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CLIMATE-SMART AGRICULTURE: A WAY TO ENSURE FOOD SECURITY

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Abstract

Climate-smart agriculture is currently gaining attention at the global level for sustainable food production and ensuring food security in a changing climate. Climate change is a major threat to agricultural systems by reducing agricultural productivity and affecting food security. Climate-smart agriculture is a practice that has proved helpful in mitigation and adaptation to changing climate, enhancement of agricultural productivity, incorporation of resilience, and reduction of greenhouse gas emissions. In this review, we have highlighted the role of different practices i.e. Plant Breeding (Crop Wild Relatives, Shuttle breeding, Genomics Selection, Genome-Wide Association Studies, Genome Editing, and Double Haploid Breeding), biotechnological approaches (Genome editing and Genetic engineering) and sensor-based precision agriculture technologies for real data about soil and crops which are helpful in changing climate scenarios. Agroforestry, crop rotation, crop diversification, laser leveling, and other advanced agronomic approaches for enhancing soil organic matter, and water holding and retention capacity of soil may lower the cost and increase food and agricultural productivity, eventually increasing farmer's income. Governments and scientists should create awareness among people about climate change and its impacts and should also devise ways to mitigate them, keeping in view the above-mentioned techniques. Adoption of climate-smart practices by the farmer community will help in reducing the negative impacts of climate change on agriculture to achieve sustainable food production.

Key words: Climate-smart, Plant breeding, Biotechnological approaches, Mitigation, Adaptation.

Introduction

It is now globally accepted by the scientific community that climate change is one of the most devastating issues of the 21st century, which is significantly hampering agricultural output efficiency by interfering with crop physiology, morphology, and biochemical constitution (Beacham *et al.,* 2018). The agricultural sector is the most vulnerable as well as a chief contributor to climate change (Lipper & Zilberman, 2018). Agricultural production has recessed by 1-5% due to biotic and abiotic stresses for the last three decades (Newbery *et al.,* 2016). Global warming is affecting cropping patterns across the globe, making crops more susceptible to abiotic stresses due to extreme weather conditions (Taranto *et al.*, 2018). Greenhouse gas (GHGs) emissions are estimated to raise the atmospheric temperature by 0.3-4.5oC, prevailing drought stress and affecting crop yield (Alam *et al.*, 2017).

Moreover, abrupt changes in weather patterns affect soil fertility, microbial activity, plant growth, and the food chain, which is quite alarming for global food security. Climate-smart agriculture (CSA) is considered a valuable strategy to deal with the challenges of changing climate, ensuring food security by increasing agricultural productivity, strengthening resilience, and reduction of GHGs emissions. Adaptation of crop plants to changing climate and mitigation of negative impacts of climate on crops and ensuring food security are considered "pillars" of CSA. CSA practices and technologies revolve around three major components: a sustainable increase in agricultural production; farmers' adoption of a changing climate; and decreasing levels of GHGs emissions (Jat *et al.*, 2020).

The purpose of this review is to elaborate the factors contributing to climate change, its positional impact on the agriculture sector, and different strategies (Fig. 1) to reduce negative impacts of changing climate on agriculture.

History of CSA: CSA refers to technologies, and agricultural and agronomic practices addressing climate challenges and food security by developing climate-resilient crops and reduction in greenhouse gas (GHGs) emissions (Lipper & Zilberman, 2018). This technique helps farmers to adapt to climatic factors mainly high temperature and low precipitation (Kumari *et al.,* 2019).

The concept and methods of climate-smart agriculture were first launched by Food and Agriculture Organization (Anon.,) in 2010 at 1st global conference on food security at Hague (Anon., 2014). The objectives of the conference were the removal or reduction of GHGs, ensuring food security (Torquebiau *et al.,* 2018), and surging yield potential of crops in the agriculture sector (Kalimba & Culas, 2020). Second and third global conferences were held in the next couple of years 2012 and 2013 which were aimed at climate-smart agriculture sourcebooks. The action plans of CSA were given in 2014 at Climate Summit, New York (Gosh, 2019).

Climate-smart approaches

Plant breeding approaches: Plant breeding has always been the right hand to cope with the changing climate, as new cultivars having resistance to stresses like drought, temperature, salinity; waterlogging, pests and diseases have been developed in several crops. To ensure food safety under harsh climatic conditions, several techniques in plant breeding i.e. crop wild relative, shuttle breeding, genomic assisted breeding, Genome-wide association studies and double haploid technology may be used to speed the variety evolution process and development of climate resilient crop varieties that will better perform under biotic and abiotic stress conditions (Blum, 2018).

