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Offsetting Climate Change Impact Through Genetic Enhancement

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Abstract

Climate change and its effects have become a burning issue of today's era. The anthropogenic activities have created many impacts on environment and on our crop plants. Crop plants are facing the problems they had never seen before. These problems are prominently water scarcity, drought, water logging, salinity, increasing temperature, terminal seasonal heat etc. Plant breeder's role is becoming very important in developing crop varieties suitable for climate resilient agriculture, understanding the genetics of novel traits, utilizing the crop germplasm which are still on breeders' shelf, and understanding the physiology of crops. Plant breeders can use crop germplasm, crop wild relatives, underutilized crops, potential plants to be developed as crops to tackle the impacts of climate change and help the farmers to feed the ever-growing population. Utilization of novel plant breeding tools such as marker assisted selection, genomic selection, transgenic, genome editing, allele mining etc. will augment the conventional plant breeding of future. Accelerated crop domestication has emerged as a new way to widen the scope of crop plants for growing demand and divergent needs of future generations. Future of plant breeding will be supplemented with the advancement of extensive, accurate, efficient and non-invasive phenotyping. The plant breeding will be assisted in future with phenomics, artificial intelligence, Internet of Things, Machine learning and Big data analysis.

Key words: Climate Change, Crop Breeding, Genomics.

I. Introduction

The anthropogenic modification of the atmosphere causes major environmental problem which leads to the global climate change. The concentration of CO₂ in the atmosphere increased almost 25% due to the fossil fuel consumption and deforestation. Over the past 100 years, increasing greenhouse gases (GHGs) concentrations resulted in global warming by 0.74°C. The Intergovernmental Panel on Climate Change (IPCC) made projections for the Indian subcontinent, which shows that a rise in temperature from 2 to 4.7°C, with the most probable level being around 3.3°C by the year 2100 (Solomon *et al.*, 2007). The gradual decrease in intensity of rainfall over the time from 1901 to 2012 (which was further confirmed by trend analysis) shows the decrease in precipitation in India. The frequent drought was also observed during the same period, with a rise in torrential and an unequal distribution of rains. A significant rise in temperature is leading to short-duration torrential rains as well as drier seasons. It is due to prolonged dry period specially in the north-eastern states of India which are known for moist weather. Extreme weather, including droughts, floods and other disasters are result of abrupt and sudden climate change. In agricultural production systems the extreme events such as heat and cold waves, flooding, hail storms, cyclones due to climatic changes are well known to adversely affect the agricultural production. Globally, the effect of climate change has been recently analysed and demonstrated in respect of production and yield of

four major crops, *i.e.*, soybean, wheat, maize and rice (Wang *et al.*, 2018). By increase of 1°C in minimum temperature above 32°C in the growing season, the average yield of rice was reduced by 10 per cent. The response of current varieties in the projected climate change scenarios of rainfed maize show the average reduction of 3.3 to 6.4% by 2030 and 5.2-12.2 % in 2050, whereas in irrigated conditions the projected average yield reduction is by 3 to 8 per cent by 2030 and 5 to 14 per cent by 2050 (Tesfaye *et al.*, 2017).

Therefore, to cope with the above climatic anomalies it is important to identify traits that maintain and promote the growth and development of plants during the stress period and pyramiding of genes governing these traits for imparting tolerance to major climatic stress, which may assist the crop plant to endure and realize the genetic potential in its yielding abilities. To achieve climate smart solutions, the development of climate-resilient high yielding varieties along with climate smart adaptation and mitigation technologies and their rapid availability to farmers' fields is necessary. Due to the various stress-adaptive mechanisms, stress uncertainty and large genotype × environment interaction, breeding for genetic enhancement for adaptation to the changing climate is however challenging.

Acquiring of modern and innovative breeding techniques, which includes precision phenotyping, rapid-cycle breeding and mining of novel genetic variation is essential for genetic enhancement program. Developing genomic approaches and methods

will need to take into account various cereals responses to climate change, some of which might be crop-specific while others can be shared between various crops (Prasanna *et al.*, 2013). Since, crop abiotic stress resistance is a polygenic complex trait, merely multi-gene synergistic effects may be efficiently accomplished (Wang *et al.*, 2018). Advantageous alleles, genes, and haplotypes should be identified from diverse germplasm (including wild races) and introgressed in to elite germplasm. For faster development and delivery of enhanced germplasm, new strategies would be necessary to combine molecular markers for accelerated breeding and development of elite germplasm using technologies such as doubled haploidy, high-throughput phenotyping, and planting in year-round nurseries for rapid generation breeding approaches. In this chapter, some of these key modern techniques and strategies for genetic enhancement in crop to offset the impact of climate change in agriculture are highlighted.

II. Impact of Climate Change on Crop Production

Climate change is a critical global threat that's likely to effect on the agricultural production system and in the end food security. It is likely to steer global average temperature, rainfall pattern and elevated carbon dioxide level, which will directly influence the crop growth and ultimately crop productivity. Climate change adversely affected agriculture system across the majority of tropical and subtropical regions in contrast to

temperate zones wherein crop yields are normally embarrassed to sowing time, crop varieties, nutrient availability, soil degradation and availability of water resources. In addition, evapo-transpiration also will be altered due to global warming; consequently, water productiveness of crops may shrink in the future. Potential climate abnormalities are coupled with global warming and crops usually come across an augmented number of abiotic and biotic stresses individually as well as in combinations, which significantly influence their growth and productivity (Prasad *et al.*, 2011; Narsai *et al.*, 2013). As climatic changes are in all likelihood to make off-putting impacts on crop growth, it could endanger the efforts to accomplish domestic and global food safety (Webber *et al.*, 2014).

II.1 Abiotic Stress

Abiotic stresses are the major stresses that plants experience specially in the area of climate change. Among the environmental stresses temperature fluctuations and variations in rainfall spells are very critical indicators, which have distressing effects on plant growth and yield. Drought, heat and their combinatorial effects on plant growth are very fatal. Apart from these the flash floods, frequent high winds and water logging are also causing severe damage to the crops standing in fields. Elevated carbon-dioxide (CO₂) and greenhouse gases (GHGs) are affecting the crop growth by jeopardizing their physiological machinery.

a. Drought

Drought is non-availability of adequate quantity of water at any growth stage of a crop plant so that the maximum crop growth and yield is hindered (Prasad *et al.*, 2011). Drought affects the crop growth by limiting the physiological and metabolic process such as mineral absorption, rate of photosynthesis, transpiration, photosynthates translocation, bud development, flowering, initiation. Drought at any critical stage of plant growth may be detrimental to yield. The severity of drought is largely unpredictable and it can be because of uneven rainfall pattern, poor rainfall, poor moisture holding capacity of soil, evapotranspiration etc. (Fahad *et al.*, 2017). Various plant species at different growth stages show different physiological and metabolic response to drought stress and deploy different mechanism to tackle it. It includes reduced absorption of photosynthetic radiation, decreased harvest index and impaired radiation use efficiency (Earl and Davis, 2003). As per the detailed analysis of data from 1980 to 2015, Daryanto, Wang and Bramely (2016) had reported a global reduction in yield of wheat and maize by 21 to 40 % due to drought. Similarly, drought stress also has significantly decreased the yield of major grain legume crops. Drought stress caused the yield decline of 26% during the reproductive phase (Baroowa and Gogoi, 2014) in black gram. Maleki *et al.* (2013) reported that 42% reduction in grain yield when Soybean crop was exposed to drought stress at grain filling stage.

