

# Chapter 1

## Stress Management in Crops by Utilizing Landraces: Genetics and Plant Breeding Perspective



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**Abstract** Native germplasm is often the untapped resource that is supposed to hold the key to unlocking nature's repository of stress overcoming genes of crop plants. With an increasing global population, crop plants are expected to yield more under a variety of environmental conditions, hence exposing them to severe stress conditions. Locally available landraces of various crop plants that are often ignored in the presence of high-yielding developed varieties, however, have survived environmental turmoil over the ages and thus are the urgent need of the hour in order to couple yield or another desirable trait with stress tolerance. To bring these landraces to use, various mechanisms by which they tolerate environmental stress need to be understood. The use of conventional breeding techniques such as hybridization, selective backcrossing, gene pyramiding, etc. along with modern techniques such as mutagenesis, use of genetic markers, development of transgenic crops, etc. enables the use of trait diversity of landraces to counter environmental stresses while maintaining crop productivity. This chapter deals with various methods for identification of causal genetic factors responsible for stress tolerance in crop landraces and the possible techniques for developing tolerant varieties in the face of increasing frequency and severity of biotic and abiotic stresses.

**Keywords** Stress management · Landraces · Genetics · Plant breeding · Domestication

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## 1 Introduction

The process of crop domestication is closely associated with the various agricultural practices, human preferences, and the changing environment (Meyer et al. 2012; Smýkal et al. 2018). With the change in climate or environment and changing patterns in the use of natural resources, plants have been subjected to a variety of stresses. This led to the process of development and evolution of different adaptive strategies that permit plant cells to sense environmental stimuli and to activate responses that allow avoidance or survival of the environmental stresses encountered. The interaction of genotype and environment, which affects both agricultural practices and crop yield, is a critical point of research during the development of stress-tolerant plants under different field regimes (Mohammed 2009; Yumurtaci 2015). In the process of domestication, plants emerged in variable types, some as wild types, landraces, or the traditional domesticated genotypes. The crops plants have been globally dispersed with the spread of humans or evolution and due to various other environmental factors such as wind, water, or different natural disaster creating a geographical barrier. The crop plants thereby varied across the world based on the different process of cultivation and in accordance served to be the landrace to a particular area. The residues of the ancient crops undergo a very slow process of domestication like that of an evolutionary process, making the crop tolerant or highly diverse (Tanno and Willcox 2006; Smýkal et al. 2018).

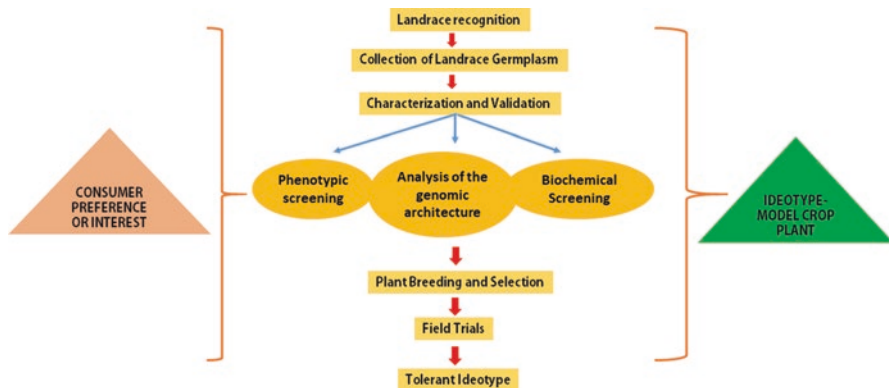
Stress can be defined, in the widest biological sense, as any factor that may produce an adverse effect in individual organisms, populations, or communities. It is also defined as the overpowering pressure that affects the normal functions of individual life or the circumstances in which plants are interrupted from fully expressing their genetic potential for overall growth, development, and reproduction (Rhodes and Nadolska-Orczyk 2001). As per the agricultural viewpoint, stress includes the external factors that limit crop productivity or destroys biomass (Grime 1979). Stress can be biotic or abiotic in nature. Biotic stresses emerge through interactions between organisms, whereas abiotic stresses are those that depend on the interaction between organisms and the physical environment. Abiotic stresses, which include the various external factors of disturbance, are often interrelated, and either individually or in combination, they hamper the physiological, biochemical, and molecular processes that adversely affect plant growth and productivity. The combined effect of the stress factors is based on its nature of interactions with its effect on the crop plants ranging from germination stage to grain filling. Crop plants in response to stress undergo a series of modifications and process of adaptations that includes both morphological and genetic changes such as genome rearrangement, induction of various tolerance genes, etc., as per its ability to tolerate the adverse effect (Tester and Bacic 2005; Pandey et al. 2017). Plants to withstand against the stress effect induce a series of regulatory mechanisms which are either constitutively expressed or induced (Roy et al. 2014; Pradhan et al. 2019). Thereby, understanding the genetic regulatory mechanism of the landraces against the stress effect and its ability to adapt to such adverse conditions serves as a source to identify or understand the process of tolerance against stress.

