



Functional Genome and Secondary Metabolome of Bast Fiber Crop

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Message from the Guest Editors

Dear Colleagues,

Plant functional genes are critical for understanding the developmental process, resistance to stresses and diseases, and the biosynthesis of bioactive compounds. Molecules with various bioactive effects in plants attribute towards preventing pathologies and decreasing therapeutic treatments in both human and animals.

Gene mining facilitates the discovery of new natural products and novel genes that regulate the synthesis of secondary metabolites and quality traits. The aim of this Special Issue is to discuss the gene mining of plant functional genes and the biosynthesis of bioactive compounds as well as their applications in medicine and animal husbandry to promote utilization and aid in harnessing maximal benefits.

We invite the submission of research articles, reviews, and short communication that address any of the following themes:

- Omics study of genes' functions and mechanisms in plants (especially bast fiber plants);
- Identification and characterization of functional genes for metabolites biosynthesis and regulation;
- Potential of plant (especially bast fiber plants) bioactive compounds in medicine and animal husbandry.





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Editor-in-Chief

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Message from the Editor-in-Chief

The metabolome is the result of the combined effects of genetic and environmental influences on metabolic processes. Metabolomic studies can provide a global view of metabolism and thereby improve our understanding of the underlying biology. Advances in metabolomic technologies have shown utility for elucidating mechanisms which underlie fundamental biological processes including disease pathology. *Metabolites* is proud to be part of the development of metabolomics and we look forward to working with many of you to publish high quality metabolomic studies.

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