

EDITORIAL

Genes, Genomes and Germplasm for Climate-Smart Agriculture- Part-I

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The world's population is projected to reach 9.1 billion by 2050 and most of this increase will be in the developing countries. In addition to the direct food grain requirement, an increase in the consumer food preference towards animal origin food requires additional fodder and feed. Furthermore, the demand for agricultural feedstocks, such as sugar, cereals, grains and oilseeds for first-generation biofuel production is predicted to increase dramatically. Thus, overall food grain production needs to be increased by 70% to meet the food, feed and biofuel demand of the world by 2050. This challenge is further exacerbated by the competition for land and water resources, global warming and the associated increase in the frequency and severity of drought and heat stress in future. Carbon dioxide concentration is expected to reach 550 and 700 ppm by 2050 and 2075, respectively. Current studies with these levels of elevated CO₂ showed that it significantly reduces the nutritional quality of crops in terms of grain protein and micronutrients. Already, "Hidden hunger," due to fewer intakes of protein, vitamin A, Zn and Fe deficiency, is a major problem in several low-income countries, including India. Moreover, India is committed to achieve Sustainable Development Goal 2 (SDG2), *i.e.*, to end hunger, achieve food security and improve nutrition and promote sustainable agriculture by 2030. Therefore, we need to produce more nutritious food in an environmentally sustainable production system. One of the solutions to this problem lies in the germplasm resources that are conserved in the Gene Banks of different countries. Detailed characterization of genes and genomes of this germplasm and their response to various abiotic stresses are necessary to identify alleles, genes, pathways and traits. Rational assembly of these alleles and genes through conventional and precision plant breeding approaches are imperative to develop climate-smart crops for sustainable food and nutritional security. Therefore, this thematic issue of *Current Genomics* on "Genes, Genomes, and Germplasm for Climate-Smart Agriculture" is a timely contribution of knowledge to develop a better and holistic understanding. This issue is a tribute to Prof. K.C. Bansal, an eminent molecular physiologist who made significant contributions towards the cause of genes and germplasm for abiotic stress tolerance and is appropriately carrying contributions of five leading specialists in the field of plant molecular physiology and biotechnology, molecular breeding, genomics, and genetics.

Prof. K.C. Bansal initiated the evaluation of all germplasm lines conserved in the National Gene Bank at ICAR-NBPGR New Delhi to identify promising genotypes for their use by breeders and researchers using modern genomics tools. During the years 2011 - 2014, a mega characterization and evaluation study with an entire cultivated gene pool of 22,469 wheat accessions conserved in the National Genebank, India was carried out and a core set, including 1,770 *T. aestivum* genotypes was developed. Furthermore, the entire wheat germplasm comprising about 22,000 accessions was evaluated for heat tolerance at ICAR-NBPGR Farm, Issapur, New Delhi, and identified several donors for heat tolerance in wheat.

Prof. K.C. Bansal has identified and functionally validated several genes for abiotic stress tolerance. Comparative transcriptome analysis of the drought-tolerant Indian landrace selection Nagina 22 (N22) and high-yielding rice variety IR 64 led to the identification of α -linolenic acid metabolic pathway, leading to jasmonic acid biosynthesis as a novel mechanism of drought tolerance. This was further validated by several researchers internationally. By using the ABA Responsive Element (ABRE) core (ACGT) containing CGMCACGTGB motif, about 402 protein-coding genes were identified as potential targets of the ABA-dependent molecular genetic network in rice. His lab also analysed MYB transcription factor family in rice and identified several over-represented *cis*-regulatory motifs in the promoter region of the MYB genes, which may be involved in stress regulation. Furthermore, the existence of OsMYBs transcriptional co-regulatory networks under drought stress was identified in rice.

His lab also identified the minimal promoter region necessary for cold stress-responsive expression of *OsMYB38* gene and using this as bait in yeast one-hybrid screen, two novel genes *OsPYL3* (*OsPYL10*) and *OsRBGD3* were identified from Nagina 22. Ectopic expression of *OsPYL3* and *OsRBGD3* under CaMV35S promoter was shown to confer cold tolerance to Arabidopsis transgenics. Both *OsPYL-3* (re-designated as *OsPYL-10*) and *OsRBGD3* could act as important targets for developing cold tolerant and early flowering crops, including rice, for increasing production in low temperature affected areas.