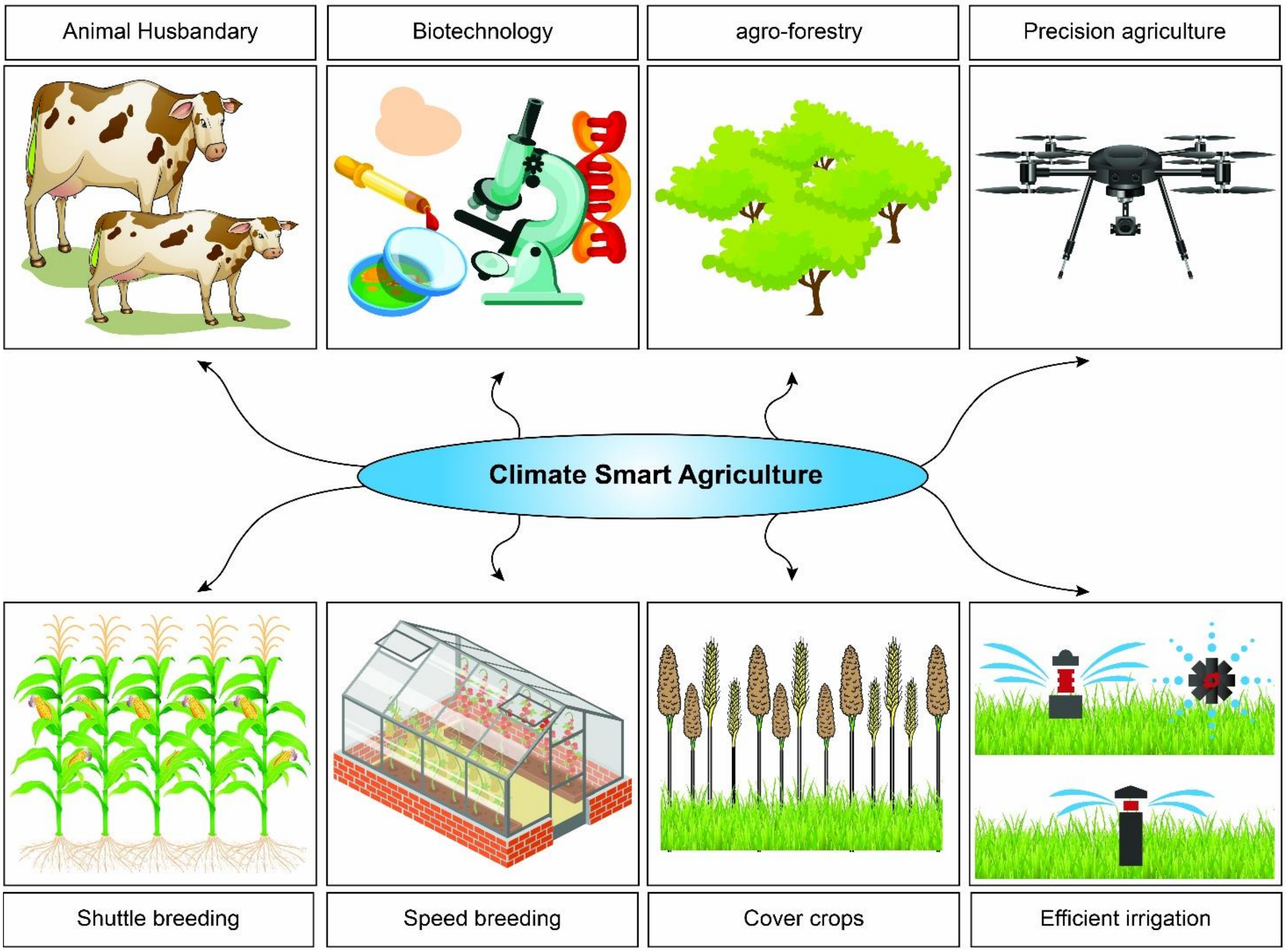

Fig. 1. Different climate-resilient strategies for Climate-Smart Agriculture.

Crop wild relatives: Crop wild relatives (CWRs) are considered sources of different biotic and abiotic stress resistance as they have evolved with time and are selected through natural selection. Nature favors CWRs in the accumulation of favorable genes through outcrossing and survival of the fittest organisms; hence, these are excellent source of genes imparting biotic and abiotic stress resistance (Prohens *et al.*, 2017). A few examples of using the CWRs in crop improvement are discussed below. *Oryza glaberrima* having the potential to tolerate drought stress was used to introgress a character in *Oryza sativa* by the interspecific backcross method. A hybrid origin species, *Helianthus anomalus* with drought resistance was used in sunflower breeding (Ndjiondjop *et al.*, 2010). In the wheat crop, *Triticum* spp., was used to introduce resistance against heat and drought stresses in durum wheat by ICARDA. Drought stress tolerance was improved in maize, potato, rice, sugarcane, wheat, cassava, lentil (Gorim & Vandenberg, 2017), and chickpea (Maphosa *et al.*, 2020) by crossing cultivars with wild relatives against biotic and abiotic stresses. In chickpea and pigeonpea, adaptability to changing climate was enhanced in cultivars by exploiting landraces in India under a project of ICAR-ICARDA (Choudhary *et al.*, 2018).