Breeding approach to enhance the crops' ability to adapt adverse stress conditions though due to various effects of cultivation bottleneck that has a negative impact on crop production must be a continuous process with an added focus on the different stress factors in addition to its yield (Bertoldo et al. 2014). Application of constant monitoring of the individuals using the modern noninvasive method as well as sequencing of the genotype helps in the proper screening of the crops for its application in breeding and development of cultivar with high adaptability. In the majority of the cases toward the increase of the agronomic value of cultivated crops, its genome structure, the type of stress factors exposed, and the variable environmental conditions help in the proper selection of the suitable strategies (Yumurtaci 2015). So there is a need to build effective crop screening methods and use the prevalent crop biodiversity on the basis of present technical advancements for the detailed evaluations of the different type of landraces which will enhance and improve the efficiency of breeding and crop improvement.

With advances in fields like physiology, molecular biology, and genetics, our understanding of crops' response to stress and the basis of varietal differences in tolerance have greatly improved. In this chapter, the biotic and abiotic stress management of crops by utilizing landraces and their wild relatives through plant breeding and genetic approaches are addressed.

## 2 Crop Landraces and Their Significance

Landraces include a group of progressive cultivated plant populations with a distinct location of origin and specific distinguishing characters, with high genetic diversity and ability to adapt variable local weather conditions. The process of landrace origin includes the set of seed selection practices or the crop domestication by farmers and the process of field management as per the different agricultural practices by farmers which vary with the area (Fuller 2007; Casañas et al. 2017). As reported by Dwivedi et al. (2016), plant landraces encompass mainly the domesticated plant species with heterogeneous local adaptations which provide the genetic elements required to meet the growing challenges of farming crops in stressful environments. These local heterogeneous genotypes with wide genetic diversity show changing phenotype with its yield ranging from low to moderate level but with high nutritional quality. Thereby, landraces with high ability to cope with stress factors include the traditional cultivars with high nutritional content and yield ability under low input system of agriculture (Zeven 1998; Azeez et al. 2018). A landrace which serves as the repository of various mechanisms of tolerance completely varies from that of the new selectively improved cultivar or variety developed by breeder taking into account a specific trait. Landraces with high genetic diversity and different traits responsible for adaptation to adverse conditions thereby serve as the source of efficient crop development using plant breeding techniques contributing mainly toward the efficient traits of nutrient uptake, utilization, and genes of tolerance against stress conditions. An unambiguous evaluation of the landrace with the



**Fig. 1.1** Schematic representation of the process of landrace utilization in crop breeding programs

improved techniques of identification (Fig. 1.1) may uncover the different patterns of diversity present, which will expedite in identifying alleles/gene loci for increasing growth, yield, and adaptation to stress, thus increasing the productivity and stability of staple crops in vulnerable environments.

Landraces are normally low yielding and less productive in comparison to the developed commercial varieties, but with the advancement in modern research in the recent years, they now serve as the repository source of genetic variability in the search for genes or traits responsible for tolerance or resistance to biotic and abiotic factors for the proper establishment of agriculture in that specific locality (Casañas et al. 2017). However, the intense use of developed varieties or transgenic plants led to decrease in use, management, and conservation of local landraces, thereby causing less presence of the agronomic or genetic data of the landraces which appear to be of great importance with changing the environment. Zeven (1998) proposed the importance and role that landraces played in the development of the crop worldwide and also its role in the improvement of crops and agricultural production which served to have been in existence since the origin of agriculture itself. Since the time of origin of agriculture, landraces have been subjected to various natural genetic modifications which include both the abiotic and biotic interventions, leading to the development of a mechanism of adaptation and tolerance (Bansal et al. 2014). Crop landraces are thereby the principal focus for the development of the agricultural system from century's immemorial (Umakanth et al. 2017). The traditional process of farmers sowing, harvesting, and storage of some proportion of seeds for sowing in the subsequent season highly enriched the genetic pools promoting intraspecific diversity (Frankel et al. 1998). This traditional concept of crop cycle for conservation and maintenance of crop landrace with the beginning of plant breeding leading to generation of generally higher-yielding cultivar resistant to specific stress subsequently replaced the traditional process leading to decrease in diversity and gene pool, thereby causing downfall to agricultural production in the present condition (Frankel and Hawkes 1975; Casañas et al. 2017).

Hawkes (1983) remarked landraces as crops associated to one specific geographical area in contrast to that of cultivars, which are bred and trialed in diverse locations seeking its ability of tolerance to that of the trait opted for. Thus, landraces of a particular location are highly specific to that particular location and with most of the landrace nomenclature taken as per the name of the location likewise the Kent Wild White Clover from Kent, UK. However, various ecological factors often led to the introduction of informal landrace varieties and migration of traditional landraces from native region to new regions.

The occurrence and maintenance of landrace germplasm include various processes like that of seed exchange or replacement among farmers in a geographical area (Louette and Smale 1996). The process of continuous cultivation by an individual farmer or discontinuous but collective cultivation of landraces also forms a significant process of maintenance. Therefore, open cultivation system with routine local or the remote introduction of landrace germplasm serves as the major process for the maintenance and occurrence of genetic diversity among landraces belonging to a particular location.

