Review Article

A review on conventional and modern breeding approaches for developing climate resilient crop varieties

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Abstract
The escalating threat of climate change is a major challenge to global food security. One of the ways to mitigate its impact is by developing crops that can withstand environmental stresses such as drought, heat, and salinity. Plant breeders have been employing conventional and modern approaches to achieve climate-resilient crops. Climate-resilient crops refer to both crop and crop varieties that exhibit improved tolerance towards biotic and abiotic stresses. These crops possess the capacity to maintain or even increase their yields when exposed to various stress conditions, such as drought, flood, heat, chilling, freezing and salinity. Conventional breeding entails selecting and crossing plants with desirable traits, while modern breeding deploys molecular techniques to identify and transfer specific genes associated with stress tolerance. However, the effectiveness of both methods is contingent on the crop species and the targeted stress. Advancements in gene editing, such as CRISPER-cas9 and genomics-assisted breeding, offer new opportunities to hasten the development of climate-resilient crops. These new technologies include Marker Assisted Selection, Genome-Wide Association Studies, Mutation breeding, Transcriptomics, Genomics, and more. The review concludes that these cutting-edge techniques have the potential to enhance the speed and precision of developing crops that can endure the challenges posed by climate change.

Keywords: Abiotic stresses, Conventional, Climate change , Mitigate

INTRODUCTION

The adverse effects of climate change, such as irregular rainfall, high temperatures, and extreme weather events, are taking a toll on global food security. These conditions can cause a decline in crop yields and quality, impacting the availability of food. Climate change can also affect the land use pattern, soil health, and nutrient availability in the soil. The variations in temperature, precipitation, and atmospheric gases can alter the water balance, leading to further changes in the ecosystem (Zhao *et al.*,2017). As a result of changing environment, the plants show altered maturing and fruiting time, alteration of floral rewards, and reduction

or increase of the growth rate. However, all these adaptive courses result in a considerable reduction in the yield of the plants. The consequence of unfavorable climatic conditions is especially prominent in crop plants, most of which have been produced for increased yield and have a decreased capacity for enduring environmental constraints. The changing environment has led to altered maturing and fruiting times and changes in plants' floral rewards and growth rates. Crop plants are vulnerable to the consequences of unfavorable climatic conditions, as they have been developed for high yields but have limited resilience to environmental stresses. Rising mean worldwide temperature is one of the ultimate alarms of mankind and can influence our most important cereals, which form the staple diet for two-thirds of the planet's population. It has been reported that even one degree-Celsius rise in worldwide mean temperature can diminish yields by 3.2% in rice, 6.0% in wheat, 7.4% in maize, and 3.1% in soyabean (Zhao *et al.*,2017). This highlights the urgent need for effective measures to mitigate the impact of climate change on global food production.

Climate change can give rise to different conditions like intermittent drought and flood, salinity, and alkalinity, which can affect the growth and productivity of crops. Additionally, it may create favorable conditions for various types of pests and diseases, may alter their habitat range and lead to significant crop damage (Luck *et al.*,2011). These factors, coupled with the increasing population of the world may develop a threat to worldwide food security. Hence, developing crops with the ability to withstand environmental stresses is crucial for building a sustainable and resilient food system. Over the years, plant breeders have employed various conventional breeding techniques, such as selection, hybridization, and mutagenesis, to produce crops with enhanced stress tolerance. The low heritability of traits has made it to develop difficult high-yielding crops that can thrive under ecological constraints. As a result, the mission of breeding crops with improved stress tolerance has been a challenging goal. Because of this reason, the scientific community is striving to identify more attributes of value that can lend tolerance to various abiotic stresses (Gaba *et al.*,2021).

Approaches, such as marker-assisted selection, genetic engineering, and genome editing, allow breeders to identify and transfer specific genes associated with stress tolerance, opening new possibilities for developing crops that can withstand environmental stresses. The recognition and mapping of various genes and quantitative trait loci (QTL) associated with biotic and abiotic stresses have resulted in the finding of abundance of DNA marker-traits. This allows plant breeders to develop new climate-resilient plants in a short span of time and with precision. The prestent review discusses different conventional and molecular methods for developing climate resilient crops.

Conventional breeding

In conventional method of crop breeding, breeders traditionally select individual plants from large segregating populations that possess desirable traits. However, these conventional breeding practices are often slow and insufficient in accelerating the development of improved crop varieties. Once crosses are made between two parent plants, subsequent generations are evaluated to identify superior plant progenies. This process involves multi-year testing of plants in replicated field trials across multiple locations to assess the genetic potential of candidate genotypes under diverse conditions. Despite its importance, this conventional approach to crop breeding lacks efficiency and expediency in achieving desired outcomes (Naqvi *et al.*, 2022).. These methods are often time-consuming and require substantial human resources (Table 1). The conventional breeding may not be effective for developing crops with complex traits, such as multiple stress tolerance. In some cases, the desired trait may be present in wild relatives of the cultivated species, and pre-breeding techniques can be used to introduce this trait into the cultivated species (Acquaah, 2015).

Pre breeding

Pre-breeding refers to transferring advantageous genes from wild or exotic plant types into accepted breeding material or agricultural backgrounds. Pre-breeding plays a critical role in developing crops that are resilient to climate change. This process entails identifying, collecting, and utilizing genetic resources to enhance crop quality and productivity (Fig. 1.). Pre-breeding strategies seek to identify and exploit wild or closely related crop species that exhibit desirable traits, such as heat or drought tolerance, to create new more robust varieties against environmental stress. Usually, the pre-breeding approach is more time-consuming (Sukumaran *et al.*, 2021). The primary goals of pre-breeding are to offer readily available genetic material to plant breeders for use in their programs, increase genetic diversity, and identify desirable traits for selecting superior parents in the crossing program. By crossing these wild relatives with cultivated crops, desirable traits can be transferred, resulting in the creation of new genetic combinations. This approach produces improved germplasm with increased diversity and enhanced biotic and abiotic stress resistance. Pre-breeding can also help to reduce linkage drag by transferring genes from primary, secondary, and tertiary gene pools, such as wild species, into better-performing elite genotypes. Pre-breeding can help to increase genetic diversity and reintroduce desirable traits from wild relatives into cultivated crops, reducing linkage drag and improving the overall performance of

Table 1. A Comparison of Conventional and Modern Breeding Approaches for Developing Climate Resilient Crop Varieties (Naqvi *et al.*, 2022; Gaba *et al.*, 2021)