Shuttle breeding: In shuttle breeding, one growing season of a crop is completed at one station, and after harvesting, the second cycle is completed in another location within the country that has optimum climatic conditions for crop growth. In this way, a breeder can get multiple generations of a crop in one year, reducing the period required for variety development. Many international organizations i.e., ICARDA practices shuttle breeding techniques involving the winter-summer period around the globe, which helped in identifying high-yielding adoptive genotypes. For wheat crop, Terbol station in Lebanon is used for the summer season and Egypt for the winter season. Norman E. Borlaug at the International Maize and Wheat Improvement Center (CIMMYT) used Toluca station for summer season and Mexico and Obregon stations for winter season for the first time. These are now being used for maize, wheat, and rice improvement by CIMMYT and IRRI (International Rice Research Institute) (Gosal & Wani, 2020).

Genomic assisted breeding: Genome selection (GS) is an innovative tool in plant breeding to speed up crop improvement and high-throughput phenotyping to identify climate-resilient genotypes for future breeding (Tadesse *et al.*, 2019). Genome Selection reduces the time and cost of selection of genotypes for varietal development (Gosal & Wani, 2020). GS is helpful for increasing genetic gain in terms of time, and speed of a breeding program. About 0.27-0.66 prediction accuracy was reported in durum wheat genotypes for grain and semolina traits by GS. Similarly, 0.138 and 0.912 prediction accuracy was reported for yield and 100 seed wt. respectively in chickpea (Muleta *et al.*, 2019). The role of genomic-assisted breeding in combating climate change and ensuring food security has soared in recent decades. The introduction of novel genes into targeted crops has been done using different breeding approaches (Table 1). First step towards development of climate resilience is, understanding the nature of stress and its repercussions. During the past decade, extensive research on QTLs has been conducted to dissect abiotic stress related plant's adaptive mechanisms using the latest genomic approaches.

For survival during prolonged submergence in rice *Sub1* QTL accounts for a major share of variability. Following the discovery of *Sub1A* QTL, three generations of backcrosses changed submergence sensitive cultivars to resistant cultivars using marker-aided backcrossing (MABC). Thus, DNA markers were also developed for further introgression in six popular cultivars. This is a good illustration of the efficiency of MAS for the introgression of agronomically valuable QTL alleles into selected material. In maize QTL for the formation of adventitious root at the soil surface, an imperative adaptation to soil waterlogging was discovered. Now numerous QTLs for this trait have been mapped. Salinity is also a consequence of climate change globally, which affects more than 20% of the world's arable land and thus affects farming. In durum wheat (genome AABB), two major QTLs related to Na+ accumulation in shoots via Na+ exclusion have been explored. Introgressions from a *Triticum monococcum* (genome AA) accession were found in both exclusion genes. Moreover, under standard conditions, the phenotypic similarity of durum wheat having salinity tolerant allele at *TmHKT; 5-A*, which is one of two salt-tolerance loci, to durum wheat that lacked favorable allele at this locus has been observed. However, under saline conditions, its performance was outstanding when compared with its durum wheat parent, which increased yields by up to 25% (Luo *et al.*, 2021).

Several intra- and inter-specific genetic maps, as well as genomic regions responsible for diverse biotic, abiotic stress tolerance and improved agronomic characters have been generated in chickpea (Bajaj *et al.*, 2016). Strategies based on genomics and NGS have accompanied sequence-based breeding schemes that may accelerate the separation and cloning of the loci governing abiotic stress tolerance, providing supreme opportunities to get into crop wild relatives, thereby escalating the genetic diversity pool for breeders (Younis *et al.*, 2020).

Genome-wide association Studies (GWAS): GWAS is an alternate technique to QTL mapping that is based on the principle of linkage disequilibrium (LD) for the detection of an association between a target trait and a DNA marker (Gómez *et al.*, 2011). GWAS requires the extensive phenotyping and genotyping of a population representing contrasting traits in a set of association mapping panels of genotypes across variable environments. GWAS has immense power to narrow down the phenotypic variation in a trait to a genetic region, followed by the identification of candidate genes involved in the expression of a particular trait in a given environment (Gupta *et al.*, 2019). GWAS is better than QTL mapping for the identification of genes associated with a trait of interest because it provides better mapping resolution owing to historical recombination and mutations in genetic lineages, which provide a strong base for identification of markers in close vicinity of genes controlling a particular trait (Challa & Neelapu, 2018).