b. Heat

Global average temperature has accelerated by 0.8°C since the 1850s and is projected to rise at the rate of 2 to 7°C by the end of this century (Allison *et al.*, 2011). Rising temperature may be a major challenge for food safety if adaptive control measures cannot be capable to lessen the expected yield losses. It has been predicted that temperatures variation of $\pm 2^\circ\text{C}$ in mean growing-season in Australia can cause up to 50% drop off in wheat yield even without differences in rainfall (Asseng *et al.*, 2011). It was concluded that the loss in yield was especially accredited to in leaf senescence as a result of extended temperature beyond 34°C. In India, reduction in wheat yield up to 20 % due to an abrupt increase in temperature through grain filling period reported by Gupta *et al.* (2010). Maize production is more susceptible towards fluctuations in temperature and rainfall amongst staple cereals (Knox *et al.*, 2012). In a study by Lobell *et al.* (2008), it was reported that, 30 % reduction in maize yield by 2030 was projected in southern Africa. The rising temperature may cause the change in cropping pattern around the globe. Growth acceleration due to above average temperature causes harm to various physiological process, less radiation interception, less biomass production, etc. (Aryal *et al.*, 2019).

c. Combined Drought and Heat

Simultaneous exposure to drought and heat stress were found to be more detrimental than these stresses occurring independently at different growth stages to crop production (Prasad *et al.*, 2011).

Water deficit and temperature extremes are mainly influencing the flowering and grain filling period due to climate change. It was delineated that the reproductive phase is severely affected by the water stress specially in case of cereal crops. Drought along with high temperatures are critical stressors with excessive impact on cereal yields. Griffin *et al.* (2004) reported that rubisco, the vital enzyme of photosynthesis is disturbed if the temperature will rise above 35°C and halt the photosynthetic process. Wheat production is influenced by drought stress throughout all the developmental stages, however, the reproductive and grain formation stage are the most crucial ones. Wheat yield declined by 30% under moderate post-anthesis drought while, decline was up to 92% in case of prolonged moderate drought stress at reproductive phases (de Oliveira *et al.*, 2013).

d. Elevated Carbon Dioxide

The atmospheric carbon dioxide (CO₂) has raised about 400 ppm from 1832 to 2014 (Wheeler and Braun, 2013). Increasing CO₂ levels in the atmosphere is a crucial factor responsible for global warming and ultimately climate change. The physiological processes of agricultural crop plants depend on the combined outcomes of climate change factors including increased CO₂ levels (Mishra and Agrawal, 2014) which will determine potential global food security. The impact of warming i.e., increased temperature and altered precipitation may be likely compensated to some degree through CO₂ fertilization effects, elevated CO₂ may have positive

impacts on crop physiology via effects on stomatal performance of plants, consequently less water loss through transpiration, resultant in improving water use efficiency as well as photosynthesis process (Lobell and Field, 2007). Balasooriya *et al.* (2018) had reported that there was yield enhancement of strawberry under elevated CO₂ concentration but with reduced fruit quality. They have also reported that the reduced yield and poor fruit quality if higher CO₂ is combined with high temperature. Similarly, Jayawardena *et al.* (2019) had reported that there was reduced yield of soybean under combinatorial effect of higher CO₂ concentration and high temperature.

e. Water Availability

Climate change has formed extreme pressure on the hydrological cycle. It is anticipated that altered hydrological cycle could ultimately impact on water availability at global level (Haddeland *et al.*, 2014).

Alteration in the water cycle which might be potentially menacing the traditional farming system. Water scarcity and irregular rainfall pattern in different parts of the globe have caused sizable reduction of yield in preceding decade. Climate change influences on agriculture depending on the degree of warming and changes in precipitation pattern between locations. The impact of climate change on precipitation pattern is not just limited to its influence on water accessibility, the increase in evapotranspiration (ET) and temperatures could add to crop irrigation needs between 5 to 20 %, by 2080 (Gornall *et al.*, 2010). Increasing water necessity and exhausting water assets has restricted

the food production beyond the present level. Consequently, consideration ought to be centred around the progression of agronomic practices and new irrigation techniques to conserve soil moisture and improve the water productivity of vegetation.

f. Flood

Flood may be of two types, viz. a frequent rain causing submergence of plants for a short period by running rainwater (flash flood) and submergence of crop field under stagnant water (by rain or river overflow) for relatively longer period. Both the conditions create anaerobic condition to the submerged plant part. It creates physiological drought condition wherein a plant is not able to absorb water by root even though water is abundant (Gautam *et al.*, 2016). The impact of waterlogging on crop growth is depending on the growth stage of plant, inherent mechanism to cope-up and duration of waterlogging. Generally, plant show quiescent strategy (minimizing the metabolism to a bare minimum and sustaining the life by saving energy while being submerged), escape strategy (plant exhaust all its energy to elongate its stem so that some plant parts can respire aerobically for survival) and alteration in physiology and metabolism (Guru and Dwivedi, 2018). Rice is a very important plant wherein mechanism of submergence tolerance has been studied significantly and several cultivars have been developed through transfer of *sub1* genes (identified in a submergence tolerant rice landrace FR13A from Odisha). In rice, several varieties such as *Swarna-sub1*, *Samba Mahsuri-Sub1* and *IR64-*

Sub1 were developed by transferring the *sub1* gene from FR13A through marker assisted backcrossing (Oladosu *et al.*, 2020).

g. Frost

Climate change brings increase in temperature and reduction in duration of cold spell. Some crop plants and trees are having physiological and metabolic requirement of undergoing summer and winter spell of particular duration. This reduced duration in cold spell because of increased temperature may bring 'false spring' within the cold spell which will damage the growing buds and subsequently affect plant physiological functions (Ma *et al.*, 2019).