Breeding Approach	Methodology	Strengths	Limitations
Conventional breeding	Selection	1.Targeted improvement of specific traits. 2.Effective in developing disease and stress resistance (Mostly oligogenic traits)	Limited genetic diversity within the selected population, Identifying phenotypes that correlate with a particular type of stress, precise trait breeding expensive, costly and labour intensive
	Hybridization	1.Enhanced yield potential and stress tolerance. 2. Increased heterosis.	Costly production of hybrid seeds. Labor intensive Time consuming
Modern	Marker-Assisted Selection (MAS)	1.Precise and efficient trait selection. 2.Accelerated breeding progress.	1.Requires prior knowledge of target genes. 2.Costly equipment and expertise.
	Genomics	1.Identification of genes associated with climate resilience. 2.Targeted manipulation of specific genomic regions.	Limited understanding of gene function and interactions.
	Phenomics	1.High-throughput assessment of plant traits. 2.Identification of novel traits related to climate resilience.	Expensive infrastructure and data analysis.
	Transcriptomics	1.Insight into molecular mechanisms of climate resilience. 2.Identification of candidate genes for breeding.	Limited understanding of gene regulation and expression.
	Mutation Breeding	1.Creation of new genetic variations when genes are not found or eroded in gene pool. 2.Potential for improved abiotic stress tolerance.	Low success rate in obtaining desired traits.
	Genome-Wide Association Studies (GWAS)	Identification of genetic variations associated with traits.	Sequencing of complex genome require more effort

modern varieties (Table 2). Wild relatives have been reported to possess significant genetic potential in various crops, including rice, wheat, maize, potato, tomato, sugarcane, and tobacco. Their genetic diversity can provide useful traits for crop improvement, such as disease resistance, abiotic stress tolerance, and yield potential. Therefore, pre-breeding approaches involving wild relatives can be an important tool for developing new crop varieties with improved traits (Bakala,2020; Singh *et al.*, 2020).

Pre-breeding approaches are crucial in developing climate-resilient crops by identifying and utilising genetic resources for crop improvement. The use of wild relatives, landraces, and gene identification can lead to the creation of new crop varieties that are better adapted to environmental stresses. Thus, pre-breeding approaches provide a valuable foundation for improving crop yields, enhancing crop quality, and mitigating the impact of climate change on agriculture.

Speed breeding

Speed breeding is a technique that involves manipulating the growth conditions of crops to accelerate the breeding process by shortening the generation time. This technique focuses on manipulating the photoperiod, which involves exposing crops to extended periods of light. By doing so, plants can complete their reproductive cycle more quickly, resulting in faster breeding cycles and more generations in a shorter time (Bhatta *et al.*,2021) The main objective of speed breeding is to accelerate the breeding process by reducing the generation time and shortening the breeding cycle. This technique rapidly produces advanced stable lines and mapping populations, allowing for faster screening and identification of donor sources for specific traits (Watson *et al.*, 2018). Speed breeding can be applicable on diverse germplasm. Unlike doubled haploid technology, which requires specific equipment for in vitro culturing to produce haploid embryos that yield
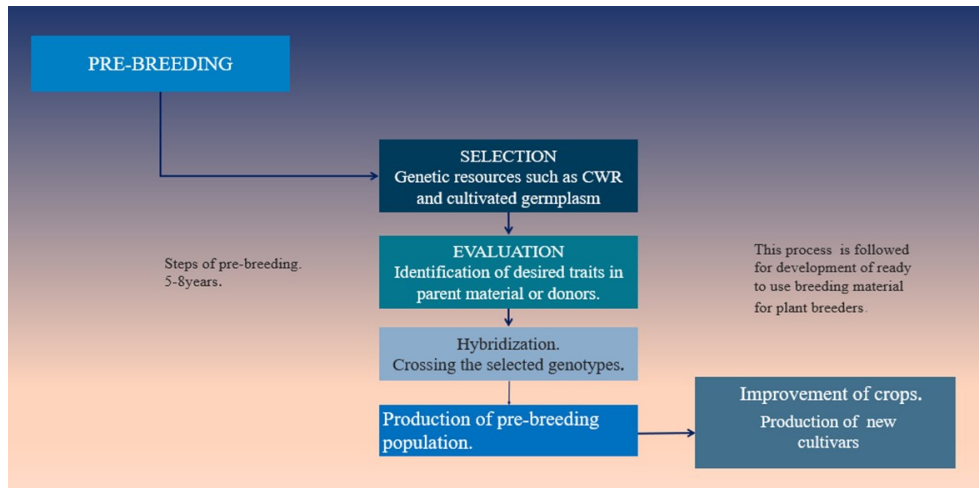
Fig. 1. *Steps involved in Pre-Breeding (Sharma et al., 2013)*

Table 2. Crops and their wild relatives possessing genes and traits for various resistance(Mammadov *et al*., 2018.)

Crop	Wild relative	Trait	Gene
Rice	*Oryza nivara* *Oryza glaberimma* *Oryza rufipogon* *Oryza officinalis* *Oryza minuta* *Oryza latifolia* *Oryza austaliensis*	Insect tolerance Resistance to brown plant hopper.	*Bph10* and *Bph18(t)(O. australiensis)*; *bph11(t), bph12(t), Bph13(t), Bph14, and Bph15 (O. officinalis)*; *Bph12 (O. latifolia)*; *Bph16(t), Bph20(t), Bph21(t), and Bph23(t) (O. minuta)*; *Bph22(t) (O. glaberrima)*; *Bph24(t), bph29 and bph30 (O. rufipogon)*
	Oryza minuta *Oryza autraliensis* *Oryza rufipogon*	Resistance to blast disease	□100 resistance (R) genes; Three major R gene clusters *(Piz, Pik, and Pita)*.
	Oryza longistaminata *Oryza rufipogon* *Oryza minuta* *Oryza officinalis* *Oryza nivara* *Oryza brachyantha*	Resistance to bacterial blight disease.	*Xa21* *Xa23* *Xa27* *Xa29(t)* *Xa30(t), Xa38* *Xa34(t)*
	Oryza nivara	Resistance to Rice grassy stunt virus.	*Gs (O. nivara)*
	Oryza longistaminata *Oryza rufipogon*	Rice tungro bacilliform virus tolerance	*O. longistaminata* and *O. rufipogon* are being used as donors in developing tolerant lines and studies are going on.
	Oryza glaberrima *Oryza barthii* *Oryza meridionalis* *Oryza australiensis* *Oryza longistaminata*	Drought and heat resistance.	Research is carried out on *O. meridionalis* .
	Oryza rufipogon	Tolerance to acid soil and aluminum.	*O. rufipogon* is being studied for QTLS.
	Oryza rufipogon (AA)	Tolerance to cold	O. rufipogon (QTLs) identified.
Maize	*Zea mays spp. parviglumis*	Fall armyworm (*Spodoptera frugiperda*) tolerance.	*wip1, RP1*, and chitinase genes when expressed in at higher intensity.
	Eastern gamagrass	Resistance to rust disease.	*Rp1td* gene
	Eastern gamagrass	Tolerance to drought.	Deep root system.
	Eastern gamagrass	Tolerance to Salinity	Ability to conserve sodium in the leaves.
	Zea nicaraguensis	Waterlogging tolerance.	Ability to develop a barrier to radial oxygen loss in basal areas of adventitious roots under stagnant deoxygenated conditions.
	Eastern gamagrass		Constitutive formation of root aerenchyma
Cotton	*Gossypium somalense*	Insect tolerance Helicoverpa Spp	Smooth leaf type
	Gossypium hirsutum "Pilose"	Tolerance to fleahopper	Pilose trait and square structure impacting stylet penetration
	Gossypium arboreum	Resistance to bacterial blight.	Bacterial blight resistance gene, *B6*.