### 3 Genetic Mechanisms of Plant Against Different Stresses

Plants respond to various stresses with alterations in different gene expressions. Genes that are induced by the effect of biotic or abiotic stresses often impart stress tolerance to the plants. Genes induced by stress include functional genes or regulatory genes. Stress response genes also induce the activation of antioxidant response pathways and protection against damage from oxidative injury. Salinity, drought, heat, cold, heavy metals, radiation, and submergence are various abiotic factors responsible for stress in plants, whereas pathogens also induce biotic stress in plants. Genes responsible for stress tolerance have been identified in many plants for a variety of stresses, and overexpression of such genes in transformed plants has been shown to result in increased tolerance.

#### 3.1 Salinity

Salinity induces both osmotic and ionic stress in plants. The salt overly sensitive (SOS) pathway is an important mechanism maintaining ion homeostasis during salt stress. The SOS signaling pathway comprises of three important genes, *SOS1*, *SOS2*, and *SOS3* (Ji et al. 2013). Maintenance of ion homeostasis is a key response to salt stress, where  $\text{Na}^+$  extrusion is the primary process, providing tolerance to the plant against salt. Elevation in  $\text{Na}^+$  levels disrupts enzymatic functions and is toxic to plant cells. During salt stress, a  $\text{Ca}^+$  spike activates the cascade of SOS signal transduction in the root cell cytoplasm. *SOS3* is responsible for activation of a primary  $\text{Ca}^+$  sensor, and with the binding of  $\text{Ca}^+$  and *SOS3*, the *SOS2* gets activated.

In shoots, however, S<sub>Ca</sub>BP8 (SOS3-like calcium-binding protein 8) is the dominant activator of SOS2. Activation of SOS2 recruits it to the plasma membrane, thereby activating the downstream target SOS1. SOS1 is a Na<sup>+</sup>/H<sup>+</sup> antiporter, and its activation leads to the extrusion of Na<sup>+</sup>. *SOS1* mutants are found to be highly sensitive to salt (Ji et al. 2013). High-affinity potassium transporter (*HKT*) genes are also involved in ion exclusion. *HKT2* has been found to increase salt tolerance through Na<sup>+</sup> exclusion (Roy et al. 2014). Tolerance to salinity is also achieved by sequestration of Na<sup>+</sup> to vacuoles by vacuolar Na<sup>+</sup>/H<sup>+</sup> antiporters such as OsNHX1, OsNHX2, OsNHX3, and OsNHX4 in rice. Activities of Na<sup>+</sup>/H<sup>+</sup> antiporters increase during salinity, and the increase is found to be more in case of tolerant plants. Increased expression of *OsNHX1* leads to increased tolerance due to Na<sup>+</sup> compartmentalization in vacuoles and also increases tolerance in transgenic rice plants. Upregulation of *OsHKT1;1*, *OsHAK10*, and *OsHAK16* leads to increased Na<sup>+</sup> accumulation in old leaves and is an important stress adaptive feature in rice (Reddy et al. 2017).

High salinity induces the biosynthesis of abscisic acid (ABA) hormone that leads to the closure of guard cells and helps plants to overcome osmotic stress occurring due to salinity. Jasmonic acid (JA) is important in the ABA-dependent regulation of salinity response genes. Homologues of the JASMONATE ZIM DOMAIN (JAZ), *OsTIFY1*, *OsTIFY6*, *OsTIFY9*, *OsTIFY10*, and *OsTIFY11* have been identified in rice. Several protein kinases (MAPK, RLK, etc.) are also parts of the ABA-dependent pathways of regulation of gene expression besides transcription factors such as *ONAC022* and microRNAs. Transcription factors such as DREB (dehydration-responsive element-binding protein) are important in ABA-independent pathways. Overexpression of *OsDREB1A*, *OsDREB1F*, and *OsDREB2A* has improved salt tolerance in transgenic rice. Genes such as *PDH45*, *OsCPK12*, etc. regulate the accumulation of ROS during salt stress and improve tolerance to salinity (Reddy et al. 2017).

### 3.2 Drought

Drought induces osmotic stress in plants. Expressions of late embryogenesis abundant (LEA) proteins involved in protection against desiccation are upregulated during drought. Overexpression of some LEA class genes has led to increased tolerance to dehydration. A gene coding for galactinol synthase (*Gols*), which is involved in the biosynthesis of raffinose family oligosaccharide, has enhanced drought tolerance in transgenic *Arabidopsis*. Gene expressing raffinose synthase is also upregulated during drought. Raffinose functions as an osmoprotectant and alleviates cellular damage during drought stress (Shinozaki and Yamaguchi-Shinozaki 2007). Methionine sulfoxide reductase (MSR) proteins encoding gene *MsrB2* induces tolerance to drought in terms of reduction of oxidative injury by ROS. *CaMsrB2* from *Capsicum annuum* overexpressed in transgenic rice has improved rice tolerance to drought (Nahar et al. 2016).

