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Omics and Breeding of Bast Fiber Crops

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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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Message from the Editor-in-Chief

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