completely homozygous lines, speed breeding does not require such equipment. The use of speed breeding to identify allelic diversity in land races and crop wild relatives is particularly important because it allows for the discovery of genetic variation that may not be present in commercial cultivars. This genetic variation can be used in breeding programs to develop new crop varieties with desirable traits such as improved stress tolerance, higher yield potential, and disease resistance (Cazzola *et al.*,2021).

Genomic assisted breeding for developing climate resilient crops

Genomic assisted breeding is a modern approach to crop breeding that utilizes molecular markers and genomic selection to expedite the development of new crop varieties with enhanced stress tolerance (Fig.2). The utilization of genomics has witnessed a remarkable surge in recent years, highlighting its significant importance and effectiveness (Varshney *et al.*, 2021). Genomics-assisted breeding (GAB) offers a viable approach to enhance crop production by developing resilient varieties that exhibit resistance to various environmental stresses such as pests, heat, cold, salt, floods, submersion, drought, and more. By employing genomic analysis, we can effectively study the stress response of crop species, along with their adaptive characteristics and wild counterparts. This analysis enables us to identify crucial genes or quantitative trait loci that underlie the desired traits, making genomics a promising tool for understanding and improving crop stress tolerance (Manickam *et al.*, 2023).

Marker-assisted selection (MAS) is a key technique in genomic-assisted breeding, which uses molecular markers to identify and select plants with desirable traits. Another important technique in genomic assisted breeding is genomic selection, which involves the use of genome-wide markers to predict the performance of untested individuals. A genomic-led breeding strategy

is employed to develop cultivars that are resilient to climate change. This strategy begins with identifying the stresses expected to impact crop production and yield under various climate change scenarios (Varshney *et al.*, 2005).The use of genetic mapping and quantitative trait loci (QTL) analysis, through bi-parental or association mapping (AM) populations, has greatly improved the ability to understand the genetic control of agricultural traits. This understanding has made it possible to employ techniques such as marker-assisted selection (MAS), QTL analysis, and AM studies, or to directly compute and employ genomic selection (GS) to produce high-value genotypes for breeding programs. (Kulwal *et al.*, 2011).

Marker assisted selection for developing climate resilient varieties

MAS is a breeding approach that involves the use of molecular markers to identify and select plants with desirable traits, including those associated with climate resilience. This technique can be used to accelerate the development of climate-resilient crops by enabling breeders to identify plants with desirable traits more accurately and efficiently than traditional breeding approaches. This approach involves identifying and utilising specific genes or genomic regions associated with desirable traits, such as abiotic stress tolerance, to improve crop performance under adverse environmental conditions. Reeta, a popular late-maturing high-yielding rice variety in eastern Indian states, is sensitive to submergence stress and phosphorus deficiency. To address these constraints, the variety was improved through marker-assisted breeding by introgressing Sub1 (for submergence tolerance), Pup1 (for low phosphorus stress tolerance), and GW5 (for narrow-grained trait) from the donor parent, Swarna-Sub1 (Barik *et al.*, 2023)

By selecting plants with desirable genes using tightly linked markers, MAS can accelerate genetic gain in
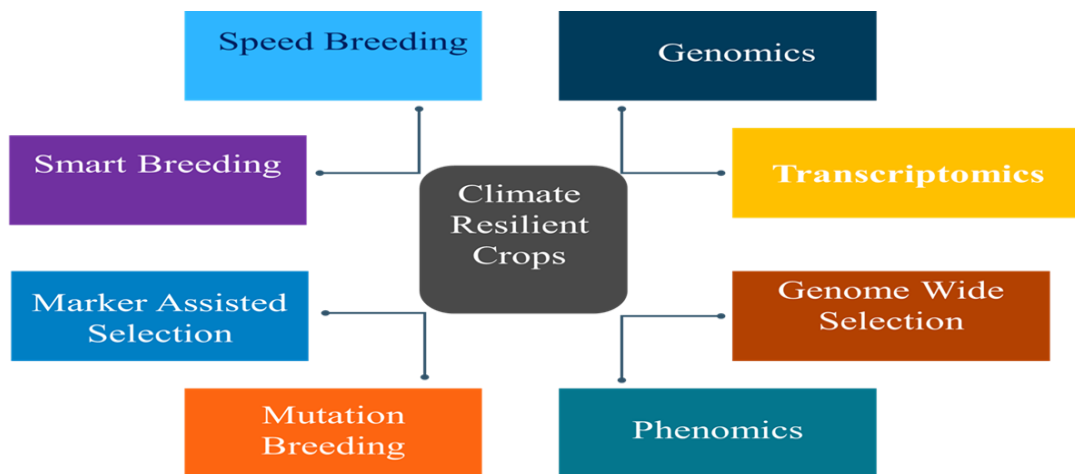
Fig. 2. *Modern Breeding Approaches for developing Cimate Resilient Crops* (Bakala *et al.*, 2020)

conventional breeding, and develop abiotic stress tolerant varieties (Kumar *et al*., 2018). Marker Assisted Backcross Breeding (MABC) is popularly utilized to produce abiotic stress resistant varieties and increase grain yield. Certain studies suggest that QTL pyramiding has increased grain yield and tiller formation under abiotic stress conditions like drought stress (Shamsudin *et al*., 2016; Anyaoha *et al*., 2019) . Incorporation of `saltol' gene through MABC in popular varieties led to formation of high yielding salt tolerant varieties which exhibited salt tolerance at seedling stage (Singh *et al*., 2016; Valarmathi *et al*.,2019) Improvement of many popular varieties was made using `sub1' gene through MAS (Dar *et al*., 2018). Rice cultivars were genetically modified by incorporating "Saltol" and "Sub1" genes and some genes for biotic stress resistance (Das *et al*., 2015). By utilizing marker assisted pyramiding, multiple drought-tolerance QTL and Sub1 were incorporated into rice varieties, leading to the development of drought- and submergence-tolerant varieties without any reduction in yield in non-stressful environments (Sandhu *et al*., 2019).