DRE/CRT (dehydration responsive element/C-repeat) regulons cooperatively with ABRE (ABA-responsive element) regulate the expression of *RD29A* gene encoding LEA-like proteins. *RD29B*, also encoding for LEA-like proteins, is regulated by ABRE elements. Drought induced *DREB* genes to regulate the expression of several drought tolerance genes. Overexpression of *DREB1A* in transgenic rice increases drought tolerance. *DREB2* genes are also induced by drought stress. However, overexpression of *DREB2* does not result in increased drought tolerance in transgenic plants, which suggests that DREB2 protein requires posttranslational activation (Nakashima and Yamaguchi-Shinozaki 2006). Two basic leucine zipper (*bZIP*) transcription factors AREB/ABF activate ABA-dependent gene expression by binding to ABRE. Overexpression of *ABF3* or *AREB2/ABF4* leads to ABA hypersensitivity and reduces transpiration, enhancing drought tolerability of transgenic *Arabidopsis* plants. Transcription factors *AtMYC2* and *AtMYB2* cooperatively activate the *RD22*, a drought-inducible gene, following the accumulation of endogenous ABA. Overexpression of both *AtMYC2* and *AtMYB2* enhanced osmotic stress tolerance in transgenic plants (Shinozaki and Yamaguchi-Shinozaki 2007).

### 3.3 Heat

Thermo-tolerance in plants is measured in terms of cell membrane thermostability (CMS). QTL and co-segregation analyses revealed several heat shock proteins to be the genetic cause of thermo-tolerance in many cereals. Thermo-tolerance is not controlled by a single gene in cereals (Maestri et al. 2002). Heat stress results in the expression of heat shock genes (*HSG*) that encode heat shock proteins (HSP). Heat shock factors (HSF) bind to the specific binding sites of Heat Shock Elements (HSE) in the promoters of HSGs, inducing the expression of HSPs on heat treatment. HSPs act as chaperones and protect intracellular proteins against denaturation, maintaining their structural stability through protein folding and keeping their functions intact. HSPs are categorized on the basis of their molecular mass, viz., HSP100, HSP90, HSP70, HSP60, and HSP20 (sHSP). Small heat shock proteins (sHSPs) show the highest diversity among all the HSPs (Hasanuzzaman et al. 2013). All sHSPs have a conserved 90-amino acid carboxyl-terminal domain, the  $\alpha$ -crystallin domain (ACD). ACD distinguishes sHSPs from other heat-induced proteins. Tolerance to heat stress is induced in sHSP-overexpressing plants (Sun et al. 2002). *HSP70* and *HSP101* are involved in heat stress tolerance in *Arabidopsis*. Three *HSP101* members, *Tahsp101a*, *Tahsp101b*, and *Tahsp101c*, have also been cloned in wheat (Maestri et al. 2002). *Hsp17.7* and *Hsp100* have been found to confer thermo-tolerance in transgenic plants overexpressing these genes. *NPK1*-related transcripts are significantly elevated by heat. Constitutive overexpression of H<sub>2</sub>O<sub>2</sub>-responsive *ANP1/NPK1* was found to increase protection against heat stress in tobacco. Overexpression of *APX1*, coding for antioxidant ascorbate peroxidase, was also found to confer moderate heat tolerance in barley (Hasanuzzaman et al. 2013).

DREB2A in its active form during high-temperature stress regulates the expression of heat shock-related genes (Sakuma et al. 2006). Heat induces the expression of many HSFs. Plants have multiple copies of HSF genes. Heat stress regulatory proteins have conferred thermo-tolerance in transformed plants. *Arabidopsis HSF1a* and *HSF1b* control early response of many genes to heat. *HSF1* has been proposed to be the master regulator of heat shock response in tomato (Hasanuzzaman et al. 2013).

### 3.4 Cold

A number of functional and regulatory genes in plants respond to cold stress. Desaturation of fatty acids is important for membrane functioning during cold stress. Glycerol-3-phosphate acyltransferase (*GPAT*) gene from *Cucurbita maxima* and *Arabidopsis thaliana*, which induces desaturation of phosphatidyl glycerol fatty acid, results in an increase in unsaturated fatty acids in transgenic tobacco plants and reduces cold sensitivity. Mutants of *FAB1* (involved in fatty acid biosynthesis), *fad5*, and *fad6* or triple mutants of genes *fad3-2*, *fad7-2*, and *fad8* (genes involved in fatty acid desaturation) lead to increase in saturated membranes and show decrease in chlorophyll content and photosynthetic efficiency and growth retardation during cold stress, suggesting their significance in low-temperature tolerance. LEA proteins functioning against cellular damage and anti-aggregation of enzymes under freezing stress increase plant cold tolerance. *Arabidopsis* genes *LOS4* and *AtNUP160* responsible for the export of RNA from the nucleus to the cytoplasm are also crucial for chilling and freezing tolerance in plants (Sanghera et al. 2011).

