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Harnessing the Power of Genome and Transcriptome Assemblies

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Message from the Guest Editor

The availability of high-quality genome and transcriptome assemblies is crucial for numerous studies of specific plant functions. Long-read sequencing technologies boost the contiguity of genome assemblies and open up novel opportunities in plant transcriptomics.

Transcriptome assemblies are a cost-effective way to access the genes of plant species with large and complex genomes. Direct RNA sequencing allows the identification of modifications on these transcripts. Deep sequencing with long reads enables detailed investigations of splicing processes, leading to a huge variety of transcript isoforms.

This Special Issue is open to all research articles providing new insights into the biology of plants based on genome or transcriptome assemblies.



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Special Issue



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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.

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