II.2 Biotic Stress

Biotic stresses include plant diseases, insects and pest of crop plants. Climate change invariably impact the growth and behaviour of all the biotic stresses. Some climatic vagaries have favourable effect on disease development while some have restrictive effect. The overall impact is unpredictable response in disease development and pest infestation.

a. Plant Diseases

Climate change may modify the growth and development rate, pathogenicity of infectious agents as well as the host plant interaction (Charkraborty and Datta, 2003). Temperature is critical factor affecting the occurrence of bacterial diseases including the ones caused by *Acidovorax avenae* (seedling blight and bacterial fruit blotch of cucurbits), *Burkholderia glumae* (bacterial panicle blight in rice) and

Ralstonia solanacearum (wilt in tomato) (Kudela, 2009). An increase in temperature could alter the life cycle of pathogens. Temperature may also influence the occurrence of vector-borne diseases through changing the population and spread of vectors. Salt stress may alter the pathogen virulence, host physiology and microbial activity in soils (Triky-Dotan *et al.*, 2005). Drought stress along with high soil temperature has resulted in increased charcoal stalk rot development in *Sorghum bicolor* (*Macrophomina phaseolina*) (Mihail, 1989). New races might also evolve swiftly under accelerated temperature and CO₂, as evolutionary forces act on massive pathogen populations underneath favourable microclimate within enlarged canopy (Chakraborty, 2013).

b. Insect-Pest

Climate change has a profound effect on insect pest. It affects the physiology, abundance, biogeography and population dynamics of insect pest of crops (Andrew and Hill, 2017). Temperature can affect directly or indirectly insect physiology, insect ecology, geographical distribution, overwintering mortality, fecundity, generations per year, active period, etc. Temperature can exert various effects which, depends on the life cycle of an insect species. Yamamura and Kiritani (1998) reported that with a 2°C temperature rise, insects might undergo one to five additional life cycles per season. Increased CO₂ concentration can affect the feeding rate of insects as well as altered chemical defence of host (Arora and Dhawan, 2013). Flooding may affect the population of soil dwelling insects. Similarly, extreme weather

events, increased precipitation and combination of other factors of climate change may bring a major change in insect pest dynamics.

III. Trait Mapping for Genetic Enhancement

Offsetting climate change through plant breeding is solely based on the plethora of genetic resources of crops and the rationale behind genes and genetics of traits affected by climate change. Crop improvement is depending on generation of variability and creation of adaptive capacity in crops to sustain the effect of climate change. Mapping of genes, studying the genetics of traits and unravelling the molecular basis of traits are important requirements to utilize them in crop breeding. In this section, various kinds of genetic resources which can be used as base material for future crop improvement are elaborated.

III.1 Wild Relatives for Tackling Climate Change

Crop wild relative (CWR) is a wild plant taxon that has an indirect use derived from its closely related species (Maxted *et al.*, 2008). Crop wild relatives are big source to combat near big challenges. CWRs possess important genes for breeding for climate tolerant varieties. The high yielding varieties has been evolving for thousands of years in adverse environmental conditions and possess a much higher degree of adaptability from CWR. Some institutional online portals serve for the use of CWR database are:

1. Crop Wild Relative Global Portal (<http://www.cropwildrelatives.org>)

Table 1: Summary of Crop Wild Relatives of Some Important Food Crops

Crop	Wild Relatives	Storage Location
Rice	<i>Oryza rufipogon</i> , <i>Oryza officinalis</i> , <i>Oryza granulata</i>	Chinese Academy of agriculture Sciences; International Rice Research Institute
Wheat	<i>Triticum</i> , <i>Aegilops</i> , <i>Dasypyrum villosum</i>	The Wheat Genetics Resource Centre (14,000)
Barley	<i>Hordeum spontaneum</i> , <i>Hordeum</i> wild species	USDA-ARS National Small Grains Collection
Sorghum	23 wild sorghum species	International Crops Research Institute for the Semi-Arid Tropics (449)
Tomato	Wild <i>Lycopersicon</i> and <i>Solanum</i> species	Tomato Genetics Resource Centre (1,196)
Potato	187 wild <i>Solanum</i> species	International Potato Centre

2. Crop Wild Relatives(CWR) and Climate Change (<http://www.cwrdiversity.org/>),
3. Gateway to Genetic Resources (<http://www.genesys-pgr.org/>),
4. Global Crop Diversity Trust (<https://www.croptrust.org/>).

A summary of crop wild relatives of some important food crops is shown in Table1 (Kaur *et al.*, 2018).

III.2 Plant Genetic Resources

Brockhaus and Oetmann (1996) defined “PGR as the reproductive or vegetative propagating material of cultivated varieties in current use and newly developed varieties, obsolete cultivars, primitive cultivars (landraces), wild and weed species, near relatives of cultivated varieties and special genetic stocks”.

Plant genetic resources are the most valuable material for climate challenge. Plant genetic resources are maintained through more than 1750 individual gene banks worldwide as shown in Table 2 (Bansal *et al.*, 2016). This table also notifies the extent of variability conserved in the form of landraces, wild and advanced research material that exists in our gene banks.

III.3 Overview of Stress Tolerance Genes

Agriculture is more prone to the climate change impacts, hence good mitigation strategies are essential for sustainable agricultural production. Climate change brought many challenges for the plant breeders. Now the breeder has to focus on how the variety that will perform in an environment with larger variability in temperature and water availability,

Table 2: Summary of Germplasm Available in Major Gene Banks of the World

Name of The Gene Bank	Number of Accessions Conserved				
	Landraces (%)	Breeding/ Research Material (%)	Wild (%)	Advanced/ Improved Material (%)	Total Accessions
International Rice Research Institute	38.2	6.91	3.74	2.92	1,31,863
N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry, Russia	28.46	12.01	7.03	15.65	3,38,592
Asian Vegetable Research and Development Centre, Taiwan	81.51	0.16	16.80	1.35	60,883
Department of Applied Genetics, John Innes Centre, Norwich Research Park, UK	14.58	1.26	1.22	29.26	26,668
ICRISAT	80.23	14.57	2.32	1.23	1,23,023
ICARDA	4.40	57.33	20.73	-	
CIMMYT	44.43	9.26	17.27	5.54	53,807

UV light, salinity and other effects of climate change (Brettell, 2008). Ozone stress is more likely to co-occur with other global climate change factors. Plant researchers have identified hundreds of genes controlling abiotic stress responses (La Pena and Hughes, 2007). These genes are classified into four major groups:

1. Genes encoding stress induced proteins such as late embryogenesis abundant proteins (LEA), response to ABA (RAB protein), dehydrin proteins and heat shock proteins (HSP).
2. Genes encoding enzymes for the synthesis of osmolytes which maintains the osmotic pressure through osmotic adjustment.

3. Genes encoding proteins or enzymes involved in scavenging the reduced oxygen species such as superoxide radical (O_2^-), hydroxyl radical (OH) and H_2O_2 .
4. Genes encoding proteins involved in ion homeostasis, ion transport and Ca^{2+} ATPase.

a. Stress Induced Regulatory Factors

Kinases or transcription factors are the regulatory elements, that are responsible to stress signals and lead to specific gene expression of stress tolerance. Four different types of regulators have been reported that are active in response to abiotic stresses. Differential screening results

suggested the existence of two separate signal transduction pathways ABA-independent pathway and ABA responsive pathway (Nordin *et al.*, 1991). In ABA independent gene expression two regulators are playing a crucial role. These are Dehydration Responsive Element Binding protein-1 (*DREB1*)/ C-repeat Binding Factor (*CBF*) and *DREB2*. Whereas in ABA-responsive gene expression, the ABA responsive element (*ABRE*) binding protein (*AREB*)/ABRE binding factor (*ABF*) is playing a crucial role (Saibo *et al.*, 2009), other regulators such as *NAC* and Myeloblastosis-Myelocytomatosis (*MYB/MYC*) are also involved in abiotic stress responsive gene expression (Nakashima *et al.*, 2007).