Transcriptional regulation during cold stress is mediated by *ICE1* [inducer of C-repeat binding factor (*CBF*) expression 1]. *ICE1* induces expression of *CBF3*, which in turn regulates transcription during cold stress. *CBFs* regulate genes involved in membrane transport and hormone metabolism, phosphoinositide metabolism, osmolyte biosynthesis, ROS detoxification, and signaling (Chinnusamy et al. 2007). *DREB1A/CBF3*, *DREB1B/CBF1*, and *DREB1C/CBF2* regulons are found to be involved in cold stress-responsive gene expression. The products of cold-induced *DREB1/CBF* genes regulate the expression of many stress-inducible genes. Overexpression of these genes in transgenic *Arabidopsis* led to increased tolerance to freezing. *ICE1* gene was found to regulate the expression of *DREB1A* promoter without affecting the other *DREB1/CBF* genes. A homologue of *DREB1/CBF*, *LeCBF1* from tomato was found to induce freezing tolerance in transgenic *Arabidopsis*. Novel *DREB1/CBF* transcription factor, *ZmDREB1A*, from maize was found to regulate cold-responsive gene expression (Nakashima and Yamaguchi-Shinozaki 2006).



### 3.5 Heavy Metal

Heavy metals lead to the onset of oxidative injury in plants (Roychowdhury and Tah 2011h; Basu et al. 2012; Roychowdhury et al. 2018, 2019). In *Arabidopsis thaliana*, cadmium uptake induces expression of *Atcys-3A*, which is involved in cysteine biosynthesis under heavy metal stress. Cysteine is the precursor in glutathione biosynthesis, which in turn is required for phytochelatin production. Phytochelatin binds to heavy metals and increases plant tolerance against heavy metal stress. Transformed *Arabidopsis* plants overexpressing *Atcys-3A* have shown increased tolerance to cadmium (Domínguez-Sofis et al. 2001). *CABPRI* overexpression in tobacco also showed increased tolerance to heavy metal stress (Sarowar et al. 2005). In rice, *OsPIP2;6* has been demonstrated to play a role in  $As^{3+}$  efflux, thereby increasing plant tolerance against arsenic. Transgenic *Arabidopsis thaliana* overexpressing *PvACR3* from *Pteris vittata*, involved in vacuole sequestration of arsenic, have been shown to have increased tolerance to arsenic (Kalita et al. 2018).

### 3.6 Radiation

Transcript levels of *PyroA*, *Ubp3*, and *MEB5.2* were found to be increased by a low dose of UV-B radiation. *PyroA*, involved in the biosynthesis of pyridoxine, is important in protection of cellular structures against singlet oxygen. *Ubp3* encodes ubiquitin, associated with protein degradation. *MEB5.2* is a novel gene with unknown function (Brosche et al. 2002). Plant flavonoids are important secondary metabolites that protect against UV-B exposure, due to its absorbance in this wavelength region and elevation of its levels in epidermal cell layers. Flavonoids are also found to inhibit oxidative stress. Flavanone 3-hydroxylase (F3H) is a key enzyme in the flavonoid biosynthetic pathway, which is encoded by *RsF3H* in *Reamuria soongorica*. *RsF3H* gene expression and enzyme activity increase rapidly under stress (Liu et al. 2013).

### 3.7 Submergence

A QTL for submergence response in rice, *Sub1*, has been identified near the centromere of chromosome 9 of rice. *Sub1A*, *Sub1B*, and *Sub1C* are three genes identified in the *Sub1* locus, of which *Sub1B* and *Sub1C* are present in all genotypes. *Sub1A* which is the variant gene has two alleles, of which *Sub1A-1* is specific for submergence tolerance and *Sub1A-2* is specific for intolerance. *Sub1A-1* overexpression has been found to confer submergence tolerance in transgenic rice (Xu et al. 2006).

### 3.8 Biotic Stress

Expressions of various regulatory genes determine tolerance or susceptibility to biotic stress caused by pathogen attack (Mamgain et al. 2013). ABA-independent dehydration-responsive *DREB2A* signaling pathways were found to crosstalk with *adr* signaling pathways, associated with disease resistance (Agarwal et al. 2006). Transgenic tobacco plants constitutively expressing *OsDREB1B* were found to induce pathogenesis-related (PR) gene expression. The promoter of *OsDREB1B* contains several disease-responsive cis-elements, and transgenic tobacco overexpressing *OsDREB1B* has shown reduced disease manifestations and delayed systemic infections with induced expression of PR genes such as *PR1b*, *PR2*, *PR-3*, *PR5*, and *CHIN50* (Gutha and Reddy 2008). Plants overexpressing *OsEREBP1* showed the reduced impact of the fungus *Magnaporthe grisea* where transcriptome analysis revealed high expression of transcription regulators belonging to the NAC and WRKY families (Jisha et al. 2015). Overexpression of *MBF1a* transcriptional coactivator gene has been found to induce resistance to fungal disease in *Arabidopsis* (Kim et al. 2007). Rice 14-3-3 family genes *GF14b*, *GF14c*, *GF14e*, and *GF14f* are differentially regulated in the interactions of rice with fungal pathogen *Magnaporthe grisea* and bacterial pathogen *Xanthomonas oryzae* pv. *oryzae*. 14-3-3 proteins act as scaffoldings for the assemblage of large signaling complexes and are potential factors in disease resistance and tolerance of stress. Response of 14-3-3s in defense against pathogens has also been reported in many other plants such as soybean, cotton, and tomato (Chen et al. 2006). Rice gene *Osmyb4* which encodes an Myb transcription factor leads to the upregulation of several genes with known functions in resistance against pathogens. Myb is effective in induction of systemic acquired resistance (SAR) (Vannini et al. 2006). Overexpression of *SIAREB1*, a member of the AREB/ABF subfamily of bZIP transcriptional factors, from *Solanum lycopersicum* has been found to enhance the expression of PR proteins (Orellana et al. 2010). NAC transcriptional factors are important in plant pathogen interactions. NAC proteins activate PR genes, induce hypersensitive response (HR), and result in cell death at the infection site. Some NAC proteins, however, also increase the susceptibility of plants against pathogens. *ATAF2* overexpression was found to increase susceptibility toward *Fusarium oxysporum* by repressing PR genes. *ATAF1* increases resistance against *Blumeria graminis* f. sp. *graminis* (Bgh) but reduces resistance against *Pseudomonas syringae*, *Botrytis cinerea*, and *Alternaria brassicicola* (Puranik et al. 2012). Overexpression of *OsNAC6* in transgenic rice has led to increased tolerance against blast disease (Nakashima et al. 2007).

