Special Issue

Omics and Breeding of Bast Fiber Crops

Message from the Guest Editors

Bast fiber is one of the most important fibers, and it is typically extracted from the stem barks and leaves of crops including jute, flax, ramie, hemp, kenaf, sisal, and so on. In the past decades, reference genomes for major bast fiber crops including jute, kenaf, ramie, hemp, and flax were released, which helped scientists to explore function genomics, genomic resequencing, pangenomics and the identification of genes linked with desired agronomic traits, as well as molecular markers such as SNPs and InDels. The referenced genomes provide an important basis for researching the methylome, modified proteome, transcriptome, non-encoding RNAs, and so on in bast fiber crops. Accordingly, omics studies help molecular breeding and genomic selection breeding come to light.

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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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