



Plant Responses to Environmental Stresses

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Message from the Guest Editors

Datasets in genomics/metagenomics, transcriptomics/meta-transcriptomics, proteomics/meta-proteomics, metabolomics, epigenomics, ionomics, phenomics—just to mention the most popular platforms—are piling up elsewhere intending to gain insights on the molecular mechanisms behind plant interaction with biotic and abiotic stresses.

Multi-Omics Integration (MOI) uses conceptual integration and element- (correlation, clustering, and multivariate analysis), pathway- (pathway mapping, co-expression analysis), or mathematical- (differential analysis, genome-scale analysis) based approaches to integrate omics datasets. MOI is facilitating the hypothesis generation leading to a further understanding of biological, molecular, and ecological functions and mechanisms, in addition to performing associations and correlations studies.

Groups applying MOI strategies to study plant responses to biotic (virus, bacteria, fungi, nematodes, insects and so on—alone or in combination) or abiotic (cold, heat, salinity, drought, heavy metals and so on—alone or in combination), or even the combination of both types of stresses, are welcome to submit the results of their studies.





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Message from the Editor-in-Chief

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