state of the art in the field of pig genetics and genomics, including the identification of gene candidates linked to important pig traits and to nutritional modifications, with the aim of collecting the most recent advances. Manuscripts focusing on high-throughput methodologies, such as RNA sequencing, ATAC-seq, MACE-seq, chip-seq, and RRBS, and covering other fields of pig genetics will be appreciated.

Guest Editors

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Deadline for manuscript submissions

closed (23 December 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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