Special Issue

Genome Assembly and Evolutionary Analysis of Brassica Crops

Message from the Guest Editors

The Brassicaceae is an important plant family with approximately 3,800species, including commercially and economically important vegetables, fodder, oilseed and ornamental crops. Recent advancements in genomics technologies, such as long-read sequencing, chromosome confirmation capture and optical mapping, have enabled the development of highly contiguous genome assemblies. These assemblies have allowed an unprecedented view of the Brassicaceae genome organisation, providing a platform for studying genome evolution, gene expression patterns and trait adaptation. In addition, the foundational resources from the closely related species and model organism, *Arabidopsis thaliana*, can be exploited to identify and confirm candidate gene function underlying traits of interest, leading to crop improvement. This Special Issue of *Plants* will highlight studies focused on recent genome assemblies of *Brassica* crops and their close relatives, encompassing comparative genomics, pan-genomes, transposable element diversity and evolution, epigenetics, gene function, global gene expression patterns, organelle genome assembly and evolution, evolutionary genomics, and polyploidization.

Guest Editors

Dr. Sampath Perumal

Global Institute for Food Security, University of Saskatchewan, 421 Downey Road, Saskatoon, SK S7N 4L8, Canada

Dr. Isobel Parkin

Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada

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Plants
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
plants@mdpi.com

mdpi.com/journal/plants

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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.

Editor-in-Chief

Prof. Dr. Dilantha Fernando
Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada

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