Genomic selection (GS)

Genomic selection is a modern breeding approach that uses genome-wide markers to predict the performance of untested individuals and select plants with desirable traits, including those associated with climate resilience. This approach relies on the identification of genomic regions associated with desirable traits, which can be used to predict the performance of plants that have not yet been phenotyped. GS relies on genomic estimated breeding values (GEBVs), calculated using genotypic and phenotypic data from a population. GEBVs can be used to predict the performance of untested individuals and prioritize those with desirable traits for further breeding . In genomic selection, individuals with the highest genome-estimated breeding values (GEBVs) are selected as parents to produce the next generation of offspring. This is done to increase the frequency of favorable alleles in the population, thereby improving the overall performance of the trait of interest (Spindel *et al*., 2018). One of the main advantages of genomic selection is its ability to predict the performance of plants in different environments. This allows breeders to develop varieties that perform well under a wide range of environmental conditions, making them more resilient to the effects of climate change. GS is a new tool for rice improvement, and research is needed to develop best-prediction models for improving abiotic stress tolerance (Onogi *et al*., 2015). Genomic selection can be combined with other breeding approaches such as marker-assisted selection or conventional breeding to accelerate the breeding process and improve selection accuracy.

Transcriptomics and proteomics

Transcriptomics is a powerful tool for understanding the genetic basis of plant stress tolerance and developing climate-resilient varieties. Transcriptomics involves the study of gene expression patterns in plants under different environmental conditions, such as drought, heat, or salinity stress. Transcriptome profiling allows the investigation of a plant's response to abiotic stresses and has ability to identify candidate genes and pathways involved in stress response, which can be targeted for breeding. For example, genes involved in stress signaling, osmotic regulation, or antioxidant defense can be targeted to improve stress tolerance in crops. In a study conducted on Arabidopsis, when Arabidopsis plants were exposed to a simultaneous stress combination of heat, drought, and virus infection, their transcriptomic analysis demonstrated suppression of transcript expression involved in the R-mediated disease response. However, there was an enhancement in the expression of transcripts associated with the heat stress response. These findings indicate that the presence of abiotic stress factors has the potential to modify pathogen-related signaling networks, subsequently leading to the suppression of defense responses (Rivero *et al*., 2022 ; Prasch and Sonnewald, 2013).

In a study by González-Schain *et al*.,2016, the authors observed the repression of various transcription factor genes, signal transduction pathways, and metabolic pathways in the heat-tolerant rice variety N22. The study also revealed that the expression of protective chaperones in anthers was crucial in mitigating heat-induced damage and facilitating fertilization.

Mutation Breeding

Mutation breeding is the method of improving the crops by inducing mutations in plant DNA to create new variations with the help of chemicals like (EMS)Ethyl Methyl Sulphonate or ionizing radiations like gamma rays (Pathirana, 2011). After the induction of the mutations in the plants the population is then inspected for mutant plants with appropriate characteristics. Mutation breeding has been successfully used to develop crops that are more resistant to diseases, pests, and environmental stresses. For example, wheat, barley, and rice varieties have been developed using mutation breeding techniques that are more tolerant to drought, heat, and salinity. The mutant variety of barley called Diamant was developed by subjecting its dormant seeds to X-ray irradiation. This resulted in a variety that exhibited superior yield characteristics, had high-quality grains, shorter stems, good malting quality, and increased resistance to lodging. (Yadav *et al*., 2016). Similarly, Calrose76, a dwarf mutant variety of japonica rice cultivar, was released in 1976 after being created through gamma irradiation. This variety had a shorter stature,

improved yield, and increased resistance to lodging (Rutger *et al*., 1976). More recently, a salt-tolerant rice variety called Kaijin was developed through mutation breeding using ethyl methane sulfonate (EMS) as the mutagen. (Takagi *et al*., 2015).

Genome-wide association studies

Genome-wide association studies (GWAS) enable high -resolution mapping in large populations by detecting statistically significant associations between phenotypes and genotypes using linkage disequilibrium (LD) (Naqvi *et al*., 2022).GWAS have been instrumental in identifying genes associated with various abiotic stress tolerances such as drought, chilling, submergence, and salinity (Ma *et al*.,2016; Pantaliao *et al*., 2016; Pandit *et al*.,2017).It has been successfully used to improve salt tolerance in Brassica, Rice and cotton, stalk lodging resistance in Maize, Karnal bunt resistance and powdery mildew resistance in wheat (Naqvi *et al*., 2022; Khalid *et al*., 2021; Khan *et al*., 2021). A study identified 146 genes that co-localized with previously reported QTL for salinity tolerance at the flowering stage in a panel of Thai varieties (Lekklar *et al*., 2019). Drought tolerance in the early growing stage of rice discovered 39 QTL for different traits in Vietnamese landraces through GWAS(Hoang *et al*., 2019). Transpiration rate, relative growth, and transpiration use efficiency (TUE) was studied from Indica and Aus rice panels under salinity and waterlogged conditions and identified previously undetected loci for TUE on chromosome 11(Al-Tamimi *et al*., 20016). Seven MTAs (Marker-Trait Associations) associated with grain yield under drought stress were identified. Genome-wide association studies (GWAS) are useful for identifying genes and alleles associated with complex traits such as abiotic stress tolerance from diverse germplasm (Swamy *et al*., 2017).

QTL Mapping

Quantitative trait loci (QTL) analysis utilizes both phenotypic and genotypic data to determine the genetic basis of variation in quantitative traits. Quantitative Trait Locus (QTL) mapping is a technique used to identify a genome's regions associated with a specific trait. It involves analysing genetic variation in a population and correlating that variation with the trait of interest. QTL mapping has been used extensively in plant breeding to identify the genetic basis of traits such as drought tolerance, heat resistance, and disease resistance (Table 3.). The DRO1 gene, a major quantitative trait locus (QTL) in rice, controls deep rooting and has been successfully cloned. It is associated with enhanced root development angles under drought stress and has shown a positive correlation with high yields. Recent research indicates that rice lines with introgressed

DRO1 exhibit improved photosynthetic rates, grain filling, and overall yield. Similar homologs of DRO1 may exist in economically important cereal crops such as wheat, barley, maize, and sorghum, making comparative genomics a promising avenue for exploration(Raj *et al*., 2023; Choudhary *et al*., 2021). To enhance drought tolerance in indica rice, researchers have investigated the co-expression of DREB2A and APX genes. The simultaneous expression of DREB2A and APX has been found to enhance drought tolerance in rice plants, offering a potential mitigation strategy against the impacts of climate change (Sandhya *et al*., 2021).

14 additive effect QTL for root and shoot traits in the cross Cocodrie × N22 were discovered, and it was found that the majority of these were clustered in chromosome 1 (Bhattarai and Subudhi, 2018). Genetics of cold tolerance at both seedling and reproductive stages has been investigated in several QTL mapping studies and several cold tolerance loci were genetically characterized (Xiao *et al*., 2018; Liu *et al* 2018). In conclusion, QTL mapping is a valuable tool for developing climate resilient varieties by identifying specific regions of the genome associated with desirable traits.