## 4 Crop Domestication and Its Impact on Genetic Diversity

Landraces with its origin and cultivation from the beginning of agriculture of about 12,000 years ago led to its domestication, thereby resulting into the conversion of wild crop plants to cultivated forms, e.g., rice landrace domestication from wild ancestor *Oryza rufipogon*. Worldwide, humans develop a special interest to a particular group of crop plants varying in location based on their taste or quality production, cultivation practices, and agricultural environments, thereby causing random selections which further led to genetic manipulation and erosion among the different landraces or crop species. Domestication indicates the approach of selective sweep on the standing as well as new variation in the genetic constituents of the landraces due to mutation or introgression (Smýkal et al. 2018). The domesticated species and its progenitor vary from each other mainly based on physiological and genetic makeup termed as domestication syndrome. Henceforth, the domestication syndrome causing loss of genetic diversity among landraces does include not only the extinction of species but the loss in allele or gene level during the process of selection trials (Flint-Garcia 2013; Karmakar et al. 2012; Roychowdhury et al. 2013; Ganie et al. 2014, 2016; Anumalla et al. 2015).

Modern cultivar developed after selection or trials, taking into account a specific trait, appears to be less tolerant to the different factors of stress in comparison to their wild relatives or the available landraces mainly because of the erosion of useful genes in the course of selection for high yield (Reif et al. 2005). In the present scenario of depleting environmental conditions and variable climatic change, modern cultivars have failed to meet the limit of tolerance, thereby developing a matter of concern among the farmers or researchers. Wild crop plants or landraces in the course of evolution without any human interference develop or adapt to different changes or stress which therefore serves as the major source to cope with the environmental stress impacts.

In the earlier period, plants breeder or researcher focused mainly on the yield and production of the crop plant, giving less importance to stress factors both abiotic and biotic. But in the present age, with an alarming increase of different abiotic and biotic factors, modern crops fail to serve with its inadequate genetic content present to cope with the different stress factors. The natural disasters due to various biotic stress-causing factors like potato blight in Ireland during the 1840s, coffee rust in Brazil, and maize leaf blight in the USA (Rogers 2004) changed the conception of the breeders toward the tolerance against stress. In the present time, along with breeding against biotic stresses, i.e., the different disease-causing pathogens, various steps have also been taken forward to aggravate the abiotic factors to improve the growth and yield of crop plants, taking into account the capacity and capability of landraces to adapt against adverse climatic conditions. Different management practices using both genetic and breeding approach against both biotic and abiotic stresses have been discussed below.

## 5 Stress Management Through Various Genetic and Breeding Approaches in Crops

Biotic stresses are resultant of the interaction of plants with other living organisms, which include pathogenic fungi, bacteria, viruses, or pests and nematodes resulting in considerable yield reduction, while abiotic stresses arise from the interaction of plants with the changing physical environment. Conventional breeding, as well as modern advanced techniques, may be used to overcome or manage the different biotic and abiotic stress undergone by the crop plants using the landrace stability.

### 5.1 Conventional Methods Used in Breeding Approaches for Stress Management

These methods bear traditional significance and have been used for long time in the past in developing disease-resistant varieties of crops. Sometimes, exotic varieties are also introduced in some areas in order to overcome biotic stress. Some of these methods are discussed here.

#### 5.1.1 Development of New Cultivars Through Crop Hybridization

This technique is used to incorporate genes for disease and insect resistance in a variety from other crops varieties belonging to the same or different genera. Introgression lines developed through hybridization of *Brassica juncea* or *Brassica napus* with *Erucastrum cardaminoides*, *Erucastrum abyssinicum*, and *Diplotaxis tenuisiliqua* showed much higher resistance to Sclerotinia rot fungus as compared to cultivars obtained from India, China, and Australia (Garg et al. 2010). Leaf spot black sigatoka caused by fungal pathogen *Mycosphaerella fijiensis* Morelet results in heavy losses in the production of banana and plantain. Hybrid progenies obtained from crossing susceptible plantains with wild resistant banana “Calcutta 4” have been found to contain partially resistant genotypes (Ortiz and Vuylsteke 1994). Identification of resistant wild varieties of crops is the important first step in the process of development of hybrids.