Single nucleotide polymorphism (SNP) genotyping arrays and genotyping by sequencing (GBS) are widely used for GWAS analysis in field crops (Arruda *et al.*, 2016). GWAS helps to identify marker trait associations using the large nucleotide variability in association mapping populations. The presence of a large number of SNPs in the mapping population is a pre-requisite for high-resolution marker trait association, which is tightly linked with the LD decay over physical distance in a population. Whereas LD decay is affected by genetic drift, recombination frequencies, selection pressure, and genetic recombination (Ruanjaichon *et al.*, 2021).

Table 1. Crop improvements against biotic and abiotic stresses using plant breeding tools.

Crop	Stress type	Method of improvement	Reference
Tomato	Tomato mosaic virus	Introgression backcrossing	(Diez & Nuez, 2008)
Wheat	Rust	Alien gene introgression	(Belhaj *et al*., 2013)
Potato	Late blight	Gene introduction from CWR	(Jo *et al*., 2014)
Rice	Bacterial leaf blight	Marker-assisted selection	(Variar and Singh, 2018)
Rice	Sheath blight	Marker-assisted selection	(Variar and Singh, 2018)
Rice	Rice blast	Marker-assisted selection	(Singh *et al*., 2013)
Chickpea	Chickpea rust	Introgression backcrossing	(Madrid *et al*., 2008)
Pinto bean	Common bacterial blight	Introgression backcrossing	(Mutlu *et al*., 2005)
Barley	Powdery mildew	Composite cross breeding	(Maroof *et al*., 1983)
Pearl millet	Rust	Backcross breeding	(Wilson *et al*., 2001)
Turnip	Turnip crinkle virus	Mutation breeding	(Lawton *et al*., 1996)
Wheat	Salt stress	Wide cross	(Zhang *et al*., 2002)
	Drought stress	Doubled haploid	(Chauhan & Khurana, 2011)
Chickpea	Drought stress	Introgression backcrossing	(Maphosa *et al*., 2020)
Sugarcane	Drought stress	Introgression backcrossing	(Gorim & Vandenberg, 2017)
Sunflower	Drought stress	Introgression backcrossing	(Ndjiondjop *et al*., 2010)

GWAS studies have been conducted in different crops and candidate genes have been mapped for several biotic and abiotic stress tolerance in different crops. GWAS was conducted in wheat for combined drought and heat stress tolerance at the maturity stage using six traits i.e., grain yield, days to heading, number of tillers per plant, plant height, spike length, and hundred grain weight using 15, 737 SNPs. A total of 205 marker trait associations were observed under stress and non-stressed conditions (Abou-Elwafa & Shehzad, 2021).

Similarly, GWAS was conducted in maize under salt stress conditions for the identification of candidate genes for salt tolerance. An association mapping panel of 305 maize inbred lines was studied under salt and normal conditions and 46, 408 SNPs were used for genotyping. Two candidate genes corresponding to salt stress i.e. GRMZM2G075104 and GRMZM2G333183 were identified (Ma *et al.,* 2015).

GWAS studies were conducted on rice to identify black-streaked dwarf virus resistance in rice. A set of 44k SNPs was used on rice diversity panel (RD1) genotypes for the identification of resistance genes. Eighty four non-redundant SNPs were found associated with RBSDV. These 84 SNPs were narrowed down to 13 QTLs associated with virus tolerance which later on were narrowed down to two QTLs i.e. qRBSDV-4.2 and qRBSDV-6.3 in rice which corresponds to resistance to RBSDV virus (Feng *et al.,* 2019).

Similarly, GWAS was conducted in sorghum for the identification of genetic regions associated with grain size. The study included 2000 association mapping panel genotypes which were surveyed using 111, 089 SNPs and extensive1 phenotype for grain size under various environments. The study resulted in 81 QTLs associated with grain size in sorghum (Tao *et al.,* 2020). The summary of above mentioned studies has concluded that GWAS has a key role in the identification of genes associated with biotic and abiotic stress tolerance and plays crucial role in the development of climate resilient crops. After identification of QTLs one has to look forward whether any transcriptional factor or gene has already been reported in that region (Shahzad *et al.,* 2021a). After gene identification, their functions may be validated through CRISPR-mediated knocking out of genes (Ahmad *et al.,* 2021). After functional validation of genes involved in stress tolerance, those may be used in different breeding programs through markers assisted breeding (Iqbal *et al.,* 2021a; Iqbal *et al.,* 2021b).

Double haploid: The doubled haploid technique involves haploid induction through wild hybridization in wheat or through inducer line mediated haploid induction in maize followed by doubling of chromosomes using colchicine to achieve 100% homozygosity in one year which was to be achieved in 7-8 years of continuous selfing. It is a quick and easy approach to get homozygous genotypes in only one generation by shortening the wheat cycle by 16-50 percent as compared to conventional breeding. In bread wheat (*Triticum estivum*) double haploids have been developed which showed higher germination and tolerance to water stress in terms of root and shoot lengths and nitrate reductase (Tadesse *et al.,* 2019).