In wheat, *TaSnRK2.7* is a multifunctional regulatory factor and involved in different activities such as carbohydrate metabolism, adjustment of osmotic potential, increasing photosystem II activity, and promoting root growth. Therefore, *TaSnRK2.7* can be potentially utilized in transgenic plant breeding to enhance abiotic stress tolerance in crop plants (Zhang *et al.*, 2011). *TaPR-1-1* is the overlapping gene within the pathogenesis-related (PR) protein family genes. Its expression is also induced by freezing, salinity, and osmotic stresses. Up regulation of *TaPR-1-1* in yeast and arabidopsis conferred tolerance to several stresses (Wang *et al.*, 2019).

Sorghum a C₄ model plant was studied for understanding molecular mechanism of resistance to stress. Three genes were highly induced (*SbIAA1*, *SbGH3-13* and *SbLBD32*) under four treatments (10 µM Indole Acetic Acid for 3 hours, 1 µM

brassinosteroid for 12 hours, 150 mM NaCl for 7 days and drought). This analysis provided new evidence for role of auxin in stress response, implied there are cross talk between auxin and abiotic stress signalling pathways (Wang *et al.*, 2010).

b. Genes and Regulatory Factors for Drought Tolerant

Drought is the common abiotic stress causing not only yield loss, but also causing yield instability. The expression of drought tolerance genes is highly complex and these genes are regulated at the transcriptional, post-transcriptional and translational levels. DREB genes regulate transcription of several genes in response to water stress. Expression of DREB genes encode transcription factors that bind to the cis-acting promoter element (DRE) of stress related genes and regulates their expression (Smirnov and Bryant, 1999). This induces synthesis of gene products for acclimatization response to low temperature and water stress conditions (Ingrain and Batels, 1996).

Over expression of Deep Rooting 1 (*DRO1*) enhances the root growth angle and promotes roots to grow more in downward direction. Introducing *DRO1* and *PSTOL1* into background of shallow rooting rice cultivar results in drought tolerance by increasing deep rooting (Uga *et al.*, 2013).

c. Genes and Regulatory Factors for Flooding and Submergence Tolerance

Flooding and submergence causes anoxic conditions in the root system. The transcription factors, such as heat shock proteins, ethylene

response binding proteins, MADS-box proteins, AP2 domain, leucine zipper, and zinc finger were enhanced in response to anoxic conditions in the root system in Arabidopsis and Rice (Lasanthi-Kudahettige *et al.*, 2007). The transcription factors in the AP2/ERF-type family are the most commonly up-regulated transcription factors followed by zinc-fingers in response to submergence tolerance. Transcription factors belonging to the basic helix-loop-helix family are the most commonly down-regulated transcription factors, together with transcription factor from the bZIP and MYB families (Licausi *et al.*, 2011).

The common problem of biotic and abiotic stresses is accumulation of ROS, including oxygen deprivation. Some of the reported redox-sensitive transcription factors are involved in the adaptive response to low oxygen. ZAT12 is a putative transcription factor, which promotes upregulation of cytosolic ascorbate peroxidase-1, a key enzyme in the removal of H₂O₂ (Rizhsky *et al.*, 2004).

The variant of ERF family genes, *Sub1A-1*, leads submergence tolerance to lowland rice. The rice gene *aie* (anaerobically inducible early) is early activated by anoxia condition and encodes for a putative protein that is involved in signalling pathways. (Huq and Hodges, 2000).

d. Genes and Regulatory Factors for Heat Tolerance

Plants under heat stress accumulate several metabolites (antioxidants, osmo-protectants, heat-shock proteins, etc.) and metabolites from different pathways (Bokszczanin *et al.*, 2013). For activation of heat induced transcription, a cis-acting

DNA sequence and the heat-shock element (HSE) are required (Nover and Baniwal, 2006). The trans-acting transcriptional factor, regulates expression of HS gene by binding the heat stress transcription factors (HSFs), to the HSE. Other transcriptional factors such as *Hsp101*, *HSA32*, *HSFA1* and *HSFA3* plays a less critical role, as knockout variants of these have small impact on heat tolerance (Yoshida *et al.*, 2011).

The over expression of Arabidopsis *HSP101* gene in rice plants, conferred high growth performance during recovery from heat stress. In Arabidopsis, 21 HSF genes are present and classified into three major classes based on structural differences. These are *HsfA*, *HsfB* and *HsfC*. *HsfAs* is responsible for heat-induced activation of heat-shock genes. *HsfBs* lacks the heat-inducible transactivation function and act as co-activators of transcription with *HsfAs* (Liu *et al.*, 2011).

e. Genes and Regulatory Factors for Chilling and Freezing Tolerance

Dehydrin proteins are produced in response to dehydration, low temperature, etc. genes such as *WCOR4106*, *WCOR413*, *Dehydrin-2*, Barley ABA inducible protein, thaumatin like protein, glucanase like protein and chitinase like protein are directly involved in chilling and freezing tolerance. Overexpression of DREB/CBF and NAC transcription factors, enhances salt, drought, and cold tolerance in rice. PR proteins with antifreeze activity can have direct effects on the stability of cellular membranes and reduce chilling injury (Yu and Griffith, 2001).

f. Genes and Regulatory Factors for Salinity Stress

Large areas of cultivated lands are affected by the high salinity which is one of the most critical environmental factors. Plants under exposure to high levels of NaCl, disturbs its water homeostasis and creates ionic stress by increasing the concentration of Cl⁻ and Na⁺ ions in cells. DRE-related binding factors, leucine zipper DNA binding proteins, putative zinc finger proteins, *myb* proteins and *bZIP/HD-ZIPs* interact with promoters of osmotic regulated genes and involved in stress responses (Hasegawa *et al.*, 2000). At transcriptional and post transcriptional level ABRE binding factors (*ABFs*)/ABA-responsive element binding (*AREBs*) proteins responds to dehydration and salt stress (Uno *et al.*, 2000). Other regulatory factors such as *SOS3*, *SOS2*, Ca²⁺-dependent protein kinases, and mitogen-activated protein kinases are involved in modulating plant salt stress responses (Halfter *et al.*, 2000). The factors such as *SOS3*, *SOS2*, and *SOS1* are components of a signal pathway. *SOS1*, encoding a Na⁺/H⁺ antiporter in plasma membrane. Na⁺/H⁺ antiporter plays a critical role in sodium extrusion and in regulating Na⁺ transport from the root to shoot. Sucrose non-fermenting-like (*SNF*) kinase encoded by *SOS2*. Ca²⁺-binding protein encode by *SOS3* with sequence similar to subunit of calcineurin and neuronal Ca²⁺ sensors (Liu *et al.*, 2000).