Genome editing

Genome editing, particularly CRISPR technology, revitalizes plant breeding by enabling precise and rapid crop modification for increased yields and enhanced stress tolerance. It offers solutions to disease resistance and other challenges, while next-generation CRISPR systems expand its applications. Crops like cereals, mushrooms, corn, and false flax have already benefited, and potato can also leverage genome editing for improved traits (Naqvi *et al*, 2022, Raza *et al*, 2021). Conventional breeding and transcriptomics studies provide a foundation for identifying gene targets and advancing crop improvement to overcome multiple challenges such as drought, heat, nutrient deficiencies, diseases, pests, and viral infections in potato through CRISPR-based genome editing (Tiwari *et al*., 2022). The involvement of Oryza sativa genes OsRAV2 and OsDST in salt and drought stress tolerance was reported. OsRAV2 is associated with salt stress response, while OsDST encodes a zinc finger transcription factor and contributes to salt and drought tolerance. Knockout experiments using NHEJ Agrobacterium mediated techniques demonstrated the role of these genes in conferring abiotic stress tolerance by inducing broad leaf area and reduced stomatal density (Gaba *et al*., 2021; Duan *et al*., 2016; Santosh *et al*., 2020). Next-generation CRISPR/Cas systems, such as prime editing, base editing, and de novo domestication, have revolutionized genome editing for crop improvement. These systems, coupled with the availability of versatile Cas orthologs

Table 3. QTL mapping of Stress-Related traits in Key Crop Species

Stress	Trait	QTL	Chromosome number	Markers	Reference
Rice Drought	Grain yield	qDTY1.1	1	RM11943-RM12091	Vikram *et al*. 2011
	Plant Height	Qtl	1	S1_19133052 S1_19791935	
	Senescence	Qtl	4	pza03231.1-pza03409.1	Almeida *et al*. 2014
	Normalized differential vegetative index (NDVI)	Qtl	5	S5_82956371 S5_64808654	Trachsel *et al*. 2016
	Grain weight per plant (g)	qGW3-2	3	RM16-RM130	Sangodele *et al*. 2014
	Panicle weight (g)	qPW8	8	RM337-RM556	Sangodele *et al*. 2014
	Grain yield	qDTY2.2, qDTY3.1, and qDTY12.1			Shamsudin *et al*. (2016)
		qSL1.38		SI-38023681	Bhattarai and Subudhi, 2018
		qTGW1, qGW3-1, qPW8		RM302-RM529 RM563-RM16 RM337-RM556	Sangodele *et al*., 2014
		qDTY3.2 and qDTY12.1, qDTY3.1 qDTY6.1		RM231, RM28099 and RM28199, RM168 and RM468 RM586-RM217	Dixit *et al*., 2014
Heat	Spikelet fertility	qHTSF3.1	3	id3001137(SNP)	Ye *et al*. 2015
	Stress susceptibility indices for yield per plant	qSSIY5.1	5	SNP8377-SNP8401	
	Maximum fluorescence (Fm)	QFm.cgb-4A	4A	Xwmc89–Xwmc420	Azam *et al*. 2015
	Thylakoid membrane damage	QHttmd.ksu-7A	7A	Xbarc121, barc49	Talukder *et al*. 2014
Cold	Seed fertility	qCT-3-2	3	Chr031934364	Zhu *et al*. 2015
	Vigor	Qtl	4	S_177665741	Allam *et al*. 2016
	Number of kernel rows per ear	Qtl	5	S_169975064	Revilla *et al*. 2016
	Early vigor	Qtl	5	PZE-105041551 (SNP)	
Waterlogging/submergence	Submergence	qSUB1.1	1	id1000556- id1003559	Gonzaga *et al*. 2016
		qSUB4.1	4	id4010621-id4012434	Gonzaga *et al*. 2016
		qsub8.1	8	id8005815- id8007472	Gonzaga *et al*. 2016
		qSUB9.1	9	id9001352-SC3	Gonzaga *et al*. 2016
Wheat					
Drought	Grain yield under drought	QRWC2AC		KSUM-119	Malik and Malik, 2015
		QHt.ccsu-2B		wPt-9423	Gahlaut *et al*., 2017
		QABA-ww-3B		Barc164-Srap19	Barakat *et al*., 2015
	ABA Content	Qtls	3B, 4A, and 5A	Wmc96, Trap9, and Barc164	(Barakat *et al*., 2015)
Terminal heat tolerance		QHthsitgw.bhu-2B	2B	Xgwm935–Xgwm1273	Paliwal *et al*.,2012.
		QHthsitgw.bhu-7B	7B	Xgwm1025–Xgwm745	Paliwal *et al*.,2012.
		QHthsitgw.bhu-7D	7D	Xgwm3062– Xgwm4335	Paliwal *et al*.,2012.
Cold tolerance		QTL (QFt5F-2/QWs5F-1)	5A	FpCBF6	(Alm *et al*., 2011).
Stay green traits	Stay green QTLs	QSg.sau-2B.1	2B.1	KASP-AX-111729522–1 KASP-AX-111729522–2 KASP-AX-111729522–3	Ren *et al*., 2021
		QSg.sau-6A.2	6A.2	KASP-AX-110040743–1 KASP-AX-110040743–2 KASP-AX-110040743–3	Ren *et al*., 2021
Salt tolerance	Proline control	QCp.iiwbr-2D	124	wmc601	Devi *et al*,.2019
	Grain yield	QCgy.iiwbr-7D	379	gwm437	Devi *et al*,.2019

(Cas9, Cas12, Cas13, and Cas14), have significantly enhanced editing efficiency. As a result, CRISPR/Cas systems now find numerous applications in crop research, successfully enabling the editing of major crops to develop resistance against both abiotic and biotic stress factors (Razzaq *et al*., 2021)

Conclusion

In conclusion, integrating conventional breeding methods and modern technologies is crucial for developing climate-resilient crop varieties to address the impacts of climate change on agriculture and ensure global food security. While conventional methods are time-consuming and labor-intensive, modern techniques such as MAS, genomics, and gene editing offer faster and more precise approaches. By integrating these approaches, diverse traits from different plant sources can be incorporated, supplemented by novel elements introduced through modern technologies. This integrated approach enhances sustainable food production and enables adaptation to changing climatic conditions. Conservation of plant genetic resources and the utilization of advanced tools like gene editing are essential for capturing valuable genetic variations and improving the resilience of crops. Understanding the underlying genetic mechanisms helps generate new cultivars capable of withstanding multiple stresses. The advancements in phenotypic and genotypic analysis and biotechnological innovations offer promising opportunities for developing and adopting climate-resilient crop varieties, ensuring a sustainable and secure global food supply.