When subjected to abiotic stresses, such as photoinhibition, high temperature, and drought, the hybrid wheat line 1–12 was found to show better tolerance compared to its parents Jing-411 and Xiaoyan-54 (Yang et al. 2006). Managed abiotic stress screening during breeding can yield resultant genotypes with adequate stress tolerance in a target environment. Breeding with stress screening for drought and low N has resulted in the development of maize lines tolerant to these stresses (Bänziger et al. 2006).

### 5.1.2 Backcrossing

Brown plant hopper-resistant rice plants were developed using a backcross breeding program involving 203 accessions from different parts of the world as donors. Backcross populations involving *indica* donors were found to produce more resistant varieties compared to *japonica* donors (Ali et al. 2006). Backcross breeding has been used for the transfer of the *cryIA* gene of transgenic cotton imparting insect's resistance in susceptible cultivars (Zhang et al. 2000). Backcrossing is particularly important in order to avoid incompatibility or sterility while developing resistant varieties when the source of the resistance gene is any related species. Backcrossing has yielded important results while breeding plants for nematode resistance (Boerma and Hussey 1992).

Backcrossing methods have also been applied in developing varieties tolerant to abiotic stresses. In a large-scale project using over 160 donor cultivars, and 3 recurrent ones, rice cultivars tolerant to drought were developed (Lafitte et al. 2006). Using backcross breeding, promising rice lines have been developed, showing tolerance to a range of stresses such as salinity, zinc deficiency and submergence, and resistance to brown leafhoppers, which depict the tremendous potential of the rice gene pool diversity in overcoming abiotic and biotic stresses (Ali et al. 2006).

### 5.1.3 Gene Pyramiding

Gene pyramiding involves incorporation of multiple genes of resistance from different genotypes in a single genotype by the process of repeated crosses and helps to build horizontal resistance in resultant plants. Resistance genes *rym4*, *rym5*, *rym9*, and *rym11* against barley yellow mosaic virus have been incorporated in barley cultivars using gene pyramiding method (Werner et al. 2005). Pyramiding has been used to incorporate resistance genes for downy and powdery mildew in *Vitis vinifera* to obtain disease-free genotypes (Eibach et al. 2007). Resistance genes *xa5*, *xa13*, and *Xa21* of rice against bacterial blight pathogen *Xanthomonas oryzae* were pyramided in the rice cultivar PR106. This resulted in increased host resistance under a combination of resistance genes against several races of the pathogen (Singh et al. 2001). Genetic markers come handy in the process of gene pyramiding by identifying desired gene combinations. Pyramiding in order to incorporate the three loci for soybean mosaic virus resistance, viz., *Rsv1*, *Rsv3*, and *Rsv4*, in a single genotype has been achieved (Shi et al. 2009). The incorporation of several resistant loci into a single line is expected to impart broad-spectrum resistance to resultant crop genotypes.

### 5.1.4 Introducing Exotic Lines

During the 1970s, Southern corn leaf blight epidemic, an exotic Texas cytoplasm, was introduced to develop hybrid maize seed in the affected regions. The hybrids contained a mitochondrial sterility gene and were resistant to the pathogen *Cochliobolus heterostrophus* and high yielding (Ullstrup 1972). Exotic maize lines were found to show higher resistance to European pod borer *Ostrinia nubilalis* (Hübner), and introduction of such varieties could be a solution to improving maize crop in affected regions (Sullivan et al. 1974). Transfer of greenbug (*Schizaphis graminum*) resistance genes from Argentinian rye to wheat was only found to be suitable via the exotic “Gaucho” *Triticale* variety as chromosome pairing was rare in rye-wheat intergeneric hybrids.

## 5.2 Application of Modern Techniques in Stress Management

Owing to various limitations of the conventional methods of breeding, such as the requirement of more time, labor, uncertainty of results, etc., various modern methods have been developed as discussed below.

### 5.2.1 Mutation Breeding

Mutation breeding involves the treatment of plant material with physical (UV, X-ray, etc.) or chemical mutagens (EMS, colchicines, etc.) and screening the mutant plants for desirable traits and homozygosity while growing them for several generations. Mutants can be used as direct mutant variety such as barley cv. “Diamant” and rice cv. “Calrose” 76, or they can be used for crossbreeding, as in linseed mutants “M1722” and “M1589” (Maluszynski et al. 1995). Mutagen benzothiadiazole (BTH) has been found to develop systemic acquired resistance (SAR) in *Arabidopsis thaliana* against turnip crinkle virus, *Pseudomonas syringae* pv tomato, and *Peronospora parasitica* (Lawton et al. 1996). Mutation breeding methods were used to develop variation in disease and pest resistance and plant stature in tropical tuber crops cassava and yam by the process of in vitro mutagenesis and then by somatic cell manipulation (Novak and Brunner 1992). Two aromatic *indica* rice varieties “RD6” and “RD15” have been developed by the process of gamma irradiation from the “KDML 105” variety. Moreover, mutant varieties have been developed in many crops such as maize, wheat, tomato, barley, soybean, carnation, brinjal, mung bean, etc. (Roychowdhury 2011; Roychowdhury and Tah 2011a, b, c, d, e, f, g, h, 2013; Roychowdhury et al. 2011a, b, c, d, 2012a, b; Oladosu et al. 2016).