In Arabidopsis, *rd29A*, *Cor6.6*, *Cor15a* and *Kin1* are stress inducible genes which contains DRE/C-repeat sequences in their promoters and are target genes of DREBs/CBFs. The gene

encoding glutathione peroxidase (Roxas *et al.*, 1997), Na⁺/H⁺ antiporter *AtNHX1* (Apse *et al.*, 1999), glycine-betaine and *LEA* (Xu *et al.*, 1996), flavoprotein *AtHAL3* (Espinosa-Ruiz *et al.*, 1999), Ca²⁺/calmodulin-dependent protein phosphatase (Pardo *et al.*, 1998) and transcription factor *Alfin1* (Bastola *et al.*, 1998) are the functional components in salt stress response of plants.

g. Genes and Regulatory Factors for High Light Tolerance

Light signals are perceived by four different families of photoreceptors. These are phytochromes (Phy), phototropins, cryptochromes and ultraviolet B (UV-B) photoreceptors. The photomorphogenesis responses of plants to light are highly complex (Kendrick *et al.*, 1994). The ROS can be produced by excess light, affecting the photosynthetic ability of a plant to utilize light energy (Shinozaki and Yamaguchi-Shinozaki, 2000). *Long After Farred Light 1 (LAF1)* transcription factors positively regulate gene expression in response to light. In the dark, *Constitutive Photomorphogenic 1 (COP1)* a ring-finger-type ubiquitin E3 ligase degrades *LAF1*. *COP1* in the darkness by targeting a bZIP transcription factor *Long Hypocotyl5 (HY5)* and *LAF1* to degradation by the 26S proteasome (Ulm *et al.*, 2004).

HY5 transcription factor is the key regulators of cryptochrome and phytochrome controlled photomorphogenesis. In UV-B induced signalling network *HY5* plays a crucial role. Mutants of *HY5* results in the down regulation of UV-B responsive genes. *HY5* also involved

in the expression of several *Arabidopsis* genes such as *CBF1*, *DREB2A*, *RD20* and *MYB59* in response to abiotic stress conditions (Lee *et al.*, 2007).

III.4 Potential Plants as Crop of Future

One of the most important problems of our present day crop plant is that, they became more human dependent, less tolerant, more prone to vagaries of climate change and more importantly having very narrowed diversity. These scenarios have been aggravated by the effects of climate change. Currently, three important crops rice, wheat and maize; accounts for most of our calorie and protein demands and unfortunately these crops are having most of the threats of climate change too. Most of our crop production is revolving around 10-50 crops. During civilization humans did the crop domestication for their potential survival on this planet and domesticated many crops plants. As per the report ~200 plants are commercially produced around the globe (which are completely domesticated) and ~2,500 plants are having potential to be developed as crop (partially domesticated) (Ferne and Yan, 2019).

The potential to be crops includes either minor crops endemic to a particular geographical area i.e. neglected crops (e.g. *Coix lacryma-jobi* - which is endemic to north-eastern states of India, guinea millet – which is endemic to Ethiopia, etc.), semi-domesticated crop (such as crop wild relatives, wild species such as *Amaranthus*, *Quinoa*, etc.) and undomesticated plants (entirely new

species for which domestication has not been reported such as *Microlaena stipoides* – a plant from grass family which can be used as grain) (Shapter *et al.*, 2013). These potential crop plants can be used for improvement of domesticated crops or itself can be used for developing into a new crop which can withstand climatic vagaries. Quinoa was cultivated in the ancient era and it is having potential to be developed as an important grain crop because of its several proven health benefit. It has been recommended for cultivation in the areas affected by climate change (Jaikishun *et al.*, 2019). A list of some plants having potential to be developed as a commercially important cereal crop in future to tackle the effects of climate change is given in Table 3.

IV. Methods of Genetic Enhancement

In general, plant breeding includes the method to improve the desired traits through selecting the desired genetic combinations. The genetic advancement of crop plants dates back from indeliberate selection of plants for cultivation by ancient farmers to the modern genomic assisted plant breeding. Therefore, the methods of genetic enhancement which can be used for tackling the climate change and developing varieties or strains of plants suitable for cultivation are explained here.

IV.1 Classical Plant Breeding Techniques

Screening and selection of the desired superior traits among several plants and combining these traits by different breeding methods into

Table 3: List of Some Plants having Potential to be Developed as a Commercially Important Cereal Crop in Future to Tackle the Effects of Climate Change

S. No.	Plant	Scientific Name	Potential Traits
1	Amaranthus	<i>Amaranthus caudatus</i>	Hardy plants, having resistance to salinity, pH change, drought etc.
2	Quinoa	<i>Chenopodium quinoa</i>	Tolerance to abiotic stresses, Highly nutritious
3	Adlay millet	<i>Coix lacryma-jobi</i>	Can be grown at higher altitude where rice and maize cannot be grown
4	Teff	<i>Eragostris teff</i>	Hardy crop, can be planted late with less rainfall
5	Fonio millet	<i>Digitaria exilis</i>	Can be grown at sea level to higher altitude, having in-depth rooting for drought tolerance
6	Buckwheat	<i>Fragopyron esculentum</i>	Gluten free, short-duration crop, can be grown in acidic soil
7	Guinea millet	<i>Brachiaria deflexa</i>	Can grow in infertile and acidic soil
8	Weeping rice grass	<i>Microlaena stipoides</i>	Rice like grain properties, so can be used in place of rice

single plant is practised under conventional plant breeding. It is the procedure of combination of different desired characters or genes at genome level. Plant breeding includes several breeding methods by which desired plant character can be combined and manipulated. It includes pure line selection in which selection is applied in genetically heterogeneous population which show desired traits and after repeated selection a pure line will develop which is genetically homozygous and homogenous and variation occurs only due to environmental. When desired traits are not found in populations then

different plant lines having desired traits can be augmented into a single genetic background through hybridization and for creating genetic variation hybridization has been extensively used as dominant method. However, when desired genes/alleles are not available in the cultivated germplasm and present in the wild relatives distant hybridization as well as somatic hybridization is practised for transferring the traits into cultivated varieties. Enhancement of vigour, viability and other desired characters by the hybridization of dissimilar inbred lines is called as heterosis. Increased number of chromosome sets per cell (both auto-

and allopolyploidy) can be artificially induced or by applying the chemical colchicine which contributes to crop improvement. Generally, the main effect of polyploidy is increase in size and genetic variability. Sudden heritable changes *i.e.* mutagenesis and by generation of variation through tissue culture *i.e.* somaclonal variation also play a crucial role in creating genetic variation and these variations are utilized in selection of desired genotypes with superior characteristics and selected genotypes are evaluated in replicated trials, preferably, over locations and years to ascertain their superiority over the existing varieties. A new superior genotype is finally multiplied and distributed for commercial cultivation.

IV.2 Precision Phenotyping for Trait Discovery

Precision phenotyping is generation of precise information to reduce the experimental “noise” introduced by uncontrolled environmental and experimental variability that are relevant and meaningful and required for improving the selection efficiency of the breeding programs for accelerating genetic gains under the conditions prevailing in farmers' fields. Various alternatives are accessible to use the data gathered through phenotypic assessment of germplasm resources (Tuberosa *et al.*, 2011). Identifying parental lines through intensive phenotypic characterization for traits imparting drought resistance allows developing new populations where segregants that combine drought-adaptive and other desirable features of parental

lines can be selected (Reynolds *et al.*, 2005). This type of breeding methodology has been successfully deployed at CIMMYT resulting several newly released improved wheat varieties across different countries. Advanced-backcross QTL analysis (ABQA) and introgression libraries (ILs) allow for proper and effective dissection of the phenotypic variability contributed by non-commercially viable parental lines (Salvi *et al.*, 2011).