Biotechnological approaches: Biotechnology has played a role in the development of climate-resilient crops through genomics, genetic engineering and genome editing.

Genomics and genetic engineering: Genomics has helped plant breeders in the early selection of desired plants through marker-assisted breeding and has helped in the assessment of genetic diversity among the source populations for designing effective crossing plans (Jamil *et al.,* 2020a; Jamil *et al.,* 2020b; Iqbal *et al.,* 2021b; Kanwal *et al.,* 2021). Genetic analysis of candidate genes that are identified through bioinformatics tools may be used in the identification of stress-tolerant genes (Pereira, 2016).

A project named Water Efficient Maize for Africa (WEMA) has developed genetically modified (GM) *BT-based* maize hybrids having resistance against drought stress and insect pests. Similarly, the genetically modified cotton crop has been developed and cultivated on large scale in different countries around the globe, which is combating the attack of bollworms and giving better yield under changing climate (Ahmad *et al.,* 2019). In millets, novel genes, alleles and QTLs have been identified which have a functional role in stress tolerance. The development of high throughput molecular markers has become possible through next-generation sequencing in millets (Bandyopadhyay *et al.,* 2017).

In in Tobacco and Arabidopsis an increase was observed in photosynthetic efficiency by engineering a Rubisco protein having high Carboxylase catalytic activity. CKX enzyme involved in cytokinin catabolism when overexpressed resulting cytokinin degradation specifically in roots showed enhanced drought resistance and agglomeration of macro and micronutrients. Climate-smart potato clones have been developed which showed high resistance to drought and heat stresses without yield penalty. The conditions given to these clones were 2–3°C increases in temperature and about 15-20% lower precipitation under the scenario of climate change (Parker *et al.,* 2019). Table 2 describes different examples of crop improvements through biotechnological techniques.

It is reported that genetically modified (GM) crops preserved about 14,200 M kg of CO_2 in 2007 which is analogous to removing 6 million cars from circulation. Growing late blight and cold storage tolerant biotech potatoes have reduced grower cost by 28%, CO_2 emissions decreased by 740 million pounds, while water use decreased by 84 billion gallons. Globally, the cultivation of Bt crops showed a reduction in pesticide and insecticide usage by 18.5% (Brookes & Barfoot, 2018).

Table 2. Crop improvements against abiotic stresses by transgenic breeding.

Crop	Stress type	Gene /Protein	Mechanism	Reference
Tomato	Drought	Δ^1-pyrroline-5-carboxylate synthase (P5CS)	Overexpression	(Hsieh *et al*., 2002)
Rice	Drought	*DREB1* gene	Overexpression	(Ito *et al*., 2006)
Arabidopsis	Drought	*DREB1A* (*CBF3*) gene	Overexpression	(Hsieh *et al*., 2002)
Wheat	Drought	*DREB1A* gene	biolistic transformation	(Pellegrineschi *et al*., 2004)
Tobacco	Drought	NADP-malic enzyme	Upregulation	(Laporte *et al*., 2002)
Arabidopsis	Drought	AVP1 protein	Overexpression	(Park *et al*., 2005)
Tomato	Drought	AVP1 protein	Upregulation	(Park *et al*., 2005)
Sugarcane	Drought and salinity	*Arabidopsis Vacuolar Pyrophosphatase* (*AVP1*) gene	Agrobacterium-mediated transformation	(Kumar *et al*., 2014)
Pigeon pea	Salinity	*P5CSF129A* ($\Delta 1$ -pyrroline-5-carboxylate synthetase gene)	Overexpression	(Surekha *et al*., 2014)
Arabidopsis	Salinity	CDR protein	Upregulation	(Tamirisa *et al*., 2014)
Rice	Cold and drought	CDR protein	Heterologous expression	(Sunitha *et al*., 2017)
Tobacco	Drought and salinity	*sbsi*-1 gene	Overexpression	(Kumari *et al*., 2017)
Maize	Drought and heat stress	Maize ubiquitin *Ubi1* promoter	Overexpression	(Casaretto *et al*., 2016)
Potato	Heat stress	Hsc70 native promoter	Upregulation	(Trapero-Mozos *et al*., 2018)
Arabidopsis	Turnip mosaic virus	*eIF(iso) 4E* locus	Site-specific mutation	(Pyott *et al*., 2016)
Tomato	Bacterial disease	*SlDMR6-1* gene	CRISPR-Cas9 mediated mutagenesis	(de Toledo Thomazella *et al*., 2016)
Wheat	Powdery mildew	*TaMLO* homoeologs	Targeted mutations	(Wang *et al*., 2014, Zhang *et al*., 2017)