Conflict of interest
The authors declare that they have no conflict of interest.

REFERENCES

1. Acquaah, G. (2015). Conventional Plant Breeding Principles and Techniques. In: Al-Khayri, J., Jain, S., Johnson, D. (eds) Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools. Springer, Cham.
2. Allam, M., Revilla, P., Djemel, A., Tracy, W. F. & Ordás, B. (2016). Identification of QTLs involved in cold tolerance in sweet× field corn. *Euphytica*, *208*, 353-365.
3. Alm, V., Busso, C. S., Ergon, Å., Rudi, H., Larsen, A., Humphreys, M. W. & Rognli, O. A. (2011). QTL analyses and comparative genetic mapping of frost tolerance, winter survival and drought tolerance in meadow fescue (*Festuca pratensis* Huds.). *Theoretical and Applied Genetics*, *123*, 369-382.
4. Almeida, G. D., Nair, S., Borém, A., Cairns, J., Trachsel, S., Ribaut, J. M., ... & Babu, R. (2014). Molecular mapping across three populations reveals a QTL hotspot region on chromosome 3 for secondary traits associated with drought tolerance in tropical maize. Molecular breeding, 34, 701-715.
5. Anyaoha, C. O., Fofana, M., Gracen, V., Tongoona, P., & Mande, S. (2019). Introgression of two drought QTLs into FUNAABOR-2 early generation backcross progenies under drought stress at reproductive stage. Rice Science, 26 (1), 32-41.
6. Al-Tamimi, N., Brien, C., Oakey, H., Berger, B., Saade, S., *et al*. (2016). Salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. *Pasture Science*, *72*(3), 165-172.
7. Azam, F. I., Chang, X. & Jing, R. (2015). Mapping QTL for chlorophyll fluorescence kinetics parameters at seedling stage as indicators of heat tolerance in wheat. *Euphytica*, 202, 245-258.
8. Bakala, H. S., Singh, G. & Srivastava, P. (2020). Smart breeding for climate resilient agriculture. In *Plant breeding -current and future views*. IntechOpen.
9. Barakat, M. N., Saleh, M. S., Al-Doss, A. A., Moustafa, K. A., Elshafei, A. A., Zakri, A. M. & Al-Qurainy, F. H. (2015). Mapping of QTLs associated with abscisic acid and water stress in wheat. *Biologia plantarum*, *59*, 291-297.
10. Barik, S. R., Moharana, A., Pandit, E., Behera, A., Mishra, A., Mohanty, S. P. & Pradhan, S. K. (2023). Transfer of Stress Resilient QTLs and Panicle Traits into the Rice Variety, Reeta through Classical and Marker-Assisted Breeding Approaches. *International Journal of Molecular Sciences*, *24*(13), 10708.
11. Bhatta, M., Sandro, P., Smith, M. R., Delaney, O., Voss-Fels, K. P., Gutierrez, L., et al. (2021). Need for speed: manipulating plant growth to accelerate breeding cycles. *Curr. Opin. Plant Biol.* 60:101986. doi: 10.1016/ j.pbi.2020.101986
12. Bhattarai, U. & Subudhi, P. K. (2018). Genetic analysis of yield and agronomic traits under reproductive-stage drought stress in rice using a high-resolution linkage map. *Gene*, *669*, 69-76.
13. Cazzola, F., Bermejo, C. J., Gatti, I. & Cointry, E. (2021). Speed breeding in pulses: an opportunity to improve the efficiency of breeding programs. *Crop and Pasture Science*, *72*(3), 165-172.
14. Choudhary, P., Pramitha, L., Rana, S., Verma, S., Aggarwal, P. R., & Muthamilarasan, M. (2021). Hormonal crosstalk in regulating salinity stress tolerance in graminaceous crops. *Physiologia Plantarum*, *173*(4), 1587-1596.
15. Dar, M. H., Zaidi, N. W., Waza, S. A., Verulkar, S. B., Ahmed, T., Singh, P. K., ... & Ismail, A. M. (2018). No yield penalty under favorable conditions paving the way for successful adoption of flood tolerant rice. *Scientific reports*, *8*(1), 1-7.
16. Devi, R., Ram, S., Rana, V., Malik, V. K., Pande, V. & Singh, G. P. (2019). QTL mapping for salt tolerance associated traits in wheat (*Triticum aestivum* L.). *Euphytica*, *215*, 1-23.
17. Dixit, S., Singh, A., Sta Cruz, M. T., Maturan, P. T., Amante, M. & Kumar, A. (2014). Multiple major QTL lead to stable yield performance of rice cultivars across varying drought intensities. *Bmc Genetics*, *15*, 1-13.
18. Duan, Y. B., Li, J., Qin, R. Y., Xu, R. F., Li, H., Yang, Y. C. ... & Yang, J. B. (2016). Identification of a regulatory element responsible for salt induction of rice OsRAV2 through ex situ and in situ promoter analysis. *Plant molecular biology*, *90*, 49-62.

19. Gaba, Y., Pareek, A., & Singla-Pareek, S. L. (2021). Raising climate-resilient crops: journey from the conventional breeding to new breeding approaches. *Current Genomics*, *22*(6), 450-467.

20. Gahlaut, V., Jaiswal, V., Tyagi, B. S., Singh, G., Sareen, S., Balyan, H. S. & Gupta, P. K. (2017). QTL mapping for nine drought-responsive agronomic traits in bread wheat under irrigated and rain-fed environments. *PloS one*, *12* (8), e0182857.

21. Gonzaga, Z. J. C., Carandang, J., Sanchez, D. L., Mackill, D. J. & Septiningsih, E. M. (2016). Mapping additional QTLs from FR13A to increase submergence tolerance in rice beyond SUB1. *Euphytica*, *209*, 627-636.

22. González-Schain, N., Dreni, L., Lawas, L. M., Galbiati, M., Colombo, L., Heuer, S.& Kater, M. M. (2016). Genome-wide transcriptome analysis during anthesis reveals new insights into the molecular basis of heat stress responses in tolerant and sensitive rice varieties. *Plant and Cell Physiology*, *57*(1), 57-68.

23. Hoang, G. T., Van Dinh, L., Nguyen, T. T., Ta, N. K., Gathignol, F., Mai, C. D., ... & Gantet, P. (2019). Genome-wide association study of a panel of Vietnamese rice landraces reveals new QTLs for tolerance to water deficit during the vegetative phase. *Rice*, *12*(1), 1-20.

24. Khalid, M. N., Amjad, I., Nyain, M. V., Saleem, M. S., Asif, M., Ammar, A. & Rasheed, Z. (2021). A review: tilling technique strategy for cereal crop development. *International Journal of Applied Chemical and Biological Sciences*, *2*(5), 8-15.