Precision phenotyping is critical for diminishing the genotype phenotype gap particularly for quantitative traits but establishment of association between a marker and a locus affecting a target trait. The use of markers linked to QTLs for the target trait helps to overcome the low heritability that is the main problems encountered in the conventional selection of quantitative traits. Selection of individuals based on their genetic makeup scores rather than their phenotypic features (Langridge, 2005). The effectiveness of marker assisted selection breeding approaches depends on how precisely the target traits have been surveyed phenotypically in mapping populations. In fact, a low heritability impairs the efficiency of detecting the presence of QTLs (Bernardo, 2004), thereby increasing Type II errors (*i.e.*, false negatives). A precise and significant phenotyping will help in selection, an approach that disregards QTLs identification and relies on the molecular profiling and accurate phenotyping of (Bernardo and Yu, 2007). Proper evaluation and control of the experimental factors that lower the heritability of traits, coupled with a wise choice of the

genetic material, can provide effective ways to increase heritability, and hence the response to phenotypic selection.

a. High-Throughput Phenomics

High-throughput phenotyping institutionalizes and improve the collection of phenotypic information and encourages the creation of archive databases useful for QTL meta-analyses (Welcker *et al.*, 2011). The best model is the SNP discovery and profiling in a number of crops (Tebbi *et al.*, 2011). High throughput phenotyping take into consideration the mechanization of methods that have just been received by various privately owned businesses and large public institutions to streamline and standardize the collection of highly accurate phenotypic data in glasshouse-grown plants (Rajendran *et al.*, 2009). However, the installation and operating cost of these platforms is still very high.

b. Digital Imaging

Digital image analysis gives an inexpensive and quick method for accurately estimating plant features whose estimation would some way or other require a lot of time. An eminent model is given by the estimation of canopy features (Fiorani *et al.*, 2012). Digital images offer advantages over other methods of light interception estimation, including the possibility of directly processing images by computer. Digital image analysis (Armengaud, 2009) takes into consideration precise analysis at higher goals scales, a significant essential to research the energy of the procedures managing root development.

IV.3 Molecular Dissection of Tolerance Traits

Recently, new molecular tools like genetic molecular maps and markers have made it possible to resolve complex traits into individual genetic components. Molecular dissection of complex traits is often referred as QTL mapping (quantitative trait locus) or QTL analysis. QTL analysis provides information about QTLs, such as the numbers of loci involved, their locations and gene effects. For QTL analysis a mapping population like RILs (Recombinant inbred lines), NILs (Near isogenic lines), CSSL (Chromosome segment substitution lines) and immortalized F₂ are developed and followed to genotyping and phenotyping to map QTLs by using single QTL mapping and multiple QTL mapping methods (Table 4). The identified QTLs are effectively used in marker-assisted selection (MAS) for further breeding programs. Molecular dissections of several complex traits have been performed using genomics and high-throughput phenotyping tools.

IV.4 Marker Assisted Breeding Approaches

Molecular markers are very efficient and powerful tool in crop improvement programmes to incorporate agronomically desired traits via marker-assisted selection (MAS). In maker-assisted breeding, selection is based on the marker tightly linked to the trait of interest so it improves the breeding efficiency many-folds and accelerates development of new varieties. By detecting any association between phenotype and genotype/markers for

Table 4: Molecular Dissection of Various Traits in Different Crops

Crop	QTLs / Candidate Genes	Chromosome	Trait	Reference
Rice	<i>qHD-6-1</i> and <i>qHD-6-2</i>	6	Heading date	Zhang <i>et al.</i> , 2018
Rice	<i>qSES2</i> , <i>qSES4</i> and <i>qChlo4</i>	2 & 4	Salt tolerance & chlorophyll content	Pang <i>et al.</i> , 2017
Rice	<i>qDT3.9</i> , <i>qDT6.3</i> & <i>qGY1</i> and <i>qSF8</i>	3, 6, 1 & 8	Drought & low nitrogen tolerance	Feng <i>et al.</i> , 2018
Rice	<i>OsDRAP1</i>	8	Drought tolerance	Huang <i>et al.</i> , 2018
Chickpea	QTL-hotspot	4	Drought related traits	Varshney <i>et al.</i> , 2014
Soybean	<i>ss245775380</i>	5	Number of days to flowering	Liu <i>et al.</i> , 2016
Wheat	<i>QGw.ccsu-1A.3</i> , <i>QGw.ccsu-5A.1</i> , <i>QGw.ccsu-6A.2</i>	1A, 5A, 6A	Grain weight	Mir <i>et al.</i> , 2012
Maize	<i>qRKP3-2</i> and <i>qKWPE9</i>	3 & 10	Mid parent heterosis	Yi <i>et al.</i> , 2019
Maize	<i>ph6-1</i> , <i>rl1-2</i> , <i>sdw4-1</i> , <i>sdw7-1</i> , <i>tdw4-1</i> and <i>tdw7-1</i>	1, 4, 6, 7 & 9	Waterlogging related traits	Osman <i>et al.</i> , 2013
Barley	<i>qRSD3</i> , <i>qTSRL3</i> & <i>qRSA6</i>	2 & 3	Root architectural traits	Jia <i>et al.</i> , 2019

any trait, QTLs are identified (Collard *et al.*, 2005). Molecular breeding includes approaches like marker assisted backcross breeding (MABB), marker-assisted recurrent selection (MARS) and genomic selection (GS). In MABB, a trait of interest is incorporated into a recurrent parent (RP) which is a superior variety except deficient in that particular trait, from a donor parent (DP) with maximum recovery of the recurrent parent genome. Molecular markers have been used for foreground selection to introgress the gene of interest (Tanksley, 1983), for background selection to recover the recurrent parent genome and for recombinant

selection to minimize the linkage drag of donor parent (Young and Tanksley, 1989).

MARS is a breeding tool that is used to accumulate favourable alleles for a particular trait into a single genetic background from several genomic regions within a single population. In MARS, markers identified for quantitative traits are used either alone or as combined selection index that includes phenotype data for the trait (Lande and Thompson, 1990). A selection index is generally defined as a numerical score obtained by integrating information from all the traits associated with the dependent trait/variable (for example, yield) and

for each trait a value is assigned based on weighted mean as per their importance. MAS is suitable for traits that are controlled by a few major genes but most of the crop traits are complex and governed by large number of genes (minor genes) thus the application of MAS in breeding practice is limited. Considering this limitation of MAS, Genomic selection (GS) is the new methodology with some modification in MAS (Meuwissen *et al.*, 2001). In GS, genome-wide markers are used to estimate the effects of all loci and compute a genomic estimated breeding value (GEBV), to achieve more reliable selection for quantitative traits.

