

Special Issue

Genome Assembly and Evolutionary Analysis of Brassica Crops

Message from the Guest Editors

The Brassicaceae is an important plant family with approximately 3,800 species, 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.

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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, and 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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