

Special Issue

Comparative Omics Analyses in Plant Evolution

Message from the Guest Editor

Studying plant evolution can reveal principles of the emergence of novel traits, such as multicellularity, sexual reproduction, and hormone signaling. Typically, the evolution of these traits is studied through comparative genomic and phylogenomic analyses, which assume that the traits emerge and evolve as gene families. However, genes and gene families form higher-order functional units (gene modules), which employ multiple genes from different gene families. These gene modules can be identified by analyzing omics data, such as protein–protein interaction networks, and by identifying transcriptionally co-regulated (co-expressed) genes, among others. Therefore, a more rewarding approach to explain the evolution of new traits, adaptations, and gene functions should by necessity compare omics data across different experiments and species. This Special Issue is poised to address the studies, approaches, and databases that compare omics data.

Guest Editor

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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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