IV.5 Genomics Tools for Genetic Enhancement

Genome-wide studies help breeders to understand the mechanism of complex traits. Earlier, genomic approaches like TILLING (targeted induced local lesions in genomes) and EcoTILLING (Ecotype TILLING), allows identification of mutant and germplasm collections for allelic variants in specific genes (McCallum *et al.*, 2000; Comai *et al.*, 2004). Nowadays, with the availability of advanced genomic tools, it is very efficient and effective to study the genotype of various traits and their interaction with phenotype. Initially, under first-generation DNA sequencing procedures, two methods were developed *i.e.* chemical and enzymatic methods and uses in vivo cloning. Being highly demanding in infrastructure, time and processing efforts (Edwards, 2013) these were soon replaced by the second-generation DNA sequencing methods

popularly known as Next Generation Sequencing (NGS) methods, which uses PCR (Polymerase chain reaction) for in-vitro cloning and are much cheaper and faster (Schendure and Ji, 2008; Edwards, 2013). Now with the advancement of technology, the Third-Generation DNA sequencing (TGS) methods are gaining popularity at commercial level. Under TGS methods there is no need of cloning and sequences a single DNA molecule at a time at broader scale (Schadt *et al.*, 2010; Giani *et al.*, 2019). Among all these methods, Next Generation Sequencing (NGS) technologies are extensively used for sequencing of genomes and transcriptomes, thus producing vast genomic data.

Analysing of NGS data by using different bioinformatics tools permits identification of various new genes and regulatory sequences. With the help of identified sequences and their positions, one can develop large collections of molecular markers that can be further utilized to improve a specific trait to offset any climate condition. For genome-wide discovery of markers like SSRs (Simple sequence repeats) and SNPs (Single nucleotide polymorphisms) or the construction of high density genetic maps, re-sequencing of genomes is very useful and amenable utilizing the genomics tools. The techniques like bulked segregant analysis (BSA) or association mapping, allows the identification of markers linked to genes and QTLs. The identified new markers can be used for marker assisted selection (MAS), marker assisted backcross selection (MABB), 'breeding by design' and genomic selection. Apart from these the physiology of stress such as drought,

high temperature, salinity, waterlogging, etc. can be dissected at molecular level using genomics tools. Currently, with the advances in genomics, new tools and methodologies are developing that allows plant breeders for genetic dissection and breeding of complex traits.

IV.6 Accelerated Crop Domestication

Crop domestication in general is a slow, continuous, difficult and environmentally dependent process. It depends on the variability present in the wild ancestor and crop wild relatives. Current crop plants are lacking diversity and have become more resistant to change. Our demands in terms of crop usage has diversified. We use now crops not only for food, feed, clothing and fodder but also for several industrial usages such as bioethanol production, biopharming, starch production, antibiotics, drugs and medicines, phytoremediation, etc. These diversified industrial revolutions have also brought some climate change effects in front of us. To tackle these, our crop usage has to be diversified and new plants must be picked as crops for future (Palmgren *et al.*, 2015).

Accelerated crop domestication is a recent method of either changing a semi-domesticated crop into a completely usable form or entirely changing a potentially usable plants into a crop of future. It is a process of using the diversity of plants for crops of future which had not been ever used before. The aim of accelerated crop domestication may also be 1) to make a new crop which are climate

resilient, 2) to improve a present day crop for the effects of climate change, 3) to gain back the QTLs or gene which were present before domestication and which may be useful in present scenario, 4) to diversify the food habits and to generate a crop with potential source of industrial demands such as biofuel.

Accelerated crop domestication methods may be partial domestication (by transfer or introgression of either of a wild gene/QTLs which have not been used before) or complete domestication of a plant (inducing the domestication syndrome by targeted mutagenesis of important homologous domestication genes identified in the related crop species) (Osterberg *et al.*, 2017). Partial domestication can be done by the methods of polyploidy, mutagenesis, introgressive hybridization, etc. The complete domestication of a plant into crop can be done by methods like site-specific mutagenesis, genome-editing tools, cis- and transgenic approaches and RNA interference (Henry, 2012). A recent example is targeting the homologues of *granule bound starch synthase 1 (GBSS1)*, encoded by the *Waxy* gene, the *Isa* gene and two gene homologues controlling seed shattering in rice, *sh4/SHA1* and *qSH1* identified in *Microlaena stipoides* (Shapter *et al.*, 2013).

V. Achievements

The effects of climate change have been tackled by the breeder in several innovative ways. As mentioned earlier, breeding of crop varieties resistant to drought, salinity, high temperature, erratic rainfall

Table 5: List of Crop Varieties Improved for Traits Affected by Climate Change

Situation	Crop	Name of Variety(ies)
Drought	Rice	Kalinga, Sahbhagi Dhan, Pradhan, Purnima, Naveen, Prabhat, ANNA4, Sabour Shree, DRR Dhan 43, DRR Dhan 50, ADT 51, CR Dhan 101, Ratnagiri-8, Jaldi Dhan-13, PNR-546
	Wheat	HD2888, C306, Sujata, HPW236, PBW644, UP2572, HI8627, Netravati, Ratan, K307, DBW17, Sabour Nirjal, Malviya 669, Pusa Bahar (HD-2987), Harshita (HI-1531), Pusa Aditya (HD-2781)
	Maize	Suvan, HQPM5, Vivek21, PMH2, Mahi Dhawal, HM4, Mukta, Suwan-1, Drona
	Pearl Millet	RHB177, HHB67, RBH173, NBH5061, PB1705, BHB1202
	Barley	PL419, K603, RD2660, RD2592, JB58
	Sorghum	Parbhani Moti, CSH5, Pant Chari 7, Phule Chitra, Phule Vasudha, Phule Anuradha, Phule Rohini, Phule Madhur
	Sugarcane	Co86032, Co 98014, CO0212, Amritha, CoVC 99463, Uphar
	Black gram	BDU1, PU31, Pant Urd 35, IPU2-43
	Chickpea	JG14, JG16, RVG203, Pratap Chana 1, Akash, Pusa 256, Pusa Chamatkar (BG-1053), Pusa 1088, Pusa 1105, Pusa 2024
	Green gram	Pusa Vishal, Pratap, RMG268, IPM205-7
	Lentil	JL3, Vamban, RVL31
	Pegion pea	Asha, UPAS 120, C11, Paras, ICPL 151, Narendra Arhar-1, JKM 189, ICPL 88039, BRG 4, Ujwala, Amrawathi, Pusa 991
	Brown Sarson	Pant Rai 20, Pusa Bold, Aravall, RGN 48, Pusa Tarak, Rohini, RH 406, RH 725
	Rai	RCC 4
	Groundnut	GG2, GG5, Gresham, Abhay, Narayani, Dharani, CO 6
	Soybean	PS 1225, MAU 71, Ahilya, JS 335, Harit Soya
Cotton	Phule Anmol, SVPR 4, Nirmal 433,	
Short Duration	Rice	PB1121, PR-124, NDR 97, Sahbhagi, Abhishek, Naveen, Anjali, Suskasamrat, Prabhat, Komal, Chandan, HUR 3020, IR64 Drt1, DRR Dhan 44, PAC 129, Daksha,
	Wheat	HD 3086, Shusk Samrat, PBW 677, HD 2967, WR 544, DBW 17, PBW 373, HI8663
	Pearl Millet	NBH 5061, PBH 306, PB 1705,
	Sorghum	CSV 32F, Phule Rohini, Phule Madhur
	Maize	HQPM1, SCMH 411, Kanchan, Shourya, Candy
	Chickpea	JG11, KWR108, RSG 963, Jaki 9218
	Indian Mustard	Laxmi Gold, Pusa Mahak, Rohini, NRCPB101, Pusa Mustard 25, Pusa Mustard 27
	Soybean	JS 335, JS 9305

