



Functional Genomics Approaches for Improving Abiotic Stress Tolerance in Crop Plants

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Message from the Guest Editors

Dear Colleagues,

In this Special Issue, contributions are invited wherein functional genomic approaches such as transcriptomics, proteomics, and metabolomics are used to identify networks of genes associated with abiotic stresses in crop plants. Omic studies that involve combinations of two or more stresses such as drought and heat, drought and salinity, and other stress combinations are strongly encouraged. Investigations on single abiotic stresses that utilize two or more omic strategies to identify key genes will be suitable for this issue. Studies using GWAS to identify genomic regions associated with stresses should include the genetic analysis of one or more genes underlying a major QTL region. The genetic analysis could be performed using mutant collections, RNAi, CRISPR, and overexpression lines.

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Guest Editors





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Message from the Editor-in-Chief

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