

## EDITORIAL

## Genes, Genomes and Germplasm for Climate-Smart Agriculture-Part-III

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UN climate change conference in Glasgow (COP26) ended with a high note on tougher pledges to end greenhouse gas emission. In this context, climate-smart agriculture assumes significance and can play a pivotal role in achieving net-zero commitments. Thus, we are happy to timely present the three parts of this thematic issue on “Genes, Genomes, and Germplasm for Climate-Smart Agriculture” which could serve as vital resource material and help in the advancement of science towards future challenges of net-zero commitments.

We wish to convey our deep gratitude to the editor-in-chief of *Current Genomics* for approving our proposal to bring this thematic issue on “Genes, Genomes, and Germplasm for Climate-Smart Agriculture” as a series in three parts. We acknowledge the contributions of all the reviewers for their time spent on insightful and impartial evaluation of the work of our contributing authors, which is critical to the improvement of all the published articles. The third and the last part of the series of this volume in honour of Prof. K.C. Bansal comprises contributions toward this thematic topic from five leading labs working on multiple facets of climate-resilient agriculture.

Drought and salinity are the key climatic factors limiting crop productivity currently and are predicted to be incurring further losses in the future. Therefore, understanding key molecular-genetic attributes of tolerance to drought and salinity is important in developing climate-resilient crops. In this volume, Ghosh *et al.* [1] highlighted key components (genes and proteins) of calcium sensors and their responders attributed to transport, environmental response and adaptation for tapping the potential of calcium signaling machinery for developing stress-tolerant crops. Further, they have described how genomics approaches can be implemented in the identification and functional characterization of these components. We are glad to present a research paper in this part, titled “Genetic dissection of epistatic interactions contributing grain yield variability in rice under drought” contributed by Majumder *et al.* [2]. In this research, the authors assessed the performance of ‘high’ and ‘low’ yielding rice lines pyramided with the same combinations of qDTYs from different genetic backgrounds and presented data on genetic interactions among QTL/genetic background affecting grain yield under reproductive stage drought stress. Developing climate-resilient crops is an urgent need for South Asia as the influence of global climate change will be prominent on the staple crops of this geography. In this context, two key contributions have been included in this part (Sukumaran *et al.* and Gaba *et al.*). Sukumaran *et al.* [3] discussed the pre-breeding methods in wheat to address the gaps in grain yield and minimize the bottleneck of genetic diversity using advanced plant breeding tools, and highlighted the importance of physiological breeding. Gaba *et al.* [4] presented genome editing using Site-Specific Nucleases (SSNs) as an alternative to plant breeding and even genetic engineering strategies, especially for multigenic traits improvement in crop plants considering the current biosafety regulations. Last but not the least, Raghuvanshi *et al.* [5] comprehended the complexities of developing salinity stress tolerance in rice using effective QTLs or genes/alleles. Taken together, this thematic issue presents an all-round account of molecular-genetic aspects related to imparting climate resilience in crops through utilizing germplasm collection by deploying modern plant breeding tools.

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