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## Comparative Omics Analyses in Plant Evolution

Guest Editor:

### **Dr. Marek Mutwil**

School of Biological Sciences,  
Nanyang Technological  
University, 60 Nanyang Drive,  
Singapore 637551, Singapore

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### **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.



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# Special Issue



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## Editor-in-Chief

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

## Message from the Editor-in-Chief

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Plants Editorial Office  
MDPI, Grosspeteranlage 5  
4052 Basel, Switzerland

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