



Genomics and Genetic Improvement of Bast Fiber Plants

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Message from the Guest Editors

Bast fiber is one of the most important fibers. With the development of sequencing technology, reference genomes for major bast fiber crops have been released. Based on the reference genome and transcriptome sequencing, a large number of candidate genes related to fiber development and specific traits have been mined. The molecular basis of the formation of agronomic traits such as fiber yield, fiber quality, disease resistance, and resistance has been systematically analyzed, contributing to the establishment of a high-throughput genotype–phenotype database, where excellent genetic resources and new germplasms have been mined to breed new varieties of bast fiber crops with high yield and high quality. This Special Issue is to gather and disseminate some of the most significant and recent contributions on the latest developments and advances in the application of the genomics and genetic breeding of bast fiber crops. The topics include, but are not limited to, the following: gathering and disseminating some of the most significant and recent contributions on the latest developments and advances in the application of the genomics and genetic breeding of bast fiber crops.





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