### 5.2.2 Marker-Assisted Selection (MAS) and QTL Mapping

DNA markers are a very important tool in plant breeding approaches as they help to identify plants containing specific DNA regions of importance which code for desired traits (Roychowdhury 2014; Roychowdhury et al. 2014). They are the most widely used types of markers predominantly due to their abundance. These markers are selectively neutral because of being usually located in coding regions. Widely used DNA markers are restriction fragment length polymorphisms (RFLP), random amplified polymorphic DNA (RAPD), and simple sequence repeats (SSR) or amplified fragment length polymorphisms (AFLP) (Collard et al. 2005). QTL mapping is an important approach required when traits are governed by more genes than one, located at particular loci within the chromosomes. QTL mapping is based on the principle that genes for specific traits segregate at the recombination events of chromosomes during meiosis. With the use of recombination frequency among progenies, the distance between markers is detected, and thereby, positions of QTLs within the genome are calculated (Collard et al. 2005). MAS can be used for screening germplasms for resistant genes (Simon-Mateo and Garcia 2011). Gene for head smut resistance in sorghum was detected using RFLP and RAPD markers (Oh et al. 1994). Ten QTLs for yellow rust resistance was detected in wheat using QTL mapping, which included five major QTLs, *QYr.sgi-4A.1*, *QYr.sgi-2B.1a*, *QYr.sgi-2B.1*, *Lr34/Yr18*, and *QYr.sgi-4A.2* (Chu et al. 2009).

### 5.2.3 Transgenic Approach

Foreign gene transfer from related or unrelated species through vectors such as *Agrobacterium tumefaciens*, gene gun, electroporation, etc. into target organisms so as to modify its genetic makeup, and introduce desirable traits, is another method of crop improvement for stress tolerance. *A. tumefaciens*-mediated gene transfer is a commonly preferred method for the purpose. Cry protein gene derived from *Bacillus thuringiensis* (Bt) has been transferred to different crops for providing resistance against chewing insects. The Cry protein disrupts the insects' guts once consumed, resulting in its death. Bt crops such as cotton, eggplant, etc. have been developed and have been proven to be commercially successful, with increasing growing areas worldwide (Romeis et al. 2006). An *Rxo1* gene for resistance against bacterial blight was transferred from maize to rice resulting in resistance against *Xanthomonas oryzae* (Zhao et al. 2005). USA and Argentina were using a total area of 30.3 and 10 million hectares of cultivated land for transgenic crops in 2000 (James 2003).

#### 5.2.4 Marker-Assisted Backcrossing (MABC)

Marker-assisted backcrossing is another convenient way of incorporating tolerance genes or QTLs into popular cultivars of crops. The widely cultivated Swarna variety of rice was incorporated with the rice submergence tolerance QTL *Sub1* in three backcrosses using polymorphic markers (Neeraja et al. 2007). Several MABC procedures have been utilized by ICRISAT in developing terminal drought tolerance in pearl millet (*Pennisetum glaucum* (L.) R. Br.) (Liu et al. 2000). *Sub1* QTL was also introgressed into the Bangladeshi mega rice variety using backcrossing assisted by SSR markers to incorporate submergence tolerance trait (Iftekharuddaula et al. 2011).

#### 5.2.5 Marker-Assisted Recurrent Selection (MARS)

MARS is used in the situation when many genes are involved in giving rise to a particular trait, in order to increase the frequency of desired alleles. Genetic gain accounting for increased grain yield of maize up to 51 kg ha<sup>-1</sup> year<sup>-1</sup> under drought stressed conditions was achieved in sub-Saharan African regions using MARS (Beyene et al. 2016).

## 6 Conclusion

During the process of crop domestication and various revolution like that of the green revolution to meet the growing demand of food based on the preference of the humans and the changing environmental conditions, different wild plants lose the natural habitat system and led to the effect of cultivation bottlenecks which later serve to be an inefficient domesticated crop. Therefore, with the evolving changes in environmental conditions and pathogenic races, untapped landraces of different crops, which were left out undomesticated during the rapid expansion of agriculture by means of high-yielding varieties and use of fertilizers and pesticides, have once again emerged as the repository source of high genetic diversity and stability. With the growing world population, and climate change pushing agricultural productivity to the edge, this genetic resource of landraces and wild varieties of crops need to be screened for tolerance or resistance traits using advanced high-throughput technologies and various procedures mentioned in the preceding sections. Stress management in the face of today's hurdles has to be an integrated approach, involving new technologies for selection and breeding using local landraces, as well as spreading of social awareness regarding the acceptance of transgenic crops that are less demanding for the environment.



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