Delayed Monsoon	Rice	Sushak Samrat, Vanaprabha, Govind, Swarna mahsuri, Ranjit, PR 113, IR 64, Nandyala Sona
	Wheat	DBW14
	Chickpea	Vijay
Heat Stress	Rice	DRR Dhan 47, DRR Dhan 52
	Wheat	Lok 1, Vidisha, PBW658, WH1124, DBW 107, HI1612, Kaushambi (HW 2045), Pusa Gold (WR-544), Pusa Basant (HD-2985), Pusa Wheat-111 (HD-2932), Harshita (HI-1531)
	Chickpea	JG14, Pusa 547
	Pigeon Pea	Bohar, UPAS120, Rajeev, Lochan
	Rapeseed/ Mustard	Urvashi, Pusa Mustard 28, Pant Rai 20,
	Cauliflower	Sabour Agrim,
	Mungbean	Pusa 9531
Cold Stress	Pearl Millet	GHB 538
	Rice	Bhrigudhan, Varun Dhan, Palam Basmati-1, Pant Dhan-11, NE Megha Rice 2
	Wheat	Buland, RSP 561, Shalimar Wheat-1
	Chickpea	PDG4
	Mungbean	Pusa 0672
Salinity	Rice	Basmati CSR 36, Panvel 3, Jarva, Luna Sampad, Luna Suvarna, Luna Sankhi, CSR 60, CSR 56, Ratnagiri 8, RD 2794
	Pigeonpea	Pusa 991
	Indian mustard	Pusa Vijay (NPI-93), CS 56, CS 58, CS 60,
	Sugarcane	Uphar, Phule 10001, Amritha, CO0212,
Water logging/ Submergence	Maize	AH-421 (PEHM-5), Pragati, Jawahar Maize 218
	Wheat	UP2338, UP2565, UP2526, UP2425
	Rice	Swarna Sub1, MTU 1010, CR Dhan 500, Jalamani, Jayantidhan, Tripura Jala, Samba Sub1, Bheema, CO43 Sub1, CR Dhan 408, DRR Dhan 50, Ranjit Sub1, Bahadur Sub1, Ashutosh, Ksheera
	Chickpea	Pusa 240
Hot and humid conditions	Cotton	PSS-2 (Arvinda)

Table 6: Examples of Crop Varieties Improved for Traits Affected by Climate Change.

S.No.	Crop	Climatic Factors	Trait	Method	Variety	Reference
1.	Rice	Drought	Root traits	MAS	Improved Kalinga III	Stele <i>et al.</i> (2006)
2.	Rice	Drought	Several traits	QTL introgression	Sahbhagi Dhan,	IRRI, Philippines (2020)
3.	Rice	Submergence	Submergence tolerance	MAS	Swarna Sub1	IRRI, Philippines (2020)
4.	Rice	Cold	Cold tolerance	QTL identification	Jimbrug, Shen-Nung89-366	IRRI, Philippines (2020)
5.	Rice	Drought	Drought tolerance	Conventional	DRR-Dhan 45	ICAR-IIRR, Hyderabad (2020)
6.	Wheat	Stresses	Chlorophyll content, stress susceptibility index, Stress intensity	Conventional	NI-5439, Raj-3765, WH-147 and HD-2733	Meena <i>et al.</i> (2015)
7.	Wheat	High temperature	Early maturing, terminal heat tolerance	Conventional	HW 2045, WR544,	IARI, New Delhi (2020)
8.	Pearl millet	Drought	Drought tolerance	Conventional	Pusa composite 443	IARI, New Delhi (2020)
9.	Maize	Temperature	High temperature	Conventional	AH-58	IARI, New Delhi (2020)
10.	Chickpea	Drought	Drought tolerance	Conventional	Pusa 1088, Pusa 1105	IARI, New Delhi (2020)
11.	Chilly	Drought	Drought tolerance	Conventional	Kashi Anmol	Maheswari <i>et al.</i> (2019)

pattern, flooding etc. has been done to tackle the effect of climate change. Advancement in precision phenotyping to accurately, effectively and efficiently measure the plant phenotype with less cost and labor by reducing the errors, utilizing advanced tools and neutralizing environmental factors has tremendously helped in the trait

dissection and mapping of underlying gene(s) (Cobb *et al.*, 2013).

Genotyping by the next-generation sequencing tools has helped the plant breeders to effectively transfer the desired QTL(s) for developing the climate resilient varieties. Trait mapping using precision phenotyping, genotyping and power to handle big data using advanced computational tools has been a boon

for plant scientist nowadays in rapid advancement of genetic gain (Araus *et al.*, 2018; Chawade *et al.*, 2019). Some achievement of breeding crop plants for offsetting the effects climate change are given in the Table 5 and 6.

VI. Conclusion and Future Prospects

Studies on climate change and creating ways to tackle it are the prime concern of today's world. Many studies have been carried out to critically measure the impact of climate change on several aspect of crop production, livelihood of small and marginal farmers, availability of resources and impact on the human life. Crop production in a broader aspect has been challenged by the effects of climate change such as drought, waterlogging, salinity, cold, unpredictable rain etc. With these problems in mind and challenges, the role of plant breeders is becoming more important day by day.

Studying the genetics of traits affected by climate changes and searching for new genes and mechanism to develop climate resilient crops are the prime concern of plant breeders nowadays. Studies on the molecular mechanism of drought tolerance, salinity tolerance, waterlogging, high temperature tolerance and increased CO₂ level have enhanced our knowledge on how to tackle the effects of climate change. Genomic assisted plant breeding (such as Marker Assisted Selection, Genomic Selection, Genome-editing, Transgenics, etc.) has created revolution in the way crop improvement is done nowadays

and in the process of creating crops which are bred-by-design (Raza *et al.*, 2019). Plant breeding for climate change is committed to develop crop plant which will be completely modelled by the breeders. The future of plant breeding for offsetting the effect of climate change can be consolidated in following points (www.cgiar.org).

1. Identification of challenge: To understand the effects of climate change and dug out the factors affecting the crop plants.
2. Identification of key important traits: Understanding the key traits in crop plant which contribute for the climate resilience such as root length, root hair density etc. for drought tolerance.
3. Identification of germplasm: Screening of germplasm for the identified traits. Searching for new genes and genotypes.
4. Popularising the underutilized crops which are climate resilient
5. Use of genomic assisted plant breeding to make crop breeding efficient, effective and accurate.
6. Utilization of phenomics tools, big data approach, Machine learning, Artificial Intelligence and Internet of Things (IoT) are the future of plant breeding and they will find appropriate uses in developing climate-smart varieties.

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