Genome editing: Advances in technology have provided numerous ways to improve food and agricultural production systems in recent years. Genome editing techniques such as meganucleases, TALENs, zinc-finger nucleases (ZFNs), and CRISPR/Cas9 are commonly employed for crop improvement (Fiaz *et al.*, 2019). CRISPR/Cas9 is a well-known genome editing tool that has transformed plant science research (Ahmad *et al.*, 2020). CRISPR/Cas9 is two acronyms for clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated endonuclease 9 (Cas9). It is used to accurately identify the function of coding and non-coding DNA sequences, to make transgene-free plants, as well as generate heritable and targeted mutations to establish novel characteristics (Monsur *et al.*, 2020). CRISPR-Cas appeal to scientists because of its ease of use, simple design, and quick delivery. The idea behind it is to deliver transformed plants with guide RNA (gRNA) based on bacteriophage resistance. The effectiveness of CRISPR/Cas is measured at the gene expression level, which encodes nucleases at various phases of the plant life cycle (Tabassum *et al.,* 2021).

CRISPR/Cas has three different mechanisms of action: 1) adaptation 2) expression and maturation 3) interference. Cas proteins are used in the first stage to identify target DNA and spacer sequences from that DNA. The spacer sequence is then used to help CRISPR array acquire immune memory. In the expression and maturation stages, precursor RNA transcripts are transcribed and tiny units known as CRISPR RNAs (crRNAs) are created. These (crRNAs) were characterized by a single spacer flanked by a repeating sequence. Furthermore, the interaction of crRNAs with Cas proteins forms an active Cas–crRNA complex. In the third phase, Cas–crRNA complex is utilized to scan cells for alien nucleic acid sequences by comparing base pair sequences to crRNA regions, then cleaving and denaturing targeted nucleic acid sequence (Ahmad *et al.,* 2021).

CRISPR-Cas systems are frequently used for development of biotic and abiotic stress resistant and nutritional enriched crop plants (Jamil *et al.*, 2020a; Shahzad *et al.*, 2021b; Zafar *et al.*, 2020). One example of enhancing disease resistance is targeting susceptibility genes (Su genes) which encode for sugar transporters. Bacterial blight is caused by *Xanthomonas oryzae* pv. *oryzae* and causes significant losses in rice yield under favorable conditions. During infection, the bacterial pathogen releases transcription activator-like effectors (TALEs) that increase transcription of genes encoding sugar transporters (i.e., *OsSWEET11*, *OsSWEET13*, *OsSWEET14*, etc.). SWEET genes are Su genes for bacterial blight disease, as they facilitate proliferation of bacteria in plant tissues. Researchers applied CRISPR-Cas system to disrupt linkage between TALEs and SWEET genes and developed rice lines with broad-spectrum resistance to bacterial blight (Oliva *et al*., 2019).

Knocking out Su loci becomes more complicated in polyploid crops such as wheat; however, CRISPR-Cas can be used to simultaneously target multiple homoeologs (copies of a gene present on multiple copies of the genome). For example, wheat lines resistant to powdery mildew were generated by simultaneous targeting of all three homoeologs of MLO and Enhanced disease resistance (Zhang *et al*., 2017) via CRISPR-Cas9.

Some plant genes enhance deleterious effects of abiotic stresses, known as sensitivity genes (Se genes). Genome editing strategies, particularly CRISPR-Cas, have been used in several plant species, including grain, vegetable, and fruit crops, to improve abiotic stress tolerance by disrupting these Se genes. For example, B-

AMYLASE (BMY) genes involved in cold tolerance in rice regulate starch degradation and accumulation of maltose to protect against cold stress. BMY function is compromised by binding a cold-responsive R2R3-type MYB transcription factor, OsMYB30, together with OsJAZ9, to promoter regions of BMY genes. Researchers used CRISPR-Cas to disrupt OsMYB30 and thus generated cold-tolerant rice lines (Zeng *et al*., 2020).

In maize, researchers have disrupted ARGOS8 via CRISPR-Cas9 to improve drought tolerance (Shi *et al*., 2017). CRISPR-based editing of *SlMAPK3* and *SlAGL6* increases tomato tolerance to heat stress, and *SlARF4* increases tolerance to salinity stresses. These CRISPR-edited mutant plants showed resistance against abiotic stresses and improved agronomic traits (Bouzroud *et al*., 2020). Several applications of CRISPR-Cas for developing plant tolerance to abiotic stress tolerance are summarized in Table 3. Recently, CRISPR-Cas9 base editing and prime editing systems were used to edit *ZmALS1* and *ZmALS2* and improved herbicide tolerance in maize (Nuccio *et al*., 2021). In rice, the fusion of Cas9 endonuclease and VirD2 facilitates the OsALS gene cleavage, and simultaneous HDR-mediated repair of the OsALS gene showed herbicide resistance in rice (Ali *et al*., 2020).

