Maize Functional Genomics, Genetics and Breeding

Guest Editor:

Prof. Dr. Xiquan Gao
State Key Laboratory of Crop Genetics & Germplasm Enhancement and Utilization, College of Agriculture, Nanjing Agricultural University, Nanjing 210095, China

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Message from the Guest Editor

Maize is one of the most important crop species worldwide. Along with the rapid progress of third generation sequencing technology in maize genome research, maize functional genomics has been significantly advanced in the last decade. Moreover, the success of whole genome sequencing of multiple maize inbred lines has promoted the cloning and functional validation of a large number of genes related to diverse traits. More and more functional genes are being applied to breeding program, targeting the improvement of maize yield and quality.

In this Special Issue, we aim to publish high-quality research articles and reviews on all aspects of maize functional genomics, genetics and breeding programs, including but not limited to, genomic characterization, genetic dissection of various traits (growth, development, abiotic stress, maize-pathogen interactions, etc.), gene cloning, and gene function study using genome editing and overexpression. The new theory and technology related to maize genetics and breeding is also within the scope of this issue.

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Special Issue

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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