25. Khan, S. U., Saeed, S., Khan, M. H. U., Fan, C., Ahmar, S., Arriagada, O. & Mora-Poblete, F. (2021). Advances and challenges for QTL analysis and GWAS in the plant-breeding of high-yielding: a focus on rapeseed. *Biomolecules,* *11*(10), 1516.

26. Kulwal, P., Thudi, M. & Varshney, R. K. (2011). Genomics interventions in crop breeding for sustainable agriculture.

27. Kumar, A., Sandhu, N., Dixit, S., Yadav, S., Swamy, B. P. M., & Shamsudin, N. A. A. (2018). Marker-assisted selection strategy to pyramid two or more QTLs for quantitative trait-grain yield under drought. *Rice*, *11*(1), 1-16.

28. Lekklar, C., Pongpanich, M., Suriya-Arunroj, D., Chinpongpanich, A., Tsai, H., Comai, L., ... & Buaboocha, T. (2019). Genome-wide association study for salinity tolerance at the flowering stage in a panel of rice accessions from Thailand. BMC genomics, 20(1), 1-18.

29. Liu, C., Ou, S., Mao, B., Tang, J., Wang, W., Wang, H., ... & Chu, C. (2018). Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. *Nature Communications,* 9(1), 3302.

30. Luck, J., Spackman, M., Freeman, A., Trebicki, P., Griffith, W., Finlay, K., Chakraborty, K. (20-11). Climate change and diseases of food crops. *Plant Pathol.,* 60, 113-121.

31. Malik, S. & Malik, T. A. (2015). Genetic mapping of potential QTLs associated with drought tolerance in wheat. *JAPS: Journal of Animal & Plant Sciences*, 25(4).

32. Mammadov, J., Buyyarapu, R., Guttikonda, S. K., Parliament, K., Abdurakhmonov, I. Y. & Kumpatla, S. P. (2018). Wild relatives of maize, rice, cotton, and soybean: treasure troves for tolerance to biotic and abiotic stresses. Frontiers in plant science, 9, 886.

33. Manickam, S., Rajagopalan, V. R., Manoharan, B., Natesan, S. & Muthurajan, R. (2023). Genomics-Assisted Breeding for Climate-Resilient Crops. In Molecular Marker Techniques: A Potential Approach of Crop Improvement (pp. 357-368). Singapore: Springer Nature Singapore.

34. Ma, X., Feng, F., Wei, H., Mei, H., Xu, K., Chen, S., ... & Luo, L. (2016). Genome-wide association study for plant height and grain yield in rice under contrasting moisture regimes. *Frontiers in Plant Science*, 7, 1801.

35. Naqvi RZ, Siddiqui HA, Mahmood MA, Najeebullah S, Ehsan A, Azhar M, Farooq M, Amin I, Asad S, Mukhtar Z, Mansoor, S. & Asif M (2022) Smart breeding approaches in post-genomics era for developing climate-resilient food crops. Front. Plant Sci. 13:972164. doi: 10.3389/fpls.2022.972164

36. Paliwal, R., Röder, M. S., Kumar, U., Srivastava, J. P. & Joshi, A. K. (2012). QTL mapping of terminal heat tolerance in hexaploid wheat (T. aestivum L.). *Theoretical and Applied Genetics,* 125, 561-575.

37. Pandit, E., Tasleem, S., Barik, S. R., Mohanty, D. P., Nayak, D. K., Mohanty, S. P., ... & Pradhan, S. K. (2017). Genome-wide association mapping reveals multiple QTLs governing tolerance response for seedling stage chilling stress in indica rice. *Frontiers in Plant Science*, 8, 552.

38. Pantaliao, G. F., Narciso, M., Guimarães, C., Castro, A., Colombari, J. M., Breseghello, F., ... & Brondani, C. (2016). Genome wide association study (GWAS) for grain yield in rice cultivated under water deficit. *Genetica,* 144, 651-664.

39. Prasch, C. M. & Sonnewald, U. (2013). Simultaneous application of heat, drought, and virus to Arabidopsis plants reveals significant shifts in signaling networks. *Plant Physiology,* 162(4), 1849-1866.

40. Pathirana, R. (2011). Plant mutation breeding in agriculture. *CABI Reviews*, (2011), 1-20.

41. Raj, S. R. G. & Nadarajah, K. (2023). QTL and candidate genes: Techniques and Advancement in abiotic stress resistance breeding of major cereals. *International Journal of Molecular Sciences*, *24*(1), 6.

42. Raza, A., Tabassum, J., Kudapa, H. & Varshney, R. K. (2021). Can omics deliver temperature resilient ready-to-grow crops?. *Critical Reviews in Biotechnology*, *41*(8), 1209-1232.

43. Razzaq, A., Kaur, P., Akhter, N., Wani, S. H. & Saleem, F. (2021). Next-generation breeding strategies for climate-ready crops. *Frontiers in Plant Science*, 12, 620420.

44. Ren, T., Fan, T., Chen, S., Chen, Y., Ou, X., Jiang, Q., ... & Li, Z. (2022). Identification and validation of quantitative trait loci for the functional stay green trait in common wheat (*Triticum aestivum* L.) via high-density SNP-based genotyping. *Theoretical and Applied Genetics*, *135*(4), 1429-1441.

45. Revilla, P., Rodríguez, V. M., Ordás, A., Rincent, R., Charcosset, A., Giauffret, C., ... & Malvar, R. A. (2016). Association mapping for cold tolerance in two large maize inbred panels. *BMC Plant Biology*, *16*, 1-10.

46. Rivero, R. M., Mittler, R., Blumwald, E. & Zandalinas, S. I. (2022). Developing climate⎕resilient crops: improving plant tolerance to stress combination. *The Plant Journal*, *109*(2), 373-389.

47. Rutger, J.N.; Peterson, M.L.; Hu, C.H.; Lehman, W.F. Induction of useful short stature and early maturing mutants in two japonica rice (*Oryza sativa* L.) cultivars. Crop Sci., 1976, 16, 631-635.

48. Sandhu, N., Dixit, S., Swamy, B. P. M., Raman, A., Kumar, S., Singh, S. P., ... & Kumar, A. (2019). Marker assisted breeding to develop multiple stress tolerant varieties for flood and drought prone areas. *Rice*, *12*(1), 1-16.

49. Sandhya, J., Ashwini, T., Manisha, R., Vinodha, M. & Srinivas, A. (2021). Drought tolerance enhancement with co-Overexpression of DREB2A and APX in indica rice (*Oryza sativa* L.). *American Journal of Plant Sciences*, *12*(2), 234-258.

50. Sangodele, E. A., Hanchinal, R. R., Hanamaratti, N. G., Shenoy, V. & Kumar, V. M. (2014). Analysis of drought tolerant QTL linked to physiological and productivity component traits under water-stress and non-stress in rice (*Oryza sativa* L.). *International Journal of Current Research and Academic Reviews*, *2*(5), 108-13.