High throughput approaches: Many practices like precision agriculture, remote sensing, the use of nanotechnology, and digital agriculture to reduce agriculture's contribution to climate change have become the need of the hour. Precision agriculture includes laser leveling, precise water, nutrients, and seed usage (Joshi *et al.,* 2017). Near and remote sensing techniques are used to take high-resolution images and real data about soil, crops, and weather based on the principle of the electromagnetic spectrum (Shafi *et al.,* 2019). This technology includes hardware as well as sensors for positioning and guidance, environmental sensing, water, crop, and yield sensing.

Nanotechnology equipped with nanotools for precision management has several beneficial impacts on agricultural and environmental problems. Nanosensors and nano-scale materials are being used to identify environmental pollution and its remediation (Iavicoli *et al.,* 2017). Another revolutionary approach is digital agriculture which involves digitization and technical optimization of different aspects of agricultural systems and value chains. It is a platform for use of innovative technologies in the agricultural system to boost profitability and productivity. Digital agriculture with sensors provides real time weather, soil, crop, and environment data. Sensor technology, robotic technology, 3D printing, and the Internet of Things (IoT) are different forms of digital agriculture (Klerkx *et al.,* 2019).

Table 3. List of climate-smart crops developed through CRISPR-Cas systems.

Crop	Improvement type	Technique	Gene/ mechanism	References
Corn	High yield	CRISPR/Cas9	Knockout of *Waxy*	(Waltz, 2016)
Rice	High-amylose and resistant starch	CRISPR/Cas9	Mutation of starch branching enzyme gene *SBEIIb*	(Sun *et al*., 2017)
Wheat	Powdery mildew resistance	CRISPR/Cas9, TALEN	knocked out six TaMLO alleles	(Wang *et al*., 2014)
Tomato	Powdery mildew resistance	CRISPR/Cas9	knockout of MLO	(Nekrasov *et al*., 2017)
Rice	Rice blast resistance	CRISPR/Cas9	knockout of OsERF922	(Wang *et al*., 2016)
Rice	Bacterial blight	CRISPR/Cas9	Deletion of the OsSWEET13 promoter	(Macovei *et al*., 2018)
Potato	Reduced toxic steroidal glycoalkaloids	CRISPR/Cas9	St16DOX gene	(Nakayasu *et al*., 2018)
Cotton	Cotton leaf curl disease–resistant	CRISPR/Cas9	CLCuMuB and Rep	(Iqbal *et al*., 2016)
Rice	Heat tolerance, high grain yield	CRISPR/Cas9 editing	pyl1/4/6 triple knockout	(Miao *et al*., 2018)
Potato tubers	Reducing enzymatic browning	CRISPR ribonucleoproteins	Polyphenol Oxidase 2 gene (*StPPO2*)	(González *et al*., 2020)
Arabidopsis	Abiotic stress	CRISPR/Cas9	UDP-glycosyltransferases	(Kumar *et al*., 2020)
Arabidopsis	Cold, salt, drought	CRISPR/Cas9	UDP-glycosyltransferases	(Zhao & Zhu, 2016)
Tomato	Chilling tolerance	CRISPR/Cas9	C-repeat-binding factor	(Li *et al*., 2018)
Rice	Atmospheric N_2 fixation	CRISPR/Cas9	Nif	(Shao *et al*., 2017)
Rice	Drought tolerance	CRISPR/Cas9	OsNAC14	(Shim *et al*., 2018)

Mitigation and adaptation practices: Improved soil fertility, plant architecture (more resilience to abiotic stresses, particularly drought and flooding), change in the cropping pattern and crop management (laser leveling, terrace farming, conservation tillage, adjustment in sowing time), regulated nutrient cycles of plants, energy and water smart activities (drip and sprinkler irrigation, rerouting of rivers, prevention of erosion and seepage), improved harvesting, post-harvesting, and storage techniques, and reducing GHGs (Altieri & Nicholls, 2017) are numerous ways of mitigation and adoption to deal with the changing environment.

A good illustration is the processing of direct seeded rice (DSR), skipping nursery raising and transplantation, seeds are directly sown in the field with minimum use of labor and irrigation as compared to transplanted rice (Laing *et al.*, 2018). It has the potential to reduce GHGs emissions and soil improvement. About 16–54% and 16–92% reductions in methane emissions have been observed with direct-seeded rice. Mitigation potential in rice crops depends on root oxidative capacity, number of productive tillers, harvest index, and small root system. The development of new climate-resilient varieties having the above-mentioned attributes may become an outstanding source of tackling climate change (Arif *et al*., 2020).

System of Rice Intensification' (SRI) with random irrigation of flooded rice showed a reduction in methane gas emission (mitigation), a decline in water usage (adaptation and resilience), and also increased yield, as well as food security (Thakur *et al*., 2016).

Climate-smart village (CSV) is a new approach at the local level to improve farmers' ability to manage climate hazards and aims to evaluate CSA technologies, services, processes, and practices for adaptation on a broader level. In South Asia, 'village' is considered a local unit to implement CSA by Climate-change, Agriculture, and Food Security (CCAFS) (Aryal *et al*., 2019).

