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Pig Genomics, Quantitative Traits and Breeding

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Deadline for manuscript submissions:

closed (10 June 2023)

Message from the Guest Editors

The last decade has witnessed great progress in the community of pig genetics and breeding. With the publication of the pig genome and the application of advanced genomics technologies, such as high-throughput sequencing, genome-wide association analysis, comparative genomics, and metagenomics, the research focus has shifted from individual genes to networks of genes with a common function. Thousands of gene mutations and gene candidates have been characterized, enabling the estimation of quantitative traits important for the breeding industry and the underlying genetic basis of quantitative traits. Moreover, rapidly evolving breeding technologies, such as genome selection and gene editing, offer exciting opportunities for molecular breeding by design. Genetically improving pig breeds is becoming feasible for more and more traits. In the Special Issue, we welcome all types of submissions, including articles, reviews, methodologies, opinion articles, and prospects in the pig breeding field, including but not limited to QTL mining, genetic dissection, genome selection, and gene editing of economically important quantitative traits.



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Special Issue



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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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