51. Santosh Kumar, V. V., Verma, R. K., Yadav, S. K., Yadav, P., Watts, A., Rao, M. V. & Chinnusamy, V. (2020). CRISPR-Cas9 mediated genome editing of drought and salt tolerance (OsDST) gene in indica mega rice cultivar MTU1010. *Physiology and Molecular Biology of Plants*, *26*, 1099-1110.

52. Shamsudin, N. A. A., Swamy, B. P., Ratnam, W., Cruz, S., Teressa, M., Sandhu, N., ... & Kumar, A. (2016). Pyramiding of drought yield QTLs into a high quality Malaysian rice cultivar MRQ74 improves yield under reproductive stage drought. *Rice*, *9*(1), 1-13.

53. Sharma, S., Upadhyaya, H. D., Varshney, R. K. & Gowda, C. L. L. (2013). Pre-breeding for diversification of primary gene pool and genetic enhancement of grain legumes. *Frontiers in Plant Science*, *4*, 309.

54. Singh, G., Singh, I., Taggar, G. K., Rani, U., Sharma, P., Gupta, M. & Singh, S. (2020). Introgression of productivity enhancing traits, resistance to pod borer and Phytopthora stem blight from Cajanus scarabaeoides to cultivated pigeonpea. *Physiology and Molecular Biology of Plants*, *26*, 1399-1410.

55. Singh, R., Singh, Y., Xalaxo, S., Verulkar, S., Yadav, N., Singh, S., ... & Singh, N. K. (2016). From QTL to variety-harnessing the benefits of QTLs for drought, flood and salt tolerance in mega rice varieties of India through a multi-institutional network. *Plant Science*, *242*, 278-287.

56. Spindel, J. & Iwata, H. (2018). Genomic selection in rice breeding. In *Rice Genomics, Genetics and Breeding* (pp. 473-496). Springer, Singapore.

57. Sukumaran, S., Krishna, H., Singh, K., Mottaleb, K. A. & Reynolds, M. (2021). Progress and prospects of developing climate resilient wheat in south asia using modern pre-breeding methods. *Current Genomics*, *22*(6), 440.

58. Swamy, B. P., Shamsudin, N. A. A., Rahman, S. N. A., Mauleon, R., Ratnam, W., Cruz, S., ... & Kumar, A. (2017). Association mapping of yield and yield-related traits under reproductive stage drought stress in rice (*Oryza sativa* L.). *Rice*, *10*(1), 1-13.

59. Takagi, H., Tamiru, M., Abe, A., Yoshida, K., Uemura, A., Yaegashi, H., ... & Terauchi, R. (2015). MutMap accelerates breeding of a salt-tolerant rice cultivar. *Nature Biotechnology*, *33*(5), 445-449.

60. Talukder, S. K., Babar, M. A., Vijayalakshmi, K., Poland, J., Prasad, P. V. V., Bowden, R., & Fritz, A. (2014). Mapping QTL for the traits associated with heat tolerance in wheat (*Triticum aestivum* L.). *BMC genetics*, 15(1), 1-13.

61. Tiwari, J. K., Buckseth, T., Challam, C., Zinta, R., Bhatia, N., Dalamu, D., ... & Kumar, M. (2022). CRISPR/Cas genome editing in potato: current status and future perspectives. *Frontiers in Genetics*, *13*, 827808.

62. Trachsel, S., Sun, D., SanVicente, F. M., Zheng, H., Atlin, G. N., Suarez, E. A., ... & Zhang, X. (2016). Identification of QTL for early vigor and stay-green conferring tolerance to drought in two connected advanced backcross populations in tropical maize (*Zea mays* L.). *PloS one*, *11*(3), e0149636.

63. Valarmathi, M., Sasikala, R., Rahman, H., Jagadeeshselvam, N., Kambale, R., & Raveendran, M. (2019). Development of salinity tolerant version of a popular rice variety improved white ponni through marker assisted back cross breeding. *Plant Physiology Reports*, *24*(2), 262-271.

64. Varshney, R. K., Bohra, A., Yu, J., Graner, A., Zhang, Q. & Sorrells, M. E. (2021). Designing future crops: genomics-assisted breeding comes of age. *Trends in Plant Science*, 26(6), 631-649.

65. Varshney, R. K., Graner, A. & Sorrells, M. E. (2005). Genomics-assisted breeding for crop improvement. *Trends in plant science*, *10*(12), 621-630.

66. Vikram, P., Swamy, B. M., Dixit, S., Ahmed, H. U., Teresa Sta Cruz, M., Singh, A. K. & Kumar, A. (2011). qDTY 1.1, a major QTL for rice grain yield under reproductive-stage drought stress with a consistent effect in multiple elite genetic backgrounds. *BMC Genetics*, *12*, 1-15.

67. Watson, A., Ghosh, S., Williams, M. J., Cuddy, W. S., Simmonds, J., Rey, M. D., ... & Hickey, L. T. (2018). Speed breeding is a powerful tool to accelerate crop research and breeding. *Nature Plants*, *4*(1), 23-29.

68. Xiao, N., Gao, Y., Qian, H., Gao, Q., Wu, Y., Zhang, D., ... & Li, A. (2018). Identification of genes related to cold tolerance and a functional allele that confers cold tolerance. *Plant Physiology*, *177*(3), 1108-1123.

69. Yadav, P., Kumar, S., & Jain, V. (2016). *Recent Advances in Plant Stress Physiology.* Daya Publishing House® A Division of Astral International Pvt. Ltd. New Delhi–110 002.

70. Ye, C., Tenorio, F. A., Argayoso, M. A., Laza, M. A., Koh, H. J., Redoña, E. D., ... & Gregorio, G. B. (2015). Identifying and confirming quantitative trait loci associated with heat tolerance at flowering stage in different rice populations. *BMC Genetics*, *16*, 1-10.

71. Zhao, C., Liu, B., Piao, S., Wang, X., Lobell, D.B., Huang, Y., Huang, M., Yao, Y., Bassu, S., Ciais, P., Durand, J.L., Elliott, J., Ewert, F., Janssens, I.A., Li, T., Lin, E., Liu, Q., Martre, P., Müller, C., Peng, S., Peñuelas, J., Ruane, A.C., Wallach, D., Wang, T., Wu, D., Liu, Z., Zhu, Y., Zhu, Z. & Asseng, S. (2017). Temperature increase reduces global yields of major crops in four independent estimates. *Proc. Natl. Acad. Sci.*, USA 114(35), 9326-9331.

72. Zhu, Y., Chen, K., Mi, X., Chen, T., Ali, J., Ye, G., ... & Li, Z. (2015). Identification and fine mapping of a stably expressed QTL for cold tolerance at the booting stage using an interconnected breeding population in rice. *PLoS One*, *10*(12), e0145704.