Special Issue

Advances in Cotton Genomics, Genetics and Breeding

Message from the Guest Editors

With the rapid development of high-throughput genome sequencing, many cotton genomes have been sequenced, assemblied and annotated, providing a great opportunity for comparative genomics research, genetic analysis and fine mapping of agronomic traits, mining genes underpinning important agronomic traits, gene functional verification, genetic transformation, etc. Molecular technology and biotechnology have achieved tremendous progress, especially gene editing technology, for instance, CRISPR/Cas9, which has enormous potential in cotton breeding through harnessing genetic diversities related to superior agronomic traits. Nowadays, marker-assisted selection, genetic transformation and genomic prediction enabled precision breeding, revolutionizing cotton breeding practices, and they are anticipated to have a profound impact on cotton production in the near future. In this Special Issue, we will report progresses on all aspects of cotton genomics, genetics and breeding.

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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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