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Plant Regulomics: Briding Transcriptional and Translational Events for Ecological Adaptation

Guest Editor:

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Deadline for manuscript submissions:

closed (28 February 2018)

Message from the Guest Editor

Plants play an important role, as food in the form of crops, and also in understanding environmental stress fluctuations. High throughput sequencing approaches have widely unravel the link between transcriptional and post-transcriptional changes at genotypic, ecotypic and phenotypic level. Several emerging technologies, such as RNA-seq, smallRNAs-seq, ribosome-mRNA-seq, metabolomics, phospho-proteomics, and single cell transcriptomics, have played major roles in defining the transcriptional and post-transcriptional regulatory events in response to environmental fluctuations or in understanding the plant system biology.

This Special Issue widely invites papers related to the identification of new and differentially regulated genes and pathways under abiotic and biotic stress through the application of RNA-seq, smallRNAs-seq, ribosome-mRNA-seq, metabolomics, phospho-proteomics, and or single cell transcriptomics, which will help to understand the genomic basis of plant adaptation to climate change.

Dr. Gaurav Sablok
Guest Editor



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Message from the Editor-in-Chief

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