Crop diversification reduces the risk of loss of total crop in case of any disaster. The introduction of new crops into existing cropping patterns helps in survival under severe stresses that may occur due to changing climate (Arif *et al*., 2020). Similarly, crop rotation, manure application, the introduction of Napier grass, and the growing of multipurpose trees like acacia spp. can increase soil carbon in contrast to BAU (Business as Usual) (Ambaw *et al*., 2019).

Crop rotation improves soil fertility, the efficiency of resource usage, and crop yield (Bowles *et al*., 2020). Composting is also reported as an adaptive option against climate change, which reduces nitrates and nitrous oxides in soil. Legumes' soil-building properties make a good combination with exhaustive cereal crops. In China, corn and alfalfa, corn and soybean, soybean and oat, soybean and rice, soybean and wheat crop rotation systems are under practice. Grain legumes, such as faba beans, peanuts, and mungbean are also in rotation with cereal crops (CSA follows the concept of conservation agriculture), which includes optimum water usage, nutrient management, zero tillage, and crop residue retention.

Agroforestry is a tree cover on agricultural land that enhances agricultural productivity by increasing the water holding and retention capacity of the soil, soil organic matter, agro biodiversity, and ultimately farmer's income. Tropical forests also play a major role in the stabilization of CO_2 concentration in the atmosphere (Baccini *et al*., 2017). A symbiotic relationship between mitigation, adaptation, and food security not only occurs but has a positive effect on one another like, nitrogen fixing trees having nodulated roots when grown with crops improve soil fertility, soil carbon (adaptation & food security) which minimizes use of fertilizers and leads to a reduction in N_2O gas emission.

In South African villages, evaluation of intercropping has been done for the period of three years 2012–2015. 210 farmers from five villages adopted resistant cereal-legume intercropping in 2012 and the number of adoptions reached 10,000 at the end of 2015. Most farmers reported 4 fold increases in sorghum yield since 2012. Coffee is sensitive to temperature fluctuations and banana is intolerant to drought stress but Coffee-banana intercropping is resilient to drought and extreme climactic conditions as banana provide shade to coffee. It showed a reduction in GHGs emissions and enhancement of carbon sequestration (Glaze-Corcoran *et al*., 2020).

Herbicide-tolerant crops have reduced weed control and fuel consumption costs in machines by up to 44% and 60% in maize and soybean crops respectively. HT canola oilseed rape variety, cultivated on about 6 million ha area in Canada showed a reduction of fuel usage for crop production by over 31,000 tons per year and CO_2 emission by 94,000 tons between 1996 and 2004 when grown under zero tillage. About 1 million tons of carbon sequestration has also been reported (Neate, 2013). In legumes, pre-flowering and post-podding are considered critical stages: managed water application at these stages may increase production rates by 15 to 25%. Similarly, a yield increase of 83-89% in maize and 90% in legumes was observed, by the use of conservation practices as compared to conventional management systems (Schaller *et al*., 2017).

Zero tillage affects nutrient availability and enzymatic activities positively in wheat crop in contrast to conventional tillage, reducing GHGs emissions (Rijal & Rijal, 2019). In canola, zero tillage practice showed soil organic matter and structure improvement, reduction of carbon emissions in the atmosphere by around 1 million tons per year, and enhanced water availability.

Conclusion and future recommendations: Climate change is an emerging issue in the 21st century globally, which is badly affecting life, especially the agricultural system. Abiotic stresses like heat and drought stress are prevailing due to climate change, severely affecting crop production by altering crop physiology, plant growth, soil fertility, diversity, and microbial activity. To overcome the adverse effects of climate, climate-smart agriculture, with high adoption and resilience, is a pressing necessity. Climate-smart agriculture's major objectives are enhancement of agricultural productivity, adaptation of food system towards changing climate, and reduction of greenhouse gas emissions. Sensor based precision agriculture technologies are used to increase profitability and environmental protection. The negative consequences of changing climate on agricultural systems can be minimized by making climate-resilient crops, changing cropping patterns, and adopting innovative crop management strategies. As a result, enhancing crop resistance to climate change is a vital component of guaranteeing food and nutritional security, which might be accomplished through genetic engineering or molecular breeding technologies. Advances in DNA sequence, as well as improved genomic methods, will speed up the identification of novel genetic and important regulatory areas of stress tolerance, paving the way for the development of new cultivars with long lasting resistance. Furthermore, high yielding cultivars boost agricultural output per unit area, reducing the need to expand production equipment. The need of the hour is to pay more attention to the impacts of climate change on the agriculture sector at the government level. Government should develop awareness schemes to make sure that climate-smart approaches are being used by the public as well as private sector. Awareness campaigns for farmers through electronic and print media can be beneficial. These initiatives will surely bring a positive change in climate as well as lessen climate change impacts.

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