His group analysed *TaHSP20* and *Clp* gene families and found that besides heat stress, these genes are also regulated by other abiotic and biotic stresses, and thus, the potential use of these genes to develop multiple stress-tolerant wheat crops was identified. In sorghum crop, Prof Bansal's group has identified stress-responsive miRNAs, tasi-RNAs, and their targets using the genome-wide approach in two sorghum genotypes, *i.e.*, M35-1 (drought tolerant) and C43 (drought susceptible).

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His lab utilised wild species of Brassica as sources of genes for abiotic stress tolerance. His lab cloned and functionally validated AtLEA4-5 homologs from *Brassica napus* and *Brassica carinata* species and was the first to demonstrate the role of Group 4 LEAs role in the abiotic stress tolerance of plants. Later, this finding was confirmed in major crop plants, including rice, by other researchers internationally. His lab also cloned *LEA4* promoter and functionally characterised it. The *BcLea4* promoter was used for driving abiotic stress-inducible expression of some of the genes encoding transcription factors like BcZFP1 and DREB1A. It was demonstrated that the LEA4 promoter-driven expression of BcZFP1 (zinc finger protein) or At-DREB1A gene confers salt and drought tolerance to transgenic crops. Under the Transgenics Network project, the gene constructs developed by Prof. Bansal were distributed to different partner centres, which led to the development of stress-tolerant transgenics in different crops.

This special issue on ‘Genes, Genomes and Germplasm for Climate-Smart Agriculture’, is divided into 3 parts (Part I to III), where several leading plant biologists have contributed their review articles in this field. Part one of this special issue comprised of five review articles where the first article is a mini-review by Joo *et al.*, [1] reviewing the progress in understanding the post-translational regulation of the bZIP family of transcription factors from model plant Arabidopsis and crops plants, such as rice, pepper, potato, and maize. Here, the authors discussed the progress in the regulation of bZIP proteins through phosphorylation, ubiquitination, and sumoylation under ABA signaling and drought stress and discussed the potential of manipulating bZIP proteins for the development of drought-tolerant crops. Tripathy *et al.* [2] have reviewed the progress in understanding the role of Ras-related in brain (RAB) GTPases, the largest family of small guanosine triphosphate (GTP)-binding proteins, in intracellular trafficking, cytokinesis, plant-microbe interactions and biotic and abiotic stress tolerance and identified potential gaps in RAB signaling for stress tolerance. Singh *et al.* [3] have detailed the role of a histidine kinase (HK) mediated phosphorylation and its role in stress tolerance. The authors have made an extensive analysis of the evolution of HKs and Response Regulators (RR) involved in a two-step phosphorelay (His–Asp) to a multi-step phosphorelay (MSP) cascade (His–Asp–His–Asp) signaling in plants and discussed the potential use of the two-component system for engineering stress-tolerant crops.

Rice is an important food crop of the world and especially in populous South-Asian countries. Drought, flood and other biotic stresses are the major climatic factor that negatively impacts crop productivity in rice. Two of the articles in this issue by Giri *et al.* [4] and Panda *et al.* [5] address these problems. Giri *et al.* summarized the progress in genes, cloned and characterised for abscisic acid signal transduction and component pathways of drought tolerance and role of microRNAs, and their target genes for drought tolerance in rice. Furthermore, the authors have reviewed the progress in the utilization of QTLs governing yield under drought (qDTY), and DEEP ROOTING 1 (DRO1) in the improvement of drought tolerance of rice. Panda *et al.* reviewed the progress in the identification of germplasm lines, mapping QTLs and genes for flooding tolerance, and successful utilization of *SUBMERGENCE 1 (SUB1)* QTL in marker-assisted backcross breeding for improving the submergence tolerance of several mega rice varieties [5].

We appreciate all the contributors of this thematic issue on “Genes, Genomes, and Germplasm for Climate-Smart Agriculture; Part I” for considering our invitation and submitting the articles on time. We acknowledge the help of members of the Editorial Board and our reviewers for all their help and cooperation. We thank the immense support provided by Mrs. Ambreen Irshad and Ms. Iqra Shafi and their team members at Bentham Science Publishers in bringing out this thematic issue.

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